ESCAIDE

ABSTRACT BOOK

European Scientific Conference on Applied Infectious Disease Epidemiology 2015

Stockholm Waterfront Congress Centre
11-13 November 2015
Stockholm, Sweden

ecdc
EUROPEAN CENTRE FOR DISEASE PREVENTION AND CONTROL

www.escaide.eu

ESCAIDE is sponsored by ECDC (European Centre of Disease Prevention and Control) and jointly organised by ECDC, EPIET (European Programme for Intervention Epidemiology), EAN (EPIET Alumni Network), TEPHINET EUROPE (Training Programmes in Epidemiology and Public Health Interventions NETwork)

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Warm welcome to ESCAIDE 2015!

This year's diverse programme is a reflection of the complexity of infectious disease surveillance, prevention and control. Each plenary session highlights the need for dedicated multidisciplinary efforts in a "one-health" approach.

The keynote at ESCAIDE 2015 will cover the global public health threat of antimicrobial resistance and its zoonotic dimension. It will inspire you with ground breaking research and examples of how new evidence informs agricultural and public health policies; and inform you of how effective these policies and countermeasures have been in Europe and globally (Plenary A).

As social media becomes an integral part of our daily life, we look closely at what the benefits are for threat detection and communicable disease surveillance (Plenary B). We will reflect on the 20th anniversary of the European Programme for Intervention Epidemiology Training (EPIET) by asking if and how we can ensure that evidence from epidemiological investigations translates into action and ultimately leads to public health protection (Plenary C). We will then discuss the emerging challenges to vaccine programmes, including antigen escape and non-specific immune effects; and how this knowledge can be used for successful vaccine development (Plenary D). The plenary sessions will end with the Public Health Event 2015, which brings two emerging viral disease back on the ESCAIDE stage. These have continued to cause loss to our society and to challenge the entire public health community, namely MERS-CoV and Ebola. We will revisit the remaining challenges and review the recent advances in a one-health approach, covering aspects of reservoirs, transmission chains and infection control.

However, the plenary sessions are only a minor component of ESCAIDE. The core of the Conference is made by your work. This year's parallel and poster sessions cover all aspects of infectious disease surveillance, prevention and control in Europe and beyond.

Many thanks to you, who submitted abstracts, irrespective of whether your submission made it into the programme or not. Please do not be discouraged as we do look forward to seeing your work at the next ESCAIDE.

The ESCAIDE Scientific Committee and the Conference's organising team extend a sincere thank you to the 218 reviewers! It is an honour to work with such dedicated public health professionals and to have your contributions to ESCAIDE 2015.

Congratulations to all graduating EPIET and EUPHEM fellows and best wishes for their continued professional development.

Last but not least, let us not forget that in addition to being a scientific Conference, ESCAIDE is also a networking and social event. With the expertise and experience that you all bring, you will make ESCAIDE 2015 an outstanding event and a lasting success! Enjoy your time at ESCAIDE 2015.

Dr Andrea Ammon
Chair, ESCAIDE Scientific Committee and Acting Director, European Centre for Disease Prevention and Control (ECDC)

Other Conference organisers

TEPHINET, the EPIET Alumni Network, national Field Epidemiology Programmes in Europe and the ECDC Fellowship Programme have always been working closely in the preparation and organisation of ESCAIDE and its predecessor, the annual EPIET Scientific Seminar. ESCAIDE is an important platform for EPIET and EUPHEM fellows to present the public health evidence resulting from their field work and discuss this with other intervention epidemiologists, public health microbiologists, fellows from other FETP's and other public health professionals. For all the institutes that invest resources on a daily basis to train EPIET and EUPHEM fellows, it is also an invaluable opportunity to meet and discuss essential topics in applied public health science. The presence of the global network TEPHINET has shown us the value of peer review of scientific output of fellowships between the member FETP's. The past 10 years of integration of EPIET in ECDC has demonstrated the added value of embedding results of fellow's field investigations in the larger community of public health professionals and European networks for disease prevention and control. I am glad that at this ESCAIDE 2015 we can look back on 20 years of achievements of the EPIET programme and look forward to a continued success of this growing scientific platform for disease prevention and control.

Dr. Arnold Bosman, Head of Public Health Training Section, ECDC

During the course of their EPIET/FETP/EUPHEM fellowship, fellows build strong networks both within and between the cohorts, fulfilling one of the purposes for which EPIET was originally built. But after those two years? How can fellows maintain such links once their official training programmes are over? This question led to the establishment of the EPIET Alumni Network (EAN) in 2000, which has now expanded to include EU FETP and EUPHEM alumni as well.

The EAN continues to grow each year, aiming always to assist in the maintenance of the network, share and exchange professional experiences, constitute and assure access to a pool of expertise, promote and deliver ongoing training for alumni, provide support to current fellows, and to contribute to both the logistical and scientific organisation of ESCAIDE.

The EAN President sits on the ESCAIDE Scientific Committee, but this is just one of the many activities of the network. The EAN board provides travel grants to our colleagues from low income countries; awards prizes for the best oral and poster presentations; and has also run a highly popular "photo from the field" competition over the past few years. None of these activities would be possible without the dedication of our members, who volunteer their time, ideas, and boundless enthusiasm to ensure that, year on year, these activities are a success.

ESCAIDE provides EAN members with the opportunity to interact with one another. We all know how easy it is to lose touch, despite the social networking platforms now available, and ESCAIDE is one highlight in the calendar at which members have the opportunity to catch up face to face. We hold our General Assembly during ESCAIDE, to which all members and current fellows are invited. Decisions affecting the network are made here, including the introduction and voting in of the new board.

We greatly anticipate ESCAIDE from year to year, knowing that it provides us the opportunity to meet new fellows, catch up with old (!) friends, and maintain those strong links between the growing family of field epidemiologists and public health microbiologists to which we belong.

ENJOY!

Dr. Naomi Boxall, EAN President

TEPHINET is the "Training Programs in Epidemiology and Public Health Interventions Network" and one of the co-organizers of ESCAIDE.

TEPHINET is an international network of field-based training programmes in applied epidemiology and public health microbiology generally called Field Epidemiology Training Programmes (FETPs) or field epidemiology and laboratory training programmes (FELTPs). The main aim of these training programmes is to build up a sufficient number of field-trained experts who are competent in the practical application of epidemiological and microbiological methods to a wide range of public health problems.

FETP and FELTP fellows are trained in a set of core competencies that are vital to the practice of public health, while providing a valuable public health service to their countries and regions.

There are five countries in the European WHO region with currently active national FETPs (Austria, Germany, Spain, Turkey and the UK). Furthermore, there are four regional programmes: the European Programme for Intervention Epidemiology Training (EPIET) which integrates the European Programme for Public Health Microbiology Training (EUPHEM), the Central Asian FELTP, the South Caucasus FELTP and the recently started Tajikistan-Afghanistan FETP.

All of them subscribe to the basic principle of "training through service". Therefore, fellows, alumni and supervisors of many of those programmes participated actively in the current fight against the West African Ebola Epidemic.

International scientific conferences offer opportunities for networking and information sharing. Also during this edition of ESCAIDE FE(L)TP fellows, alumni and other PH professionals will hopefully be able to show their achievements and learn from each other's experience in order to acquire new ideas and skills that can be put into action.

In this sense we wish all the participants a successful conference with many interesting discussions and inspirations for your daily work.

Dr. Katharina Alpers, TEPHINET Representative, European Region

Scientific Committee

Andrea Ammon – ECDC, Chair of ESCAIDE Scientific Committee

Andrea is the Acting Director of ECDC. Prior to joining ECDC, Andrea served in several roles at the Robert Koch-Institute, in Berlin, Germany, most recently as Head of Department for Infectious Disease Epidemiology. She has published over 90 peer-reviewed journal articles related to her work.

Mike Catchpole – ECDC

Mike is the Chief Scientist at the ECDC. As Head of the Office of the Chief Scientist he is responsible for driving the scientific agenda of the ECDC, and overseeing the quality of the scientific outputs of the Centre. Prior to joining ECDC in 2014, he was the Director of Public Health England's national Centre for Infectious Disease Surveillance and Control. He is a medical doctor with over 20 years of experience of working in infectious disease epidemiology at a national and international level. His main research interests have been in the fields of sexual health, major incident and disaster response, and medical information systems.

Johan Giesecke – Karolinska Institute, Sweden

Johan is a Professor of Epidemiology at the Karolinska Institute, Sweden, and the first Chief Scientist at the ECDC, a position he held from 2005 until his recent retirement in September 2014. From a background as an infectious disease clinician, his research interests include: epidemic modelling, HIV/STIs and late sequelae of acute infections. He has published some 150 scientific papers, has written a textbook on infectious disease epidemiology and co-edited another.

Naomi Boxall – President of the EPIET Alumni Network (EAN).

Naomi is a Senior Epidemiologist at Mapi since 2013, having left Public Health England, where she had been for 6 years. From a background that includes a PhD in veterinary epidemiology supported by a biochemistry and genetics undergraduate degree, her research interests now include non-infectious topics to supplement previous experience in gastrointestinal and health-care acquired infections. As president of the EAN board, she represents the vast alumni of EPIET, EU-FETP and (now) EUPHEM on the scientific committee and remains committed to training in field epidemiology.

Aftab Jasir – ECDC/EUPHEM

Aftab is an associate professor, expert public health microbiologist and chief scientific coordinator of European Public Health Microbiology training programme (EUPHEM) at ECDC. In addition to many years professional work as a university teacher and coordinating European projects, Aftab has worked in many public health bodies/organisations (including Lund University hospital, Sweden; HPA, UK and CDC, US). Specialisations include health care associated infections and antibiotic resistance, monitoring and evaluating QA/QC systems, molecular typing, and vaccine and antimicrobial drug development. Aftab is a member of many scientific societies and international advisory boards.

Scientific Committee

Polya Rosin – ECDC

Polya is the project manager for ESCAIDE since January 2015. Her responsibilities at ECDC include surveillance of food- and waterborne parasitic diseases, scientific advice coordination, and the application of evidence-based methods in scientific opinions. Previously, Polya has worked in microbiology coordination and scientific liaison. Her background is in biotechnology, molecular biology and parasitology.

Panayotis T. Tassios – University of Athens, Greece (ESCMID representative)

Panayotis is Associate Professor in Molecular Microbiology at the National & Kapodistrian University of Athens, Greece. His research focuses on the molecular typing of bacterial strains and their antimicrobial drug resistance mechanisms, to assist epidemiological investigations and infection control. He is also active in lifelong teaching, on his scientific interests as well as on scientific writing, aided by his experience as Associate Editor of several journals. Panayotis represents the European Society of Clinical Microbiology and Infectious Diseases (ESCMID) on the Scientific Committee.

Mira Kojouharova – NCIPD, Bulgaria (AF Representative)

Mira is the Deputy Director of the National Centre of Infectious and Parasitic Diseases (NCIPD) in Sofia, Bulgaria, and Head of the Epidemiology and Communicable Disease Surveillance Department. Mira holds a professorship, and leads research and teaching in the field of post-graduate education in epidemiology, surveillance and control of communicable diseases and practical work related to the surveillance of communicable diseases in Bulgaria. Mira's research interests are particularly focused on influenza and acute respiratory diseases in adults and children, poliomyelitis and viral hepatitis. Mira is an ECDC Advisory Forum (AF) member, and represents the AF in the ESCAIDE Scientific Committee.

Arnold Bosman – ECDC

Arnold is a Public Health Specialist, trained in The Netherlands, focused on providing specialised training in Intervention Epidemiology to public health professionals. He is a member of the EPIET Scientific Conference committee. Currently he is a manager of Public Health Training at ECDC aiming to establish an effective network of training in applied public health (e.g. epidemiology, public health microbiology) in order to strengthen the work force in the EU.

Thea Kølsen Fischer – SSI (NMFP representative)

Thea is a public health virologist heading the Virology Surveillance and Research Unit at the Statens Serum Institut (SSI) and a Professor in Global Health and Infectious Diseases. Thea's research has focused on global high-incidence viruses such as influenza, EVs and rotavirus combining epidemiology, molecular profiling and vaccinology. She is specialised in epidemiology and laboratory outbreak management as an EIS Officer at CDC (2003-2005). Thea represents the ECDC National Microbiology Focal points (NMFP) in the ESCAIDE Scientific Committee.

Scientific Committee

Yvan J Hutin – WHO

Yvan is in charge of Strategic Information at WHO's Global Hepatitis Programme after having worked with ECDC as Chief Coordinator of the European Programme for Intervention Epidemiology Training (EPIET) from 2012 to 2015. After an MD and a residency in hepato-gastroenterology, he joined the Epidemic Intelligence Service (EIS) of the United States' Centers for Disease Control and Prevention (CDC). As part of his public health career, he worked in Burkina Faso, Uganda and at the World Health Organization in Geneva, India and China.

Denis Coulombier – ECDC

Denis is a medical doctor, specialist in tropical diseases and in public health. He has an extensive international experience worldwide, including preparing for large sporting events in the field of communicable disease and response, acquired as a surveillance manager in 1996 Olympic Games in Atlanta, as a coordinator of public health surveillance and response in the 1998 FIFA world cup in France and as a WHO advisor for public health surveillance in the 2004 Athens Olympic Games. He joined the Epidemic Intelligence Service of the US Centres for Disease Control and Prevention in 1991 and subsequently worked in the Epidemiology Programme Office of the CDC in health. In 2000, Dr Coulombier was seconded to the World Health Organisation to lead the team in charge of epidemiology capacity strengthening. Since the start-up of the European Centre for Disease Prevention and Control (ECDC) in May 2005 and until March 2011, Dr Coulombier was the head of unit for preparedness and response and since April 2011 he is the head of unit for Surveillance and Response Support.

Katharina Alpers – RKI, Germany (TEPHINET representative)

Katharina is the Coordinator for the Postgraduate Training for Applied Epidemiology (PAE), the German Field Epidemiology Training Programme (FETP) and is based at Robert Koch-Institute (RKI) in Berlin. She is currently representing all European FETP in the advisory board of the global FETP network called TEPHINET (Training Programs in Epidemiology and Public Health Interventions Network). Katharina represents TEPHINET in the ESCAIDE Scientific Committee.

Fortunato (Paolo) D'Ancona – ISS, Italy (ETSF representative)

Paolo is a Doctor and Communicable disease epidemiologist at the National Centre for Epidemiology, Surveillance and Health Promotion at the Istituto Superiore di Sanità, Italy. Among several activities, he leads the Italian Network on the surveillance of antimicrobial resistance, and is project leader for the VENICE III project that supports vaccine programmes in the EU. Paolo is also training site supervisor for the EPIET programme at Istituto Superiore di Sanità, and is Chair of the EPIET Training Site Forum (ETSF). Paolo represents the ETSF in the ESCAIDE Scientific Committee.

Marc Struelens – ECDC

Marc is the Chief Microbiologist at ECDC. He is a former President of the European Society of Clinical Microbiology and Infectious Diseases (ESCMID), and Professor of Medical Microbiology at the Faculty of Medicine of the Université Libre de Bruxelles (ULB) in Belgium. Marc has authored over 200 peer-reviewed articles and 20 book chapters across many disciplines, including molecular epidemiology, control of nosocomial infections, and antimicrobial resistance. He has served as editor of several international scientific journals, been a member of several national and international advisory boards, European Union (EU)-supported research and public health networks, and has served as consultant to the WHO and EU.

Abstract Reviewers

The Scientific Committee warmly thanks everyone who participated in the reviewing of the abstracts submitted for ESCAIDE 2015

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Elton Rogozi

Austria
Michael Kunze

Barbados
Angela MC Rose

Belgium
Silvia Villanueva

Bulgaria
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Anna Kurchatova

Canada
Nawal Farhat
April Hexemer
Leah Martin
Robert Stirling

China
Bao Chang-jun
Lijie Zhang

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Sophia Kyradji

Czech Republic
Jozef Dlhy
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Nina Stock

Denmark
Thea Kølsen Fischer
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Egypt
Ahmed Zaghloul

Estonia
Kuulo Kutsar

Ethiopia
Abadit Niguse

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Georgia
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Germany
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Andreas Jansen
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Jaishri Mehraj
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Ute Rexroth
Bettina Rosner
Jamela Seedat
Miriam Wiese-Posselt
Florian Burckhardt
Guenter Pfaffy

Ghana
Joseph Kwadwo Larbi Opare

Greece
Maria Keramarou
Konstantinos Kesanopoulos
Georgia Mandilara
Kassiani Mellou
Dimitrios Paraskevis
Vana Sypsa
Panayotis T. Tassios
Georgina Tzanakaki
Alkiviadis Vatopoulos
Loukia Zerva
Agoritsa Baka

Hungary
Ivelina Damjanova
Rita Szabo

India
Himanshu Nayak

Ireland
Martin Cormican
Suzanne Cotter
Derval Igoe
Aileen Kitching
Darina O'Flanagan

Israel
Jacob Moran-Gilad

Italy
Fabrizio Bruschi
Fortunato D'Ancona
Antonietta Filia
Enrico Girardi
Loredana Ingrosso
Domenico Martinelli
Annalisa Pantosti
Giovanni Rezza
Lara Ricotta
Michela Sabbatucci
Monica Sane Schepisi
Nikolaos Stilianakis
Roberto Novati

Lao People's Democratic Republic
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Latvia
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Lithuania
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Luxembourg
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Malta
Charmaine Gauci
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Olukemi Olugbade
Aishat Usman

Norway
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Karin Nygård
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Poland
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Paulo J Nogueira
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Beatriz Pérez Gorricho
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Maria Fernandez Prada
Leticia Franco

Sweden – ECDC
Barbara Albiger
Julien Beauté
Arnold Bosman
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Niklas Danielsson
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Tarik Derrough
Irina Dinca
Dragoslav Domanovic
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Edit Szegedi
Johanna Takkinen
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Sweden
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Otilia Mårdh
Sybille Rehmet
Claes Schalen
Anders Tegnell
Katherina Zakikhany

Switzerland
Olivier Ronveaux

The Netherlands
Saverio Caini
Susan Hahne
Annick Lenglet
Ellen Stobberingh
Marianne van der Sande

Trinidad and Tobago
Lisa Hansen

Turkey
Osman Sezer Cirit

United Kingdom
A-Lan Banks
Paul Cleary
Paul Crook
Gavin Dabrera
Lorraine Doherty
Michael Edelstein
Androulla Efstratiou
Naomh Gallagher
Maya Gobin
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David Jenkins
Silvia Jiménez Jorge
Ioannis Karagiannis
Alper Kilic
Samia Latif
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Sophia Makki
Jim McMenamin
Anna Molesworth
Irvine Neil
Isabel Oliver
Arlene Reynolds
Giri Shankar
James Stuart
Daniel Thomas
Chris Williams
Julie Wilson

USA
Peter Gerner-Smidt
Britta Lassmann
David Perlman
Richard Goering
Ashly Jordan

Information Stands

ECDC

European Centre for Disease Prevention and Control

The European Centre of Disease Prevention and Control (ECDC) was established in 2005. It is an EU agency which aims to strengthen Europe's defences against infectious diseases. It is seated in Stockholm, Sweden.

ecdc.europa.eu

ECDC Survey

You have the expertise and knowledge we need, so please visit our info-stand for an ongoing ECDC-project on prioritization of infectious diseases to support preparedness planning. We want to know the revealed importance of public health professionals for attributes on disease priorities and public perception. You can help us out by completing a survey in about 5-10 min and collect a memorable Dutch treat while helping out!

ecdc.europa.eu

EPIET & EUPHEM

Epidemiology Training & European Programme for Public Health Microbiology Training

The European Programme for Intervention Epidemiology Training (EPIET) and the European Programme for Public Health Microbiology Training (EUPHEM) are two-year fellowship programmes that provide training and practical experience in intervention epidemiology at the national and regional centres for surveillance and control of communicable diseases (EPIET) and in laboratories with public health function (EUPHEM) at collaborative Training Sites in the European Union (EU) and European Economic Area (EEA) Member States.

ecdc.europa.eu/en/epiet/

Training Network Strengthening (TNS) Group

Public Health Training Section, Public Health Capacity and Communication Unit, ECDC

The Training Network Strengthening Group (TNS) works in close collaboration with ECDC Disease Programmes and core functions as a reference team for adult learning methodology and quality assurance of ECDC training activities (EPIET, EUPHEM and the Continuous Professional Development Programme, with the ECDC Summer School and Senior Exchange). Key areas of work include: training resources and needs assessment, development of sets of competencies for ECDC training programmes, instructional design (including E-learning), evaluation and accreditation of training, and networking/partnerships with national, European and international stakeholders.

ecdc.europa.eu

ECDC Reinbursements

The European Centre of Disease Prevention and Control (ECDC) was established in 2005. It is an EU agency which aims to strengthen Europe's defences against infectious diseases. It is seated in Stockholm, Sweden.

ecdc.europa.eu

EAN

EPIET Alumni Network

The EPIET Alumni Network (EAN) was created to help develop and maintain a network of European public health epidemiologists that have participated in the European Programme for Intervention Epidemiology Training (EPIET) or other European Field Epidemiology Training Programmes (FETP).

epietalumni.net/

EC CHAFEA

Consumers, Health, Agriculture and Food Executive Agency

The Consumers, Health, Agriculture and Food Executive Agency - CHAFEA - was created on 1 January 2005. Chafea implements the EU Health Programme, the Consumer Programme and the Better Training for Safer Food initiative.

ec.europa.eu/chafea/

AIRSAN

The objective of the AIRSAN project is to ensure an efficient, multi-sector, multi-stakeholder, coherent response at the EU level to public health threats (PHTs) in air transport.

www.airsan.eu/

EMCDDA

European Monitoring Centre for Drugs and Drug Addiction

The European Monitoring Centre for Drugs and Drug Addiction (EMCDDA) was established in 1993. Inaugurated in Lisbon in 1995, it is one of the EU's decentralised agencies. The EMCDDA exists to provide the EU and its Member States with a factual overview of European drug problems and a solid evidence base to support the drugs debate.

www.emcdda.europa.eu/

ECCMID

European Congress of Clinical Microbiology and Infectious Diseases

The 26th European Congress of Clinical Microbiology and Infectious Diseases will take place in Istanbul, Turkey, from 9 - 12 April 2016. We are looking forward to bringing the world's leading experts and innovative research to ECCMID. The Programme Committee is preparing keynote lectures, symposium, educational workshops and meet-the-expert sessions on parallel tracks, covering the latest developments in the field of infectious diseases and clinical microbiology.

www.eccmid.org

HZI

Helmholtz Zentrum für Infektionsforschung

The PhD Programme "Epidemiology" at the Helmholtz Centre for Infection Research in Braunschweig, Germany, includes thorough mentoring of research projects and a structured teaching programme in English. The programme does not require tuition fees and facilitates participation for PhD students residing in cities other than Braunschweig. Currently 14 PhD students from 8 different countries are enrolled

www.helmholtz-hzi.de/en/

Invited Speaker Biographies

Plenary Session A: Key Note Address
Global public health threat of antimicrobial resistance

Prof. Jan Kluytmans
Amphia Hospital, Breda/Oosterhout, St. Elisabeth Hospital and TweeSteden Hospital, Tilburg

Prof. Jan Kluytmans did his medical training as well as specialization in Clinical Microbiology at Erasmus Medical University, Rotterdam, The Netherlands. The title of his PhD thesis in 1996 was: Nasal carriage of Staphylococcus aureus: the key to preventing staphylo-coccal disease. His scientific career focuses on the epidemiology and control of nosocomial infections, with a special interest in Staphylococcus aureus, surgical site infections and catheter related infections. He discovered the concept of perioperative eradication of nasal carriage as an infection control measure. More recently he focused on antimicrobial resistance in humans in relation to the food chain.

He has been involved in many national and international guidelines on infection control, especially those dealing with the control of MRSA. He has been the chair of the Dutch Working Party on Infection Control for many years. Since 2013 he is the president of the Dutch society of Medical microbiology.

At present he is working in the Amphia Hospital in Breda/Oosterhout, St. Elisabeth Hospital and TweeSteden Hospital in Tilburg. Since 2006 he holds a position as a Professor of Medical Microbiology and Infection Control at the VUmc medical university, Amsterdam. In 2014 he moved to the Julius Center for Healthcare Epidemiology at the University Medical Center in Utrecht where he is leading several workpackages of the COMBACTE network (part of the Innovative Medicne Initiative). He has published more than 200 papers in peer-reviewed journals.

Plenary B:
Social Media: a toy or a useful tool?

Dr. John Brownstein
Boston Children's Hospital, USA

Dr. John Brownstein is the Chief Innovation Officer at Boston Children's Hospital, USA. He is a global leader in Healthcare Information Technology and, in particular, the emerging fields of informatics and big data analytics. He runs a 50-person multi-disciplinary team focused on digital innovations that span clinicians and consumers. His group is supported by a multi-million dollar budget including grants from NIH, USAID, DoD, IARPA, CDC, Google, Skoll and Gates Foundation. His work has pioneered 'digital epidemiology'- utilizing diverse digital data sources to understand population health. His work is published in over a 150 peer-reviewed papers, all focused on new methods and applications in digital health. This work was recognized by the White House with the Presidential Early Career Award for Scientists and Engineers.

He also leads the development of several novel patient facing public health systems, including HealthMap, Vaccine Finder and MedWatcher. The systems are considered premier global public health tools in use by millions of patients each year and endorsed by numerous public health agencies including CDC, WHO, DHS, DOD, HHS, and EU, and has been recognized by the National Library of Congress and the Smithsonian. In addition to research achievements, this translational impact comes from playing an advisory role to numerous agencies on real-time public health surveillance including HHS, DHS, CDC, IOM, WHO and the White House.

Prof. Ingemar J. Cox
University College London, United Kingdom & University of Copenhagen, Denmark

Prof. Ingemar J. Cox is currently a Professor in the Department of Computer Science at University College London (UCL). He is also a Professor in the Department of Computer Science at the University of Copenhagen. He is Head of the Future Media Group at UCL. Between 2003 and 2008, he was Director of UCL's Adastral Park Campus. His current research interests involve data analytics of online social media, Twitter and query logs, for healthcare purposes.He has been a recipient of a Royal Society Wolfson Fellowship (2002-2007).

He received his B.Sc. from University College London and Ph.D. from Oxford University. He was a member of the Technical Staff at AT&T Bell Labs at Murray Hill from 1984 until 1989 where his research interests were focused on mobile robots. In 1989 he joined NEC Research Institute in Princeton, NJ as a senior research scientist in the computer science division. At NEC, his research shifted to problems in computer vision and he was responsible for creating the computer vision group at NECI. He has worked on problems to do with stereo and motion correspondence and multimedia issues of image database retrieval and watermarking. In 1999, he was awarded the IEEE Signal Processing Society Best Paper Award (Image and Multidimensional Signal Processing Area) for a paper he co-authored on watermarking. From 1997-1999, he served as Chief Technical Officer of Signafy, Inc, a subsidiary of NEC responsible for the commercialization of watermarking. Between 1996 and 1999, he led the design of NEC's watermarking proposal for DVD video disks and later colloborated with IBM in developing the technology behind the joint "Galaxy" proposal supported by Hitachi, IBM, NEC, Pioneer and Sony. In 1999, he returned to NEC Research Institute as a Research Fellow. He is a Fellow of the ACM, IEEE, the IET (formerly IEE), and the British Computer Society. He is a member of the UK Computing Research Committee. He was founding co-editor in chief of the IEE Proc. on Information Security and is an associate editor of the IEEE Trans. on Information Forensics and Security. He is co-author of a book entitled "Digital Watermarking" and its second edition "Digital Watermarking and Steganography", and the co-editor of two books, `Autonomous Robots Vehicles' and `Partitioning Data Sets: With Applications to Psychology, Computer Vision and Target Tracking'.

Plenary Session C: Ensuring that evidence leads to public health protection – special session on occasion of the 20th EPIET anniversary

Dr. Johanna Takkinen
European Centre for Disease Prevention and Control (ECDC)

Dr. Johanna Takkinen is a Doctor of Veterinary Medicine (1989) with a special degree in food- and environmental hygiene from the Faculty of Veterinary Medicine in the University of Helsinki (2005). While doing practice mainly with large animals, she has worked in different food-, water- and environmental laboratories for several years since 1983, first as a laboratory technician and later as a Head of food laboratory in Porvoo, Finland, with a responsibility of all laboratory services and accreditation of several microbiological and chemical methods for food, water and indoor air samples.

In 1999, Dr. Takkinen joined the European Intervention Epidemiology Training programme (EPIET) in the Robert Koch Institut in Germany, and moved to work at the National Public Health Instute (KTL at the time, THL nowadays) in Finland in 2002. She was recognised de facto Diplomate for Food Science in the European College of Veterinary Public Health in 2005 and in the same year, she finished her Master of Public Health studies for the Nordic School of Public Health in Gothenburg, Sweden. In October 2005, Dr. Takkinen started to work as a Senior Expert in the European Centre for Disease Prevention and Control (ECDC) and since 2006, she has been leading the coordination of ECDC Food- and Waterborne Diseases and Zoonoses (FWD) programme.

As a Head of ECDC FWD programme covering 22 bacterial, viral, parasitic and prion diseases, Dr. Takkinen has a deep interest to understand and explore the epidemiology of these diseases in a holistic way so that important gaps in the prevention and control can be identified and appropriately addressed. The FWD programme has three main pillars for activities: 1) Strengthen and develop surveillance for FWD, including molecular-based surveillance, so that it supports monitoring of trends and detection of emergence of new pathogenic strains in humans in European Union (EU) and European Economic Area (EEA); 2) strengthen the detection of and response to multi-state foodborne outbreaks through indicator- and event-based surveillance/monitoring and promoting the collaboration between food safety and public health authorities; and 3) strengthen the public health microbiology capacity and capability particularly in the field of molecular typing.

Dr. Jane Richardson
European Food Safety Authority (EFSA)

Dr. Jane Richardson has a degree in Molecular Biology from the University of Edinburgh (1994) and a PhD in Microbiology from the Imperial College of Science, Technology and Medicine (2000). She spent three years training as an Analyst/Programmer, developing patient management systems for the Welsh Radiology Service

In 2003 she joined the UK Health Protection Agency in the North West of England. In her role as Epidemiology and surveillance analyst she worked on both infectious diseases and chemical exposure events, developing expertise in the use of routine health data to support exposure assessments for contaminated land incidents and airborne releases.

In 2007 she joined the European Food Safety Authority (EFSA) in Italy. Combining her scientific training with experience gained in an IT environment, she has worked as a senior database manager on a number of multinational monitoring surveillance programmes.

She is participating in three joint initiatives with the European Centre for Disease Prevention and Control (ECDC), namely molecular typing, geographical distribution of arthropod vectors and multinational outbreak of hepatitis A.

Dr. Gaia Scavia
Istituto Superiore di Sanità, Italy

Dr. Gaia Scavia (DVM) is a veterinary epidemiologist working at the National Italian Public Health Institute (ISS), Department of Veterinary Public Health and Food Safety. She has been involved since 2003 in epidemiology and surveillance of FWD in both human and food / veterinary fields, including outbreak detection and investigation and implementation of integrated alert systems.

In 2013 and 2014 she has been involved in the National Task Force for the investigation of the large community-wide outbreak of Hepatits A linked to frozen berries. Her specific task was the assessment of the risk for public health posed by frozen berries with particular focus on food tracing-back, in order to support the adoption of specific outbreak control measures. This task was also carried out in collaboration with ECDC and EFSA which coordinated the investigation of the Hepatitis A outbreak at the European Union level.

Invited Speaker Biographies

Plenary Session D:
Emerging challenges to vaccine programmes: antigen escape and non-specific immune effects

Prof. Nicole Guiso
Pasteur Institute, France

Prof. Nicole Guiso joined the Institut Pasteur in 1972 as a voluntary trainee, having obtained a Master's Degree in biochemistry. She obtained her first PhD in 1976 and the second one in 1980. She left the Institut Pasteur, between 1986-1987, to take up the position of Visiting Lecturer at the National Jewish Hospital in Denver, Colorado, USA, to study Archaebacteria. She rejoined the Institute in 1988 and was appointed Laboratory Head in 1991 followed by positions of director of two National Reference Centres, Pertussis and Diphtheria. She took up the position of Head of the department of "Ecosystems and Epidemiology of Infectious Diseases" department in 2002.

Nicole Guiso has authored more than 300 articles in international peer-reviewed journals, several book chapters; moreover she has been involved as principal investigator in more than 300 international colloquia and seminars and has been invited by many international organisations as an expert on pertussis.

Nicole Guiso was actively involved in research, directing studies of post-graduate students, post-doctoral investigators and trainees. She has been a member of the Scientific Council of the Institut Pasteur in Paris and of several Instituts Pasteur around the world. She was awarded the Nicloux Prize of the French Chemical Society in 1984, the Dr Darolles Prize of the Academy of Medicine in 1998, "Grade de Chevalier dans l'ordre National du Mérite" in 2001 and "Grade de Chevalier dans l'ordre National de la Legion d'Honneur" in 2006.

Prof. Annette Mankertz
Robert Koch Institute, Germany

Professor Annette Mankertz is a biochemist and received a diploma from Berlin Free University in 1987. She joined Prof. Walter Messer at the Max Planck Institute for Molecular Genetics in Berlin and was awarded PhD for studies of bacterial viruses in 1990. Since then, she worked at the Robert Koch Institute.

First, she became interested in the molecular biology of porcine circoviruses and investigated the mechanisms of pathogenicity and the interaction of circoviruses with their hosts. Meanwhile, Annette Mankertz switched gears and nowadays works with viruses inducing the childhood diseases measles, mumps and rubella (MMR). As Head of the National Reference Centre MMR she cooperates closely with the ECDC and the WHO, and her lab serves as one of three WHO Regional Reference Labs in Europe. Besides her commitment to public health and laboratory diagnostic she is still highly interested in basic science, especially in molecular virology.

In 2011, Annette Mankertz has been appointed the Head of Unit "Viral infections" and Deputy Head of the "Department of Infectious Diseases" in RKI. In 2014, she became Professor at the Free University. She enjoys teaching and working in the area of interface between public health, diagnostic and basic science.

Prof. Christine Stabell Benn
University of Southern Denmark, Denmark

Prof. Christine Stabell Benn is a medical doctor (1996), PhD (2003) and Doctor of Medical Science (2011) from University of Copenhagen. She has worked at the Bandim Health Project in Guinea-Bissau (BHP) since 1993, starting as a medical student. She has spent post doctoral time at the Danish National Hospital, Department for Infectious Diseases and at Stanford University. In 2010 Prof. Benn received an ERC Starting Grant. In 2012, Prof. Benn was selected by the Danish National Research Foundation to establish and lead a Center of Excellence, the "Research Center for Vitamins and Vaccines" (CVIVA). Since 2013, she has held the position of Professor in Global Health at the University of Southern Denmark.

Prof. Benn's research aims to document that vaccines and vitamins affect the immune system in a much more general way than previously thought. With regard to childhood vaccines, they are usually implemented without prior trials documenting their effect on overall health. It is assumed that if a vaccine prevents a target disease, then the effect on overall mortality is beneficial and proportional to the number of deaths caused by the disease. However, sometimes this turns out not to be the case. For instance, in low-income countries with high infectious disease mortality, Bacille Calmette-Guérin (BCG) against tuberculosis and measles vaccines have stronger mortality-reducing effects than can be ascribed to prevention of tuberculosis and measles infections, i.e. they also protect against other infectious diseases. In other words they have beneficial heterologous or non-specific effects. Recent studies conducted in Denmark have shown that the measles-mumps-rubella vaccine may have similar beneficial non-specific effects on morbidity in high-income countries.

These observations tend to be dismissed because they do not fit assumptions. However, we need to draw lessons also from the unexpected and even "unbelievable" observations. If vaccines have non-specific effects and modulate the immune system in more general ways, immunization programmes designed to take into account and optimise both specific and non-specific effects of vaccines hold the potential for greatly improving health.

Plenary Session E: Public Health Event 2015: Ebola and MERS-CoV – recent advances and remaining challenges

Dr. Maria Van Kerkhove
Institut Pasteur, France

Dr Maria Van Kerkhove is the Head of the Outbreak Investigation Task Force at Institut Pasteur's Center for Global Health. She is an experienced infectious disease epidemiologist with strong field experience in infectious disease outbreaks and epidemiologic investigations. Her main research interests include zoonotic, respiratory and emerging/re-emerging viruses such as avian influenza, MERS-CoV, Ebola and Marburg.

Dr Van Kerkhove is also currently a technical consultant for WHO as a member of the MERS-CoV task force. She has worked with WHO to routinely analyze available data from countries and conduct risk assessments, and regularly participates in Missions to affected member states.

Dr Van Kerkhove was previously employed by Imperial College London in the MRC Center for Outbreak Analysis and Modelling where she worked closely with WHO on influenza, yellow fever, meningitis, MERS-CoV and Ebola Virus Disease.

Prof. Stephan Günther
Bernhard-Nocht-Institute for Tropical Medicine in Hamburg, Germany

Prof. Stephan Günther is a specialist in Medical Microbiology, Virology, and Infection Epidemiology at the Bernhard-Nocht-Institute for Tropical Medicine in Hamburg, Germany. He has a medical degree from the Humboldt-University Berlin (Charité) and holds a professor position at the University of Hamburg.

His research is dedicated to hemorrhagic fever viruses in Africa, in particular the investigation of virus replication using molecular and structural biological approaches and studying pathogenesis in small animal models. Major focus of clinical virology is molecular epidemiology, diagnostics, and therapy of hemorrhagic fever viruses in Africa.

He is coordinating several European project consortia, including:

- European Mobile Laboratory project funded by European Commission, Development and Cooperation Office, DEVCO „Establishment of Mobile Laboratories up to Risk Group 4 in combination with CBRN Capacity Building in sub-Saharan Africa" (EMLab) 2012-2015
- Horizon 2020 project "Ebola Virus Disease – Correlates of protection, determinants of outcome, and clinical management" (EVIDENT) 2014-2016

Dr. Pierre Formenty
World Health Organization (WHO)

Dr. Formenty has been working for the World Health Organization (WHO) since January 1996. Within WHO, he is leading the "Viral Haemorrhagic Fevers and other emerging zoonotic diseases" group. He is a field epidemiologist specialized in Public Health (infectious diseases surveillance and outbreak response) and in Medical Virology with special focus on viral haemorrhagic fever (notably Filovirus). He is also a Veterinary Officer, specialized in virology and epidemiology for domestic and wild animals. He has more than seventeen years' experience in tropical animal pathology and tropical medicine. Since 1996, Dr. Pierre Formenty has participated in the control activities of more than 29 outbreaks of international importance. During these missions he supported outbreak response activities for the following diseases: Chikungunya (2 times), Cholera (1), Dengue (1), Ebola (9), Marburg (4), Monkeypox (2), Nipah (1), Plague (1), Rift Valley Fever (4), SARS (1) and Yellow Fever (2).

Dr. Gunnstein Norheim
Norwegian Institute of Public Health

Gunnstein Norheim, MSc Pharm, PhD, is a staff scientist at the Division for Infectious Control at the Norwegian Institute of Public Health. He has a PhD from University of Oslo on meningococcal vaccines development and bacterial meningitis in Africa, and served as a consultant for WHO in Burkina Faso. He has worked as a post doc at the Oxford Vaccine Group, University of Oxford, on pre-clinical and clinical development of serogroup B and X meningococcal vaccines. Current research areas include meningococcal vaccine development for the African meningitis belt, molecular epidemiology of tuberculosis and clinical evaluation of Ebola vaccines. During the last year he has worked on the coordination, planning and implementation of the phase III clinical trial with a novel vaccine against Ebola in Guinea, and is a member of the Study Steering Group for this trial.

Plenary Session Abstracts

18	PLENARY SESSION A	WEDNESDAY 11 NOVEMBER	9:00-10:30
18	PLENARY SESSION B	WEDNESDAY 11 NOVEMBER	16:30-18:00
19	PLENARY SESSION C	THURSDAY 12 NOVEMBER	9:00-10:30
20	PLENARY SESSION D	FRIDAY 13 NOVEMBER	9:00-10:30
22	PLENARY SESSION E	FRIDAY 13 NOVEMBER	16:30-18:00

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Plenary Session Abstracts

Plenary Session A
Wednesday 11 November
9:00-10:30

Plenary Session A: Keynote

Antibiotic resistance: A tragedy of the commons

Presented by

Prof. Jan Kluytmans

Affiliation

University Medical Center of Utrecht, Julius Center for Health Sciences and Primary Care, Amphia Hospital Breda, The Netherlands

Abstract

The discovery of penicillin in 1928 marked the beginning of the age of antibiotics, a revolution in healthcare that has been the cornerstone in decreasing the morbidity and mortality of major bacterial infectious diseases in humans and other animals in the last six decades. Antibiotics allowed major advances in medically complex treatments, such as organ transplantation and immunosuppressive cancer treatment (e.g. chemotherapy), by controlling the risk of (opportunistic) bacterial infections.

Over time bacteria have developed resistant to the existing antibiotics and new antibiotics have hardly been developed during the last three decades. Experts and leaders around the globe have recently recognized antimicrobial resistance as one of the major threats to human health in the near future.

Studies of ECDC have estimated that the current number of annual deaths due to infections caused by drug-resistant bacteria in Europe alone was 25 000 and that the associated costs amounted to 1.5 billion euros per year. In a recent review, a continued rise in resistance by 2050 is estimated to lead to 10 million deaths every year worldwide and an increase of 2% to 3.5% in gross domestic product (GDP), costing the world up to 100 trillion USD.

This lecture will describe the use of antimicrobials in humans and animals, the consequences of this use, the political and economic barriers to improve prudent use and possible solutions for this problem.

Plenary Session B
Wednesday 11 November
16:30-18:00

Plenary Session B: Social Media: a toy or a useful tool?

Digital Disease Detection

Presented by

Dr. John Brownstein

Affiliation

Boston Children's Hospital, The United States of America

Abstract

Over the past fifteen years, Internet technology has significantly changed the landscape of public health surveillance and epidemic intelligence gathering. Disease and outbreak data is disseminated not only through formal online announcements by government agencies, but also through informal channels such as social networking sites, blogs, chat rooms, Web searches, local news media and crowdsourcing platforms. These data streams have been credited with decreasing the time between an outbreak and formal recognition of an outbreak, allowing for an expedited response to the public health threat. Collectively, these online sources create an image of global public health that is fundamentally different from the one produced by traditional public health surveillance infrastructure. The talk will discuss the current capabilities and future directions in the use of the non-traditional data sources for the purposes of public health surveillance and rapid detection of emerging infectious diseases.

How to use Internet data for public health purposes: current limitations and possible solutions?

Presented by

Prof. Ingemar Cox

Affiliation

University College London, United Kingdom & University of Copenhagen, Denmark

Abstract

Around 80% of US Internet users consult the Internet, via traditional search engines and social media, when they require medical information. The digital trails people leave on social media and search engines can be used for a variety of health purposes. These include infectious disease surveillance, alternative non-pharmacological means of intervention, and facilitating a number of epidemiological investigations. Research has addressed public-health questions such as the effect of media on development of anorexia, developed tools for measuring influenza rates and assessing drug safety, and examined the effects of health information on individual wellbeing.

This talk will show how Internet data can facilitate medical research, providing an overview of the area. We will discuss the types of information which can be inferred from a variety of Internet data sources, including social media, search engines, and specialized medical websites. We will briefly summarize analysis methods used in recent literature, and show how results can be evaluated. Finally, we will discuss current limitations, including ethical and privacy issues, and possible technological solutions.

Plenary session C
Thursday 12 November
9:00-10:30

Plenary Session C: Ensuring that evidence leads to public health protection – special session on occasion of the 20th EPIET anniversary

Recurring hepatitis A outbreaks in the EU/EEA: summary of the recommendations

Presented by

Dr. Johanna Takkinen

Affiliation

European Centre for Disease Prevention and Control (ECDC)

After several years of decreasing trend, foodborne hepatitis A virus (HAV) infection has re-emerged as a public health problem in EU/EEA since 2011. Several consecutive multi-country foodborne HAV outbreaks were experienced in Europe 2012-2014. The first such outbreak started in October 2012 affecting citizens in Nordic countries. By June 2013, 103 HAV cases of infection with two strains of HAV genotype 1B were identified with suspected exposure to contaminated frozen strawberries, most likely imported from Egypt or Morocco. The second outbreak of 107 cases was recorded between 1 November 2012 and 30 April 2013 among tourists from 14 countries after their return from holidays in Egypt. The outbreak was caused by a HAV strain of genotype 1B but with different sequence type from the first outbreak strains. International outbreak team concluded that these cases were associated with exposure to locally produced fresh strawberries. Based on the comparison in the international HAVNET sequence database, hosted by the National Institute for Public Health and Environment in the Netherlands, all three strains involved in the first two outbreaks were closely related and clustered with other strains isolated from travellers returning from Egypt. A third and by far the largest documented foodborne hepatitis A outbreak occurred between January 2013 and August 2014 with over 1500 cases reported in 13 countries. The outbreak strain was of genotype 1A and suspected vehicles were mixed frozen berries, mostly linked to freezing processors in Poland and berry suppliers from Bulgaria. These outbreaks highlight the increasing importance of foodborne transmission of HAV through berry products, the vulnerability of EU population due to low endemicity and lack of vaccination in European travellers. In the second outbreak, travellers had no vaccination as they perceived the risk for HAV infection low in all-inclusive luxury resorts even in endemic countries. These outbreaks were successfully investigated by different international outbreak investigation teams, with invaluable support from several EPIET fellows in various countries, public health and food safety authorities in the EU Member States, ECDC and EFSA.

Recurring hepatitis A outbreaks in the EU/EEA: food tracing activities

Presented by

Dr. Jane Richardson

Affiliation

European Food Safety Authority (EFSA)

Abstract

In July 2013 EFSA was requested by the European Commission to coordinate tracing activities in relation to a multinational outbreak of hepatitis A. Confirmed cases (outbreak strain KF182323) were reported in ten European countries (331 cases). Analysis of food histories and questionnaires identified consumption of berries and berry products. HAV contamination was detected in frozen mixed berries (14 lots) and mixed berry cakes/pastries (2 lots). Tracing began with 38 lots/cases from Italy, Ireland and the Netherlands, an additional 5 lots/cases were added from France, Norway and Sweden in spring 2014. These starting points for tracing were classified based on the strength of evidence of the association between food vehicle (berries) and the HAV outbreak. The tracing data were exchanged via the European Rapid Alert System for Food and Feed. The final dataset comprised 6227 transactions among 1974 food operators. Bulgarian blackberries and Polish redcurrants were the most common ingredients in the traced lots/cases; however, Poland is the largest producer of redcurrants in Europe, and Bulgaria is a major exporter of frozen blackberries. No single point source of contamination linking all 43 lots/cases could be identified. HAV cases/lots in five countries could be linked to seven Polish freezing processors and/or to five frozen berry suppliers in Bulgaria. Indicating that HAV contamination could have occurred at the freezing processor or in primary production of berries and therefore compliance with Good Hygiene Practice, Good Manufacturing Practice and Good Agricultural Practice is recommended

Recurring hepatitis A outbreaks in the EU/EEA: a national perspective

Presented by

Dr. Gaia Scavia

Affiliation

Istituto Superiore di Sanità, Department of Veterinary Public Health and food Safety, Rome, Italy

Abstract

In 2013/2014 Italy experienced one of the largest community-wide outbreak of Hepatitis A causing 247 confirmed cases of infection with Hepatitis A virus (HAV) genotype IA and 1435 probable cases. Soon after the outbreak was detected in May 2013, mixed frozen berries contaminated with HAV were identified as the source of the outbreak. Epidemiological evidence obtained through a case-control study was supported by the finding of a 100% nucleotide similarity of the VP1-2A sequences of HAVs detected in the human and in frozen berries samples. A range of Public Health actions were then undertaken to prevent the occurrence of new cases of HAV infection, based on the outcomes of the investigation coordinated by a multidisciplinary National Task Force, in collaboration with regional and local public health authorities. The investigation revealed a widespread and prolonged pattern of HAV contamination of imported frozen berries, with several manufacturing companies, brands and lots implicated in the outbreak since February 2012. Trace-back investigation also revealed an extremely complex network of frozen berries suppliers from 19 different countries and with no possibility for a single point source to potentially explain the vast contamination of berries found in Italy. These aspects made the adoption of control options in the frozen berries production and manufacturing chain, particularly challenging and confirmed the high microbiological risk profile of frozen berries. The importance of a multi-disciplinary approach to outbreak investigation, HAV contamination assessment, and control measures adoption, including consumers' risk communication, is the most important point of the lesson learned from this outbreak.

Plenary Session D
Friday 13 November
9:00-10:30

Plenary Session D: Emerging challenges to vaccine programmes: antigen escape and non-specific immune effects

Impact of immunization with different pertussis vaccines on selection of escape mutants and reduction in vaccine effectiveness

Presented by

Prof. Nicole Guiso

Affiliation

Institut Pasteur, France

Abstract

Bordetella pertussis, and to a lesser extent Bordetella parapertussis, cause whooping cough in humans, a highly transmissible respiratory disease, life threatening for unvaccinated subjects. Vaccination strategies were thus introduced worldwide with whole-cell pertussis (wP) vaccines with great success in regions reaching high vaccine coverage with efficacious vaccines. In the late 20th -early 21st century, subunit or acellular pertussis (aP) vaccines replaced wP vaccines in industrialized countries. Since the introduction of vaccination the incidence of the disease has dramatically decreased. However, (i) B. pertussis still circulates and evolves in humans, its only known reservoir, (ii) the disease still occurs through epidemic cycles every 3-5 years and vaccination didn't change this frequency.

B. pertussis and B. parapertussis, two species issued from the animal species B. bronchiseptica, have adapted to their unique host but also evolved according to the herd immunity i.e. according to the vaccine coverage, vaccine type and vaccine strategy as demonstrated by comparing bacteria circulating in high or low vaccine coverage. The latest transformation of B. pertussis is the loss of production of a virulence factor included in different aP vaccines, pertactin (PRN). The direct relation between aP vaccine introduction and increase in B. pertussis PRN-deficient isolate prevalence is still speculative although highly probable. However, B. parapertussis isolates presenting the same phenotype are also collected although this species shouldn't be impacted by aP vaccine induced-immunity. This phenotype might thus as well be a transient evolution of this species or an on-going adaptation to its human host.

The lack of PRN production does not impact the virulence or transmission of B. pertussis however, we recently demonstrated that B. pertussis PRN-deficient isolates are capable of sustaining longer infection as compared to PRN-producing isolates in an in vivo model of aP immunization. Loosing PRN production might thus provide a selective advantage to these isolates on aP vaccine effectiveness. A recent study performed in United States suggests also that aP vaccinated persons might have a greater susceptibility to PRN- isolates compared with PRN+ isolates. Pursuit of the epidemiological, clinical and microbiological studies is urgently needed.

Establishing worldwide reference laboratories, harmonizing epidemiological studies and collecting B. pertussis and B. parapertussis isolates should be a priority to better understand the impact of vaccination on Bordetella populations or the role of Bordetella species evolution on pertussis vaccines effectiveness.

Measles and mumps, two related viruses with distinct challenges for global vaccination programs

Presented by

Prof. Annette Mankertz

Affiliation

Robert Koch Institute, Berlin, Germany

Abstract:

Measles and mumps viruses both belong to the family paramyxovirus and are transmitted by droplet infection. Contraction of measles virus results in maculo-papular rash, high fever and strong malaise. Approximately one in 1,000 infections will lead to death. In contrast, mumps virus shows a lower index of contagiosity and manifestation, and cases present more benignly with painful swelling of the parotid gland. Fatal progression is estimated to occur in one in 10,000 cases. Live attenuated vaccines were developed in the 1950s and 60s by John F. Enders and Maurice Hilleman. Descendants of these vaccines are still in use today and have led to a dramatic decrease in global incidence. Moreover, WHO has launched an elimination program for measles and rubella.

Measles vaccine evokes a robust immune response which is supposed to last lifelong. Use of the vaccine has led to a massive reduction of the death toll. As we know of today, there are no indications for a loss of vaccine efficacy despite the fact that vaccine and virus have co-circulated for decades and changes in neutralizing epitopes have been detected. However it is not clear whether a lack of natural boostering will influence longtime immunity against measles. Investigation of recent outbreaks indicates a slight increase in secondary vaccination failure. Since plaque neutralization test of 2xMMR vaccinated showed protection against measles and rubella despite a negative ELISA titer, German guidelines for virus diagnostic in pregnant women now recommend assessing immunity by controlling the vaccination card rather than measuring IgG-titers. Serological surveillance should be performed nevertheless when vaccination documents are not available.

Mumps outbreaks in highly vaccinated groups were recorded throughout the world during recent years. Outbreak investigations have revealed frequent secondary vaccine failure. In general, mumps immunity after vaccination seems to be more individual when compared to measles and rubella since PNT and EIA do not correlate well. The underlying cause, including antigen escape or waning immunity, will be discussed.

In conclusion, I find it important to stress that the MMR-vaccine was and is one of the best buys in public health. Administering the MMR-vaccine twice is the best measure to protect children against measles and women of child-bearing age against rubella and is a prerequisite to fulfill the WHO elimination goal for measles and rubella. The mumps component of the MMR-vaccine can be considered just as worthy of improvement.

Non-specific effects of neonatal and infant vaccination: Public-health, immunological and conceptual challenges

Presented by

Dr Christine Stabell Benn

Affiliation

Research Center for Vitamins and Vaccines, Statens Serum Institut, Denmark, and University of Southern Denmark/Odense University Hospital.

Abstract

Can tuberculosis vaccine protect neonates against septicaemia? Can measles vaccine protect against pneumonia in the absence of measles? Is smallpox vaccine the best vaccine against HIV infection so far? Are these vaccine effects different for males and females?

The speaker will argue that the answer to these questions is yes. Her group's research on vaccines in the world's poorest countries has provided insight into the vaccines multifaceted effects. A growing number of observational studies and randomised trials show that in addition to the specific disease-protective effect, vaccines also confer non-specific effects – they affect the immune system's ability to respond to unrelated pathogens. Live attenuated vaccines seem to improve the immune system's ability to handle other pathogens. However, inactivated vaccines, while inducing specific protection, may reduce the immune system's ability to fight other pathogens. Both positive and negative non-specific effects seem strongest for females. Emerging immunological studies suggest that mechanisms such as heterologous T-cell immunity and innate immune training are implied.

The findings open the door to a new understanding of how vaccines can modulate the immune system. They are controversial, and they are not yet widely recognized. However, in 2014 WHO acknowledged that non-specific effects of vaccines warrant further research.

Plenary Session E
Friday 13 November
16:30-18:00

Plenary E: Public Health Event 2015: Ebola and MERS-CoV – recent advances and remaining challenge

On the animal-human interface – reservoirs & transmission chains; challenges for infection control and development of vaccines in the context of an outbreak

Presented by

Dr. Maria Van Kerkhove, Institut Pasteur, France
Dr. Pierre Formenty, World Health Organization (WHO)
Stefan Günther, Bernhard-Nocht-Institute for Tropical Medicine in Hamburg, Germany
Gunnstein Norheim, Norwegian Institute of Public Health

Parallel Session Abstracts

24	PARALLEL SESSION PROGRAMME	WEDNESDAY 11 NOVEMBER	10:50-12:30
24	Parallel Session 1: Antimicrobial Resistance		
26	Parallel Session 2: Outbreaks I		
29	Parallel Session 3: Influenza		
31	PARALLEL SESSION PROGRAMME	WEDNESDAY 11 NOVEMBER	13:30-14:50
31	Parallel Session 4: Healthcare Associated Infections		
33	Parallel Session 5: International Health		
35	Parallel Session 6: Emerging and Vector-borne diseases		
37	PARALLEL SESSION PROGRAMME	THURSDAY 12 NOVEMBER	10:50-12:30
37	Parallel Session 7: HIV-STI		
40	Parallel Session 8: Outbreaks II		
42	Parallel Session 9: Burden of Disease		
45	PARALLEL SESSION PROGRAMME	THURSDAY 12 NOVEMBER	14:00-15:20
45	Parallel Session 10: Food and Waterborne diseases		
47	Parallel Session 11: Vaccine-preventable Diseases I		
49	Parallel Session 12: Novel Methodological Approaches		
51	PARALLEL SESSION PROGRAMME	THURSDAY 12 NOVEMBER	17:00-18:10
51	Parallel Session 13: Late Breakers		
53	Parallel Session 14: Vaccine-preventable diseases II		
55	Parallel Session 15: Public Health Microbiology and Molecular Epidemiology		
57	PARALLEL SESSION PROGRAMME	FRIDAY 13 NOVEMBER	10:50-12:30
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Parallel Session Programme
Wednesday 11 November
10:50-12:30

Parallel Session 1: Antimicrobial Resistance

MODERATOR: Panayotis Tassios (ESCAIDE Scientific Committee, Greece)

Survey of carbapenemase-producing Klebsiella pneumoniae in Romania, 2013-2014

Ani Isidro Cotar (1,3), Brandusa Elena Lixandru (1), Monica Straut (1), Codruta Romanita Usein (1), Dana Cristea (1), Simona Ciontea (1), Dorina Tatu-Chitoiu (1), Irina Codita (1), Aftab Jasir (2), Maria Damian (1)

1. Cantacuzino National Institute of Research-Development for Microbiology and Immunology, Splaiul Independentei 103, Bucharest, Romania
2. The European Programme for Public Health Microbiology Training (EUPHEM), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
3. European Program for Intervention Epidemiology Training, ECDC, Stockholm, Sweden

Background

This study aims to provide a snapshot of the distribution and dissemination of carbapenemase-producing Klebsiella pneumoniae isolates collected during six months starting from October 2013 till April 2014 from hospitalised patients in eight Romanian hospitals.

Methods

The antimicrobial susceptibility testing of K. pneumoniae isolates was performed by disk diffusion method, whereas screening for carbapenemases production was done by a combination of Kirby-Bauer disk-diffusion methods, MastDisc ID inhibitor combination disks and the biochemical Carba NP II tests. Confirmation of carbapenemases was performed by amplification of the genes blaOXA-48-like, blaNDM, blaKPC and blaVIM. Sequencing of the PCR products was used for determination of sub-type of carbapenemase gene, whereas genetic relatedness among carbapenem non-susceptible isolates was evaluated using Pulsed Field Gel Electrophoresis (PFGE).

Results

Among 75 investigated carbapenem non-susceptible K. pneumoniae isolates 65 contained one of three Ambler classes of carbapenemase, A (KPC-type), B (metallo-beta-lactamase) or D (OXA-type), whereas for 10 isolates no carbapenemase activity was detected. PCR results showed that 51 strains harbored blaOXA-48 gene, 8 strains had the blaNDM gene, whereas the blaKPC and blaVIM genes were present in 4 and 2 strains, respectively. The analysis of PFGE profiles of OXA-48 and NDM-1 producing K. pneumoniae suggests inter-hospital and regional transmission of epidemic clones.

Conclusion

This study presents the first detection of K. pneumoniae strains harbouring blaKPC-2 and blaVIM-1 genes in Romania. The PFGE results of this study are testimony of a clonal dissemination of K. pneumoniae harbouring all of the four carbapenemase genes across the sample of Romanian hospitals enrolled. There is urgent need for strengthening of hospital infection control measures to protect patients from these multiple resistant bacteria in Romanian hospitals.

Keywords: carbapenemase-producing K. pneumoniae, molecular detection, PFGE analysis, epidemic clone

PRESENTED BY: Ani Ioana Cotar (aniioana@gmail.com)

REFERENCE NUMBER: 3000

Salmonella enterica isolates, Greece

Kyriaki Tryfinopoulou (1,2), Georgia Mandilara (3), Eleni Valkanou (4), Panagiota Giakkoupi (2), Kleon Karadimas (3), Alkiviadis Vatopoulos (3,2)

1. European Public Health Microbiology Training programme (EUPHEM), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
2. Antimicrobial Resistance and HAI Laboratory, National School of Public Health- CPHL-HSDCP – Vari , Attica-Greece
3. National Reference Centre for Salmonella-National School of Public Health-CPHL-HSDCP – Vari , Attica-Greece
4. National Reference Veterinary Laboratory for Salmonella and Antimicrobial Resistance, Chalkida, Greece

Background

Our study aims to identify the underlying ESBL and AmpC genes in ESCs resistant human and food-producing animal Salmonella enterica isolates collected in Greece from January 2008 to December 2014

Methods

Clinical isolates (2808) and isolates from food and food-producing animals throughout Greece (599) were tested for antimicrobial resistance. Characterization and antimicrobial susceptibility were performed by standard methods. Isolates resistant to cefotaxime and/or ceftazidime were screened for the detection of ESBLs and AmpC-β-lactamases using the double-disk synergy interpreted along with cefoxitine susceptibility for the presumptive identification of ESBL, pAmpC or ESBL+pAmpC phenotypes. PCR and subsequent DNA sequencing of the PCR products were applied for detection and characterization of the ESBL genes $bla_{TEM\text{-}type}$, $bla_{SHV\text{-}type}$, $bla_{CTX\text{-}M\text{-}type}$, $bla_{IBC/GES\text{-}type}$ and plasmid-mediated AmpC genes.

Results

In total 14 Salmonella isolates, [12 human and 2 of poultry origin (broiler laying hens)] with resistance to third generation cephalosporins were identified, assigned to ten different serotypes. Ten isolates (9 human and 1 poultry) produced ESBLs and 4 (3 human, 1 poultry) produced AmpC enzymes. Three different ESBLs genes [blaCTX-M-group 1 (n=5), SHV-5-like (n=4) and blaIBC1/GES-7 (n=1)] and three different AmpC β-lactamase genes [blaCMY-2 (n=2), blaDHA-1 (n=1), blaMIR/ACT (n=1)] were identified, with bla CTX-M-group 1 and blaCMY-2 found in both human and poultry isolates.

Conclusion

The presence of ESBLs and plasmid-acquired AmpC-β-lactamases in human and poultry Salmonella isolates in Greece is still rare. Nevertheless, the observed diversity of these enzymes in various Salmonella serotypes emphasizes the multiplicity of the respective blagene acquisition events. Also, highlights the need for close monitoring of ESCs resistance mechanisms in both clinical and veterinary contexts, since food-producing animals could become an important reservoir and potential vehicle for these ESCs-resistant strains to humans.

Keywords: Salmonella spp, ESBLs, AmpCs

PRESENTED BY: Kyriaki Tryfinopoulou (k.tryfinopoulou@otenet.gr)

REFERENCE NUMBER: 2915

Mandatory reporting of carbapenem-resistant Gram-negative bacteria in Hesse, Germany suggests rising trends and a decreasing role of international travel

Anja Hauri (1), M. M. Kaase (2), K.-P. Hunfeld (3), C. Imirzalioglu (4), P. Heinmueller (5), T.A. Wichelhaus (6), U. Heudorf (7), J Bremer (7), A. Wirtz (8)

1. HLPUG
2. Department of Medical Microbiology, Ruhr-University Bochum, Bochum, Germany
3. Central Institute of Laboratory Medicine, Microbiology & Hospital Hygiene, Krankenhaus Nordwest, Frankfurt am Main, Germany
4. Institute of Medical Microbiology at the Biomedical Research Centre Seltersberg (BFS) University-Hospital Giessen and Marburg, Campus Giessen, Germany
5. Hesse State Health Office, Dillenburg, Germany
6. Institute for Medical Microbiology and Infection Control, Hospital of Johann Wolfgang Goethe University, Frankfurt, Germany
7. Public Health Office, Gie
8. Hesse Ministry of Health, Wiesbaden, Germany

Background

Carbapenems are potent broad spectrum β-lactam antibiotics that are used as the last resort treatment for many Gram-negative bacteria. Carbapenem-resistant gram-negative bacteria (CR-GN) have emerged as a global threat. In November 2011, mandatory reporting of CR-GN was introduced in Hesse, one of the German federal states with a population of 6.1 million.

Methods

The case definition includes isolates resistant to the four major antibiotic classes acylureidopenicillins, third- and fourth-generation cephalosporins, carbapenems and fluoroquinolone. For Pseudomonas aeruginosa isolates from blood or cerebrospinal fluid and for all other CR-GN isolates from any specimen are notifiable. We defined as possibly travel-associated patients with non-German residency or any stay outside Germany during the 12 preceding months. We extracted from the Hessian CR-GN database all patients notified between 1 January 2012 and 30 April 2015. We counted as CR-GN isolates notifications of the first isolate, identified at species level, per patient.

Results

Of the 865 patients reported during the study period, 135 patients were associated with a foodborne outbreak and excluded from further analysis. Of the remaining 730 patients 152 were notified in 2012, 199 in 2013, 277 in 2014 and 102 in the first four months of 2015. Information on travel history was available for 501 patients. From 2012 to 2015, 54.6%, 47.2%, 38.1% and 39.3% of patients were possibly travel-associated. Proportion of possibly travel-associated isolates was highest for Acinetobacter baumannii (67.7%; 113/167) and lowest for Pseudomonas aeruginosa (27.8%; 13/35) and Enterobacter spp. (12.9 %; 9/70).

Conclusion

Preliminary data suggest rising trends of CR-GN notifications and decreasing associations with international travel, in line with ongoing autochthones transmission in Hesse. Good infection control measures are needed to contain this spread.

Keywords: Surveillance, Multidrug-resistant gram-negative bacteria, Carbapenem-resistance, Mandatory reporting, international travel

PRESENTED BY: Anja Hauri (anja.hauri@hlpug.hessen.de)

REFERENCE NUMBER: 3198

Evaluation of the Antibiotic Guardian campaign to help tackle antimicrobial resistance

Katerina Chaintarli (1), Suzanne M. Ingle (2), Alex Bhattacharya (3), Diane Ashiru-Oredope (3), Isabel Oliver (1), Maya Gobin (1)

1. Public Health England, Field Epidemiology Services, Bristol, UK
2. Health Protection Research Unit in Evaluation of Interventions, School of Social and Community Medicine, University of Bristol, UK
3. Public Health England, AMRs and HCAI Programme Team, London, UK

Background

As part of the 2014 European Antibiotic Awareness Day, an online pledge system was launched in the UK to increase people's commitment to reduce Anti-microbial Resistance (AMR).The aim of this evaluation was to determine whether the Antibiotic Guardian (AG) campaign improved AMR awareness and behaviour.

Methods

An online survey was sent to all 11,833 Antibiotic Guardians (AGs) to assess changes in knowledge and behaviour (outcomes) before and after the AG campaign. Logistic regression models, adjusted for age, sex and pledge group (members of public or healthcare professionals), were used to estimate associations between outcomes and AG characteristics.

Results

2478 AGs responded to the survey (21% response rate) from which 1696 (68%) pledged as healthcare professionals and 782 (32%) as members of public. These were similar to proportions seen in the whole population of 11,833 AGs. 76.9% of respondents were connected to the healthcare system and 96.3% of all AGs had prior knowledge of AMR. 66.9% of respondents were female and respondents were most commonly between 45-54 years old (25.1%). Two thirds (63.4%) of respondents reported always acting according to their pledge. Healthcare professionals were less likely to act according to their pledge than members of the public (Odds Ratio (OR)=0.31, 95% Confidence Interval (CI): 0.25-0.38). People that were confused about AMR prior to the AG campaign acquired more knowledge after the campaign (OR=3.2, 95% CI: 1.39-7.23).

Conclusion

This large study demonstrated that the campaign increased knowledge and changed behaviour particularly among members of public. Qualitative methods are being applied to explore the results from the quantitative analysis. This campaign should continue but needs to consider the lessons learnt from this evaluation.

Keywords: Public Health, Antimicrobial Drug resistance, Quantitative Evaluation, Behavioural medicine

PRESENTED BY: Katerina Chaintarli (katerinachaintarli@gmail.com)

REFERENCE NUMBER: 3016

Antimicrobial Resistance and Causes of Non-prudent Use of Antibiotics in the European Union, the ARNA project: Translating Research into Policy Actions

John Paget (1), Dominique Lescure (1), Anna de Jong (1), Natasja van der Laan (2), Ann Versporten (3), Herman Goossens (3), Francois Schellevis (1), Liset van Dijk (1)

1. Netherlands Institute for Health Services Research (NIVEL), The Netherlands
2. TNS-NIPO, The Netherlands
3. University of Antwerp, Belgium

Background

The objective of ARNA (Antimicrobial Resistance and Causes of Non-prudent Use of Antibiotics in the European Union) is to contribute to a more prudent use of antibiotics in the EU, with a special focus on the use of non-prescribed antibiotics. The project will run over a two year period (July 2014-June 2016) and is funded by the EC.

Methods

In year 1 ARNA will: 1) assess the non-prudent use of antibiotics in all EU Member States, with a special focus on Cyprus, Estonia, Greece, Hungary, Italy, Romania and Spain; 2) carry out a survey of Ministries of Health and relevant regulatory authorities; 3) carry out two literature reviews. In year 2 (July 2015-June 2016), ARNA will: 1) analyse the collected data and define policy options using the Multiple-Criteria Decision Analysis technique; 2) hold national policy dialogues and a consensus conference.

Results

To date (1 May 2015), ARNA has collected data on the non-prudent use of antibiotics among patients (N=65,103), general practitioners (N=712), and pharmacists (N=702) in the seven EU countries. A systematic literature review has been completed (n=59 studies) on the frequency and causes of non-prudent use of antibiotics. Finally, the web-based survey has been completed by representatives from 15 (of 28) Ministries of Health / relevant regulatory authorities in the EU.

Conclusion

The ARNA project is implementing research to assess and define the causes of non-prudent use of antibiotics in the EU. We will present the research findings and then describe the different policy options. The policy options will form the basis for the national policy dialogue meetings and the consensus conference in 2016, all of which will be carried out in collaboration with the EC.

Keywords: Drug Resistance, Microbial, European Union, prescriptions, Anti-Bacterial Agents

PRESENTED BY: John Paget (j.paget@nivel.nl)

REFERENCE NUMBER: 3161

Parallel Session 2: Outbreaks I

MODERATOR: Kåre Mølbak (ECDC Advisory Forum, Denmark)

Should seasonal workers feel worried about rodents present at the field? – Lesson learnt from the leptospirosis outbreak among Polish seasonal strawberries harvesters in Germany in 2014

Zuzana Klochanova (1,2), Salla Toikkanen (3,2), Michal Czerwinski (1), Beata Fiecek (1), Tomasz Chmielewski (1), Stanislawa Tylewska-Wierzbanowska (1), Johannes Dreesman (3), Malgorzata Sadkowska-Todys (1)

1. National Institute of Public Health - National Institute of Hygiene, Warsaw, Poland
2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden
3. Governmental Institute of Public Health of Lower Saxony, Hannover, Germany

Background

Leptospirosis is a zoonotic disease usually transmitted through contact with water or soil contaminated with urine of infected rodents. In August 2014, Germany informed Poland via Focal point for Early Warning Response System about an outbreak of leptospirosis among Polish seasonal strawberry harvesters working in Germany, similar to outbreak from 2007. We investigated to identify the risk factors in order to prevent future outbreaks.

Methods

We conducted case-control study among Polish harvesters who worked at German strawberry farms between May-September 2014 and retrospectively inquired about their exposures using a standardized questionnaire. A case was a harvester with leptospirosis-compatible symptoms onsetting minimum 2 days after beginning and maximum 2 weeks after terminating work at a farm, and with a physician's diagnosis or a laboratory-confirmation. We described severity of the outbreak and calculated adjusted odds ratios (aOR) and 95% confidence intervals (CI) using logistic regression.

Results

We identified 40 cases (6 cases laboratory confirmed) and 124 controls working at two strawberry farms those we included in the study. Overall, 24 cases were hospitalized, from those 5 cases developed meningitis and 2 cases renal dysfunction. In multivariable analysis, illness was significantly associated with presence of live or lifeless rodents in the field (aOR=4.24; 95%CI: 1.76-10.25), exposure to standing water in ditches by washing hands, feet or passing through (aOR=3.15; 95%CI: 1.27-7.79), and work during or after rain (aOR=1.11; 95%CI: 1.03-1.20 per day).

Conclusion

Our results suggest that rodents in the field and rainy weather conditions are risk factors for leptospirosis infection. Due to prevent re-emergence of the outbreak we recommend to monitor occurrence of the rodents at the area and to increase awareness among seasonal workers, strawberry farmers and local doctors.

Keywords: leptospirosis, strawberries, harvesting, rodents, rain

PRESENTED BY: Zuzana Klochanova (zklochan@gmail.com)

REFERENCE NUMBER: 3185

Two consecutive outbreaks of Salmonella Muenchen linked to pig farming in Germany 2013-2014: Is something missing in our regulatory framework?

Anika Schielke (1,2,3), Wolfgang Rabsch (1), Rita Prager (1), Sandra Simon (1), Angelika Fruth (1), Rüdiger Helling (4), Martin Schnabel (4), Claudia Siffczyk (5), Sina Wieczorek (6), Sabine Schroeder (7), Beate Ahrens (6), Hanna Oppermann (7), Stefan Pfeiffer (8), Sophie-Susann Merbecks (9), Andreas Gilsdorf (1), Klaus Stark (1), Dirk Werber (1,10)

1. Robert Koch Institute (RKI), Berlin, Germany
2. Postgraduate Training for Applied Epidemiology (PAE, German Field Epidemiology Training Programme), Robert Koch Institute, Berlin, Germany
3. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
4. Saxon State Ministry of Social Affairs and Consumer Protection, Dresden, Germany
5. Brandenburg State Office of Environment, Health and Consumer Protection, Potsdam, Germany
6. Thuringian State Authority for Consumer Protection, Bad Langensalza, Germany
7. Agency for Consumer Protection of the Federal State of Saxony-Anhalt, Magdeburg, Germany
8. Ministry of Labour and Social Affairs Saxony-Anhalt, Magdeburg, Germany
9. State Health Authority Saxony, Chemnitz, Germany
10. State Office for Health and Social Affairs, Berlin, Germany

Background In 2013, raw pork was the suspected vehicle in an outbreak of Salmonella (S.) Muenchen in Saxony. Current European regulations do not make provision for regulatory control measures on pig farms where salmonella is detected – not even when associated with human disease. In 2014, we investigated an outbreak of the same rare serovar affecting Saxony and 3 other federal states in Eastern Germany.

Methods
We defined cases as infections notified with S. Muenchen or Salmonella of group C/C2-C3 in affected states with onset between 2014/05/26-2014/08/03. Staff of an affected nursing home completed an online survey about their food consumption. Local food safety authorities tested raw pork products for S. Muenchen and traced back positive food specimens to farms investigated on-site. The National Reference Centre for Salmonella subtyped human, food and environmental isolates by pulsed-field gel electrophoresis (PFGE).

Results
Four affected states notified 247 cases (54% male; median age: 56 years; 4 deaths; highest reported incidence in Saxony, 3.4/100,000 population). Nursing home staff having breakfast at work, where raw pork was offered, was more likely to become cases compared with others (relative risk: 10; 95% confidence interval: 1.4-73). Isolates from humans in 2013 and 2014, raw pork sausages and surface swabs from three interacting pig farms shared indistinguishable PFGE patterns. One of the farms was already the suspected source of the 2013 outbreak on the basis of trace back and positive S. Muenchen environmental samples.

Conclusion
Epidemiological, microbiological and trace back evidence suggested that a common source in pig farming explains the 2013 and 2014 outbreaks. As current regulatory framework does not require effective measures at the farming stage, legislators should consider tightening regulations for salmonella in pigs.

Keywords: Salmonella, Outbreaks, Food-borne Diseases, Pigs

PRESENTED BY: Anika Schielke (schielkea@rki.de)

REFERENCE NUMBER: 3090

Outbreak of Hepatitis B in a German nursing home 2011 associated with blood glucose monitoring

Jane Hecht (1,2,3), Christoph Ziesch (4), Christian G Schüttler (5), Dieter Glebe (5), Claudia Santos-Hövener (1), Osamah Hamouda (1), Ruth Offergeld (1)

1. Robert Koch-Institut Berlin, Department of Infectious Disease Epidemiology
2. Postgraduate Training for Applied Epidemiology (PAE- German Field Epidemiology Training Programme), Robert Koch Institute (RKI), Berlin, Germany
3. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
4. Local health authority (Gesundheitsamt), Görlitz, Außenstelle Löbau, Germany
5. National Reference Laboratory (NRL) for Hepatitis B and D, German Centre for Infection Research, Institute for Medical Virology Justus-Liebig-University Gießen, Germany

Background
From June to November 2011, a nursing home in Saxony, Germany, reported eight cases of acute hepatitis B virus (HBV) infection. We investigated to identify the mode of transmission and prevent further infections.

Methods
We used electronic nursing home data to include residents of 2011 in a retrospective cohort study. We defined cases as being HBs-antigen anti-HBc-IgM positive (ELISA). HBV genomes in the positive serum specimens were cloned and sequenced. We collected information regarding possible exposures and analysed data using Exact Poisson regression.

Results
We identified eight cases among 82 residents (attack rate: 10%, 3 deaths, case fatality ratio (CFR): 37%). In univariable analysis, blood glucose monitoring (BGM, relative risk (RR) 21.3,CI3,3-∞), insulin injection (RR 6.9,CI 1.5-31.6) and chiropody (RR 6.7,CI1.1-∞) were associated with being a case. Only BGM was associated in multivariable Poisson regression (p=0.03). Infection control review revealed that nurses probably used one BGM device for more than one patient. Five positive specimens had high viral load (› 10^7 genomes/ml), were HBeAg-negative (subgenotype D2, rare in Germany) and shared up to 99.6 % genomic sequence. One of these five patients, a to the nursing home unknown HBs-antigen carrier, could be identified as the probable source of the outbreak on the basis of phylogenetic analysis.

Conclusion
Re-use of BGM devices may have caused this hepatitis B outbreak with a chronically infected resident as the source. The high CFR may be explained by the HBeAg-negative nature of the HBV variant. Our investigation shows, that nursing homes remain vulnerable to BGM-associated hepatitis B outbreaks despite existing recommendations. Strict implementation of universal precautions needs to be applied by everyone on every patient at any time, irrespective of the status of infection.

Keywords: Disease, Outbreak, Hepatitis B, nursing home, blood glucose monitoring

PRESENTED BY: Jane Hecht (hechtj@rki.de)

REFERENCE NUMBER: 3078

Bubonic plague outbreak investigation in the endemic district of Tsiroanomandidy - Madagascar, October 2014

Alain Rakotoarisoa (1,2), Maherisoa Ratsitorahina (3), Patrice Piola (3), Ariane Halm (4), Mino Rajerison (5)

1. Indian Ocean Field Epidemiology Programme, Indian Ocean Commission, Mauritius
2. Epidemiological Surveillance Department, Ministry of Health, Madagascar
3. Epidemiology Unit, Pasteur Institute, Madagascar
4. Health Surveillance Unit, Indian Ocean Commission, Mauritius
5. Plague Unit, Pasteur Institute, Madagascar

Background

Plague remains a major public health problem in Madagascar, endemic in 44 of 111 districts, with multiple epidemics every year. Our aim was to describe an outbreak reported by local health authorities between August 1 and October 12, 2014 in the district Tsiroanomandidy and look at previously reported associated factors to improve plague control strategies.

Methods

Suspected cases were individuals with sudden fever with lymphadenopathy or cough with hemoptysis and/or chest pain and/or breathing difficulty, probable cases were patients with positive test strip and confirmed cases were patients with positive culture. We identified cases from health registers and used a questionnaire to collect socio-demographic and clinical information, and performed a retrospective environmental survey of rodents and vectors in five villages.

Results

We identified 30 cases of bubonic plague, 28 probable and two suspected, including 14 deaths (46.7%) in four of the district's 17 municipalities. Median age was 15 years and 56.7% (17/30) of cases were under 15 years. The sex ratio (male/female) was 4:1. Ninety percent (27/30) of cases occurred in two municipalities (Tsinjoarivo and Ambatolampy). Recent murine mortality was reported and Yersinia pestis was isolated from four out of 42 rodents in two villages. A flee trap set in a house 10 hours after insecticide spraying still collected 45 fleas. Slash and burn culture, cohabitation with animals and generalized poor sanitation were observed or reported.

Conclusion

In this outbreak the majority of cases were young men and nearly half of the cases died. Insecticides used appeared to be inefficient. Raising awareness among the population, establishment of community surveillance, rodent and vector control are crucial prevention strategies, as well as controlled use of insecticides to ensure their effectiveness.

Keywords Madagascar, bubonic plague, epidemic, fleas, insecticide

PRESENTED BY: Alain Rakotoarisoa (arissoa@gmail.com)

REFERENCE NUMBER: 3085

Outbreak of Mycoplasma pneumoniae infection in a school in Baden Wuerttenberg - Germany, 2014-2015

Nobila Ouedraogo (1,2,5), Alexandra Lang (3), Nadja Muerter (3), Guenter Pfaff (1), Enno Jacobs (4), Elisabeth Aichinger (1), Christiane Wagner-Wiening (1,5)

1. Baden-Wuerttemberg State Health Office, Stuttgart, Germany
2. Postgraduate Training for Applied Epidemiology (PAE, German FETP), Robert Koch-Institute, Berlin, Germany
3. Public Health Office Goeppingen, Germany
4. National Consultant Laboratory for Mycoplasma, Dresden, Germany
5. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden

Background

Disease caused by Mycoplasma pneumoniae is not mandatory notifiable in Germany, and outbreaks are rarely investigated. Therefore, its public health impact is not well understood. In December 2014, a cluster of pneumonia cases was observed in a school in Baden-Wuerttemberg with 527 students aged 6 to 18 years and 60 teachers. We investigated the outbreak to determine its extent and conducted a cohort study among all students and teachers to identify risk factors.

Methods

We defined probable cases as students/teachers with pneumonia or fever and cough or shivering occurring between 15/10/2014 and 15/01/2015. Confirmed cases were those with throat swabs or blood samples positive for M. pneumoniae by PCR or serology respectively. Students' parents and teachers completed a questionnaire on symptoms and contacts with infected persons within the preceding two months. We calculated attack rates (AR) and adjusted risk ratios (RR) using univariate analysis.

Results

We received 311 replies (53%) and identified 48 probable and 10 confirmed cases. The AR was 15% (44/302) among students and 44% (4/9) among teachers. The mean duration of disease was 11 days (range: 2-30). The main risk factors for infection included prior contact with family members with a respiratory infection (RR=3.0; 95%CI=1.8-5.0), being a teacher (RR=3.0; 95%CI=1.4-6.6) and sitting in the most crowded classroom (6th grade) (RR=2.3; 95%CI=1.4-3.8).

Conclusion

The high AR and the long duration of the disease suggest that the public health impact of M. pneumoniae related diseases in crowded settings such as schools might be considerable. We recommend routine testing for M. pneumoniae by physicians in case of respiratory infections in similar settings in order to guide early infection control measures and prevent future outbreaks.

Keywords: Mycoplasma pneumoniae, outbreak, respiratory tract infection, cohort study, prevention and control measures

PRESENTED BY: Nobila Ouédraogo (OuedraogoN@rki.de)

REFERENCE NUMBER: 3163

Parallel Session 3: Influenza

MODERATOR: Mira Kojouharova (ESCAIDE Scientific Committee, Bulgaria)

Waning immunity of the influenza vaccine against laboratory confirmed A(H3N2) and B Influenza, Spain, season 2014/15

Alin Manuel Gherasim (1), Salvador de Mateo (1,2), Amparo Larrauri (1,2), The Spanish cycEVA team (3)

1. National Centre of Epidemiology, Institute of Health Carlos III, Madrid, Spain
2. CIBERESP, Institute of Health Carlos III, Madrid, Spain
3. The Spanish cycEVA team

Background

The Spanish 2014/15 influenza season was dominated by the co-circulation of A(H3N2) and B viruses. Using data from cycEVA study (the Spanish component of I-MOVE), we aimed to determine the influenza vaccine effectiveness (IVE) against medically-attended influenza-like illness (ILI) with laboratory-confirmed influenza and to evaluate its evolution according to the time since vaccination.

Methods

Between weeks 50/2014 and 16/2015 ILI patients attending the primary healthcare sentinel general practitioners (GP) were systematically swabbed. We used a test negative design to compare influenza positive cases with negative controls. We estimated the adjusted IVE (aIVE) by virus type using logistic regression and controlling for potential confounders (age, sex, time of symptoms onset, sentinel region, chronic conditions, GP visits and smoking). We determined the VE considering the tertiles (days) of the time since vaccination using not vaccinated as reference group.

Results

In the final analysis we included 799 confirmed influenza cases (54,8% A(H3N2)) and 439 controls. At week 16/2015, the overall aIVE was 0.3% (95%CI: -70%; 42) and 50% (95%CI: 6; 73) against influenza A(H3N2) and B respectively. The aIVE against A(H3N2) declined from 49% (95%CI: -17; 78) before 88 days since vaccination, to -91% (95%CI: -356; 20) after 106 days, while the aVE against B influenza declined from 72% (95%CI: 10; 91) to -12% (95%CI: -187; 56) in similar periods.

Conclusion

Finishing influenza season 2014-15, the trivalent influenza vaccine had no protection against A(H3N2) and a moderate protective effect against B influenza. Against both viruses we registered a decline of the aIVE with time since the vaccination, effect that seemed more pronounced for A(H3N2). Influenza vaccines should maintain their protective effect through the whole influenza season.

Keywords: Human Influenza, influenza virus A(H3N2), influenza vaccines, vaccine effectiveness, test-negative design

PRESENTED BY: Alin Manuel Gherasim (amgherasim@externos.isciii.es)

REFERENCE NUMBER: 3060

Influenza vaccine effectiveness (VE) estimates from the I-MOVE multicentre case control study in Europe, 2014-15: low vaccine effectiveness against A(H3N2) and moderate vaccine effectiveness against A(H1N1)pdm09 and B

Esther Kissling (1), Marta Valenciano (1), Udo Buchholz (2), Amparo Larrauri (3), Caterina Rizzo (4), Beatrix Oroszi (5), Ausenda Machado (6), Coralie Giese (7,8), Daniela Pitigoi (9,10), Iwona Paradowska-Stankiewicz (11), Annicka Reuss (2), Alin Manuel Gherasim (3), Antonino Bella (4), Judit Krisztina Horváth (5), Raquel Guiomar (6), Lisa Domegan (7), Emilia Lupulescu (9), Monika Korczynska (11), Alain Moren (1), IMOVE multicentre case control team (12)

1. EpiConcept, Paris, France
2. Robert Koch Institute, Berlin, Germany
3. National Centre for Epidemiology, Instituto de Salud Carlos III, Madrid, Spain
4. Istituto Superiore di Sanit
5. Office of the Chief Medical Officer, Budapest, Hungary
6. Instituto Nacional de Sa
7. Health Protection Surveillance Centre, Dublin, Ireland
8. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, Stockholm, Sweden
9. Cantacuzino Institute, National Institute of Research
10. Universitatea de Medicina si Farmacie Carol Davila, Bucharest, Romania
11. National Institute of Public Health-National Institute of Hygiene, Warsaw, Poland
12. I-MOVE multicentre case control team

Background

In the seventh I-MOVE (Influenza Monitoring Vaccine Effectiveness in Europe) season, we undertook a multicentre case-control study based on sentinel practitioner surveillance networks in eight European Union (EU) countries to measure 2014/15 influenza vaccine effectiveness against medically-attended influenza-like illness (ILI) laboratory-confirmed as influenza. The season was characterised at European level by co-circulation of influenza A(H1N1)pdm09, B and mismatched A(H3N2) viruses.

Methods

Practitioners systematically selected ILI patients to swab within eight days of symptom onset. We compared influenza type/subtype positive patients to influenza-negative patients among those meeting the EU ILI case definition. Using logistic regression we calculated adjusted vaccine effectiveness (AVE) by influenza type/subtype, controlling for potential confounders (age, sex, time of onset and presence of chronic conditions) and study site. We calculated AVE overall and by age group.

Results

We included 4410 ILI patients, among whom there were 1400 A(H3N2), 375 A(H1N1)pdm09 and 580 B cases. AVE against A(H3N2) was 22.8% (95%CI: 0.1-40.4) overall, 36.9% (95%CI: -8.1-63.2), 18.4% (95%CI :-26.0-47.1) and 29.4% (95% CI: -8.9-54.2) among those aged 0-14, 15-59 and 60+ years respectively. AVE against A(H1N1)pdm09 was 43.7% (95%CI: 8.7-65.3) overall, 83.6% (95%CI: 49.6-94.7), 46.7% (95%CI: -25.7-77.4), and 13.2% (95%CI: -98.1-62) among those aged 0-14, 15-59 and 60+ years respectively. AVE against B was 55.4% (95%CI: 31.6-70.9) overall, 67.0% (95%CI: -1.2-89.3), 53.4% (95%CI: 9.1-76.1) and 51.2% (95%CI: 6.6-74.5) among those aged 0-14, 15-59 and 60+ years respectively.

Conclusion

Results indicate a low AVE against A(H3N2), overall and by age group. This is in line with a reported mismatch between circulating and vaccine strain. AVE against A(H1N1)pdm09 and B was moderate. The low and moderate estimates indicate seasonal influenza vaccines should be improved to achieve acceptable protection levels.

Keywords: Influenza, Influenza vaccine, prevention & control, multicentre studies, case control studies

PRESENTED BY: Esther Kissling (e.kissling@epiconcept.fr)

REFERENCE NUMBER: 2921

Pilot study to harmonize the reported influenza intensity levels and trends within the Spanish Influenza Sentinel Surveillance System using the Moving Epidemic Method (MEM)

Horacio Gil (1,2), Mathieu Bangert (1), Concepcion Delgado (3), Salvador de Mateo (3), Amparo Larrauri (3), SISSS (4)

1. European Program for Public Health Microbiology Training (EUPHEM), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden
2. Centro Nacional de Microbiología, Instituto de Salud Carlos III (ISCIII), Madrid, Spain
3. Centro Nacional de Epidemiología, ISCIII, Madrid, Spain
4. Spanish Influenza Sentinel Surveillance System, Spain

Background

Assessment of the intensity and trend of influenza activity is currently estimated using historical data from the Spanish Influenza Sentinel Surveillance System (SISSS) using qualitative indicators from the European Influenza Surveillance Network. These indicators are subjective and prone to their own interpretation. The MEM has been proposed by ECDC for harmonizing the reporting of intensity and trend indicators. This pilot study explores the impact of implementing MEM within the SISSS.

Methods

Intensity and trend indicators for the influenza season 2014-2015 in the 17 sentinel networks of the SISSS were estimated with thresholds and values (δ and n) calculated using the R-MEM package and weekly incidence rates from the previous ten seasons, excluding the pandemic season (2009-2010). MEM estimated indicators were compared with those reported by the networks. The specific intensity level during the epidemic peak calculated by MEM was compared to the one reported by each network using the Wilcoxon signed-rank test.

Results

Five networks reported higher pre-epidemic thresholds in comparison with the MEM. Ten of 17 sentinel networks, and also nationally, reported a peak intensity level that differed to the level calculated with the MEM. However, these discrepancies were not statistically significant for intensity levels (p=0.74). Influenza trends reported from 13 networks were increasing prior to the start of the epidemic wave, in contrast to the stable trend estimated with MEM.

Conclusion

MEM intensity levels showed non-significant differences with the SISSS reported levels. However, MEM will allow objective influenza surveillance monitoring and standardization of criteria for comparing the intensity of influenza epidemics among regions in Spain and different countries. This is considered crucial for guiding timely influenza control and prevention measures.

Keywords: Influenza, MEM, Intensity, Trend, Spain

PRESENTED BY: Horacio Gil (hgil@isciii.es)

REFERENCE NUMBER: 2897

Low seasonal influenza vaccine effectiveness in Ireland: a test-negative case-control study, I-MOVE project, 2014/2015

Coralie Giese (1,2), Lisa Domegan (2), Joan O'Donnell (2), Derval Igoe (2), Claire Collins (3), Michael Joyce (3), Olga Levis (3), Suzie Coughlan (4), Allison Waters (4), Margaret Duffy (4), Grainne Tuite (4), Linda Dunford (4), Darina O'Flanagan (2)

1. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden
2. Health Protection Surveillance Centre, Dublin, Ireland
3. Irish College of General Practitioners, Dublin, Ireland
4. National Virus Reference Laboratory, University College, Dublin, Ireland

Background

Within the Influenza Monitoring Vaccine Effectiveness in Europe (I–MOVE), we undertook a test-negative case-control study to estimate 2014/15 influenza vaccine effectiveness (VE) in Ireland.

Methods

Sentinel general practitioners (GPs) swabbed influenza-like illness (ILI) patients within seven days of symptom onset using systematic sampling. We compared influenza vaccination status between laboratory confirmed cases for influenza and test-negative controls among patients fitting the EU ILI case definition. Patients were considered vaccinated if the interval between vaccination and symptom onset was ›14 days. We used logistic regression to calculate influenza VE and 95% confidence intervals (95%CI) overall and among target group for vaccination, adjusting for age, symptom onset month, medical conditions and number of GP visits.

Results

We included 171 cases and 108 controls from 25 practices. Vaccination coverage was 15%. Adjusted VE was -14% (95%CI -186%–55%) overall, -36% (95%CI -285%–52%) against influenza A(H3) and -59% (95%CI -611%–65%) against influenza B. Crude VE for individuals vaccinated during current season only was 61% (95%CI -42%–89%) , and 56% (95%CI -100%–90%) for those vaccinated during the previous season only. The target group for vaccine included 57 cases and 31 controls and vaccination coverage was 41%; adjusted VE was - 81% (95%CI -638%–46%).

Conclusion

The A(H3N2) vaccine mismatch reported during the 2014/2105 season contributed to the poor effectiveness of the influenza vaccine against laboratory-confirmed influenza in Ireland. Vaccine uptake among recruited patients was low resulting in wide CI for all estimates. VE point estimates appeared to decrease with repeated immunisation. Because low VE may lead to negative perceptions of influenza vaccination by the public, efforts to improve influenza VE have to be prioritised. The effect of repeated immunization requires further investigation.

Keywords: Influenza, influenza vaccine, vaccine effectiveness, case control studies

PRESENTED BY: Coralie Giese (coraliegiese@hotmail.com)

REFERENCE NUMBER: 3174

A time-series analysis of the 2009 influenza A/H1N1 epidemiology, media attention, risk-perception and public reaction in 5 European countries

Amena Ahmad (1), Nadine Froehlich (1), Enny Das (2), Celine Klemm (3), Verena Kessler (1), Jan Hendrik Richardus (4), Ralf Reintjes (1,5)

1. Hamburg University of Applied Sciences, Germany
2. Radboud University Nijmegen, the Netherlands
3. VU University Amsterdam, the Netherlands
4. Erasmus MC Rotterdam, the Netherlands
5. University of Tampere, Finland

Background
In 2009, influenza A/H1N1 caused the first pandemic of the 21st century. As part of the EU funded project E-com@EU – this study aims to explore the time-dependent interplay between the changing influenza A/H1N1 epidemiology, media attention, public risk perception and behaviour in terms of vaccine uptake along the pandemic time-line in five European countries (Czech Republic, Denmark, Germany, Spain and UK).

Methods
Data on the 2009 A/H1N1 epidemiology (reported number of cases/deaths), the A/H1N1 vaccine uptake and public risk perception (from Apr.2009 – Mar.2010) were retrieved from various published literature sources. Media attention was estimated by the number of influenza A/H1N1 related news reports in selected print-media and TV-newscasts in the five countries. The dynamics and interactions of these elements were analysed along the epidemic time-line.

Results
All five countries were significantly affected by two influenza A/H1N1 waves – the first in spring followed by the second, larger wave in autumn/winter 2009. Vaccine uptake among the general population and at risk groups including health care workers was low and occurred mainly within a short period of around four weeks after the vaccine became available. Media attention surged with the WHO declarations of the pandemic, before the actual pandemic started to spread across European countries, and dropped to lower levels thereafter.

Conclusion
The combined analysis primarily shows that media logic does not equate epidemiological logic i.e. media attention does not necessarily increase with increased numbers of infections but spotlights certain key events based on their news value. These media attention time-periods however posit windows of opportunity to inform the public about resources where they can seek reliable information once it becomes available and when public interest rises.

Keywords: Influenza A Virus H1N1, Epidemiology, Media, Communication, Risk

PRESENTED BY: Amena Ahmad (amenaalmes.ahmad@haw-hamburg.de)
REFERENCE NUMBER: 3002

Parallel Session Programme
Wednesday 11 November
13:30-14:50

Parallel Session 4: Healthcare Associated Infections

MODERATOR: Naomi Boxall (ESCAIDE Scientific Committee, EAN Board, UK)

A pseudo-outbreak of Stenotrophomonas maltophilia linked to bronchoscopy in an Intensive Care Unit (ICU) in England, 2014

Thomas Waite (1,2), Katerina Chaintarli (3), Janet McCulloch (3), Charles Beck (3)

1. Public Health England Field Epidemiology Training Programme (FETP), Bristol, UK
2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden
3. Public Health England Field Epidemiology Service, Bristol, UK

Background
Stenotrophomonas maltophilia is an emerging multidrug-resistant pathogen causing severe healthcare-associated infections including pneumonia and meningitis. Risk factors include age, intubation and long ICU admission. An exceedance of S.maltophilia was reported in 18 bronchoalveolar lavage (BAL) specimens from an ICU between 01/10/13-31/10/14. We investigated the potential outbreak to determine risk factors and inform control measures.

Methods
We conducted a cohort study of ICU patients for whom a BAL specimen was submitted to the hospital laboratory. Cases were patients with a S.maltophilia positive BAL. We calculated the association between infection and clinical/demographic risk factors (admission length, bed location, bronchoscope used and disinfection method, inpatient antibiotic use) by comparing exposed and non-exposed individuals and calculating risk ratios (RR) with 95% confidence intervals using univariate logistic regression. Specimens were typed using pulse-field gel electrophoresis (PFGE).

Results
47 patients had a BAL sample submitted; 18 met the case definition. None had symptoms suggesting S.maltophilia infection. Known risk factors for S.maltophilia were not associated with being a case. PFGE typing revealed clusters of two strain types; seven isolates of 'type A' and five 'type B'. We found elevated risks of isolation of 'type A' in patients exposed to bronchoscope 1 (RR 13.56, 95%CI 1.82-100) and of 'type B' in patients exposed to bronchoscope 2 (RR 16.89, 95%CI 2.14-133). No association with disinfection method, bed location or antibiotic use was found. No microbiological samples were obtained from bronchoscopes.

Conclusion
Due to the absence of symptoms, results from our epidemiological investigation and association of strain types with particular bronchoscopes we concluded that this was a pseudo-outbreak where specimens had been contaminated by bronchoscopes. We recommended use of single-use bronchoscopes, which was an effective control measure.

Keywords: Stenotrophomonas maltophilia, Intensive Care, Bronchoscopes, Disinfection

PRESENTED BY: Thomas Waite (thomas.waite@phe.gov.uk)
REFERENCE NUMBER: 2877

Hospital-internal microbiological surveillance of multi-resistant Klebsiella pneumoniae and Escherichia coli: a pilot study

Nina Stock (1,2), Vaclav Vanis (1,3), Marek Maly (1), Gabriela Kapounova (3), Petra Vopalkova (3), Zuzana Zemanova (3), Jan Kubele (3), Vlastimil Jindrak (1,3)

1. National Institute of Public Health, Prague, Czech Republic
2. European Program for Public Health Microbiology, ECDC, Sweden
3. Centre for Clinical Microbiology and Antibiotic Surveillance, Hospital Na Homolce, Prague, Czech Republic

Background

In 2013, 13% of invasive E.coli and 52% of K.pneumoniae isolates in the Czech Republic were resistant to third generation cephalosporins. This study investigates the prevalence of ESBL- and AmpC-producing K.pneumoniae and E.coli in a Czech hospital, as well as possible risk factors associated with cases positive at admission (import).

Methods

Rectal swabs were taken for a three month period from all patients admitted to a 65-bed surgical department at admission and discharge, and three times weekly during their ICU stay. Patients with ESBL- or AmpC-producing K.pneumoniae or E.coli were further classified into imported and hospital-acquired cases.Demographic and clinical data were obtained through the hospital database. Data acquisition for risk factor analyses occurred through patient interviews examining profession, previous hospitalisation, antibiotic treatment and invasive devices. A cohort study design was applied.

Results

522 patients were included in the study (average age: 58y; average length of stay: 8 days). Sixty patients (11%) were positive according to the case definition, whereof 63% were imported cases. 65% of cases were positive for E.coli and 42% for K.pneumoniae (includes multiple colonisation). 85% of cases would have been missed without rectal screening procedures. Previous hospitalisation was the most important risk factor associated with imported cases (RR=2.6, p<0.001). Stratification demonstrated a high association with K.pneumoniae (RR=18.5, p<0.001), but not with E.coli (RR=1.2, p=0.6).

Conclusion

The prevalence of ESBL- and AmpC-producing K.pneumoniae and E.coli was greatly underestimated. K.pneumoniae-colonization at admission was highly associated with previous hospitalisation; E.coli-colonization was not associated with any risk factor.Due to absence of risk factors at admission for certain pathogens, a high overall compliance to standard precautions is crucial to control the spread of multi-resistant gram-negative bacteria.

Keywords: multi-drug resistance, E.coli, K.pneumoniae, microbiological surveillance, screening, hospital

PRESENTED BY: Nina Stock (nina.stock@web.de)

REFERENCE NUMBER: 2925

National automated real-time surveillance of hospital-acquired bacteraemia in Denmark

Sophie Gubbels (1), Jens Nielsen (1), Marianne Voldstedlund (1), Kenn Schultz Nielsen (2), Brian Kristensen (3), Kåre Mølbak (1), . The HAIBA stakeholder group (4)

1. Department of Infectious Disease Epidemiology, Statens Serum Institut, Copenhagen, Denmark
2. Department of IT development and projects, Statens Serum Institut, Copenhagen, Denmark
3. Department of Microbiology and Infection Control, Statens Serum Institut, Copenhagen, Denmark
4. Representatives from the Capital Region of Denmark, Region Zealand, Region of Southern Denmark, Central Denmark Region, North Denmark Region

Background

Bacteraemia is one of the most frequent and severe hospital-acquired infections. Since March 2015 national surveillance data are publicly available for bacteraemia through the Hospital Acquired Infections Database (HAIBA, www.haiba.dk). HAIBA provides automatic, continuous and timely surveillance data using existing data sources.

Methods

Data from the National Patient Registry and the Danish Microbiology Database were available from 1 January 2010. The case definition for bacteraemia was the yield of at least one pathogenic bacteria from a blood culture. A bacteraemia was considered hospital-acquired if the sample for blood culture was taken more than 48 hours after admission and less than 48 hours after discharge. The denominator for incidence calculations was defined as risk days between 48 hours after admission and 48 hours after discharge or until a bacteraemia occurred. Only the first episode during an admission was included in the incidence. The online surveillance system shows data for the entire country as well as by region, hospital, department and by public or private hospitals.

Results

Between 2010 and 2014, 13,730 hospital-acquired bacteraemia were identified, with an incidence of 7.29 per 10,000 risk days. The incidence varied among the five Danish regions between 5.99 and 8.03 per 10,000 risk days. Trends over time varied between hospitals and departments and need to be evaluated for each location individually.

Conclusion

HAIBA is envisioned to be a practical infection control tool for microbiologists, infection control nurses and clinicians, but also to provide transparency towards regional and national politicians as well as citizens. These data on bacteraemia will provide a dynamic way for hospitals and individual departments to monitor their trends, discuss the potential reasons for these trends and initiate and evaluate interventions.

Keywords: bacteremia, hospital, infection control, surveillance, Denmark

PRESENTED BY: Sophie Gubbels (gub@ssi.dk)

REFERENCE NUMBER: 3080

Measles outbreak among vaccinated healthcare workers in a hospital in the Netherlands, April 2014: Implications for measles control?

Laura Nic Lochlainn (1,2), Jussi Sane (1,2), Nathalie van Burgel (3), Rob van Binnendijk (1), Susan Hahne (1)

1. National Institute for Public Health and the Environment (RIVM), Centre for Infectious Disease Control, Bilthoven, the Netherlands
2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, Stockholm, Sweden
3. Department of Medical Microbiology, Haga Hospital, The Hague, the Netherlands

Background

In 2013, the Dutch National Institute for Public Health published advice for protection of healthcare workers (HCWs) against measles through catch-up vaccinations. In April 2014, two measles patients in a Dutch hospital initiated a cluster among HCWs. We investigated this cluster and estimated vaccine effectiveness (VE) to assess the appropriateness of current advice.

Methods

We defined potentially exposed HCWs as those in departments with measles patients between 23/03/2014 and 11/04/2014. We investigated cases' clinical severity, close contacts, and vaccination history via questionnaire. We calculated attack rates (AR) and VE as one minus the relative risk. We tested cases' sera for measles IgG and IgM, IgG avidity (high-avidity if >50%) and measles-virus–neutralising antibodies (mnAbs) in stored occupational pre-illness and per-illness sera.

Results

Between 04/04/2014 and 24/04/2014, eight of 64 potentially exposed HCWs were notified with measles (AR=13%). Cases' median age was 27 years (range 25-43); 50% were female. Six cases occurred among 47 twice-vaccinated HCWs (AR=13%); one case among eight once-vaccinated HCWs (AR=13%); one case among four unvaccinated HCWs (AR=25%). The two-dose measles VE was 49% (95%CI -226-92%). Twice-vaccinated cases reported mild measles symptoms and no secondary transmission. Three of four cases with stored pre-illness sera had mnAbs titers above the suggested cut-off for protection (120mIU/mL). Six twice-vaccinated cases had high per-illness avidity, indicating secondary vaccine failure; the once-vaccinated case had primary vaccine failure.

Conclusion

In this outbreak, six twice-vaccinated HCWs had secondary vaccine failure. Presence of mnAbs in three cases prior to measles exposure did not prevent infection. Insight into correlates of immune protection and enhanced surveillance of measles vaccine failure is necessary to assess whether measles booster vaccinations should be considered for HCWs.

Keywords: Measles, outbreak, healthcare workers, the Netherlands, vaccine failure

PRESENTED BY: Laura Nic Lochlainn (laura.nic.lochlainn@rivm.nl)

REFERENCE NUMBER: 3128

Parallel Session 5: International Health

MODERATOR: Kølsen Fischer (ESCAIDE SC, ECDC National Microbiology Focal Point, Denmark)

What are the most important infectious disease threats facing Europe? A ranking study.

Martijn Bouwknegt (1), Arie Havelaar (1,2), Rabin Neslo (3), Ana Maria de Roda Husman (1,4), Lenny Hogerwerf (1), Jim van Steenbergen (1), Mirjam Kretzschmar (1,3), Massimo Ciotti (5), Jonathan Evan Suk (5)

1. National Institute for Public Health and the Environment, Bilthoven, the Netherlands;
2. Emerging Pathogens Institute, University of Florida, Gainesville, USA
3. Julius Centre, Utrecht University, Utrecht, the Netherlands
4. Institute for Risk Assessment Sciences, Utrecht University, Utrecht, The Netherlands;
5. European Centre for Disease Prevention and Control, Stockholm, Sweden

Background

Emerging infectious diseases pose a continuing threat, the magnitude depending not only on pathogen characteristics and environmental determinants, but also on the abilities of health systems to anticipate and prepare for emerging risks. The need to identify and prioritise infectious disease threats has thus emerged as an important area for public health action, and one that requires strengthened collaboration across sectors and disciplines. The European Centre for Disease Prevention and Control (ECDC) launched a risk ranking study.

Methods

The methodology is based on multicriteria decision analysis. Two stakeholder meetings were used to identify and refine criteria to be used in the ranking system. Ten final criteria were grouped into a risk model consisting of three categories: likelihood of pathogen emergence; magnitude of the threat; and current level of health system preparedness/resilience to mitigate threats. Expert panels were used to provide weights for each criteria. The final list of criteria and criteria weights was employed by multi-disciplinary panels of experts to score a wide range of infectious diseases. These scores were standardized and analysed, leading to an overall risk ranking.

Results

A novel methodology for the ranking of emerging was developed. Over 100 experts were invited to participate, representing every EU Member State. The final ranking (results to be available by September, 2015) provides a basis for prioritisation of emerging infectious disease threats.

Conclusion

Rapid changes in infectious disease transmission pose continue threats to health security in Europe. Public health preparedness, which is predicated upon anticipation and strategic planning, can be strengthened by processes which engage multiple disciplines to prioritise emerging risks. Harnessing multidisciplinary expertise through multicriteria decision analysis is a potentially powerful approach for doing so.

Keywords: Emerging infectious disease, risk, decision analysis, emergency preparedness,

PRESENTED BY: Jonathan Evan Suk (jonathan.suk@ecdc.europa.eu)

REFERENCE NUMBER: 2968

A mixed-methods tool to assess Public Health surveillance systems.

Matthias Nachtnebel (1), Christian Winter (1), Barbara Buerkin (1), Ute Rexroth (1), Andreas Gilsdorf (1)

1. Robert Koch-Institute, Germany

Background

The German Partnership Program for Excellence in Biological and Health Security supports efforts to strengthen infectious disease control in the main partner countries, Sudan, Morocco and Tunisia; ultimately to improve global health security (non-proliferation) but simultaneously stipulated by the International Health Regulations (IHR 2005). This goal required initial assessments of Public Health (PH)-surveillance systems as starting points for the identification of elements pliable to improvements through capacity building and for the mapping of training needs.

Methods

To facilitate a systematic process we developed a mixed-methods tool for the assessment of PH-surveillance systems. Essentially a semi-structured questionnaire, the tool combines quantitative and qualitative aspects addressing surveillance staff at all levels. It covers comprehensively all areas of PH-surveillance, ranging from routine tasks for indicator-based surveillance, management, analysis and flow of data, over event-based surveillance, outbreak detection and response, to intra- and inter-organisational communication channels.

Results

The tool proved highly useful for the first assessment of a national surveillance system, covering all involved levels and including data collection sites, district, state and finally national surveillance offices. The tool enabled with reasonable input a systematic assessment while proving flexible enough to accommodate needs specific to different levels of the system. Qualitative sections were particularly relevant as they helped to untangle informal communication processes and hierarchical relationships inherent to the system. Eventually, the tool equipped us with the information necessary to formulate recommendations culminating in a package of tailored capacity building activities.

Conclusion

The IHR (2005), the global health security agenda but also the recent Ebola epidemic all call for strengthening PH-surveillance. The development of efficient and systematic assessment tools, especially covering quantitative and qualitative aspects, are crucial to make these improvements happen.

Keywords: surveillance, research design, Africa, Northern, public health, capacity building

PRESENTED BY: Matthias Nachtnebel (nachtnebelm@rki.de)

REFERENCE NUMBER: 3105

Inventory of advisory reports issued and the methodology applied by five NITAGs between 2011-2014, to assess possible modes of collaboration.

Daniëlle Nijsten (1), Hans Houweling (2), Antoine Durupt (1), Alex Adjagba (1)

1. Agence de Médecine Préventive, Paris, France
2. Health Council of the Netherlands, The Hague, The Netherlands

Background

National Immunization Technical Advisory Groups (NITAGs) are facing difficulties in terms of growing complexity of vaccination issues and a lack of human resources. Sharing the preparatory work for advisory reports may partially solve these problems and ensure that recommendations made are based on the best available evidence. We assessed the feasibility of collaboration by identifying concrete elements of advisory processes in the recent past that could have been subject of such collaboration.

Methods

We made an inventory of all advisory reports issued between 2011-2014 by five well-established European NITAGs, to assess overlap in topics and activities. Relevant data was extracted from each report to identify the (type of) question posed, key-factors considered, and evidence used in the decision-making process. Recommendations dealing with the same question were compared to identify overlap in activities and processes applied, to identify areas for potential collaboration or exchange of evidence.

Results

A total of 104 recommendations were retrieved. One question was discussed by three NITAGs and five questions by two NITAGs. The advisory reports for these six questions showed overlap in key-factors considered, such as disease burden, epidemiology, results from mathematical modelling, vaccine effectiveness and vaccine safety. However, all NITAGs involved used different types of evidence to support these key-factors. The remaining 98 advisory reports were specific to only one country.

Conclusion

Even though collaboration is a clear goal, advisory reports issued by these five NITAGs show little overlap in topics and processes applied. A first step to collaboration would be to establish an independent platform, enabling insight into each other's work and exchange of future working programs, questions to be addressed, assessment frameworks to be applied and evidence to be used.

Keywords: Vaccination, immunization, decision making, recommendation, Europe

PRESENTED BY: Daniëlle Nijsten (danielle.nijsten@rivm.nl)

REFERENCE NUMBER: 3089

Public preferences for vaccination programmes during pandemic outbreaks – a discrete choice experiment in four European countries

Domino Determann (1,2), Ida Korfage (1), Angela Fagerlin (3,4), Ewout W. Steyerberg (1), Michiel Bliemer (5), Helene Voeten (6), Jan Hendrik Richardus (1,6), Mattijs S. Lambooij (2), Esther W. de Bekker-Grob (1)

1. Department of Public Health, Erasmus MC University Medical Center Rotterdam, Rotterdam, the Netherlands
2. Centre for Prevention and Health Services Research, National Institute for Public Health and the Environment (RIVM), Bilthoven, the Netherlands
3. Department of Internal Medicine and Psychology and Center for Bioethics and Social Sciences in Medicine, University of Michigan, Ann Arbor, United States of America
4. Ann Arbor Center for Clinical Management Research, Ann Arbor, United States of America
5. Institute of Transport and Logistics Studies, The University of Sydney Business School, Sydney, Australia
6. Rotterdam-Rijnmond Municipal Public Health Service, Rotterdam, the Netherlands

Background

The success of mitigating communicable disease outbreaks is dependent upon the uptake of preventive measures by the public. Thus far, formal quantitative techniques such as discrete choice experiments (DCE) have not yet been used to quantify and compare pandemic vaccination programme preferences of members of the public of European countries.

Methods

Representatives of four European countries (the Netherlands, Poland, Spain, and Sweden, N=2,068) participated in an online DCE. A disease scenario was presented in each choice set, for which respondents were asked to choose between two vaccination alternatives, with systematically varying characteristics, and one opt-out alternative. Panel latent class models were used to estimate the relative importance of vaccination programme characteristics (effectiveness, safety, advice, media attention, and out-of-pocket costs) and to predict uptake.

Results

In the case of a severe outbreak, vaccine effectiveness was the most important characteristic determining vaccination preferences in all countries, followed by the body that advises the vaccine. In Sweden, the advice of family and/or friends and the advice of physicians strongly affect vaccine preferences, in contrast to Poland and Spain, where the advice of (international) health authorities was more decisive. In the case of a mild outbreak, vaccination advice and costs were most important in the Netherlands and Sweden, while vaccine effectiveness and vaccination advice were most important in Poland and Spain. Irrespective of disease scenario or programme characteristics, the predicted vaccination uptakes were lowest in Sweden, and highest in Poland.

Conclusion

This study shows inter-country differences in vaccination preferences, especially regarding effectiveness, costs and advice. To increase uptake, the most important representative within each European country will need to step forward to advise the public on vaccinations during future pandemic outbreaks.

Keywords: Vaccination, Pandemics, Choice behaviour, Public health

PRESENTED BY: Domino Determann (d.determann@erasmusmc.nl)

REFERENCE NUMBER: 2888

Parallel Session 6: Emerging and Vector-borne diseases

MODERATOR: Maria Zambon (Eurosurveillance Seminar speaker, ECDC National Microbiology Focal Point, UK)

Risk factors for severe West Nile virus neuroinvasive disease, Greece, 2010-2014

Chrysovalantis Silvestros (1,2), Danai Pervanidou (2), Angeliki Lambrou (2), Agoritsa Baka (2), Annita Vakali (2), Konstandinos Danis (1), Christopher Williams (1), Theano Georgakopoulou (2), christos Hadjichristodoulou (2,3)

1. EPIET: European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden
2. Hellenic Center for Disease Control & Prevention, Athens, Greece
3. Medical Faculty, University of Thessaly, Larissa, Greece

Background

Since 2010, West Nile virus (WNV) human infection emerged in Greece and has become established with human and animal cases. The epidemiology and risk factors for severe WNV disease have been well documented for lineage 1, but not for lineage 2 the only one found in Greece. We aimed to identify risk factors for severe West Nile virus neuroinvasive disease (WNND) in order to better target prevention measures.

Methods

We used the data derived from the WNV database of the Unit of Vector-borne Diseases of the Hellenic Center for Disease Control and Prevention (KEELPNO). These data were received from the mandatory notification system and the active laboratory surveillance system. A detailed questionnaire was used during telephone interviews with the cases and the treated physicians to collect demographic information, and information on clinical presentation, underlying diseases (including immunosuppression), treatment and outcome of every WNV case. Encephalitis, meningitis or acute flaccid paralysis cases were classified as WNND cases. All WNND cases hospitalised in the intensive care unit (ICU) or died were classified as severe. We estimated odds ratios adjusted for possible confounders (aOR) and 95% confidence intervals (CI) for severe outcome using multivariable logistic regression models.

Results

Out of the 446 WNND cases included in the analysis, 112 (25%) were classified as severe, including 76 fatalities. Age (aOR per year: 1.05, 95% CI: 1.03-1.07) and coronary artery disease (aOR: 1.81, 95% CI: 1.02-3.20) were independently associated with severe outcome on multivariable analysis adjusted for diabetes.

Conclusion

Elderly people and people with coronary heart disease are more likely to develop severe disease among WNND patients. Communication campaigns on personal protective measures against mosquito bites should primarily target the high-risk groups.

Keywords: West Nile virus, vector-borne disease, Greece, neuroinvasive disease

PRESENTED BY: Chrysovalantis Silvestros (silvestros@keelpno.gr)

REFERENCE NUMBER: 3098

Active entomological surveillance following West Nile virus (WNV) emergence, Greece, 2014

Annita Vakali (1), Danai Pervanidou (1), Eleni Patsoula (2), George Balatsos (2), Stavroula Beleri (2), Nikos Tegos (2), Agoritsa Baka (1), Theano Georgakopoulou (1), Christos Hadjichristodoulou (3)

1. Hellenic Center for Disease Control and Prevention (KEELPNO), Athens, Greece
2. Department of Parasitology, Entomology and Tropical Diseases, National School of Public Health, Athens, Greece
3. University of Thessaly, School of Medicine, Department of Hygiene and Epidemiology, Larissa, Greece

Background

Active systematic entomological surveillance constitutes key element of integrated vector control programs. Following the report of human WNV cases in 2010, entomological surveillance is implemented annually. In 2014, the entomological surveillance program aimed to record the native mosquito species, their abundance and seasonal distribution, as well as identify areas with WNV infected Culex pipiens and Ochlerotatus (Aedes) caspius mosquitoes

Methods

We approached subcontractors awarded vector control tenders in 28 Regional Units to place 54 (range: 7-68) CO2 or Triple traps every fifteen days from May to November and send the mosquitoes to the laboratory for species identification and WNV testing. Minimum infection rate(MIR) was calculated and compared with data from previous years.

Results

A total of 47,039 mosquitoes were collected, 45,011 (95%) of which were identified up to species level. Overall, 14 species were identified. The most abundant were C.pipiens(89%), followed by Ochlerotatus (Aedes) caspius(9%) collected in all study areas. Aedes albopictus mosquitoes were collected in 12 Regional Units, even if not the targeted species. Six mosquito pools were positive for WNV, in areas where no human cases were recorded in 2014. MIR was 0.18 (95%CI= 0.04-0.32) from May to November.

Conclusion

C.pipiens, the main WNV vector in Greece, has the greater geographical distribution and abundance. MIR declined compared to 2012 (MIR=2.03, 95%CI=1.73-2.33) as did the recorded human cases. Data collected from 2012 and 2014 indicate a positive linear correlation between MIR and the number of human cases, while the same correlation was not identified in data obtained from other years. Further study is needed for the level of correlation between mosquito infection indicators, the number of human cases and their impact on targeted public health interventions.

Keywords: Greece, West Nile Virus, Culex pipiens

PRESENTED BY: Elina Patsoula (epatsoula@esdy.edu.gr)

REFERENCE NUMBER: 3101

Clinico-epidemiological characteristics of the cases of Ebola Virus disease - Nigeria, July - September, 2014.

Abimbola Aman-Oloniyo (1), Peter Adewuyi (1), Mahmood Dalhat (1), Saheed Gidado (1), Patrick Nguku (1), Gabriele Poggensse (1)

1. Nigeria Field Epidemiology and Laboratory Training Program

Background

By 14th September, 2014, 4507 confirmed and probable cases and 2296 deaths reported from five countries in West Africa in the ongoing 2014 Ebola Virus Disease (EVD) outbreak. Nigeria reported the first confirmed EVD on 20th July 2014 and declared EVD-free by WHO 20th October 2014. We conducted a descriptive cross-sectional study of the clinico-epidemiological profile of EVD cases in Nigeria.

Methods

We defined a suspected EVD case as any person, alive or dead, with sudden onset of high fever who had contact with a suspected, probable, or confirmed EVD case; probable was any deceased suspected case with epidemiological linkage with a confirmed case; confirmed case was either of these with a positive laboratory result for EVD antigen (detection of virus RNA or IgM antibodies).

Results

There were 20 EVD cases (19 (95%) confirmed, 1 probable) 8 died (case fatality rate (CFR): 40%); eleven (55%) were females. Mean age was 39.6(+12.4) years. Most 8 (40%) were between 30 and 39 years old. Twelve (60%) cases, 5 deaths were Healthcare Workers (HCWs) (CFR:41.6%); 9(75%) were primary contacts of index case. Sixteen (80%) cases were detected in Lagos State; 4 (20%) in Rivers. Dates of onset (17th July to 26th August, 2014) to date of report/hospitalization ranged from 1-9 days; 9 (69%) cases reported between days 5 and 9. Presentations included fever 15 (75%); fatigue 9 (45%); anorexia 8 (40%); vomiting 8 (40%); headache 3 (15%); joint pain 3 (15%); muscle pain 2 (10%); conjunctivitis 2 (10%); sore-throat 2 (5%). Age was statistically related to outcome ($p<0.05$) (alive/ dead).

Conclusion

Many EVD cases reported at late stage; HCWs were mostly affected. Infection Prevention and Control practices are recommended.

Keywords: Ebola Virus Disease, health care workers, Lagos, Rivers, Nigeria.

PRESENTED BY: Abimbola Aman-Oloniyo (bimboaman@gmail.com)

REFERENCE NUMBER: 2890

Malaria prevalence decreased following mass drug administration of malaria chemoprevention during the Ebola outbreak, Monrovia, Liberia, 2014

Anna Kuehne (1,2,3), Amanda Tiffany (4), Konstandinos Danis (2,5), Michel Janssens (6), Estrella Lasry (6), Chibuzo Okonta (7), Clement Besse (6), Victor Koko (8), Alfred Pah (8), Kwabena Larbi (8), Klaudia Porten (3)

1. Postgraduate Training for Applied Epidemiology (PAE), Robert Koch Institute, Berlin, Germany
2. European Programme for Intervention Epidemiology Training (EPIET), ECDC, Stockholm, Sweden
3. Epicentre, Paris, France
4. Epicentre, Geneva, Switzerland
5. Institut de Veille Sanitaire, Paris, France
6. Médecins Sans Frontières, Operational Centre Paris, Monrovia Project, Monrovia, Liberia
7. M Médecins Sans Frontières, Operational Centre Paris, Tropical Medicine, New York, USA
8. Liberian National Malaria Control Programme, Ministry of Health and Social Welfare, Monrovia, Liberia

Background

In 2014, Médecins Sans Frontières implemented a mass drug administration (MDA) of Artesunate/Amodiaquine (ASAQ) malaria chemoprevention to reduce admissions for fever to Ebola-treatment-centres (ETC) and malaria-associated morbidity in Monrovia, Liberia. To inform future MDAs targeting the reduction of malaria, we estimated the number of malaria cases prevented.

Methods

We systematically included every 20oth household in the distribution area (target population 551,971) to monitor two rounds of ASAQ-MDA, one month apart. We collected information on age, self-reported adherence and self-reported malaria in the previous month for all household members (HM) after both rounds. We calculated prevalence differences (PD) and 95% confidence intervals (95%-CIs) of malaria prevalence before the first (r1) and the second round (r2), stratified by adherence and age-group. We extrapolated the differences to the target population.

Results

Of 1229 HM, 4.2% reported malaria prior to r1, and 1.5% prior to r2 (PD=2.7%; 95%-CI 1.4-4.0%; p<0.0001), suggesting that 14,821 (95%-CI 4,801-24,840) malaria cases were averted in the target population. Reported malaria among children <=5 years of age completing a full course of ASAQ in r1, was 9.7% before r1 and 1.1% after r1 (PD=8.6%; 95%-CI 2.2-15.0%; p=0.009); among children not completing the course 3.8% and 1.3%, respectively (PD=2.5%; 95%-CI -2.3-7.3%; p=0.3112). Among HM > 5 years old completing treatment, 5.8% reported malaria before r1 and 1.6% after r1 (PD=4.2%; 95%-CI 1.9-6.5%; p=0.0004); among those not completing treatment 2.0% and 1.8%, respectively (PD=0.2%; 96%-CI -1.4-1.9; p=0.8168).

Conclusion

Self-reported malaria decreased significantly after the first round of ASAQ-MDA among individuals reporting to complete the full course. Further research into the extent to which MDAs are independently associated with the reduction in malaria prevalence and ETC admissions for fever is needed.

Keywords: Malaria, Chemoprevention, Liberia, Ebola, Prevalence

PRESENTED BY: Anna Kuehne (KuehneAn@rki.de)

REFERENCE NUMBER: 3115

Parallel Session Programme
Thursday 12 November
10:50-12:30

Parallel Session 7: HIV-STI

MODERATOR: Lorraine Doherty (EPIET supervisor, UK)

High prevalence of Mycoplasma genitalium in women with a previous STI history and female sex workers visiting HIV counselling institutions in North-Rhine-Westphalia, Germany (STI-HIT study) 2012-2013

Anne Lallemand (1,2), Viviane Bremer (1), Klaus Jansen (1), Stine Nielsen (1), Dieter Muenstermann (3), Andreas Lucht (3), Carsten Tiemann (3)

1. Robert Koch Institute, Berlin, Germany
2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
3. Labor Krone, Bad Salzuflen, Germany

Background

Mycoplasma genitalium (Mg) can cause urethritis in women and has been associated with cervicitis and pelvic inflammatory disease. Women asking for a free anonymous HIV test may have other STIs such as Mg, yet prevalence in that population is unknown. We assessed the prevalence and factors associated with Mg infection in women seeking HIV testing at local public health authorities (LPHA) to inform decision making regarding Mg screening in HIV counselling institutions.

Methods

LPHA in North Rhine-Westphalia screened women for Mg infection using self-collected vaginal swabs, analysed by transcription-mediated amplification assays (APTIMA® Mycoplasma genitalium, RUO). LPHA staff collected self-reported information on socio-demographic characteristics, sexual and HIV testing behaviours, previous STI history and clinical symptoms. We assessed Mg prevalence and 95% confidence intervals (95%CI). Using univariate and multivariable binomial regression, we calculated adjusted prevalence ratios (aPR) and 95%CI to identify associations between potential risk factors and Mg infection.

Results

Eighteen LPHA recruited 1430 women, including 286 female sex workers (FSW). Median age was 30 years [25-38]. Mg prevalence was 13.6% (39/286; 95%CI:9.9-18.2%) in FSW and 3.6% (41/1144; 95%CI:2.6-4.8%) in other women. Of 80 Mg positive women, 74.2% were asymptomatic. Among FSW, positivity was inversely associated with reporting at least one previous STI (ref.: no previous STI; aPR=0.38, 95%CI:0.15-0.93). Among the other women, positivity was associated with at least one previous STI (aPR=3.1, 95%CI:1.7-5.8) and a lower level of school education (ref.: high-school diploma completed; secondary school diploma: aPR=3.1, 95%CI:1.5-6.4; secondary school education: aPR=4.7, 95%CI:2.0-10; no diploma: aPR=5.4, 95%CI:1.4-21).

Conclusion

Mg prevalence was high, particularly in FSW. Even in the absence of symptoms, LPHA may consider testing for Mg FSW as well as other women with a previous STI history.

Keywords: Mycoplasma genitalium, Prevalence, STI, HIV test, Sex workers

PRESENTED BY: Anne Lallemand (lallemanda@rki.de)

REFERENCE NUMBER: 3084

High prevalence of genital infections with Mycoplasma genitalium in female sex workers reached at their working place in Germany: the STI-Outreach study

Klaus Jansen (1), Viviane Bremer (1), Gyde Steffen (1), Navina Sarma (1), Stine Nielsen (1), Dieter Muenstermann (2), Andreas Lucht (2), Carsten Tiemann (2)

1. Robert Koch-Institut, Berlin, Germany
2. Labor Krone, Bad Salzuflen, Germany

Background

Data on Mycoplasma genitalium (MG) in female sex workers (FSW) is scarce. FSW without regular contact to health services may be at high risk for STI. Amongst other STI, we measured MG-prevalence among FSW at their workplace to identify most vulnerable subgroups and to plan effective interventions.

Methods

Outreach-workers screened FSW in Berlin, Hamburg, and North Rhine-Westphalia for MG using self-collected vaginal swabs. Swabs were analysed by TMA (APTIMA® Mycoplasma genitalium-assay, RUO). We collected data on sociodemographics, duration of sex work and access to medical care through cultural mediators. We fitted multivariate logistic regression models to calculate adjusted odds ratios (aOR) and 95%-confidence intervals (95CI) for diagnosis of MG.

Results

We enrolled 1,445 FSW at 292 working places. 88% of FSW were born abroad. 41% of non-Germans had no German language skills. German and non-German FSW differed regarding existing health insurance (89% vs. 21%, p<0.01) and ever attending low threshold STI clinics (70% vs. 43%, p<0.01). FSW worked in brothels (26%), clubs/bars (20%), rented rooms inside brothels (18%), apartments (14%), saunaclubs (9%) and on the street (7%).Prevalence of MG was 18%. Of MG-positive FSW, 18% were coinfected with chlamydia or trichomonas respectively, 9% with gonorrhea. Diagnosis of MG was associated with younger age (aOR=0.97; 95CI=0.95-0.99, per year increasing), being born in Bulgaria (aOR=2.9; 95CI=1.2-7.2) or Romania (aOR=3.4; 95CI=1.4-8.3; reference Germany), having no German skills (aOR=3.1; 95CI=1.2-8.0), and having no health insurance (aOR=1.8; 95CI=1.0-3.2)

Conclusion

Prevalences of MG and STI-coinfections were high, especially in younger, migrated FSW, without German skills and health insurance. Tests for MG, and if tested positive, for chlamydia, trichomonas and gonorrhoea, may be considered for FSW, combined with cultural mediation.

Keywords: Mycoplasma genitalium, prevalence, sex worker, Germany

PRESENTED BY: Klaus Jansen (jansenk@rki.de)

REFERENCE NUMBER: 3019

HIV surveillance in Ireland: a timely system for timely trend analysis, 2012-13

Coralie GIESE (1,2), Derval Igoe (2), Kate O'Donnell (2), Gillian Cullen (2), Joanne Moran (3), Cillian de Gascun (3), Darina O'Flanagan (2)

1. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden
2. Health Protection Surveillance Centre, Dublin, Ireland
3. National Virus Reference Laboratory, University College, Dublin, Ireland

Background

HIV is notifiable in Ireland since 2011. Local laboratories send positive HIV tests to the National Virus Reference Laboratory (NVRL) for confirmation. NVRL notifies confirmed cases to Departments of Public Health (DPH) via the national Computerised Infectious Disease Reporting System (CIDR). Pre notification, NVRL requires two separate samples from most local laboratories to ensure provenance of the sample. NVRL sends an enhanced surveillance form to clinicians; this information is entered into CIDR by DPH. We evaluated HIV surveillance to assess its timeliness, identify delays and inform interpretation of trends.

Methods

We calculated median time intervals (inter-quartiles; range) in HIV surveillance steps, from HIV first sample confirmation to completion of enhanced information in CIDR, for cases notified in 2012/2013 using CIDR and NVRL databases.

Results

We analysed 665 of 669 HIV notifications. For 72% of notifications requiring two samples, there was a ten-day interval (4–19;0–2996) between first and second sample confirmation; a nine-day interval (6–14;0–386) in notification following confirmation, and an 18-day interval (8–60;0–523) in form completion. Overall, 81% of notifications had enhanced surveillance information within six months of diagnosis. The interval between diagnosis at NVRL and form completion varied from 20(14–117;11–239) to 49(27–125;12–252) days by DPH area.

Conclusion

Timeliness of the HIV surveillance system was in line with the international standard of 66% of cases reported within six months of diagnosis; reliable analysis of trends could be undertaken within six months. NVRL should notify on first sample detection of HIV from all laboratories. Sources and strategies for resolving longer delays identified in some sites need to be further explored.

Keywords: Human Immunodeficiency Virus, surveillance, timeliness, evaluation

PRESENTED BY: Coralie Giese (coraliegiese@hotmail.com)

REFERENCE NUMBER: 3112

Antimicrobial resistance of Neisseria gonorrhoea in Germany, results from the Gonococcal Resistance Network (GORENET)

Sandra Dudareva-Vizules (1), Susanne Buder (2), Klaus Jansen (1), Anna Loenenbach (1), Sergejs Nikisins (1,3,4), Andrea Sailer (1), Eva Guhl (2), Peter Karl Kohl (2), Viviane Bremer (1)

1. Department for Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany
2. German Reference Laboratory for Gonococci, Department of Dermatology and Venerology, Vivantes Hospital Berlin, Germany
3. Department of Infectious Diseases, Robert Koch Institute, Berlin, Germany
4. European Public Health Microbiology Training (EUPHEM) programme, European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden

Background

Neisseria gonorrhoeae (NG)-infections are not reportable in Germany and limited data on NG-epidemiology and antimicrobial resistance (AMR) are available. With GORENET we monitor the NG-AMR in Germany to guide treatment algorithms and targeted prevention strategies.

Methods

Between April and December 2014 data onNG-AMR-tests and patient related information was collected from participating laboratories nationwide.Laboratories were asked to send isolates to the reference laboratory (NRL) for AMR-testing towards ceftriaxone, cefixime, azithromycin, ciprofloxacin, and penicillin by using E-Test, and beta-lactamase. Results were interpreted according to EUCAST 4.0. We described all reported isolates by sex, age and tested material. We characterized isolates tested in NRL by resistance patterns. We calculated proportions, medians, and interquartile range (IQR).

Results

We received information on 651 isolates from 19 laboratories. Altogether, 90% isolates were from men. Median age of tested men was 36 (IQR 29-49) and women 28 (IQR 22-41) years. Tested materials among men were urethral (98%) and rectal swabs (2%), among women mainly endocervical (74%) and vaginal swabs (17%). Of 253 isolates tested in NRL none were resistant towards ceftriaxone, 1.6% were resistant towards cefixime, 11.1% towards azithromycin, 73.1% towards ciprofloxacin, and 30.4% towards penicillin. Further 37.9% and 50.6% isolates showed intermediate susceptibility to azithromycin and to penicillin. From 205 isolates tested for beta-lactamase, 25.9% were positive.

Conclusion

Isolates tested for NG-AMR were mostly from men. A substantial proportion may be attributable to men having sex with men. Among men urethral swabs are most frequently tested for NG-AMR, as urethral infections are more often symptomatic. NG-AMR to ceftriaxone and cefixime remains low, while resistance and intermediate susceptibility to azithromycin, ciprofloxacin and penicillin is substantial. Monitoring of NG-AMR should be highly prioritised.

Keywords: Antibiotic resistance, Neisseria gonorrhoeae, Germany

PRESENTED BY: Sandra Dudareva-Vizules (dudareva-vizules@rki.de)

REFERENCE NUMBER: 2959

Late Breaker: Injection of a new psychoactive substance (NPS) snow blow is associated with recent HIV infections amongst homeless and chaotic people who inject drugs (PWID) in Dublin, Ireland, 2015

Coralie GIESE (1,2), Derval Igoe (2), Zorina Gibbons (3), Caroline Hurley (4), Siobhan Stokes (3), Sinead McNamara (3), Orla Ennis (4), Kate O'Donnell (2), Eamon Keenan (3), Cillian De Gascun (5,6), Fiona Lyons (7), Mary Ward (4), Kostas Danis (1), Ronan Glynn (4), Allison Waters (5), Margaret Fitzgerald (4)

1. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden
2. HSE Health Protection Surveillance Centre, Dublin, Ireland
3. HSE National Drug Treatment Centre, Dublin, Ireland
4. Department of Public Health, Dublin, Ireland
5. National Virus Reference Laboratory, University College Dublin
6. School of Medicine, University College Dublin
7. St. James's Hospital, Dublin 8

Background

In early 2015, the Health Service Executive in Dublin detected a sudden increase in acute HIV infections among PWID: three cases were diagnosed p24 antigen positive. We investigated to identify the source of infection.

Methods

We conducted a case-control study among homeless, chaotic (using several drugs in an intense and chaotic way) PWID in Dublin, injecting in the previous 12 months. Cases were recent HIV infections (either p24 positive, negative test within 12 months of diagnosis, acute sero-conversion illness, or recency assay test showing evidence of recent infection) or diagnoses with epidemiological link to recent infections, diagnosed since June 2014. Controls were randomly selected from a list of homeless chaotic HIV test-negative PWID (within three months), requiring daily attendance at the National Drug Treatment Centre (NDTC). We interviewed cases and controls to collect information on living conditions, drug use, sexual and injecting practices. We calculated crude and adjusted odds ratios (OR) using logistic regression. Urine samples from cases were tested for NPS.

Results

We included 15 cases and 39 controls. Injection of snow blow(α-PVP) was associated with HIV (adjusted-OR: 49[95%CI:3.6-669]) with a dose response effect (occasional (OR:13[95%CI:2.1-85]), daily (OR:128[95%CI:10-1594])). Having a PWID sex partner (adjusted-OR:36[95%CI:1.6-782]) and re-using needles/syringes (adjusted-OR:13[95%CI:1.01-177]) were also independently associated with HIV. Alpha-PVP was detected in 42% (5/12) of screened cases.

Conclusion

This is the first evidence of an association between the NPS snow blow and HIV. Measures have been taken in Dublin to ensure adequate access to needle exchange programmes and condoms, and to raise awareness of the risks posed by synthetic cathinones. In light of outbreaks in Romania and Greece (2011) and Glasgow (2015), prevention efforts among PWID may be needed in Europe.

Keywords: HIV, drug users, disease outbreaks, case-control studies

PRESENTED BY: Coralie Giese (coraliegiese@hotmail.com)

Parallel Session 8: Outbreaks II

MODERATOR: Ettore Severi (ECDC, Expert Outbreak Response)

Every way the wind blows: using meteorological analysis to investigate unexplained community outbreaks of Legionnaires' disease in Nottingham City, 2012 and 2014

John Mair-Jenkins (1,2), Vanessa MacGregor (3), Wendy Mears (3), Neil Anstey (3), Rob Johnston (4), Charles Beck (2), Keith Neal (2), Laura Bayliss (2), Jonathan Lloyd (2), James Thompson (5), Ian Hall (5), Jonathan Van-Tam (6), Richard Puleston (2)

1. Field Epidemiology Training Programme, Public Health England, UK
2. Field Epidemiology Services, Public Health England, UK
3. Health Protection Team - East Midlands, Public Health England, UK
4. Specialist Microbiology Services, Food, Water and Environmental Microbiology, Public Health England, UK
5. Microbial Risk Assessment and Behavioural Science Group, Public Health England, UK
6. Division of Epidemiology and Public Health, University of Nottingham, UK

Background
The incidence of Legionnaires' disease is consistently higher in Nottingham (14.2/1,000,000, 2009-2011) than England and Wales (4.9/1,000,000). Previous outbreak investigations, including 14 cases in 2012, were inconclusive. In March-April 2014, Public Health England investigated 7 laboratory-confirmed cases clustered in Nottingham, supplementing traditional methods with meteorological analysis.

Methods
We collected 14-day case histories to identify common exposures, locations visited, and routes used. We conducted environmental investigations of domestic properties and suspected commercial sources. We hypothesised a point source and modelled the epidemic curve as the convolution of the known incubation period with an infection-time distribution to estimate the start and end of the exposure window. We used local weather station data to calculate wind roses for the exposure window. We repeated the meteorological analysis for the 2012 cases to identify common patterns between outbreaks.

Results
Traditional investigations failed to identify common or individual sources. Modelling estimated the 2014 exposure window from 17/02/14 to 7/04/14. We identified a shifting wind-direction from prevailing south-westerly (normally occurring 58% of year) to less common north-easterly winds (23% of year). North-easterly winds coincided with the incubation periods of 71% (5/7) of the 2014 cases; and 79% (11/14) of the 2012 cases. We redefined our geographical investigation area looking for common exposure patterns between outbreaks, new potential sources north-east of Nottingham, carried out environmental investigations and water sampling. Despite more focussed investigation no sources were identified.

Conclusion
Our investigation shows that meteorological analysis is an important tool which can supplement tradition epidemiological methods in narrowing the geographical investigation area and may help link unresolved outbreaks. Whilst we have not identified a source, we recommend that meteorological analysis is incorporated into future legionella outbreak investigations.

Keywords: Legionnaires' Disease, Legionella pneumophila, meteorology, disease outbreaks

PRESENTED BY: John Mair-Jenkins (john.mairjenkins@phe.gov.uk)

REFERENCE NUMBER: 2883

Waterborne acute gastroenteritis outbreak in a South West mountain village, March 2014, France

Aurelie Fischer (1), christine castor (1), Patrick Bonilla (2), Michel Noussitou (2), Loic Rambaud (3), Patrick Rolland (1)

1. French Institute of Public Health Surveillance, Department of Coordination of Alerts and Regions Regional office in Aquitaine, Bordeaux, France
2. Regional Health Agency of Aquitaine, Delegation of Pyr
3. French Institute of Public Health Surveillance, Department of environmental health, Saint-Maurice, France

Background
In March 2014, an acute gastroenteritis (AGE) outbreak in a middle school of a French mountain village was reported to the local health authorities as well as non-conformities of the tap water, non-treated. Epidemiological and environmental investigations were carried out to describe the outbreak, determine the source of contamination and adapt control measures.

Methods
A cohort study was conducted in the middle school to collect AGE symptoms and water consumption data between February and March. In addition, microbiological analyses were performed on stool samples of AGE cases and on samples from the communal water supply network. To evaluate the magnitude of the outbreak, health insurance reimbursements of AGE drugs delivered by the pharmacy's village were retrospectively compared to those of 3 nearby villages.

Results
At the middle school, 73 people among 79 responded to the questionnaire; 93% declared AGE symptoms with recurrences for 73%, and 96% consummated tap water at school. The number of glasses drank was associated with the number of recurrences (p=0.004). Drug reimbursement data confirmed an epidemic episode of AGE in the village which lasted 3 months from mid-February until mid-April (6% of AGE cases at the village versus 2% in the 3 nearby villages (p<10-3)). Different enteric viruses were isolated from cases' stool samples, and fecal coliforms and enterococci were found in the water. Despite chlorination, water contamination persisted during months. A dysfunction was identified in the connection of the municipal waste water treatment plant to the water supply network.

Conclusion
The investigations confirmed a large waterborne outbreak and highlighted the need to treat water and install protective devices in the water treatment plant.

Keywords: acute gastroenteritis, waterborne outbreak, waste water treatment plant, water supply, enteric virus, health insurance reimbursements

PRESENTED BY: Christine Castor (Christine.CASTOR@ars.sante.fr)

REFERENCE NUMBER: 3124

Multinational Salmonella Chester outbreak associated with travel to Morocco, 2014

Laure Fonteneau (1,2), Simon Le Hello (3), Sophie Bertrand (4), Wesley Mattheus(4), Laetitia Fabre (3), Mia Torpdahl (5), Aphrodite Smpiraki (6), Ingrid Friesema (7), Moa Rehn (8), Carmen Varela Martínez (9), Etorre Severi (10), Céline Gossner (10,11), Nathalie Jourdan-Da Silva (1)

1. French Institute for Public Health Surveillance, France
2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden
3. National Reference Laboratory Salmonella, France
4. National Reference Laboratory Salmonella, Institute of Public Health, Belgium
5. Statens Serum institute, Denmark
6. National Reference Laboratory Salmonella, Greece
7. National Institute for Public Health and the Environment, The Netherlands
8. Public Health Agency of Sweden, Sweden
9. Instituto de Salud Carlos III, CIBER Epidemiología y Salud Pública, Spain
10. European Centre for Disease Prevention and Control, Stockholm, Sweden
11. School of Public Health and Primary Care, Maastricht University Medical Center, Maastricht, The Netherlands

Background

In September 2014, six countries reported an unusually high number of Salmonella Chester cases to the European Centre for Disease Prevention and Control. We undertook investigations to identify a common exposure.

Methods

We defined a case as a European Union (EU) resident with symptoms onset after 05/05/2014 and S. Chester laboratory confirmation. We interviewed EU cases about their travel history. We conducted a case-case study among French patients with salmonellosis who travelled recently to Morocco. We compared notified S. Chester cases with other notified salmonellosis cases frequency matched for age and week of onset. We calculated Odds Ratios (ORs). We compared 32 isolates from EU cases, and 4 food isolates from Morocco by Whole Genome Sequencing using Single Nucleotide Polymorphisms (SNP) analysis.

Results

Between 05/05/2014 and 22/10/2014, countries notified 156 cases in the EU including 90 cases in France. Among the 54 interviewed cases, 87% had travelled to Morocco. We compared 14 S. Chester cases and 26 cases with other salmonellosis. We did not identify a common place of exposure or a common means of transport from/to Morocco. Compared to other salmonellosis, cases of S. Chester were more likely to have eaten shrimps (OR=5.6; 95%CI [1.1-28]), eaten in any restaurant (OR=6.2; 95%CI [1.1-295]) and to have visited the coast (OR=15.9; 95%CI [1.6-735]). A comparison of sequences showed two epidemic sub-clusters with 40 SNPs difference harboring two different antibiotic resistance plasmids.

Conclusion

The source of the outbreak was likely contaminated food distributed throughout the coastal areas of Morocco. We recommend to European countries strengthening the surveillance of cases to rapidly detect and investigate a reemergence of cases in view of increasing tourist traffic between Morocco and Europe next summer.

Keywords: Salmonella, Outbreak, Foodborne Diseases, Morocco

PRESENTED BY: Laure Fonteneau (l.fonteneau@invs.sante.fr)

REFERENCE NUMBER: 3137

An investigation of an enteroviral meningitis outbreak-Karaganda City, Kazakhstan, June-August 2014

Nazym Tleumbetova (1,2), Nazira Kerimbekova (3,2)

1. Epidemiologist, Toldikurgan City Department of Consumer Protection
2. Central Asia Filed Epidemiology and Laboratory Training Program
3. National Reference Laboratory for Viral Infections

Background

During June–July, 2014, 189 people with suspected viral meningitis were hospitalized in Karaganda city in Kazakhstan; 75% (142) of them were aged 4-14 years. In 2013, only 18 cases were reported. Upon request by the Kazakh public health administration, we conducted a hospital-based case-control study to identify the causative agent and risk factors for disease transmission

Methods

As cases, we enrolled all patients (n=93), aged 4-14 years, who were hospitalized during June-August, 2014 with sudden onset of fever, neck rigidity, vomiting, and headache. Controls were randomly selected children (n=103), aged 4-14 years, and hospitalized during June-August for acute, non-infectious conditions. We collected information on outdoor activities, water sources, and contact with individuals with fever. Exposures within three weeks of case-patient's disease onset and control selection were collected through parents' interviews. Logistic regression was used to study the disease-exposure associations

Results

Case-patients lived in different parts of the city; 39 (42%) of them swam in open water ponds, 38 (41%) visited shopping malls, 22 (24%) swam in public pools. In the multivariate analysis, risk factors for disease were: swimming in public pools (OR 3.3; 95% CI=1.4-7.6) or in open ponds (2.6; 95% CI=1.3-5.2), and visiting malls (OR 3.2, 95% CI=1.6-6.5). Cerebrospinal fluid was collected from 21 case-patients, 18 (86%) of them gave positive PCR tests for enteroviruses only

Conclusion

There is evidence that waterborne transmission through swimming was a risk factor in this enteroviral outbreak. Visiting shopping malls also played a role in disease transmission. We recommended that people should refrain from swimming in open water ponds and that sanitary inspection of public swimming pools should be intensified. Also, good personal hygiene practices are recommended when visiting malls

Keywords: viral meningitis, enteroviruses, Kazakhstan, case-control

PRESENTED BY: Nazym Tleumbetova

REFERENCE NUMBER: 2988

Could whey powder be the source of an eight-month low-intensity outbreak with Salmonella Agona, Denmark, 2013-2014?

Luise Müller (1), Charlottte Kjelsø, (1), Søren Persson (2), Mia Torpdahl (2), Tenna Jensen (3), Gitte Sørensen (4), Steen Ethelberg (1)

1. Department of Infectious Disease Epidemiology, Statens Serum Institut, Denmark
2. Department of Bacteriology, Mycology and Parasitology, Statens Serum Institut, Denmark
3. Division of Food and Feed Safety, Danish Veterinary and Food Administration, Denmark
4. Division of Food Microbiology, National Food Institute, Technical University of Denmark, Denmark

Background
In October 2013, we identified a cluster of five Salmonella Agona patients in Denmark. This Salmonella serotype is able to survive in dried products such as infant formula. An outbreak investigation was initiated to reveal the source in order to stop the outbreak.

Methods
All human Salmonella serotype Agona isolates from 2013-2014, were subtyped by Pulsed-Field Gel Electrophoresis (PFGE) and Whole Genome Sequencing (WGS). We defined a case as a laboratory-confirmed Salmonella Agona patient in Denmark from August 2013 with a specific PFGE pattern. Following hypothesis-generating interviews, we performed a case-control study. In addition, food sampling and trace-back investigations were conducted.

Results
In total, we identified 21 Salmonella Agona cases with the same PFGE and WGS type. Cases were 0-81 years and occurred with 1-4 per month from August 2013 to April 2014. Whey powder appeared as an ingredient in products consumed by cases in all the affected age groups: infant formula and premade baby-food, and protein shake consumed when working out or during hospital admission. The case-control study showed that adult cases were more likely to consume protein shake than controls (OR=35, 95% CI 2.3-1700). Matched analyses were not possible. Samples of protein powder tested negative. It was not possible to identify a common product or supplier of whey powder.

Conclusion
The case-control investigation could not prove whey powder as the source since the number of cases was too small. However, the long duration, the skewed age distribution and previous findings of Salmonella Agona in powdered products support this hypothesis. Protein shake has to our knowledge not previously been identified as a possible vehicle for Salmonella outbreaks, but should be considered in future Salmonella Agona outbreaks.

Keywords: Salmonella, Disease Outbreak, Case-control study

PRESENTED BY: Luise Müller (lum@ssi.dk)

REFERENCE NUMBER: 3193

Parallel Session 9: Burden of Disease

MODERATOR: Osamah Hamouda (Robert Koch Institute, Germany)

Estimating the average annual burden of tick-borne encephalitis in Slovenia to guide vaccination policy, 2009-2013

Mario Fafangel (1,2), Alessandro Cassini (3), Edoardo Colzani (3), Irena Klavs (1), Marta Grgič Vitek (1), veronika u?akar (1), Marion Muehlen (3), Marko Vudrag (1)

1. National Institute of Public Health (NIJZ), Ljubljana, Slovenia
2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden
3. European Centre for Disease Prevention and Control, Stockholm, Sweden

Background
With a mean annual incidence of 11.6/100,000 from 2009-2013, Slovenia has one of the highest incidences of tick-borne encephalitis (TBE) in Europe. TBE vaccination coverage remains low. The objective of this study was to estimate the mean annual burden of TBE virus (TBEV) infection in Slovenia to target limited resources for vaccination more effectively.

Methods
We used the 2009-2013 Slovenian surveillance data, to calculate the mean annual incidence of TBE/100,000 population by age, sex and region and estimated Disability-Adjusted Life Years (DALYs) with 95% uncertainty intervals (UI), using the Burden of Communicable Diseases in Europe (BCoDE) toolkit developed by ECDC.

Results
We estimated an overall loss of 225 DALYs/year (95% UI: 210-239) for TBEV infections or 10.9 DALYs/100,000 (95% UI: 10.2-11.6) per year. The mean annual TBE incidence was the highest among 40-79 year-olds (16/100,000 population) while relatively low among 5-9 year-olds (11/100,000). Among those aged ≥40 years, DALYs/100,000 point-estimates were the highest in 50-54 year-old males (14.1 DALYs/100,000 (95% UI: 9.9-19.0)) and 55-59 year-old females (16.2 DALYs/100,000 (95% UI: 11.4-21.8)). However, the highest burden point-estimate was among 5-9 year-olds (females: 15.8 DALYs/100,000 (95% UI: 11.1-21.3), males: 20.7 DALYs/100,000 (95% UI: 14.6-27.8)). The Gorenjska region had the highest mean annual incidence (29/100,000) and the highest burden (26.2 DALYs/100,000 (95% UI: 24.5-28.0)).

Conclusion
The estimated burden of infection was the highest among 5-9 year-olds, despite low TBE incidence, suggesting that incidence data alone does not fully reflect the disease burden and might not be the best indicator to guide vaccination policy. Health authorities are advised to consider prioritisation of the 5-9 year-old age group in efforts to increase vaccine coverage.

Keywords: Burden of Illness, Tick-Borne Encephalitis, Viral Encephalitis, Vaccination

PRESENTED BY: Mario Fafangel (mario.fafangel@nijz.si)

REFERENCE NUMBER: 3096

Online syndromic surveillance was suitable to estimate community incidence of Acute Gastrointestinal illness (AGI), influenza-Like Illness (ILI) and Acute Respiratory Illness (ARI), Sweden, 2013-2014.

Alessandro Pini (1,2), Hanna Merk (2), Edward van Straten (2), Annasara Carnahan (2), Ilias Galanis (2), Anders Wallensten (2)

1. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden
2. The Public Health Agency of Sweden, Stockholm, Sweden

Background

The Public Health Agency of Sweden implemented an online syndromic surveillance system (Hälsorapport) to estimate weekly community incidence of AGI, ARI and ILI. Participants, selected using a stratified random sample from a population-based register, completed weekly online health questionnaires. We evaluated acceptability, representativeness and validity of the system.

Methods

We calculated the overall proportion of invited people who participated and weekly reporting proportions. We used chi-square test to compare sex and age of participants with the Swedish population. We calculated Spearman correlation coefficients (r) with a lag of ± 5 weeks to assess the agreement of the estimated weekly incidence of ILI, ARI and AGI, standardized for the Swedish population age distribution, with a routine internet search-based surveillance system that analyses trends of queries for specific terms.

Results

Of the 34,748 invited, 3,258 (9.4%) participated. On average, 78% of participants answered the weekly questionnaires. Compared with the general population, males were under-represented (47% vs 50% in the general population; p<0.01) and under-five participants were over-represented (47% vs 6%; p<0.01). The AGI and ARI incidence correlated significantly with routine surveillance data (r=0.79 and 0.83; p<0.01), when no lag was applied. ILI incidence correlated with influenza surveillance data with the largest coefficient (r=0.69; p<0.01) when traditional surveillance data were shifted back by three weeks.

Conclusion

Acceptance to the weekly reporting questionnaire was high. Participants were not representative of the general population in terms of age and sex, but age-standardized data produced incidences that agreed with routine surveillance. The system was suitable for estimating the community incidence of ARI, ILI and AGI and could be introduced in Sweden and in countries with high internet penetration and up-to-date population registers.

Keywords: Illness Burden, Influenza, Gastrointestinal Disease, Cohort Study, Sweden

PRESENTED BY: Alessandro Pini (alessandro.pini@folkhalsomyndigheten.se)

REFERENCE NUMBER: 3088

Prevalence of carriage of extended-spectrum beta-lactamase-producing Enterobacteriaceae and shiga toxin-producing Escherichia coli in asymptomatic day-care children in Lower Saxony (Germany), 2014

Manuela Harries (1,2,3), Johannes Dreesman (1), Katja Claußen (1), Sophie Rettenbacher-Riefler (1), Elke Mertens (1)

1. Governmental Institute of Public Health of Lower Saxony, Hanover, Germany
2. Postgraduate Training for Applied Epidemiology (PAE, German Field Epidemiology Training Programme), Robert Koch-Institute, Berlin, Germany
3. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden

Background

In Germany asymptomatic carriers of shiga toxin-producing Escherichia coli (STEC), identified during contact screening of notified cases, need permission of the heath office to attend nurseries. A presumed high STEC prevalence of unknown STEC-carriers would make a prolonged exclusion (until two consecutive negative stool cultures) difficult. Furthermore, hospitals are developing strategies to reduce the risk of infection caused by admission of carriers of extended-spectrum beta-lactamase-producing Enterobacteriaceae (ESBL-E). We aimed to estimate the prevalence of ESBL-E and STEC in healthy children and identify predictors for carriage to guide risk assessment and management.

Methods

During April-September 2014, we collected stool specimens from children without diarrhoea in voluntarily participating nurseries in Lower Saxony. We analysed STEC by PCR and ESBL-E on chromogenic agar. Parents completed questionnaires on nutrition, lifestyle, prior antibiotic treatment and animal contact. We compared ESBL-E-carriers and non-carriers by univariable analysis.

Results

Of 223 participants, 44% were female and median age was 3.5 years (range 0-6). Five children were colonized with ESBL-E (prevalence: 2.2%, 95%CI: 0.3-4.2). One child tested positive for STEC (prevalence 0.5%, 95%CI: 0-1.3). Twenty-seven participants (12%) indicated drinking raw milk: 3/5 ESBL-E-carriers versus 24/218 non-carriers (OR=14; 95%CI: 2.1-95). ESBL-E-carriage was also associated with antibiotic intake (4 vs 51; OR=13; 95%CI: 1.4-126) and having contact to pet rodents (3 vs 36; OR=7.6; 95%CI: 1.2-49).

Conclusion

The low STEC-prevalence in asymptomatic children supports the current practise of exclusion of STEC-carriers from nurseries.The association between ESBL-E-carriage and raw milk consumption and contact to pet rodents needs further investigation but could be considered relevant for admission screening in hospitals.The overall high proportion of participants drinking raw milk suggests prevention messages regarding this habit need to be reinforced.

Keywords: Prevalence, EHEC, ESBL, children, raw milk, antibiotics, Germany

PRESENTED BY: Manuela Harries (Manuela.Harries@gmx.de)

REFERENCE NUMBER: 3196

The burden of paediatric invasive meningococcal disease in Spain (2008-2013). MENDICOS Project

Irene Rivero (1,2), Lucía Vilanova (2,3), Jacobo Pardo (2), Federico Martinón-Torres (1,2,3)

1. Translational Pediatrics and Infectious Diseases Section Pediatrics Department, Hospital Clínico Universitario de Santiago de Compostela, Santiago de Compostela, Spain
2. Genetics Vaccines Infections and Pediatrics Research Group (GENVIP), Healthcare Research Institute of Santiago de Compostela, Santiago de Compostela, Spain.
3. MENDICOS research network is composed by: Martinón-Torres, F.; Palacios, A.; Prieto, LM.; Grasa, CD.; Llorente, M.; Perez, B.; Tagarro, A.; Orío, M.; Baquero, F.; Bueno, M.; Saavedra, J.; Calvo Rey, C.; Piñeiro, R.; Mate, I.; Jensen, JM.; Bello, P.; Aleo, E.; Blumenfeld, J.; Badillo, K.; Fernandez, E.; La Orden, E.; Perez, R.; Navas, A.; Feito, C.; Otheo, E.; Jimenez, A.; Alvarez, C.; Calvo Monge,

Background

Invasive meningococcal disease remains a rare infectious disease with high mortality but also with important morbidity. Until recently no universal vaccine existed against B serogroup, which explains most of the cases in settings like Europe. The aim of this study is to analyse the clinical course and sequelae of meningococcal disease in Spain.

Methods

Retrospective review of all children aged under 15 years admitted to any of the 36 hospitals in the MENDICOS Spanish network (www.mendicos.org) with confirmed or probable invasive meningococcal disease between January 2008 and December 2013.

Results

A total of 465 cases were identified across the country, most of them occurring in previously healthy children (91,6% (n=426)). Mean age (standard deviation) was 1.3 years (SD 0.5), with 53.3% (n=248) of the cases occurring in infants below 2 years. 81.8% (n=372) were laboratory confirmed cases. 95.2% (n=256) of those serogrouped were B serogroup. The diagnosis was meningitis in 24.7% (n=115) of the cases, sepsis in 36.8% (n=171) and both in 38.5% (n=179). Mean hospital length of stay was 11.5 (10.8) days. 81.7% (n=380) of the patients required PICU admission, with a mean PICU stay of 3.9 (4.9) days. 3.4% (n=16) were exitus. 12.7% (n=59) of the survivors were discharged with any kind of physical sequelae, mainly neurological (n=22).

Conclusion

Serogroup B invasive meningococcal infection explains substantial morbidity and mortality in Spain, occurring mainly in infants. The recent availability of a vaccine against B serogroup may change this scenario, and its inclusion in the national immunization program should be carefully considered, moreover given that the vast majority of the cases occur in otherwise healthy children.

Keywords: Meningococcal disease, Neisseria meningitidis, Burden of disease, vaccine-preventable disease

PRESENTED BY: Irene Rivero (irina667@hotmail.com)

REFERENCE NUMBER: 3045

Reduction in attendance of health care centres, during Ebola outbreak in N'zérékoré prefecture, Guinea, November 2013 – March 2015

Emilie Johanna Peron (1,2), Laure Fonteneau (1,3), Abdoulaye Bhoye Bah (4), Gadiry Bah Abdoul (4), Cristina Valencia (1,5), Enock Haba (6), Adama Kaba (7), Laurence Marrama (8), Boubacar Diallo (4), Kone Moussa (4), Guenael Rodier (4), Thomas Mollet (8), Bertrand Sudre (8)

1. European Programme for Interventional Epidemiology Training (EPIET), ECDC Stockholm, Sweden
2. Department for Infectious Disease Epidemiology, Robert Koch Institute, Berlin Germany
3. Institut de Veille Sanitaire (IVS), Paris, France
4. World Health Organization, Conakry, Guinea
5. Scientific Institute of Public Health, Brussels, Belgium
6. Department of Health, N
7. Ministry of Health, Guinea
8. European Centre for disease prevention and control (ECDC), Stockholm, Sweden

Background

The epidemic of Ebola Virus Disease (EVD) in Guinea has had an unmeasured impact on healthcare access, through changes in healthcare-seeking behaviour and staffing of health centres, which could adversely affect health outcomes in diseases such as childhood malaria. To assess this impact in primary care, we compared healthcare attendances before, during and after the epidemic in the area of N'zérékoré.

Methods

We obtained aggregate figures for healthcare attendances in the 16 primary healthcare centres, stratified by age group and reason for attendance, from the routine surveillance system. We compared monthly consultations in three periods: pre-epidemic (November 2013-August 2014), epidemic (September 2014-February 2015) and post-epidemic (March 2015) according to the occurrence of EVD in the area. We searched the EVD surveillance records for cases among healthcare staff in the area, and identified any interruptions to centre function.

Results

During the epidemic, the monthly number of consultations for all causes dropped by 44% (from 6675 to 3746), by 52% among the under-fives (from 1989 to 962) and by 18% for antenatal care visits (from 1636 to 1344). Post-epidemic, attendances increased to 5392 for all causes, 1591 for the under-fives and 1744 for antenatal care visits. Two healthcare staff were reported as EVD cases, and only two one-month clinic closures were identified.

Conclusion

Healthcare attendances decreased by around half during the epidemic, increasing afterward but not fully returning to pre-epidemic levels. The effect was greatest among the under-fives, the highest risk group for fatal malaria. This change, occurring despite evidence of health service continuity, suggests a change in health-seeking behaviour during the epidemic. During epidemics, interventions to maintain access to routine healthcare should be implemented to avoid adverse health outcomes.

Keywords: EVD outbreak, Guinea, healthcare, consultations, surveillance system, vaccination

PRESENTED BY: Emilie Johanna Peron (emilie.peron@free.fr)

REFERENCE NUMBER: 3106

Parallel Session Programme
Thursday 12 November
14:00-15:20

Parallel Session 10: Food and Waterborne diseases

MODERATOR: Katharina Alpers (ESCAIDE Scientific Committee, TEPHINET, Germany)

High proportion of asymptomatic infections in an outbreak of hepatitis E associated with a spit-roasted piglet, France, 2013.

Yvonnick Guillois (1), Florence Abravanel (2), Takayuki Miura (3), Nicole Pavio (4), Véronique Vaillant (5), Sébastien Lhomme (2), Françoise S. Le Guyader (3), Nicolas Rose (6), Jean-Claude Le Saux (3), Lisa King (1), Jacques Izopet (2), Elisabeth Couturier (5)

1. Regional Epidemiology Unit for the Brittany region, Institut de veille sanitaire, Rennes, France
2. National Reference Center for HEV, Centre hospitalier universitaire, Toulouse, France
3. Microbiology Laboratory, LSEM-SG2M, Ifremer, Nantes, France
4. UMR 1161 Virology, Animal Health Laboratory, Agence nationale de sécurité sanitaire de l'alimentation, de l'environnement et du travail, Maisons-Alfort, France
5. Department of Infectious diseases, Institut de veille sanitaire, Saint-Maurice, France
6. Swine Epidemiology and Welfare unit, Agence nationale de sécurité sanitaire de l'alimentation, de l'environnement et du travail, Ploufragan/Plouzané laboratory, France

Background
On 11 December 2013, 3 clustered cases of hepatitis E were reported on a French coastal island. They had taken part in a wedding meal where one of the courses was a spit-roasted piglet. The piglet had been stuffed with a raw stuffing partly made from the liver. Investigations were carried out to identify the vehicle of contamination and evaluate the dispersion of the Hepatitis E virus (HEV) in the environment.

Methods
A questionnaire was administered to 98 wedding participants who were asked to give a blood sample. Cases were identified by reverse transcription – polymerase chain reaction and serological tests. A retrospective cohort study was conducted among 38 blood sampled participants after the exclusion of 14 participants with evidence of past HEV infection. Crude relative risks and 95% confidence intervals were calculated by food item consumed during the wedding.Phylogenetic analyses were performed to compare the clinical HEV strains, with strains isolated from the liquid manure sampled at the farm where the piglet was born and from the untreated island wastewater.

Results
Seventeen cases were identified, 70.6 % were asymptomatic. No at risk exposure was significantly associated with acute hepatitis E infection at the p=0.05 level. The stuffing had the most significant association (p=0.10).Clinical strains from the index cases, veterinary and environmental HEV strains were identical.

Conclusion
Our investigation attributed this large HEV outbreak to the consumption of an undercooked pig liver-based stuffing and provides further evidence for the need to cook thoroughly pig liver-based food.After infection, the cases became a temporary reservoir for HEV, which was isolated in 4 samples of untreated wastewater collected at two wastewater treatment plants located in the island.

Keywords: Hepatitis E virus, outbreak, asymptomatic infection, pork liver, wastewater

PRESENTED BY: Lisa King (Lisa.KING@ars.sante.fr)

REFERENCE NUMBER: 2935

Environmental drivers of Legionnaires' disease in four European countries, 2007-2012

Julien Beauté (1,2), Sven Sandin (2), Soren Anker Uldum (3), Bonita Brodhun (4), Maria Cristina Rota (5), Petra Brandsema (6), Johan Giesecke (2), Par Sparen (2)

1. European Centre for Disease Prevention and Control (ECDC), Sweden
2. Medical Epidemiology and Biostatistics, Karolinska Institutet, Sweden
3. Statens Serum Institut (SSI), Denmark
4. Robert Koch Institute (RKI), Germany
5. Istituto Superiore di Sanit
6. Rijksinstituut voor Volksgezondheid en Milieu (RIVM), the Netherlands

Background
Legionnaires' disease (LD) is an important cause of potentially preventable morbidity and mortality in Europe. The disease is caused by inhalation of aerosols containing Legionella, a gram-negative bacteria. Previous findings have suggested an impact of climate on LD incidence. This study aimed to determine the contribution of weather parameters to LD incidence to improve awareness and preparedness.

Methods
Once annually, EU Member States, Iceland and Norway report their LD surveillance data to the ECDC. For this study, community-acquired LD cases reported by Denmark, Germany, Italy, and the Netherlands with onset date between 2007 and 2012 were aggregated by onset week and region of residence. Weather variables were extracted from the European Climate Assessment & Dataset project for 2007–2012. General linear models assuming a Poisson distribution were used to estimate incidence risk ratio (IRR). Given the known median incubation period, a lag of one week between exposure and disease onset was assumed.

Results
7 787 community-acquired LD cases were reported with a region of residence and onset date. In multivariate analysis, cumulative precipitation was positively associated with LD notification rates. A residual seasonality was observed with IRR two to threefold higher from June to October compared to January. Humid subtropical climate was associated with a two-fold higher IRR compared with oceanic climate.

Conclusion
Our findings confirm the dominant role of precipitation as a significant factor associated with an increased incidence of community-acquired LD. Older patients with pneumonia should be systematically tested for Legionella during the warm season especially after heavy rainfall. Further studies should try to better understand the behavioural factors associated with community-acquired LD infections and their seasonal changes.

Keywords: Legionnaires' disease, Surveillance, Environment, Weather, Europe

PRESENTED BY: Julien Beauté (julien.beaute@ecdc.europa.eu)

REFERENCE NUMBER: 2871

Outbreak of food-poisoning after a wedding feast; Karakurt Village, Manisa Province, Turkey, 2014

Huseyin Ozturk (1), GURCAN PARACIKLI (1), Gonca Atasoylu (2), Serap Cetin Coban (1), Fehminaz Temel (1), Mehmet Besir Algan (3), BAHADIR SUCAKLI (1)

1. Public Health Institution of Turkey, Early Warning Response and Field Epidemiology Department
2. Provincial Public Health Directorate of Manisa
3. İzmir Food Control Laboratory Directorate

Background

On 09 June 2014, Provincial Public Health Directorate reported an acute gastroenteritis outbreak of 138 residents. An investigation was performed to identify the cause, mode of transmission and to prevent the recurrence of similar outbreaks.

Methods

In this retrospective cohort investigation, we interviewed 457 residents who had lunch at the wedding feast including groom, bride, relatives and cook. We reviewed hospital records. Probable case was defined as onset of abdominal pain and nausea or vomiting and who consumed meal at feast (Soup, pickle, chicken with potatoes, chickpea, rice, compote, keskek and hosmerim –traditional meals). We detected 108 probable cases. We tested stool, water and food specimens for pathogen identification. Odds ratios (ORadj) were obtained through logistic regression model including keskek, chickpea, hosmerim.

Results

The attack rate was 23.6%(108/457). Main symptoms were abdominal pain (100.0%), nausea (98.1%), vomiting (74.1%), diarrhea (73.1%) and fever (31.5%). Epidemic curve showed a peak after meal. Main incubation period was 4.9 hours (min:0.5, max:15.0). Meals were prepared outside, at the soil ground early in the morning and served at noon. Only hosmerim was prepared by caterer a day ago and was stored outside. Probable cases who ate hosmerim developed the disease 2.9(95%CI:1.6-5.1) times more compared to ones who did not. After controlling other factors, consuming hosmerim was 3.5 times more (ORadj: 3.5, 95%CI: 1.8-6.8). Bacillus cereus and was detected in hosmerim, chickpea, keskek; Staphylococcus aureus was positive in hosmerim, keskek. Water, stool specimens were tested negative.

Conclusion

Symptoms, incubation period, unsafe food preparation conditions, lack of information on hosmerim storage conditions and epidemiological evidence suggest that this outbreak was due to contaminated hosmerim. Village residents were educated on safe food preparation and preservation practices.

Keywords: Outbreaks, Foodborne Diseases, Cohort Studies, Bacillus cereus, Staphylococcus aureus

PRESENTED BY: Huseyin Ozturk (dr.huseyin.ozturk.85@gmail.com)

REFERENCE NUMBER: 3033

What is the incubation period and symptoms of Enteroinvasive Escherichia coli? A detailed review of two outbreaks in England during 2014 and a systematic review of the literature.

Sophie Newitt (1,2), Vanessa MacGregor (3), Vivienne Robbins (3), Laura Bayliss (2), Marie Chattaway (4), Tim Dallman (4), Richard Puleston (2), Jeremy Hawker (2)

1. Field Epidemiology Training Programme (FETP), Public Health England, UK
2. Field Epidemiology Service, Public Health England, UK
3. East Midlands Public Health England Centre, Public Health England, UK
4. Gastrointestinal Bacterial Reference Unit, Public Health England, UK

Background

Enteroinvasive Escherichia coli (EIEC) outbreaks are rare in the UK. In June 2014, two EIEC outbreaks occurred in Nottingham, England, the first reported in Northern Europe to our knowledge. This provided an opportunity to improve the knowledge base about the natural history of EIEC.

Methods

We telephone interviewed laboratory-confirmed (EIEC isolated or PCR detected) and probable cases (clinical case-definition) using a bespoke structured questionnaire covering all potential symptoms and their onset, severity and duration. We analysed cases' clinical characteristics, incubation periods and duration of illness descriptively. We performed a systematic literature review to identify previous reports of incubation periods and symptom profiles.

Results

We identified 157 cases (37 confirmed and 120 probable) and interviewed 122 (78%), providing the second largest dataset globally on EIEC incubation period and third largest on symptoms. The median incubation period was 21 hours (95%CI 20 to 26), with a range of 6 to 168 hours (7 days). 121 cases (99%) experienced diarrhoea, 99 malaise (94%), 109 abdominal pain (91%), 92 fever (75%) and 73 chills (72%). Cases experiencing diarrhoea reported it as watery (89%) with a frequency of up to every 10 to 15 minutes; 12 (12%) experienced bloody diarrhoea. Illness was fairly severe; 63 cases consulted their GP and 21 attended hospital. The median duration of illness was seven days (95%CI: 5-7) but four cases reported ongoing symptoms one month after onset.

Conclusion

We observed a slightly longer incubation period than previously reported outbreaks and malaise, abdominal pain and chills were more prominent symptoms than previously reported. Reviewing these outbreaks alongside the literature provided greater insight into EIEC which may help improve the prompt recognition of future outbreaks caused by this pathogen.

Keywords: Enteroinvasive Escherichia coli, EIEC, outbreak, systematic review

PRESENTED BY: Sophie Newitt (sophie.newitt@phe.gov.uk)

REFERENCE NUMBER: 3032

Parallel Session 11: Vaccine-preventable Diseases I

MODERATOR: Christine Stabel Benn (Plenary session D speaker, Denmark)

Indirect effect of childhood PCV10/13 vaccination on invasive pneumococcal disease among seniors 65 years old and over in six European countries (Spidnet network): Implications for PCV13 vaccination of the elderly

Germaine Hanquet (1), Agnes Lepoutre (2), Pilar Ciruela (3), Didrik Frimann Vestrheim (4), Alison Smith-Palmer (5), Pavla Krizova (6), Suzanne Cotter (7), Marcela Guevara (8,9), Emmanuelle Varon (10), Carmen Munoz-Almagro (11), Brita Winje (4), Andrew Smith (12), Jana Kozakova (6), Jolita Mereckiene (7), Jesus Castilla (8,9), Anca Sirbu (13), Maria Ordobas (14), Eva Morfeldt (15), Marina Pana (16), Birgitta Henriques (15,17,18), Lucia Pastore-Celentano (19), Camelia Savulescu (1), and SpIDnet group (19)

1. EpiConcept, France
2. Institut de Veille Sanitaire, Saint-Maurice, France
3. Public Health Agency of Catalunya, Barcelona, Spain
4. Norwegian Institute of Public Health, Division of Infectious Disease Control, Oslo, Norway
5. Health Protection Scotland, National Services Scotland, Glasgow, Scotland, UK
6. National Institute of Public Health, Prague, Czech Republic
7. Health Protection Surveillance Centre, Dublin, Ireland
8. Instituto de Salud P
9. CIBER Epidemiolog
10. Centre National de Référence des Pneumocoques, AP-HP, Hôpital Européen Georges Pompidou, Paris, France
11. Hospital Sant Joan de D
12. Scottish Haemophilus, Legionella, Meningococcus and Pneumococcus Reference Laboratory, Glasgow, Scotland, UK
13. National Institute of Public Health, Bucharest, Romania
14. Sub-directorate of Health Promotion and Prevention, Madrid, Spain
15. Public Health Agency of Sweden, Solna, Sweden
16. INCDMI Cantacuzino, Bucharest, Romania
17. Karolinska Institutet, Solna, Sweden
18. Karolinska University hospital, Solna, Sweden
19. European Centre for Disease Prevention and Control, Stockholm, Sweden

Background

The SpIDnet network conducts population-based surveillance for invasive pneumococcal disease (IPD) in eight European countries. In seven sites (six countries) in which PCV7 (7-valent pneumococcal conjugate vaccine) was replaced by PCV13 and/or PCV10, we measured the indirect effect of PCV10/13 childhood vaccination on IPD in elderly, to inform decisions on elderly PCV13 vaccination. The childhood vaccination uptake was 93-97% in four sites with universal PCV13 vaccination versus 50-77% in the three sites where PCV10/13 were used without universal vaccination.

Methods

We compared IPD incidence between each PCV10/13 year and the PCV7 period in elderly ≥65 year-old by calculating incidence rate ratios (IRR) pooled across sites, using random effect meta-analysis.

Results

After four PCV10/13 years, overall IPD incidence decreased by 13% (IRR 0.87, 95%CI:0.74-1.03). The incidence of PCV7 and additional six PCV13 serotype IPD decreased by 71% (IRR 0.29, 95%CI:0.15-0.56) and 21% (IRR 0.79, 95%CI:0.68-0.93), respectively. PCV7 serotype IPD incidence decreased by 83% (IRR 0.17, 95%CI:0.14-0.22) in sites with universal PCV13 vaccination and by 47% (IRR 0.54, 95%CI:0.42-0.68) in sites without universal vaccination. Incidence of nonPCV13 serotype IPD gradually increased, up to +43% in year 4 (IRR 1.43, 95%CI:1.21-1.68).

Conclusion

Results indicate an indirect effect of childhood PCV10/13 vaccination on vaccine serotype IPD in elderly, which was higher in sites with universal vaccination. However, the gradual nonPCV13 IPD increase, suggesting serotype replacement, partly countered PCV10/13 effect on overall IPD. Declines in PCV13 serotypes and increases in non-PCV13 serotypes decrease the potential benefit of elderly PCV13 vaccination. Further monitoring of IPD serotype trends in elderly as more cohorts of children receive higher valency PCV is essential to better estimate the additional benefit of elderly PCV13 vaccination over childhood vaccination.

Keywords: Streptococcus pneumoniae, Pneumococcal Infections, Pneumococcal Vaccines, Vaccine effectiveness, Population Surveillance, elderly

PRESENTED BY: Germaine Hanquet

REFERENCE NUMBER: 3064

Men-C vaccination and changing trends in invasive meningococcal disease in EU/EEA Member States, 2004 - 2014

Miriam Ramliden (1), Netta Beer (1), Joana Gomes Dias (1), Robert Whittaker (1), Assimoula Economopoulou (1), Csaba Ködmön (1), Lucia Pastore-Celentano (1)

1. ECDC

Background

Since 1999, 15 of 31 EU/EEA Member States (MS) have introduced meningococcal C (Men-C) vaccination into their national vaccination programmes. We analysed trends of invasive meningococcal disease (IMD) in laboratory-confirmed cases reported to the European Surveillance System (TESSy) by 24 MS from 2004-2014. We calculated proportions and notification rates (NR) by age, gender and serogroup.

Methods

We analyzed trends of invasive meningococcal disease (IMD) in laboratory-confirmed cases reported to the European Surveillance System (TESSy) by 24 MS from 2004 – 2014. We calculated proportions and notification rates (NR) by age, gender and serogroup. The percentage change in annual NR was estimated using linear regression analysis of the log of the annual NR.

Results

45,544 cases of IMD with known age and gender were reported. The mean annual NR was 0.9/100,000, with the highest burden in children under five (7.1/100,000), and an overall annual decrease of 6.2% (95%CI: -7.4%;-5.0%). Serogroup B accounted for 69% of cases with a mean annual NR of 0.6/100,000, and a significant decrease of 7.2% (95%CI: -9.0%;-5.5%). In serogroup C, which accounted for 14% of cases (mean annual NR= 0.13/100,000), a statistically significant reduction was seen in MS who started a routine Men-C vaccinating policy prior to 2004 (12.4% reduction (95%CI: -16.7%;-7.9%)) and between 2004 and 2014 (9.1% reduction (95%CI: -11.2%;-6.9%)). The reduction in countries without routine vaccination policy was not significant (0.7% reduction (95%CI: -4.9%;-3.7%)). The mean annual rates of serogroup Y and W remain low (0.04/100,000 and 0.02/100,000, respectively), although there is an increasing trend for both serogroups (9.7% (95%CI: 6.3%;13.2%) and 3.8% (95%CI: -2.3%;10.3%).

Conclusion

The significant serogroup C decrease in MS with Men-C vaccination and stable trends in MS without, underscores the impact of the vaccination. This, along with the high proportion of serogroup B across Europe and increasing trends serogroups Y and W, will need to be considered in future policy decisions on vaccination.

Keywords: Neisseria meningitidis, invasive meningococcal disease, serogroup, epidemiology, vaccination

PRESENTED BY: Robert Whittaker (robert.whittaker@ecdc.europa.eu)

REFERENCE NUMBER: 2942

Reporting of laboratory-confirmed deaths to monitor the impact of the 2009 influenza pandemic in Europe: was this an effective strategy?

John Paget (1), Peter Spreeuwenberg (1), Robert Taylor (2), Yung-Ching Lin (3), Pasi Penttinen (4), Lone Simonsen (5)

1. Netherlands Institute for Health Services Research (NIVEL), The Netherlands
2. Sage Analytica, Bethesda, United States of America
3. Austrian Agency for Health and Food Safety, Austria
4. European Centre for Disease Prevention and Control (ECDC), Sweden
5. George Washington University School of Public Health and Health Services, United States of America

Background

Although ECDC and WHO monitored the 2009 influenza AH1N1 pandemic using laboratory-confirmed deaths, modelling studies indicate that such deaths only account for about 10% of all pandemic respiratory deaths globally. We investigated whether this was also true in the European Union (EU), where the 2009 pandemic was particularly mild.

Methods

The WHO-sponsored GlaMOR study generated excess pandemic respiratory mortality estimates using a two-stage approach: we first estimated pandemic respiratory mortality in 20 countries (covering ~35% of the world population) using a multivariate linear regression model and weekly virology and respiratory mortality time series data for 2005-2009. We then used a multiple indicator imputation model to project the mortality burden to all world countries, and compared the sum of modelled pandemic excess deaths to the sum of laboratory confirmed deaths in all EU countries.

Results

In 2009, ECDC reported 2,269 laboratory-confirmed influenza deaths in the EU, ranging from 3 deaths in Luxembourg to 362 deaths in the United Kingdom. The GLaMOR study estimated a total of 3,369 pandemic respiratory deaths for the EU, ranging from 3 deaths in Luxembourg to 489 deaths in Italy. Overall, the ECDC laboratory-confirmed pandemic influenza death count was 2/3 (67%) of the modelled EU respiratory pandemic mortality estimate.

Conclusion

In conclusion, whilst laboratory-confirmed pandemic mortality surveillance only captured 10% of pandemic deaths globally, in the EU laboratory-confirmed deaths may have captured up to 67% of cases. This suggests that during a less-severe pandemic in a region with excellent laboratory testing capabilities, tracking laboratory-confirmed deaths may in fact be an effective and timely tool to monitor the impact of an influenza pandemic.

Keywords: Influenza, Human, Population Surveillance, Europe, Pandemics

PRESENTED BY: John Paget (j.paget@nivel.nl)

REFERENCE NUMBER: 3166

Parallel Session 12: Novel Methodological Approaches

MODERATOR: Andreas Gilsdorf (ECDC National Coordinator, Germany)

Event-based surveillance in hotels in South East Wales (UK) during the 2014 NATO Summit

Daniel Thomas (1), Sarah Jones (2), Clare Elliott (3), Lisa Holley (4), Jason Austin (5), Maria Pinch (6), Diane Thomas (7), Marc Carrington (8), Hannah Evans (1), Simon Cottrell (1), Christopher Williams (1)

1. Public Health Wales Communicable Disease Surveillance Centre, Cardiff, Wales, UK
2. Cardiff City Council, Cardiff, Wales, UK
3. Public Health Wales Informatics, Cardiff, Wales, UK
4. Newport City Council, Newport, Wales, UK
5. Torfaen Borough Council, Pontypool, Wales, UK
6. Caerphilly County Borough Council, Wales UK
7. Monmouth Borough Council, Monmouth, Wales, UK
8. Vale of Glamorgan Borough Council, Barry, Wales, UK

Background

On September 4 and 5 2014, a NATO Summit took place in Newport, Wales (UK). This was the largest gathering of international leaders ever to take place in the UK. Delegates, media, police and others were accommodated in hotels and student residences, and an estimated 24,000 room nights in 80 hotels were reserved in Newport, Cardiff and surrounding areas. Intelligence from a number of sources indicated an early increase in seasonal norovirus activity, presenting a theoretical risk to people gathering for the event.

Methods

In order to quickly identify any unusual patterns of illness amongst delegates and others attending the 2014 NATO Summit, we set up a simple event-based surveillance system in hotels in South East Wales. Hotels were recruited by local government environmental health teams and asked to report daily, by web form, any health-related incidents in the preceding 24 hours. These reports were assessed by the health protection team, and if necessary, acted on.

Results

Fifty one hotels in six local government areas participated in the scheme. Between Tuesday 25 August to Friday 12 September 2014, ten events were reported, of which six were considered of public health significance. Five of these six events were of incidents of vomiting and/or diarrhoea in staff or residents. One event was a fire. The remaining events were predominantly public order incidents.

Conclusion

Intensive multi-source surveillance was implemented in response to the NATO Summit. Event-based surveillance in hotels proved one of the more useful sources of intelligence, and led to direct public health action during the Summit. This scheme indicates the value of working with the commercial hotel sector to obtain health intelligence during large events.

Keywords: Surveillance, Mass gathering events, Norovirus, Hotels

PRESENTED BY: Daniel Thomas (daniel.thomas@wales.nhs.uk)

REFERENCE NUMBER: 3067

Development and evaluation of a register-based surveillance system for severe influenza virus infections in Denmark

Annika Wendland (1,2), Jens Nielsen (1), Manon CHAINE (1), Hanne-Dorthe Emborg (1), Sophie Gubbels (1), Marianne Voldstedlund (1), Tyra Grove Krause (1)

1. Statens Serum Institut, Copenhagen, Denmark
2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden

Background

Following the 2009/10 influenza pandemic, WHO identified the lack of robust surveillance systems for severe courses of influenza as a weakness in pandemic preparedness.Until 2013/14, Denmark used weekly active reporting of patients admitted with laboratory-confirmed influenza to Intensive Care Units (ICU) during the influenza season. This manual system was time consuming and difficult to operate during high-burden seasons. We aimed to develop an automatic, timely and more complete surveillance system of influenza patients receiving intensive care, based on data capture from existing registers, to monitor the severity of an influenza season.

Methods

Using the Danish personal identification number, we linked national data from the Danish microbiology database with data from the Civil Registration-, National Patient-, and Vaccination Register. We defined cases as influenza infections that were laboratory-confirmed within 4 days of a hospital admission including ICU treatment. We extracted information on underlying conditions, vaccinations and vital status from the aforementioned registers. We calculated the sensitivity of both systems for season 2013/14, using Chapman's formula for two-source capture-recapture studies. We compared the delay from admission to reporting between the two systems.

Results

The new system was more sensitive (sensitivity 146/153 vs 108/153), detecting 42 previously unreported cases. The median delay between admission and reporting in the old system was 6 days (IQR: 4-8 days) compared to 13 days (IQR: 6-24 days) in the new system.

Conclusion

The register-based surveillance system is simple to operate, providing surveillance data with higher sensitivity than the previous system. We could improve timeliness by running the system every day. The system is flexible, can cope with high case numbers and can be adapted for surveillance of severe outcomes of other pathogens.

Keywords: Influenza, intensive care, register-based surveillance, data capture

PRESENTED BY: Annika Wendland (annikawendland@hotmail.com)

REFERENCE NUMBER: 2900

Insights for outbreak response: understanding the chains of Ebola virus disease (EVD) transmission in N'zérékoré, Guinea; February 2015

Cristina Valencia (1,2), Hawa Bah (3), Barry Fatoumata (3), William Perea (3), Barry Diallo (3), Moussa Kone (3), Coralie GIESE (1,4), Lila Lucie Conde (5), Emmanuel Ronan Malano (6), Thomas Mollet (7), Bertrand Sudre (7), Josep Jansa (7), Denis Coulombier (7)

1. European Programme for Interventional Epidemiology Training (EPIET), ECDC Stockholm, Sweden
2. Scientific Institute of Public Health, Brussels, Belgium
3. World Health Organization, Conakry, Guinea
4. Health Protection Surveillance Centre, Dublin, Ireland
5. Department of Health, N'zérékoré prefecture, Guinea
6. Ministry of Health, Guinea
7. European Centre for disease prevention and control (ECDC), Stockholm, Sweden

Background

During the 2014-2015 outbreak in Nzérékoré, Guinea, modes of transmission remained unexamined for a number of new cases. We investigated EVD transmission chain (TC) in eight sub-prefectures of Nzérékoré in order to adapt response.

Methods

Between August 2014 and February 2015, the Direction Prefectorale de la Santé routinely collected information among new cases regarding hospital visits, cases among household members, participation in burials, as well as dates of onset and exposure. We used dates of exposure and dates of onset to calculate serial intervals between consecutive cases [SI]. Cases who reported hospital visits, contact with a case in the household or participating in burials were attributed to these exposures.

Results

We identified 8 TC (2 urban and 6 rural; 103 probable/confirmed cases). With respect to urban chains (17 cases, SI range: 7-20 days), 50% were hospital-related, 50% were household-related and none were burial-related. With respect to rural chains (86 cases, SI range: 7-30 days), none were hospital-related, 50% were household-related and 50% were burial-related. No cases reported multiple exposures.

Conclusion

While household exposures accounted for 50% of transmission in all settings, the other half was explained by burials in rural areas and hospitals in urban areas. Serial intervals exceeding the 21-days incubation in rural areas suggested intermediary hosts that may have been missed. Health authorities need to prevent household transmission everywhere. Urban areas need to address hospital transmission. Rural areas must focus on safe burials and search for possible persons missing in the chain of transmission.

Keywords: Ebola virus disease (EVD), chains of transmission, Guinea, Nzérékoré, outbreak

PRESENTED BY: Cristina Valencia (cristina.valencia@wiv-isp.be)

REFERENCE NUMBER: 3077

Improving mapping for Ebola response in Tonkolili District, Sierra Leone through mobilisation of local people and smartphone technology, January 2015

Laura Nic Lochlainn (1,2,3), Ivan Gayton (4), Georgios Theocharopoulos (2,3,5), Stanley Bockarie (6), grazia Caleo (4)

1. National Institute for Public Health and the Environment (RIVM), Centre for Infectious Disease Control, Bilthoven, the Netherlands
2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, Stockholm, Sweden
3. Medecins Sans Frontieres, Operational Center Amsterdam, Amsterdam, the Netherlands
4. Manson Unit, Medecins Sans Frontieres, London, UK
5. Institut de Veille Sanitaire (InVS), Departement des Maladies Infectieuses, Cedex, France
6. Ebola Management Centre, M

Background

In January 2015, the Magburaka Ebola Management Centre (EMC) operated by Médecins Sans Frontières in Tonkolili district, Sierra Leone, identified that available maps lacked up-to-date village information. This delayed follow-up of Ebola cases and their contacts. We undertook a survey that aimed to collect mapping, population and health-care access data for Tonkolili district in order to improve Ebola response.

Methods

We recruited 12 local people with self-owned Android smartphones and paired them with 12 motorbike drivers. Smartphones were installed with open-source survey software, OpenDataKit (ODK) and open-source navigation software, OpenStreetMap Automated Navigation Directions (OsmAnd). The teams received basic training and surveyed villages throughout Tonkolili district (area: 7,003km²). Teams collected GPS coordinates; village name(s); health-care facility locations; population estimates; contact information of village leaders and health-care workers. Pre-existing village data from the 2010 census or prior OpenStreetMap contributions were used to check data quality. Maps were created using QGIS™ open-source mapping software.

Results

The teams mastered the ODK and OsmAnd software within 1-2 hours. No device training was necessary. Tonkolili district was surveyed within two weeks, collecting data from 950 villages. Ninety-five percent of village names collected agreed with pre-existing village data. We submitted our validated data to OpenStreetMap to update their mapping database. Villages of Ebola cases from the Magburaka EMC or Ebola cases who sought care outside of Tonkolili district were mapped to allow for rapid response, hygiene-kit distribution, outcome follow-up or survivor support.

Conclusion

Involving local people and using accessible technology allowed rapid implementation of a survey to collect geographic and population data, as well as creation of new maps for improved Ebola response. These methods could be used for future emergencies to improve response actions.

Keywords: Ebola virus, mapping, Sierra Leone, infection control

PRESENTED BY: Laura Nic Lochlainn (laura.nic.lochlainn@rivm.nl)

REFERENCE NUMBER: 3127

Parallel Session Programme
Thursday 12 November
17:00-18:10

Parallel Session 13: Late Breakers

MODERATOR: Viviane Bremer (Robert Koch Institute, Germany)

Uncovering the scale of a reptile associated salmonellosis outbreak in United Kingdom (UK), 2015: a recent history

Sanch Kanagarajah (1), Isidro Carrion (1), Adedoyin Awofisayo-Okuyelu (1), Philip Ashton (1), Tim Dallman (1), Jeremy Hawker (1), Richard Elson (1)

1. Public Health England, UK

Background

Salmonella enterica serotype Enteritidis has been associated with reptiles in the United States, but until now not documented in UK. Transmission of reptile associated salmonellosis occurs through contact with reptiles or contaminated reptile feed such as feeder mice. Severe and invasive disease is more frequent in children aged under five years. A cluster of cases of Salmonella Enteritidis was detected using whole genome sequencing (WGS) in August 2015. We investigated the event to identify the source..

Methods

Review of routinely collected information suggested the hypothesis of a possible link with reptiles. We conducted a case-control study. A case was defined as a laboratory-confirmed Salmonella Enteritidis within a five single-nucleotide polymorphisms difference of the outbreak WGS profile. We randomly recruited controls from a consumer survey panel frequency matching by age group (three controls per case). Cases and controls with history of travel within seven days of onset or interview were excluded. Standardised questionnaires on food and animal contact were completed online. We used multivariable logistic regression to calculate (adjusted) odds ratios ((a)OR) and 95% confidence intervals (95%CI).

Preliminary Results

During January- August 2015, 70 cases were reported; median age was 18 years (range: 1-72), 36% were <10 years of age and 54% were females. 28 cases and 180 controls were included. Compared with controls, cases were more likely to have contact with snake (aOR: 810, 95%CI: 85-7715), and with feeder-mice (OR: 322, 95%CI: 40-13482).

Conclusion

Cases were associated with owning a reptile. We believe this to be the first reported S. Enteritidis outbreak associated with snakes. Further microbiological and environmental investigation is essential to identify the source and the real extent of this outbreak.

Keywords: outbreak, salmonella, reptiles, United Kingdom

PRESENTED BY: Isidro Carrion (isidro.carrion@phe.gov.uk)

First case of diphtheria in Spain since 1986

Magda Campins Marti (1), Joan Balcells (2), Maria Teresa Martin (3), Tomas Pumarola (3), Silvia Herrera (4), Mireia Jane (5), Neus Camps (5), Jose Fernando Cordero (6)

1. Preventive Medicine and Epidemiology Department. Hospital Universitario Vall Hebron. Barcelona
2. Pediatric Intensive Care Unit. Hospital Universitario Vall Hebron. Barcelona.
3. Microbiology Laboratory. Hospital Universitario Vall Hebron. Barcelona, Spain
4. Unidad de Enterobacterias, Centro Nacional de Microbiologia, Instituto de Salud Carlos III. Majadahonda, Madrid, Spain
5. Subdirecci
6. Graduate School of Public Health. University of Puerto Rico

Background

Diphtheria was eliminated from Spain for almost 30 years due to the high vaccination coverage reached in children. The last reported case was in 1986. We report the clinical, epidemiological and control measures following an autochthonous case of toxigenic Corynebacterium diphtheria recently diagnosed in Catalonia (Spain).

Methods

On May 28, 2015, a 6-year-old unvaccinated child presents to the emergency department of a rural hospital complaining of a four-day history of severe sore throat, general malaise, low-grade fever and progressive neck swelling. Clinical examination shows pseudo-membranes covering the tonsils. Toxigenic C. diphtheria was confirmed by PCR on May 30.

Results

The child was transferred to a tertiary care hospital and despite treatment with penicillin G, administration of equine diphtheria antitoxin (DAT) and intensive care support, patient developed myocarditis, renal failure and finally died on June 27. Contact tracing revealed 8 vaccinated children and 1 vaccinated adult asymptomatic carriers of toxigenic C. diphtheria.

Conclusion

Some major difficulties for the proper management of this case and the corresponding epidemiological investigation should be acquainted by the international community in order to improve preparedness against diphtheria in the European Union. We highlight the lessons learned and the challenges for clinical management, preparedness and public health response:1. To guarantee accessibility to DAT for early administration to the potential patients. 2. To ensure availability of microbiological techniques and locally appropriate kits for transport of samples to the reference laboratory.3. To facilitate early detection of unvaccinated clusters and the educational efforts implemented to improve immunization coverage in these groups.4. To assure the training of clinicians in some almost forgotten preventable diseases as diphtheria or poliomyelitis, for timely detection and diagnosis.

Keywords: Diphtheria, Spain, Public health, Diphtheria antitoxin

PRESENTED BY: Magda Campins Marti (mcampins@vhebron.net)

REFERENCE NUMBR: 3481

Surveillance and Outbreak Response Management and Analysis System (SORMAS) for outbreak control of Ebola virus and other diseases - results of a field pilot in Nigeria, 2015

Celestine Ameh (1), Sabine Mall (2,3), Olewunmi Adeoye (1), Sandra Beermann (4), Justus Benzler (4), Hermann Claus (4), Kerstin Denecke (2,3), Elsie Ilori (5), Goeran Kirchner (4), Todd Laedtke (6), Maike Lamshoeft (7,3), David Moyer (6), Connor Nelson (6), Olubunmi Ojo (5), Cindy Perscheid (8), Norbert Schwarz (7,3), Daniel Tom-Aba (1), Sebastian Yennan (5), Gabriele Poggensee (1), Gerard Krause (2,9,3)

1. Nigeria Field Epidemiology and Laboratory Training Program, Abuja, Nigeria
2. Helmholtz-Centre for Infection Research, Braunschweig, Germany
3. German Centre for Infection Research (DZIF), Braunschweig, Germany
4. Robert Koch Institute, Berlin, Germany
5. Surveillance/IHR, NCDC, Federal Ministry of Health, Abuja, Nigeria
6. SAP America SE & Co. KG, Philadelphia, PA, USA
7. Bernhard Nocht Institute for Tropical Medicine, Hamburg, Germany
8. Hasso Plattner Institute, Potsdam, Germany
9. Hannover Medical School, Hannover, Germany

Background

During the Ebolavirus (EVD) outbreak in West Africa 2014/15, response management posed serious challenges. We developed the IT Surveillance and Outbreak Response Management and Analysis System (SORMAS) in order to improve detection and control of outbreaks in low resource settings.

Methods

We analyzed Nigerian EVD-outbreak control procedures and designed process models compliant with the Integrated Disease Surveillance and Response (IDSR) standard, with dedicated interfaces for 7 different kinds of public health officers (PHO). Mobile phone apps for field-PHO connected via cloud technology to an in-memory database assured bi-directional information and management functionalities. We piloted SORMAS in randomly selected local government administrations (LGA) of two Nigerian states. Through an agent-based model we simulated an EVD-outbreak generating daily injects for SORMAS-users and processed real cholera and measles notifications via SORMAS. The evaluation consisted in: A) anonymous user-surveys, B) comparing SORMAS-with conventional IDSR-notifications, C) observation protocols from supervisory field visits.

Results

The pilot took place from July 6 to August 9, 2015 in 32 private and 32 public health facilities of 16 randomly selected LGA of Oyo and Kano State and the respective public health departments. A) Among 103 participants, 87 (85%) would recommend the use of SORMAS to their colleagues. On a scale from 1 (difficult) to 10 (easy to use SORMAS) the median value was 8. B) SORMAS processed 94 measles- and 16 cholera-cases compared to 84 and 18 respectively via conventional IDSR-notification. C) Mobile apps worked well for contact-officers and need improvement for rumor- and surveillance-officers.

Conclusion

The conceptual approach of SORMAS was functional and well accepted under field conditions in Nigeria. SORMAS may contribute to significant improvement of surveillance and control of infectious diseases.

Keywords: Ebolavirus, disease, outbreaks, mobile applications, surveillance, organization & administration, medical informatics

PRESENTED BY: Gerard Krause (gerard.krause@helmholtz-hzi.de)

REFERENCE NUMBER: 3509

Assessing the threat of Mycobacterium chimaera infection in patients undergoing open heart surgery in England and Wales

Theresa Lamagni (1), Katharina Kranzer (1), Sonia Bhatt (1), Isidro Carrion-Martin (5), Katherine Russell (1), David Pearce (1), Brendan Mason (2), Christopher Williams (2), Gayle Dolan (1), Tim Brown (1), Grace Smith (1), Peter Hoffman (1), Bennett Allan (1), James Walker (1), Samuel Collins (1), Ginny Moore (1), Simon Parks (1), Stephen Robins (3), Alicia Yeap (1), Nada Ahmed (1), Andre Charlett (1), Eleri Davies (2,4), Meera Chand (1)

1. Public Health England, UK
2. Public Health Wales, UK
3. Society of Clinical Perfusion Scientists of Great Britain and Ireland, UK
4. Cardiff and Vale University Health Board
5. European Programme for Intervention Epidemiology Training, European Centre for Disease Prevention and Control, Stockholm, Sweden

Background

Following alerts from Switzerland and The Netherlands, PHE in collaboration with partner organisations investigated the risk of invasive Mycobacterium chimaera infection through exposure to contaminated water circuits in heater cooler units (HCUs) used in theatre for cardiopulmonary bypass.

Methods

We identified potential cases of invasive (sterile site) M. chimaera infection associated with cardiopulmonary bypass using linked hospital admission and laboratory surveillance data. Surgical procedure coding was used to identify cases involving bypass, and risk assessment assuming 5y risk period undertaken in hospitals with implicated devices. Clinical and environmental isolates were characterised and aerobiological investigations undertaken to identify mechanisms of transmission.

Results

We identified 17 cases of endocarditis, disseminated infection, discitis and sternal wound infections due to Mycobacterium avium complex diagnosed between 2008 and 2015, of which 14 have been confirmed to date as M. chimaera. All except one were adults with a median interval between surgery and infection of 19 months (range 3 months to 5 years). Patients had undergone cardiac valve surgery in 10 different hospitals all of whom used a specific HCU brand. The risk of infection following such procedures in England between 2007 and 2014 was 0.4/10,000 person-years. Examination of water circuits and air generated by HCUs in five hospitals identified M. chimaera contamination. Aerobiological testing identified a potential mechanism for aerosolisation of tank water.

Conclusion

We identified a number of cardiothoracic patients with post-surgical infections possibly resulting from direct inoculation of the surgical field from aerosols generated by contaminated HCUs in theatre. Whilst our risk estimate is undoubtedly an underestimate due to diagnostic practices in the UK, it is likely to be lower than that of delaying surgery for most patients.

Keywords: Mycobacterium chimaera infection, cardiopulmonary bypass, Cardiac Surgical Procedures, Equipment, Contamination, England

PRESENTED BY: Theresa Lamagni (theresa.lamagni@phe.gov.uk)

Parallel Session 14: Vaccine-preventable diseases II

MODERATOR: Susan Hahne (EPIET alumni, the Netherlands)

A systematic review for the basic reproductive number for measles: implications for measles elimination

Gillian H. Lim (1), Fiona Guerra (1), Shelley L. Deeks (1,2), Natasha Crowcroft (1,2)

1. Public Health Ontario, Canada
2. University of Toronto, Canada

Background

Achieving measles elimination requires accurate estimates of basic reproductive numbers (Ro) to determine herd immunity and targets for immunization coverage. Ro is frequently cited as ranging between 12-18, however this is based on limited studies. Population immunity, Ro, the effective reproductive number (Re) and vaccine effectiveness (VE) are interdependent. We present updated estimates of measles Ro and Re using recent data from published literature and from Ontario (Canada's most populous province), where measles is eliminated.

Methods

A systematic literature review was conducted to derive updated estimates of Ro. English abstracts from MEDLINE, Embase and Global Health were retrieved and screened by two reviewers. A preliminary meta-analysis was conducted to derive overall estimates of Ro weighted by study size, stratified by jurisdictions with high/low birthrates (20 births/1,000 population). Confirmed measles cases reported through the integrated Public Health Information System between 2006-2014 were analysed to derive estimates of Re in Ontario by modeling the distribution of outbreak sizes. The interdependency between population immunity (coverage´VE), Ro and Re was examined: Ro=Re/(1-population immunity).

Results

From the 14,700 abstracts retrieved, 18 papers were selected. A wide range of Ro estimates was reported across jurisdictions and study periods (1.4-770.4); the overall weighted estimate for Ro was lower in jurisdictions with low birthrates (8.0 versus 20.1). Analysis of Ontario measles cases yielded Re=0.68, 95% confidence interval of 0.55 to 0.84, indicating a theoretical Ro = 3.9.

Conclusion

A wide range of Ro estimates was reported in the literature, with a high degree of heterogeneity by jurisdiction and time period. Ontario data suggest previous Ro estimates may be too high. These findings have global implications as accurate estimates of Ro are critical in achieving elimination goals.

Keywords: measles, basic reproduction number, disease eradication, disease transmission

PRESENTED BY: Natasha Crowcroft (natasha.crowcroft@oahpp.ca)

REFERENCE NUMBER: 3141

Risk perception and willingness to perform preventive measures in case of pandemic influenza; comparison of 4 European countries

Helene Voeten (1,2), Bram Meima (1), Marloes Bults (1,2), Domino Determann (2), Ida Korfage (2), Amena Ahmad (3), Jan Hendrik Richardus (1,2)

1. Municipal Public Health Service Rotterdam-Rijnmond, Rotterdam, The Netherlands
2. Erasmus MC, University Medical Center Rotterdam, The Netherlands
3. Hamburg University of Applied Sciences, Hamburg, Germany

Background

Research into risk perception and behavioural responses of the public is important in preparing outbreak management. The aim of this study was to investigate risk perception of the general public in 4 European countries with regard to a hypothetical outbreak (pandemic) of a new influenza virus.

Methods

We performed a cross-sectional online survey among a representative internet panel in 4 European countries (UK, Sweden, Poland, Spain). Respondents (n=2004) were randomly shown 1 of 3 imaginary newspaper articles, all describing the outbreak of a new influenza virus in their country, but varying with regard to severity of the outbreak (i.e. number of deaths, percentage ill, and spread across continents).

Results

Risk perception of a hypothetical flu outbreak differed more between countries than between outbreak scenarios (mild, intermediate, severe). Perceived severity, perceived vulnerability and anxiety were lowest in Sweden, as was perceived efficacy of preventive measures and intention to perform these measures. UK respondents scored highest regarding perceived severity/vulnerability and intention to perform measures. Practicing better hygiene, avoiding crowded places, and avoiding people who are coughing/sneezing were considered more effective measures than vaccination in all countries. Swedish respondents were most concerned about side-effects of vaccination, whereas Polish respondents were most concerned about vaccine effectiveness. In Sweden, trust in the government was highest and the preferred source of information was the Department of Health; in Poland, trust in the government was lowest and the preferred source of information was the family doctor.

Conclusion

In case of pandemic influenza, risk perception and willingness to perform preventive measures may vary considerably across European countries. Content and source of information about pandemics should be adapted to the risk perception in the specific country.

Keywords: Risk perception, influenza, prevention, outbreak management, Europe, pandemic

PRESENTED BY: Helene Voeten (h.voeten@rotterdam.nl)

REFERENCE NUMBER: 3199

What is the impact of offering healthy school-age children influenza vaccine: an inter-country comparison of influenza-related morbidity and mortality across the UK and Ireland in 2014/15

Helen K Green (1), Lisa Domegan (2), Joan O'Donnell (2), Ajay Oza (2), Naomh Gallagher (3), Jillian Johnston (3), Jim McMenamin (4), Arlene Reynolds (4), Simon Cottrell (5), Daniel Thomas (5), Fiona Warburton (1), Nick Andrews (1), Joanna Ellis (6), Richard Pebody (1)

1. Public Health England Centre of Infectious Disease Surveillance and Control, London, UK
2. Health Protection Surveillance Centre, Health Service Executive, Dublin, Ireland
3. Public Health Agency Northern Ireland, Belfast, UK
4. Health Protection Scotland, Glasgow, UK
5. Public Health Wales Molecular Diagnostics Unit, Cardiff , UK
6. Public Health England Operations Directorate, Microbiology Services, Colindale, London, UK

Background

Countries within the UK, unlike Ireland, are extending the routine selective influenza vaccination programme to include healthy children. It is predicted that in addition to direct protection, the programme will provide indirect protection to the wider community by reducing transmission. In 2014/15 different age-cohorts were targeted in each country, providing a unique opportunity to compare overall programme impact through standardised approaches.

Methods

Influenza activity in 2014/15 was assessed for England (no universal schoolchildren programme), Wales (targeting all 11-12yrs), Scotland and Northern Ireland (both targeting all 5-11yrs), with Ireland as a control. The Moving Epidemic Method and ECDC-defined thresholds were applied to influenza-like illness (ILI) consultation rates in primary care to assess weekly intensity level. Influenza-attributable mortality was estimated through a European multivariable Poisson regression model, FluMOMO, adjusting for trend, seasonality and extreme temperature.

Results

2014/15 was dominated by influenza A(H3N2), with similar proportions of vaccine-mismatched viruses circulating across countries. ILI rates peaked at medium intensity in Ireland and Wales being above baseline for 11 and 12 weeks respectively. Activity peaked at low intensity in England (with activity above baseline for 14 weeks), Scotland (one week) and Northern Ireland (two weeks). Significant influenza-attributable mortality was seen across all countries, with the lowest rate in Ireland and the highest in England.

Conclusion

Preliminary standardised assessment of influenza activity across the UK and Ireland suggests an ILI rate reduction in countries targeting all primary schoolchildren for vaccination relative to countries targeting only healthy secondary schoolchildren or not targeting healthy children. However there was no clear pattern in influenza-attributable mortality by vaccination strategy. Continued assessment can help determine suitability of these endpoints for measuring impact and inform optimal rollout of such programmes.

Keywords: United Kingdom, Ireland, Influenza, Vaccination, Child, Impact

PRESENTED BY: Helen K Green (helenkaygreen@gmail.com)

REFERENCE NUMBER: 3059

Late Breaker: Insufficient Measles Coverage in Refugees coming to Rhineland Palatinate, Germany from March 2015 until September 2015 highlights vaccination priority

Florian Burckhardt (1), Wilma Heinen (2), Manfred Vogt (1)

1. Landesuntersuchungsamt Rheinland-Pfalz, Germany
2. Gesundheitsamt Kreisverwaltung Trier-Saarburg, Germany

Background

In 2015, Germany has received an unprecedented influx of refugees. The German State of Rhineland-Palatinate hosts about 5% of all refugees coming to Germany. Refugees in Germany have the legal entitlement for an initial health screening which includes protection against vaccine preventable diseases. Refugees of age 15 and younger receive vaccinations (including MMR) according to national guidelines. Starting from March 2015, refugees older than 15 were screened at the Landesuntersuchungsamt (LUA) serologically for measles antibodies. A herd immunity of 95% is required in order to prevent measles outbreaks in a normal population without crowding.

Methods

We classified serologically borderline results as susceptible against measles. We calculated one-sided confidence intervals using Poisson distribution for measles susceptibility upper bound (SUB), stratified by age and nationality.

Results

From March until September 2015 LUA received 9129 serological samples of which 7524 (82%) were positive, 1118 (12%) negative and 487 (5%) borderline. The majority of samples came from Syrian (n=2828; 31%; SUB:15%), Albanian (n=2184; 24%; SUB:30%) and Afghani (n=959; 11%, SUB:16%) refugees. Only 5% of refugees grouped by nationality had a SUB of less than 5%, i.e. had sufficient herd immunity as a population. Distribution among age-groups were n=3733 (41%) for 16-24y (SUB: 26%), n=3156 (35%) for 25-34y (SUB: 18%), n=1454 (16%) for 35-44y (SUB: 9%) and n=786 (9%) for 45y and older (SUB: 5%). Total SUB was 18%.

Conclusion

The classic herd immunity threshold of 95% against measles does not accommodate for assortative mixing in crowded refugee shelters. With a total SUB of 18%, immediate and universal vaccination against measles for all refugees coming to Germany remains a very urgent priority in order to prevent outbreaks among a vulnerable population.

Keywords: refugees, measles, vaccination, Germany

PRESENTED BY: Florian Burckhardt (florian.burckhardt@lua.rlp.de)

Parallel Session 15: Public Health Microbiology and Molecular Epidemiology

MODERATOR: Jacob Moran-Gilad (Eurosurveillance Seminar speaker, Israel)

Microbiological characteristics of group B streptococcal isolates (GBS) submitted during enhanced surveillance of infant disease, United Kingdom, 2014-2015

Darshana Patel (1), Theresa Lamagni (1), Paul Heath (2), Catherine O'Sullivan (2), Victoria Chalker (1), Georgia Kapatai (1), Androulla Efstratiou (1)

1. Public Health England, London, United Kingdom
2. St George's University Hospitals NHS Foundation Trust, London, United Kingdom

Background

Neonatal GBS infections present as early onset disease (EOD) at 0-6 days which is commonly associated with sepsis and pneumonia or late onset disease (LOD) at 7-89 days which is often associated with meningitis. UK recommendations for prevention of EOD (2003) were in part based on a 2000-2001 enhanced surveillance study of invasive GBS disease and identified 568 cases, of those 53 (9%) resulted in death.

Methods

Cases (April 2014–April 2015) identified via the British Paediatric Surveillance Unit and microbiologists were defined as infants, aged ‹90 days from whom GBS was isolated from a normally sterile site. GBS isolates were characterised by serotyping and multilocus sequence typing (MLST) based on whole-genome sequencing.

Results

GBS from 274 of 314 cases reported from April 2014-March 2015 were characterised. Of 274 cases, 147 were EOD (54%) and 127 LOD (46%). Serotype III (n=161) and Ia (n=46) were the prevalent serotypes; the greater proportion of serotype Ib, II and V isolates (≥72%) were from EOD. EOD Isolates (n=82) were assigned to 20 STs (index of discrimination (D)=0.85) and LOD (n=66) to 13 (D=0.74). Isolates assigned to ST17 (n=60), ST23 (n=19) and ST1 (n=14) were prevalent equivalently in EOD and LOD (X^2=2.75, p=0.25). Most frequently detected STs among serotype III were ST17 (n=57) and ST19 (n=10); for serotype V, ST1 (n=12). The majority of Ia, ST23 (n=13) were from EOD.

Conclusion

Differences in MLST and serotypes between EOD and LOD isolates were indicated. Our surveillance data should contribute towards the current national guidelines for invasive GBS infections in neonates and aid in implementation of a GBS vaccine programme.

Keywords: Streptococcus agalactiae, streptococcal infections, infant, newborn, incidence

PRESENTED BY: Darshana Patel (darshana.patel@phe.gov.uk)

REFERENCE NUMBER: 2971

Unraveling an 11-year Community-Acquired MRSA Outbreak by Whole-Genome Sequencing

Robert Skov (1), Marc Stegger (1), Andreas Petersen (1), Anders Rhod Larsen (1), Lance B Price (2), Paal Skytt Andersen (1)

1. Statens Serum Institut
2. George Washington University, Washington, DC, USA

Background

Methicillin-resistant Staphylococcus aureus (MRSA) infections are increasing in most parts of the world, with outbreaks posing a problem in both hospitals and the community. Surveillance and outbreak analysis is a cornerstone in fighting outbreaks and determining relatedness of isolates, by using epidemiological investigations, phenotypic and genotypic typing characterization of the infectious agent. With the improved resolution obtained by using whole genome sequencing (WGS) this would allow a better tracing of transmission routes among more outbreaks including complex community associated MRSA (CA-MRSA) outbreaks.

Methods

We applied WGS to 82 isolates belonging to the European CA-MRSA CC80 clone from a low prevalence region of Denmark from 1997 to 2009. Detailed epidemiological data and phylogenetic analyses were used to understand genetic relationships and reconstruct transmissions between human cases confirming or refuting epidemiological based possible transmission routes.

Results

Phylogenetic analyses identified 52 cases of the CC80 clone over nine years, belonging to one prolonged transmission chain / outbreak containing two distinct subclades. The analyses confirmed all but one of the suspected epidemiologically transmission chains including household-, kindergarten-, school-, health-care- and workplace-related transmissions. Multiple cases previously unrecognized as being part of the transmission chain were assigned to the outbreak and a few could be refuted.

Conclusion

This population-based investigation of a community-acquired MRSA outbreak over a thirteen-year period underscores the strength of WGS for surveillance and outbreak investigations. Our analyses confirmed suspected transmission routes, but more importantly, the increased resolution allowed multiple additional cases to be linked to the outbreak and thereby indicating additional transmission routes.

Keywords: Staphylococcus aureus, MRSA, whole genome sequencing, outbreak

PRESENTED BY: Robert Skov (rsk@ssi.dk)

REFERENCE NUMBER: 3148

Detection of epidemiologically linked clusters of Salmonellosis identified using whole genome sequencing; a retrospective epidemiological analysis in England and Wales, 2014

Gayle Dolan (1,2), Alison Waldram (1,2), Philip Ashton (3), Tim Dallman (3)

1. UK Field Epidemiology Training Programme, Public Health England (PHE), London, UK
2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden
3. Gastrointestinal Bacteria Reference Unit, Public Health England (PHE), London, UK

Background

Validation of whole genome sequencing (WGS) for Salmonella characterisation and typing was implemented in England and Wales in April 2014. In this study, we define clusters of genetically similar isolates and use routinely collected exposure information to identify potential epidemiological links.

Methods

We obtained WGS data for all Salmonella isolates sequenced April-August 2014. Clusters were defined as 5+ isolates with a matching single nucleotide polymorphism (SNP) address at the 0, 5 or 10 SNP level, when compared with a serotype specific reference genome; controls as isolates with more than 50 SNP differences from any other isolate. We described clusters by number, size, duration and demographics of their cases and extracted exposure information from case questionnaires (including travel, animal contact, foods etc.). A retrospective case-case design (2 controls per case) was used to examine associations with illness, calculating odds ratios and p values (Fisher's exact test).

Results

1510 isolates were reviewed and 32 unique clusters (566 cases, 418 with exposure information) were identified. The number of cases per cluster was 5-145 and duration 6-106 days. In 14 clusters the majority (>85%) of cases had exposure to foreign travel; an association with travel was found in 8/9 of these investigated analytically. Twelve of the 18 remaining clusters were investigated and an association found in 9 (food n=3, eating out n=4, animal contact n=1, ill contact n=1). Cases in 5 clusters had previously been linked through conventional outbreak detection methods.

Conclusion

WGS may facilitate the identification of previously undetected clusters. Further prospective validation is required in order to explore the utility of this in directing future investigation.

Keywords: Salmonella, Genomics Cluster Analysis, Epidemiology

PRESENTED BY: Alison Waldram (Alison.Waldram@phe.gov.uk)

REFERENCE NUMBER: 2939

Integrating routine whole genome sequencing (WGS) into an outbreak investigation of Salmonella enterica serovar Typhimurium linked to a carvery buffet at a restaurant in Leicestershire, February - March 2015

John Mair-Jenkins (1,2), Roberta Borges-Stewart (3), Laura Baylis (2), Deborah Modha (4), Tim Dallman (5), Elizabeth De Pinna (5), Philip Monk (3), Richard Puleston (2)

1. Field Epidemiology Training Programme, Public Health England, UK
2. Field Epidemiology Services - East Midlands, Public Health England, UK
3. Health Protection Team - East Midlands, Public Health England, UK
4. Medical Microbiology, Leicester Royal Infirmary, University Hospitals of Leicester NHS Trust, UK
5. Gastrointestinal Bacteria Reference Unit, Public Health England, UK

Background

On 7th March 2015 University Hospitals Leicester reported 17 cases of S. Typhimurium to Public Health England. We conducted an epidemiological investigation to identify and control the source.

Methods

We identified salmonellosis cases using statutory notifications and case interviews. Hypothesis generation questionnaires linked eating restaurant food with illness. All clinical isolates were characterised using phage-typing, MLVA profiling and whole genome sequencing (WGS). We conducted a case-control study collecting exposure information using internet-based questionnaires. We calculated adjusted odds ratios (aOR) using multivariable exact logistic regression, comparing exposures between cases (confirmed: matching WGS, possible: symptomatic) and case-nominated controls (1:1), all of whom had eaten at restaurant after 1st February. We obtained restaurant environmental surface swabs and staff stool samples.

Results

Case finding identified 46 confirmed cases with a nationally unique WGS clade (including three staff; two carvery staff – symptomatic during the outbreak; the other asymptomatic) and 7 possible cases; 86% (43/53) reported eating at the restaurant. Twenty-one cases (49%) and 10 controls completed case-control questionnaires. Eating carvery food was the only significant exposure after adjustment for sex and recent antibiotic treatment (aOR 20.9, 95% CI 2.2-∞). No food samples were available and environmental investigations were inconclusive; however staff may have not declared illness as sickness-absence was unpaid.

Conclusion

Our investigation confirmed an outbreak related to the restaurant carvery. This was unexpected in a newly-built restaurant with modern facilities which appeared well run. Timely WGS results confirmed case linkage and supported epidemiological evidence of the restaurant as the only plausible source. Contamination of food by staff may have been a factor. The number of cases declined after we recommended the restaurant retrain and supervise staff prior to a busy holiday weekend.

Keywords: salmonella, disease outbreaks, food-borne infection, phylogeny

PRESENTED BY: John Mair-Jenkins (john.mairjenkins@phe.gov.uk)

REFERENCE NUMBER: 3136

Parallel Session Programme
Friday 13 November
10:50-12:30

Parallel Session 16: Vaccine-preventable diseases III

MODERATOR: Lucia Pastore Celentano (ECDC, acting Head of Disease Programme VPD)

A unique measles B3-cluster in the United Kingdom and the Netherlands linked to air travel and transit at a large international airport in 2014: implications for public health follow-up of exposed travellers

Laura Nic Lochlainn (1,2), Sema Mandal (3), Rita de Sousa (1,4), Karthik Paranthaman (5), Rob van Binnendijk (1), Mary Ramsay (3), Susan Hahne (1), Kevin E Brown (6)

1. National Institute for Public Health and the Environment (RIVM), Centre for Infectious Disease Control, Bilthoven, the Netherlands
2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, Stockholm, Sweden
3. Centre for Infectious Disease Surveillance and Control, Public Health England, London, UK
4. European Programme for Public Health Microbiology Training (EUPHEM), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
5. Kent, Surrey and Sussex Public Health England Centre, Ashford, Kent, UK
6. Virus Reference Department, Public Health England, London, UK

Background
Between February-April 2014, measles cases with the unique B3 strain in the United Kingdom (UK) and the Netherlands were epidemiologically linked to a 45-year-old unvaccinated adult who, during week 5/2014, travelled from the Philippines to London via Amsterdam while infectious with measles. We investigated the cases to highlight improvements needed in public health follow-up of travellers exposed to measles.

Methods
We included laboratory confirmed measles cases in the UK and the Netherlands with the B3 genotype MVs/Tonbridge.GBR/5.14 or any laboratory confirmed measles cases with an epidemiological link to the index case. Cases were identified through surveillance activities at public health institutes in the UK and the Netherlands.

Results
Between epidemiological weeks 7-14/2014, 17 UK and 15 Dutch cases were detected with an indistinguishable measles sequence of the B3 strain, MVs/Tonbridge.GBR/5.14. Of those, nine were epidemiologically linked with the index case; six UK cases were at Amsterdam airport or on the same flight as the index case; one UK case was a household contact and two Dutch cases worked at Amsterdam airport. The remaining 10 UK and 13 Dutch cases were investigated, but could not be linked to the index case. Obtaining passenger information from the airline was challenging, and delayed alerting 61/72 (85%) passengers with available contact information.

Conclusion
In this investigation, 32 measles cases occurred following introduction of measles from the Philippines. Delay in obtaining passenger information from the airline hampered timely public health investigation and response. A rapid and efficient method for obtaining passenger information and contact details in situations of public health urgency is needed, that is globally adopted by airline companies and enforced by their regulatory authorities.

Keywords: Measles, United Kingdom, the Netherlands, unvaccinated, travellers, airport

PRESENTED BY: Laura Nic Lochlainn (laura.nic.lochlainn@rivm.nl)

REFERENCE NUMBER: 3135

A large and foreseeable outbreak of measles in Wales

Simon Cottrell (1,2), Hannah Evans (1,2), Catherine Moore (3), Jorg Hoffmann (4), Sara Hayes (5), Clare Elliott (6), Claire Midgley (7), Daniel Thomas (1), Rachel Jones (3), Marion Lyons (4), Richard Roberts (2), Christopher Williams (1)

1. Communicable Diseases Surveillance Centre, Public Health Wales, Temple of Peace and Health, Cardiff, UK
2. Vaccine Preventable Disease Programme, Public Health Wales, Temple of Peace and Health, Cardiff, UK
3. Microbiology Services Cardiff, Public Health Wales, University Hospital of Wales, Cardiff, UK
4. Health Protection Team, Public Health Wales, Swansea/Cardiff, UK
5. Abertawe Bro Morgannwg University Health Board, 1 Talbot Gateway, Port Talbot, UK
6. Informatics, Public Health Wales, Temple of Peace and Health, Cardiff, UK
7. CDC Epidemic Intelligence Service, 1600 Clifton Road, NE Mailstop E-92, Atlanta, USA

Background
From 2012-2013, Wales (population 3.1 million) saw its largest outbreak in 18 years; affecting a large but defined area and not confined to any religious, ethnic or societal group. We used multi-source reconciled data to describe the outbreak and actions taken.

Methods
Clinically suspected cases were notified through the statutory system. Confirmed cases were notified cases with a measles PCR or oral fluid test result consistent with recent measles. Immunisation data were ascertained through local child health information systems or primary care surveillance. We calculated vaccine effectiveness using the screening method.

Results
The outbreak lasted from 26/10/2012 to 02/07/2013, peaking on 16/04/2013, centering on three Mid/West Wales health boards. There were 1,211 notified cases (median age 10 years) and 447 confirmed. Confirmed cases were older than unconfirmed notifications (median 13 vs 5 years, Kruskal-Wallis p<0.001). Numbers of confirmed cases were similarly distributed across socio-economic deprivation quintiles. The highest proportion of suspected cases not providing test samples (31%) were from the most deprived quintile. Prior vaccination with two MMR doses was 99.0% effective. There were 64 admissions (53 per 1000 cases) and one death (case fatality ratio 0.0008). Children 10-18y had the highest age-specific attack rate (0.3%) and lowest pre-outbreak MMR coverage (9.9% unvaccinated) . A national catch-up programme and media campaign were implemented. Vaccines (77,805) were delivered through schools, general practice and ad-hoc community clinics.

Conclusion
The outbreak was a foreseeable consequence of low historic levels of MMR vaccination uptake in the area, temporally associated with local press coverage of alleged MMR side-effects in 1998-2001. The successful catch-up campaign in response to the outbreak reduced the potential for future outbreaks of measles, likely helped by extensive media coverage.

Keywords: measles, MMR, Wales, vaccination, uptake

PRESENTED BY: Simon Cottrell (simon.cottrell@wales.nhs.uk)

REFERENCE NUMBER: 3143

Multiregional secondary measles transmission linked to a Slovenian international dog show, Italy 2014-2015

Flavia Riccardo (1,2), Del Manso Martina (2), Antonietta Filia (2), Antonino Bella (2), Pierlanfranco D'agaro (3), Fabio Magurano (2), Silvia Declich (2)

1. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden
2. Istituto Superiore di Sanità, Rome, Italy 3. Department of Medical, Surgical and Health Sciences, University of Trieste, Trieste, Italy

Background

On December 2nd 2014, Slovenian authorities reported 17 confirmed measles cases linked to an international dog show with 366 registered participants from Italy, 304 from 26 other European countries, and an unknown number of unregistered participants. We investigated to identify measles cases among Italian participants and potential further transmission.

Methods

We defined a case as any person with fever and rash and cough, coryza, or conjunctivitis in Italy since 1 November 2014 linked with the dog show. Italian regional health authorities interviewed registered participants, using a standardized questionnaire on symptoms/diagnosis, vaccination history and contact details of accompanying non-registered participants, who were also interviewed. We retrieved additional information on cases from the national surveillance system including laboratory results (IgM/PCR/genotyping) and investigated transmission chains.

Results

Overall, 304/538 (57%) dog-show participants from 14 regions were interviewed. Of 245 who self-reported measles vaccination status, 56 (23%) were vaccinated. Among unvaccinated participants, 144/169 (85%) reported prior disease. Eighteen cases (median age 31 years; range 5-52, 89% female) were identified in four regions. Seventeen cases were laboratory confirmed. Fifteen of those were unvaccinated and two had received one dose. Eleven cases were primary, three secondary and four tertiary. One primary case, a high-school teacher, transmitted the virus to one of her students who then infected two siblings and two classmates, all unvaccinated. Genotype D8 viruses isolated from three primary cases were identical to those isolated in Slovenia.

Conclusion

Epidemiological and laboratory evidence suggested spread of measles in four regions in Italy linked to the international dog show in Slovenia. Health authorities should raise awareness of the risk of measles outbreaks among participants of large public gatherings and promote vaccination.

Keywords: Measles/epidemiology, Measles/transmission, Crowding, Travel

PRESENTED BY: Flavia Riccardo (flavia.riccardo@iss.it)

REFERENCE NUMBER: 3046

Large measles outbreak in Berlin 2014/2015 - Many cases not opposed to vaccination, yet unvaccinated

Alexandra Hoffmann (1,2,3), Daniel Sagebiel (1), Kathrin Hentschel (1), Dirk Werber (1)

1. State Office for Health and Social Affairs, Berlin, Germany
2. Postgraduate Training for Applied Epidemiology (PAE), Robert Koch-Institut, Berlin, Germany
3. European Programme for Intervention Epidemiology Training (EPIET), ECDC, Sweden

Background

Measles is a notifiable vaccine-preventable disease in Germany. Two vaccinations are recommended at the ages 11-14 months and 15-23 months. The largest measles outbreak in Berlin since 2001 started in October 2014 and is ongoing. We aimed to understand reasons for non-vaccination in German-born measles cases eligible for vaccination to inform intervention strategies.

Methods

We provided Local Health Authorities (LHA) with spreadsheets to assess the main reason for non-vaccination among measles cases, pre-defining the categories "critical attitude towards vaccination", "not opposed to vaccination", "vaccination discouraged by physician", "unknown". We allowed for the collection of additional qualitative information. Cases were unvaccinated persons (1 to 45 years) of German nationality notified to Berlin LHA's with measles since October 2014. Excluded from the analysis were cases from Berlin districts where response was ≤75%.

Results

In 10/12 Berlin districts 433 cases were ascertained until 31/07/2015, 57% (n=246) were adults. Incidence was highest among children aged 1 year (766/100,000). Main reason for non-vaccination: 169 (39%) reported not to be opposed to vaccination, 115 (27%) a critical attitude towards vaccinations, 8 (2%) were discouraged by physicians. For 141 (33%) the reason was unknown. Reasons for non-vaccination were age-dependent. Most parents of one year olds (63%, 15/24) as well as adults (50%, 123/246) but less than 25% in 2-17 year-olds was not opposed to vaccination. "Vaccination postponed", "lack of knowledge" and "forgotten to get vaccinated" were reasons mentioned by those not opposed to vaccination.

Conclusion

Many German measles cases in Berlin were not opposed to vaccination indicating their accessibility for interventions, eg recall systems or catch-up campaigns for adults. Pediatricians need to vaccinate as early as recommended.

Keywords: Measles, Disease Outbreak, Berlin, Germany, Vaccinations

PRESENTED BY: Alexandra Hoffmann (alexandra.hoffmann@lageso.berlin.de)

REFERENCE NUMBER: 3082

Estimation of the incidence of pertussis requiring hospitalization in infants using capture-recapture methodology, Germany, 2013-2014.

Anika Schielke (1,2,3), Anja Takla (1), Rüdiger von Kries (4), Ole Wichmann (1), Wiebke Hellenbrand (1)

1. Robert Koch Institute (RKI), Berlin, Germany
2. Postgraduate Training for Applied Epidemiology (PAE, German Field Epidemiology Training Programme), Robert Koch Institute, Berlin, Germany
3. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
4. Ludwig-Maximilians-University of Munich, Munich, Germany

Background

Pertussis became notifiable in Eastern German federal states in 2002 and nationwide in March 2013. Infants are at greatest risk for severe disease, the majority requiring hospitalization. We performed active pertussis surveillance in a pediatric sentinel hospital network 2013-2014 to quantify the degree of under-reporting in the statutory notification system and to obtain a better incidence estimate of pertussis requiring hospitalization among infants in Germany.

Methods

We applied the capture-recapture methodology to cases defined as children aged r hospitalized because of laboratory-confirmed pertussis with disease onset from 01/07/2013-31/12/2014 from two sources: (1) participating sentinel hospitals (n=387) and (2) the national notification system. Information on age, sex, disease onset and vaccination status were available from both. Local health departments were asked to validate the hospitalization status of notified cases. Cases from both sources were finally matched by month/year of birth, sex, reporting district and disease onset.

Results

For 2013, we estimated an incidence of 57 hospitalized pertussis cases per 100,000 infants (95% confidence interval [CI] 46-67/100,000), revealing under-reporting to the national notification system of 50%. In 2014, estimated incidence increased to 70/100,000 (95% CI 60-79/100,000); under-reporting decreased slightly (46%). Validation of the hospitalization status decreased under-reporting by 6% in 2013 and 1% in 2014. Under-reporting was lower in Eastern than Western federal states (24% vs. 50%).

Conclusion

Our study revealed marked under-reporting of severe pertussis in infants in Germany, especially in Western federal states where notification was newly established. The high estimated burden of severe pertussis in infants underlines the need to reevaluate and potentially adapt the current preventive strategy in Germany - immunization of infants and their close contacts, the so-called cocoon strategy.

Keywords: Pertussis, infants, hospitalization, capture-recapture

PRESENTED BY: Anika Schielke (schielkea@rki.de)

REFERENCE NUMBER: 3097

Parallel Session 17: Outbreaks III

MODERATOR: Chris Williams (EPIET supervisor, UK)

Outbreak of Multiple Salmonella Serotype Infections Linked to Sprouted Chia Seed Powder -Canada, 2014

Meghan Hamel (1), Jennifer Cutler (1), Leah Isaac (2,3), Kashmeera Meghnath (1), Joanne Tataryn (1), Investigative Team (3)

1. Public Health Agency of Canada, Guelph, Ontario, Canada
2. Canadian Food Inspection Agency, Ottawa, Ontario, Canada
3. Public Health Agency of Canada; Health Canada; Canadian Food Inspection Agency; British Columbia Centre for Disease Control; British Columbia Public Health Microbiology and Reference Laboratory; Alberta Health; Alberta Health Services; Provincial Laboratory for Public Health in Alberta; Public Health Ontario; Public Health Ontario Laboratory; Ontario Ministry of Health

Background

In the spring of 2014, increases in cases of Salmonella Hartford and Saintpaul were observed in Canada, however investigators were unable to hypothesize a source. In May 2014, the Public Health Agency of Canada was notified of a Salmonella Newport outbreak in the United States linked to sprouted chia powder. A link was made between this outbreak and the previously observed Canadian Salmonella increases, and an investigation was initiated.

Methods

Cases were defined as a resident or visitor to Canada with one of the Salmonella outbreak strains. Cases were interviewed using a questionnaire specific to chia products. Frequency of chia consumption reported by cases was compared to a baseline frequency derived from a population-based telephone survey in Canada. The Canadian Food Inspection Agency(CFIA) conducted a food safety investigation at the processor.

Results

A total of 63 confirmed cases of Salmonella were identified in 4 provinces, with symptom onset ranging from December 4, 2013 to June 22, 2014. Four Salmonella serovars (Newport, Hartford, Oranienburg, Saintpaul) and 12 PFGE patterns were associated with human illness in this investigation. Seventy-three percent of cases with available exposure information reported consuming sprouted chia seed powder. Ten unique Salmonella serovars were observed across 30 positive product samples. The investigation at the processing facility revealed that several steps during chia powder production were conducive to pathogen growth and that the process lacked any treatment that would be lethal to Salmonella.

Conclusion

This is the first time sprouted chia seed powder has been implicated in a foodborne outbreak. CFIA is reviewing industry practices through establishment inspections as well as implementing various sampling programs for sprouted and dried products in order to inform a risk mitigation strategy.

Keywords: Outbreak, chia, Salmonella, Canada, sprout

PRESENTED BY: Melissa Phypers (melissa.phypers@phac-aspc.gc.ca)

REFERENCE NUMBER: 3184

Pneumonic plague outbreak following case migration from the endemic highlands – municipality of Ambaohoabe, Madagascar, December 2013

Lala Harisoa Rabetaliana (1,2), Charles Ramarokoto (3), M. Ratsimba (4), A. Randriamanantena (3), A.R. Babity (5), S. Rabesahala (2), V. Maheriniaina (2), Patrice Piola (3), Ariane Halm (6), Christophe Rogier (7), Mino Rajerison (4)

1. Indian Ocean Field Epidemiology Training Programme, Indian Ocean Commission, Mauritius
2. Epidemiological Surveillance Department, Ministry of Health, Madagascar
3. Epidemiology Unit, Pasteur Institute, Madagascar
4. Plague Unit, Pasteur Institute, Madagascar
5. District health Office, Ministry of Health, Madagascar
6. Health Surveillance Unit, Indian Ocean Commission, Madagascar
7. Pasteur Institute, Madagascar

Background

Around 40% of documented plague cases worldwide occur in Madagascar with seasonal epidemics in the central highlands. Local media reported several plague-related deaths in a normally plague-free area. We conducted an investigation aiming to confirm and describe the outbreak and to identify its origin.

Methods

We performed active case finding with a suspected case defined as a person with sudden fever and cough with hemoptysis and/or chest pain and/or breathing difficulty from 18 November 2013 in Ambodirafia. Probable cases had a positive rapid diagnostic (RDT) or serology test and confirmed cases had positive culture of Yersinia pestis. Demographic and clinical data were collected using a questionnaire. Sputum and blood samples were collected for RDT, serology and bacterial culture testing.

Results

We identified 16 cases of pneumonic plague of which 12 suspected and four probable. The overall attack rate was 10.2 per 1000 and case fatality 56.2% (9/16). The sex ratio (male/female) was 0.7, median age 35 years (range: 10-60 years). All seven surviving patients had fever, chest pain and hemoptysis and received antibiotic treatment. One out of seven sputa (14.3%) was RDT positive and 57.1% (4/7) of serum samples were positive; no Yersinia pestis was isolated. The local index case was infected by a case from a neighbouring plague-stricken region. Several secondary cases among family and contacts resulted from the patients' quest for adequate treatment.

Conclusion

This highly contagious and lethal pneumonic plague outbreak occurred in a remote rural area in the non-endemic lowlands. Prior treatment of patients with antibiotics might have impeded culture, not allowing us to confirm the pathogen. Community health workers should be sensitised to plague symptoms, trained to perform surveillance and treat suspected cases.

Keywords: Madagascar, outbreak, pneumonic plague, secondary case

PRESENTED BY: Lala Rabetaliana (lalarabet@gmail.com)

REFERENCE NUMBER: 3147

An outbreak of the newly recognised Shigella boydii serotype 20 amongst UK military personnel involved in the Ebola response, Sierra Leone, December 2014 and January 2015

Daniel Todkill (1,2), Rohini Manuel (3), Claire Jenkins (4), Catherine Ryan (3), Richard Puleston (2), Jeremy Hawker (2)

1. Field Epidemiology Training Programme Fellow, Public Health England, UK
2. Field Epidemiology Service, Public Health England, UK
3. Public Health Laboratory London, Public Health England, UK
4. Gastrointestinal Bacteria Reference Unit, Public Health England, UK

Background

In January 2015, Public Health England (PHE) and the UK Ministry of Defence were alerted to cases of diarrhoea and fever in military personnel who were present in Benguema transit camp, Sierra Leone or had recently returned to the UK via Benguema.

Methods

An outbreak control team was convened; hypothesis-generating questionnaires conducted in symptomatic individuals and faecal samples taken for polymerase chain reaction (PCR) and culture. This pointed to food consumed in Benguema between 30 December 2014 and 1 January 2015 as the probable source. A case-control study was undertaken; possible cases had three or more loose stools in 24 hours or any two from; one or more episodes of loose stools, fever, abdominal pain/cramps, nausea/vomiting or blood in stools. Probable cases had a PCR-positive faecal sample for ipaH gene and confirmed cases were culture positive for Shigella boydii serotype 20. Controls were sampled randomly from personnel who returned to the UK on the same flight as cases and personnel remaining at the camp who were present during the period of putative exposure. Univariate, stratified and multivariable logistic regression was used to calculate crude and adjusted odds ratios and 95% confidence intervals.

Results

Seven cases were confirmed, three probable and two possible. Ten confirmed or probable cases and 43 controls were included in the case-control study. Multivariable analysis demonstrated the Coronation Chicken lunch on 1 January (aOR: 28.15, 95% CI: 1.87-423) was significantly associated with disease, and could account for the 6 earliest cases, suggesting this was the most likely source of infection for them.

Conclusion

This is the first reported epidemiological investigation of an outbreak of the newly recognised pathogen Shigella boydii serotype 20.

Keywords: Shigella, Shigella boydii, Disease outbreaks, Food-borne Diseases

PRESENTED BY: Daniel Todkill (dan.todkill@phe.gov.uk)

REFERENCE NUMBER: 3152

Cholera outbreak from contamination of surface well; the importance of hand washing - Bwari, Abuja, Nigeria, 2014

Abimbola Aman-Oloniyo (1), Zaiki Balogun (1), Abiodun Egwuenu-Oladejo1 (1), Godwin Okezue (1), Samuel Sha'aibu (1), Lydia Taiwo (1), Benson Udu (2), Patrick Nguku (1), Gabriele Poggensse (1)

1. Nigeria Field Epidemiology and Laboratory Training Program
2. Mpape Primary Healthcare Center, Bwari

Background

Cholera outbreaks cause high morbidity and mortality without effective interventions. In 2014, 35,974 suspected cholera cases (305 laboratory-confirmed) and753 deaths (CFR 2.1%) were reported in Nigeria. In April, 2014 we investigated a cholera outbreak in sub-urban slum in Abuja, Nigeria, to identify the risk factors for infection.

Methods

We conducted a 1:3 unmatched case-control study. A case was defined as any person aged 2 years and above (community or hospital-based) who had acute watery diarrhea with(out) vomiting in Bwari between 17th March and 10th April, 2014; a control was any resident of Bwari 2years and above without these symptoms during same period. We recruited 37 cases, 119 controls and used structured questionnaire to collect data on risk factors; odds ratios (OR) were calculated using Epi-Info 3.5.4. We analyzed 10 stool samples and samples from7 water sources using rapid diagnostic tests kits and thiosulfate-citrate-bile-sucrose agar respectively.

Results

Females constituted 54.3% cases and 61.3% controls. The mean age of cases and controls were 17.6 years and 28.1 years respectively ($p<0.05$). Cases were less likely to have washed hands with soap after toilet use (OR = 0.014, 95% confidence interval (CI): 0.16 – 0.77) and more likely to have eaten cold fried fish (OR=3.372, 95% CI: 1.20 – 9.51). Four (40%) stool specimens and 2 samples collected from open-well within homes in the community tested positive for Vibrio cholerae.

Conclusion

Contaminated surface-wells and poor personal hygiene (indicated by protectiveness of hand washing) likely propagated the outbreak. As immediate public health action surface-wells were sealed off and treated by the local environmental health unit. Intensive health education emphasizing importance of water purification and hand washing with soap and water were conducted.

Keywords: Cholera, Infection control, Personal hygiene, Nigeria

PRESENTED BY: Abimbola Aman-Oloniyo (bimboaman@gmail.com)

REFERENCE NUMBER: 2867

Outbreak Investigation Of Anthrax, Kuruchdega Village In Simdega District Of Jharkhand, India 2014

Priyakanta Nayak (1), Achelal R Pasi (1), Aakash Shrivastava (1), Shaikh S Hossain (2), Kayla Laserson (2), Samir V Sodha (2), Anil Kumar (1), Srinivas R Venkatesh (1)

1. National Centre for Disease Control
2. Centers for Disease Control and Prevention, India

Background

An outbreak of cutaneous anthrax was reported from a remote district of Jharkhand in India.We investigated the outbreak and evaluated potential risk factors to guide public health intervention

Methods

We conducted a detailed evaluation of the cases using medical record review and interviews.Venous blood specimens were obtained and evaluated using blood culture in RIMS microbiology laboratory, Ranchi. We ascertained additional cases and conducted a 1:2 case control study to assess risk factors

Results

Thirteen patients (all male; median age 30 years; range 18-58 years) including 5 deaths were reported; the attack rate was 11.1% and case fatality rate was 38%.In one/three blood cultures, Bacillus anthracis was confirmed.Among the 13 case-patients, 77% had cutaneous lesions in the upper extremities.All cases and controls (13/26) had consumed dead bull meat; 77% of cases (10/13) were involved in the slaughtering, chopping and handling the dead bull meat.Slaughtering, handling or chopping dead bull meat were actions significantly associated with having anthrax (Odds Ratio (OR) 74; 95 % confidence interval (CI): 19.5 – 845.9). Men were 35 times more likely than females to have anthrax (95 % CI: 3.9 – 312.2).People with an agricultural occupation were 25 times more likely to have anthrax as compared to those working as labourer (95 % CI: 2.8 – 200.6)

Conclusion

In this outbreak, anthrax was likely transmitted through unprotected contact with anthrax- affected animal hide and meat.We recommended screening of cattle, sheep and goats for any symptoms, and administration of 1 ml anthrax spore vaccine subcutaneously to each animal within 5 km radius.We educated the community regarding disposal of dead carcases, handling and slaughtering of infected animal and personal hygiene

Keywords: Anthrax, Jharkhand, India, RIMS

PRESENTED BY: Priyakanta Nayak (pikoo.2007@gmail.com)

REFERENCE NUMBER: 3081

Parallel Session 18: Epidemiology and Microbiology Driving Public Health Policy

MODERATOR: Aftab Jasir (ESCAIDE Scientific Committee & Head of EUPHEM, ECDC)

Different risk factors for infection with Giardia lamblia assemblages A and B in children attending day-care centres

Roan Pijnacker (1), Lapo Mughini-Gras (1), Moniek Heusinkveld (1), Jeroen Roelfsema (1), Titia Kortbeek (1), Wilfrid van Pelt (1)

1. Center for Infectious Disease Control, National Institute for Public Health and the Environment (RIVM), The Netherlands

Background

Giardia lamblia is a common human enteric parasite and can cause diarrhoea in children. Pre-school children attending day-care centres (DCCs) are twice as likely to be G. lamblia-positive compared to those home-cared. Different G. lamblia assemblages are found in various animals, but only assemblages A and B are detected in humans and are known to have zoonotic potential. We aim at determining risk factors for infection with assemblages A and B in DCC-attending children.

Methods

Monthly stool sampling of ≤4-year-old children attending a laboratory surveillance network of 44 DCCs in the Netherlands was performed during 2010-2013. Additionally, basic child- and extensive DCC-level epidemiological data were collected. 226 out of 5015 (4.5%) tested stool samples were positive for G. lamblia using RT-PCR. Assemblages could be determined for 138 G. lamblia-positive samples. Risk factors for infection with assemblages A or B as compared to G. lamblia-negative children were assessed using mixed-effects logistic regression models.

Results

In total, 62 (45%) samples were assemblage A and 76 (55%) were assemblage B. Risk factors for assemblage A were attending DCCs with sandpits, specifically during spring/summer (OR 3.5, 95%CI 1.1-11.0), and with >90 children (OR 10.9, 95%CI 1.4-87.7). For assemblage B, risk factors were attending DCCs with pets (OR 2.1, 95%CI 1.1-3.8) and with a room dedicated to diaper-changing (OR 3.0, 95%CI 1.5-6.0) and laundry (OR 2.4, 95%CI 1.2-4.5). Excluding sick children and having cloth-towels were protective for assemblage B (OR 0.2, 95%CI 0.1-0.4 and 0.05, 95%CI 0.0-0.4, respectively).

Conclusion

Risk factors for assemblages A and B were found to be different, with assemblage B being more related to DCC hygiene than assemblage A, indicating that their reservoirs and transmission routes might be different.

Keywords: Giardia, epidemiology, child day care centers, parasitology

PRESENTED BY: Roan Pijnacker (roan.pijnacker@rivm.nl)

REFERENCE NUMBER: 2966

Marked decrease in rotavirus detections among young children in the Netherlands in 2014

Roan Pijnacker (1), Lapo Mughini-Gras (1), Harry Vennema (1), Erwin Duizer (1), Wilfrid van Pelt (1)

1. Center for Infectious Disease Control, National Institute for Public Health and the Environment (RIVM), The Netherlands

Background

Rotavirus is the most common cause of diarrhoea in young children. An exceptionally low rotavirus incidence was reported in January-April 2014 in the Netherlands, a country where rotavirus vaccination is not enforced. The aim of this study was to use passive-surveillance-independent data to examine whether this decrease was caused by e.g. a relatively mild course of the disease resulting in less rotavirus-related hospitalizations and GP visits, or by an actual drop in rotavirus circulation in the child population.

Methods

Data from two comparable studies were used. The first study consisted of monthly faecal sampling of ≤4-year-old children attending a network of 44 Dutch day-care centres participating to laboratory surveillance of enteropathogens during 2010-2013. The second study was a monthly-repeated cross-sectional survey (2012-2014) of enteropathogens in 8768 Dutch households with preschool children. In both studies, children were sampled at random and regardless of symptoms, and faecal samples were analysed for the presence of rotavirus using an internally controlled multiplex RT-PCR. Rotavirus detections in ≤4-year-old children in January-April 2014 were compared with those of the same period in previous years using logistic regression models, while adjusting for child's age, gender, and day-care attendance.

Results

In total, 195/6569 (3%) faecal samples were positive for rotavirus. The adjusted rotavirus detection rate during January-April 2014 (0.4%, 95%CI 0-1.3%) was significantly lower than 2010 (11.5%, 95%CI 8.0-15.1%), 2011 (7.1%, 95%CI 4.8-9.5%), 2012 (7.1%, 95%CI 4.9-9.4%), and 2013 (6.8%, 95%CI 3.9-9.7%).

Conclusion

The evidenced decrease in rotavirus detections in 2014 confirmed that the concurrent decrease in the reported rotavirus incidence was due to a genuine drop in rotavirus circulation in the child population rather than the result of a less severe course of the disease.

Keywords: epidemiology, rotavirus, gastroenteritis, netherlands, communicable diseases

PRESENTED BY: Roan Pijnacker (roan.pijnacker@rivm.nl)

REFERENCE NUMBER: 3091

Insight into the natural and treated history of hepatitis C virus (HCV); a cohort study of women infected with contaminated anti-D immunoglobulin in Ireland between 1977 and 1979

Patricia Garvey (1), Lelia Thornton (1), Niamh Murphy (1), Paula Flanagan (1)

1. Health Protection Surveillance Centre, 25-27 Middle Gardiner Street, Dublin 1, Ireland

Background

In the mid 1990s, a group of women were diagnosed with HCV genotype 1b infection following administration of contaminated anti-D immunoglobulin between 1977 and 1979. Our objectives were to describe their disease history and estimate the effect of selected host factors on disease progression to provide information for HCV treatment strategies.

Methods

We conducted a cohort study on women that developed chronic infection with HCV. A research nurse collected information from records at seven HCV treatment centres on demographics, health status, and known risk factors in 2005, 2007, 2008, 2009 and 2013. We calculated prevalence, case fatality, relative risks (RR) for treatment success, and hazard ratios (HR) for disease progression using Cox regression.

Results

374 participants were recruited to the study. 321 (86%) participants remained alive, 247 (77%) of whom were still chronically infected. At the end of 2013 the prevalence of cirrhosis and liver-related case fatality were 19% and 5%, respectively, compared with 10% and 2.4% at the end of 2008. 131/365 (35%) have completed antiviral treatment; 55/131 (42%) had a sustained virological response (SVR). SVR rates recorded after triple therapy were higher compared to ribavirin/pegylated interferon therapies (RR= 2.0; 95%CI 0.8-4.3) or earlier monotherapy (RR=3.2; 95%CI 1.8-5.8). Remaining chronically infected (HR=3.8; 95%CI 2.3–6.3) and high alcohol intake (HR=6.8; 95%CI 3.5–13) were independently associated with higher cirrhosis risk

Conclusion

Risk of cirrhosis and liver-related case fatality in this group were lower than those reported in some previous studies of HCV cohorts, however, disease progression is accelerating. With the advent of new HCV therapies with higher success rates, timely intervention could benefit a high proportion of this cohort.

Keywords: Hepatitis C, Cohort Study, Disease Progression, Cirrhosis.

PRESENTED BY: Patricia Garvey (patricia.garvey@hse.ie)

REFERENCE NUMBER: 3039

Internalized homonegativity and consequent sexual orientation concealment as a barrier for recent HIV-testing in Poland

Zuzana Klochanova (1,2), Magdalena Rosinska (1), Axel J. Schmidt (3), Lukasz Henszel (1)

1. National Institute of Public Health - National Institute of Hygiene, Warsaw, Poland
2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden
3. Department of Social & Environmental Health Research, London School of Hygiene and Tropical Medicine, London, United Kingdom

Background

In Poland, the rate of new HIV diagnoses among men-who-have-sex-with-men (MSM) increased 14-fold between 2000 and 2011. Testing levels remain insufficient despite previous education campaigns and increasing availability of voluntary counselling and testing sites operating in large cities. We aimed to identify possible barriers to recent HIV-testing among MSM in Poland, beyond knowledge and availability of services.

Methods

We reanalysed European MSM Internet Survey (EMIS) data collected in June-August 2010 of MSM residing Poland (N=2746). We restricted the analysis to non-transgender men predominantly attracted to men, aged 15-70. We further excluded men with missing data on HIV-testing history, or who had their HIV diagnosis prior to 12 months preceding the survey. We calculated adjusted prevalence ratios (aPR) and 95% confidence intervals (CI) using binominal regression to explain lack of recent (within the last 12 months) HIV-testing.

Results

From the sample of 2141 MSM, 912 (43%) were recent testers. Lack of recent testing was significantly associated with high-risk sexual behaviour (aPR=1.47;95%CI:1.37-1.58), concealment of same-sex sexual attraction (none has the knowledge vs. most: aPR=1.41; 95%CI:1.24-1.60), smaller settlement size (‹100,000 inhabitants vs. more; aPR=1.22; 95%CI:1.11-1.35), being in longer steady relationship (›12 months vs. shorter; aPR=1.18; 95%CI:1.02-1.36), and insufficient knowledge about HIV-testing (aPR=1.09; 95%CI:1.02-1.17).

Conclusion

Concealment of same-sex sexual attraction and residing smaller settlements were strong predictors of poor HIV-testing, suggesting that prevention efforts may be hampered by stigmatizing environment. Reducing society-level homophobia, and peer-based HIV-testing offers could help to reach areas with poorer testing access and to those MSM who might delay testing due to fear of disclosure of their sexual attraction. Association with high-risk sexual behaviour and insufficient testing-related knowledge suggest a need to focus on specific MSM sub-groups.

Keywords: MSM, HIV, testing, homophobia

PRESENTED BY: Zuzana Klochanova (zklochan@gmail.com)

REFERENCE NUMBER: 3181

Parallel Session Programme
Friday 13 November
13:30-14:50

Parallel Session 19: Vaccine Coverage, Effectiveness and Safety

MODERATOR: Niklas Danielsson (ECDC, Group leader Reponse)

Vaccination coverage of young people aged 16 to 18 estimated using the novel approach of the electronic immunisation record of MesVaccins.net, South West France, 2013.

Gaelle Gault (1), Aurelie Fischer (1), Annie Burbaud (2), Jean-Paul Guthmann (3), Flavie Burelle (4), Elisabeth Nicand (4), Patrick Rolland (1), Jean-Louis Koeck (5)

1. French Institute of Public Health Surveillance, Department of Coordination of Alerts and Regions Regional office in Aquitaine, Bordeaux, France
2. Regional Health Agency of Aquitaine
3. French Institute of Public Health Surveillance, Unit of vaccine preventable diseases, Saint-Maurice, France
4. Study Group in Preventology, Villenave d'ornon, France
5. French Army Hospital, Robert Picqu

Background

Vaccination coverage (VC) of young people is not routinely recorded in France and the scarce available data shows insufficient VC. We used the new electronic immunisation record (EIR) of MesVaccins.net, developed for individual follow-up, to estimate VC among young people.

Methods

We considered the 16-18 years old who participated to the mandatory national citizenship day (NCD) in South West France from April to October 2013. People invited to the NCDs received a letter that explains how to create an EIR. Created EIRs were validated by health practitioners by checking EIR data against the vaccination booklet. VC was estimated for 8 routine vaccinations.

Results

Among the 18,714 participants, 9,636 (51%) accepted to create an EIR of which 2,781 (29%) had an EIR validated. VC was above 90% for 3 vaccinations (diphtheria/tetanus/poliomyelitis, tuberculosis, measles/mumps/rubella) and between 80% and 90% for pertussis and Haemophilus influenzae type b vaccinations. VC was low for meningococcal meningitis C (37%), hepatitis B (54%) and human papilloma virus infections (47%).

Conclusion

VCs estimated through EIR were close to those estimated from other available sources, although sometimes higher than expected, reflecting a probable selection bias. These results provided relevant VC estimates to health authorities useful for vaccination prevention programs. Further evaluations of this novel and reactive tool for VC surveillance are ongoing.

Keywords: vaccination coverage, young people, electronic immunisation record

PRESENTED BY: Aurelie Fischer (aurelie.fischer@ars.sante.fr)

REFERENCE NUMBER: 3131

No increased incidence of new-onset autoimmune disease in vulnerable girls and women after quadrivalent human papillomavirus vaccination

Olof Grönlund (1), Eva Herweijer (1), Karin Sundström (2), Lisen Arnheim Dahlström (1)

1. Dept. of Medical Epidemiology and Biostatistics, Karolinska Institutet, Stockholm, Sweden
2. Dept of Laboratory Medicine, Karolinska University Hospital Huddinge, Stockholm, Sweden

Background

We aimed to assess if quadrivalent human papillomavirus (qHPV) vaccination is associated with an increased incidence of new-onset autoimmune disease in girls and women previously diagnosed with at least one autoimmune disease.

Methods

A nationwide register-based cohort study in Sweden including all girls and women ages 10-30 and diagnosed with at least one of 49 pre-specified autoimmune diseases. Study period was 2006-2012. Main outcome measures were incident new-onset autoimmune disease within 180 days of each dose of qHPV vaccination. Incidence rate ratios (IRR) were estimated using Poisson regression adjusting for demographic factors and socioeconomic status.

Results

In total, 70 265 girls and women had at least one of the 49 predefined autoimmune diseases. Of those, 16% received at least one dose qHPV vaccine. In unvaccinated, 5428 new-onset autoimmune diseases occurred during 245 807 person-years of follow-up at a rate of 22.1 (95% CI = 21.5 to 22.7) new events per 1000 person-years. In girls and women vaccinated with at least one dose of qHPV, 124 new events occurred during 7848 person years of follow-up at a rate of 15.8 (95% CI = 13.2 to 18.8) new events per 1000 person-years. There was no increase in the incidence of new-onset autoimmune disease associated with qHPV vaccination during the risk period, on the contrary; a slightly lower IRR was observed (0.77, 95% CI = 0.65 to 0.93).

Conclusion

In this first nationwide study investigating qHPV vaccine safety in this vulnerable population, qHPV vaccination was not associated with an increased incidence of new-onset autoimmune disease. Therefore, the risk-benefit ratio of vaccination in these individuals may be more favourable than currently known.

Keywords: Papillomavirus Vaccines, Safety, Autoimmune Diseases, Cohort Studies

PRESENTED BY: Lisen Arnheim Dahlström (lisen.arnheim.dahlstrom@ki.se)

REFERENCE NUMBER: 2934

Factors associated with delayed vaccination leading to measles outbreak, Chennai, India, 2013

Tony Fredrick (1), Yuvaraj Jayaraman (1), Manoj Murhekar (1), Manickam Ponnaiha (1), Joseph David (1), Kamaraj Pattabi (1)

1. National Institute Of Epidemiology,India

Background

Chennai, in India had been reporting measles cases and outbreaks since 2006, despite achieving 95% vaccination coverage. We surveyed one administrative area in Chennai to estimate the measles vaccine coverage and identify reasons for delayed vaccination

Methods

We required to recruit 370 mothers of children aged 12-23 months from 10 clusters (slums) with the assumptions of 85% coverage, 5 % absolute precision, 95% confidence interval (CI) and design effect two. We selected clusters through probability proportional to size and households by random start point. We interviewed the mothers to collect information on vaccination status, socio-demographic, economic status and reasons for delayed vaccination. We estimated the coverage with 95% CI. We computed adjusted odds ratios (AOR) and 95% CI for factors independently associated with delayed vaccination using multiple-logistic regression analysis.

Results

Among the study participants 70% belonged to low socio-economic group and 51% children were males. Overall 92% (95% CI = 88–94) had their first dose measles vaccination. Nearly 44% (95% CI = 39.2–49.7) amongst immunized had delayed measles vaccination with a median delay time of ›35 days. Only 27% (95% CI = 23–33) received second dose measles vaccination. Factors independently associated with delayed vaccination were mothers age ‹ 25 years (AOR=2.1; 95% CI: 1.4-3.4), working mother (AOR=1.3, 95% CI: 1.1-2.6), migrant status (AOR=1.7; 95% CI: 1.7-2.6), immunization post › 5 km (AOR=2.2; 95% CI: 1.2-4.2) and delayed vaccine spacing (AOR=3.5; 95% CI: 1.7 -6.6).

Conclusion

Delayed vaccination was the cause of under immunization leading to outbreaks. We recommend perinatal counselling for mothers regarding timely vaccination compliance, targeted outreach immunization sessions for children of working and migrant mothers and re-orientating health workers on reducing vaccine spacing.

Keywords: Measles Vaccination, Delayed vaccination, Risk factors

PRESENTED BY: Tony Fredrick (tony_fredrick@yahoo.com)

REFERENCE NUMBER: 3056

Convincing German parents to get vaccinated during school entry health examinations, 2014/2015

Jakob Schumacher (1,2,3), Daniel Sagebiel (4), Susann Sroka-Rodrigues (5), Juan Carlos Ramirez-Henao (6), Anette Siedler (1)

1. Robert Koch Institute, Department for infectious diseases epidemiology, Seestra
2. Postgraduate Training for Applied Epidemiology (PAE, German FETP)
3. European Programme for Intervention Epidemiology Training (EPIET)
4. Federal state public health agency Berlin (Landesamtes f
5. Local public health agency Charlottenburg-Wilmersdorf (Bezirksamt Charlottenburg-Wilmersdorf), Otto-Suhr-Allee 100 10585 Berlin
6. Local public health agency Marzahn-Hellersdorf (Bezirksamt Marzahn-Hellersdorf), Alice-Salomon-Platz 3, 12627 Berlin

Background

Parents can transmit vaccine-preventable diseases to unprotected children. In Germany parents belong to age groups with high proportions of immunisation gaps. Our objective was to measure the efficiency of a pilot information campaign on parental vaccination, targeting parents that accompany their children to school entry health examinations in two districts in Berlin.

Methods

From 25/05/2014 – 31/07/14, in district A and from 15/11/2015–31/04/2015 in district B, physicians informed the targeted parents about the importance of parental vaccination, handed out a pre-paid envelope and a self-administered questionnaire. Parents checked their diphtheria, tetanus, pertussis and measles vaccination status using their vaccination records and reported whether they planned to get vaccinated in case they found missing vaccinations. Physicians estimated the time spent for informing parents. We calculated proportions and 95% confidence intervals (95%CI).

Results

Overall, 162 of 1306 (12%) parents replied. Out of 162 parents 103 (64%; 95%CI 56%-71%) were fully vaccinated, 133 (82%) had a complete vaccination for tetanus, 131 (81%) for diphtheria, 115 (71%) for pertussis and 125 (77%) for measles. Thirty-four of the 59 (58%; 95%CI 45%-70%) not fully vaccinated parents reported that they planned to get vaccinated. The time spent for informing parents reported by physicians was 3 minutes per parent.

Conclusion

With this efficient approach we could increase awareness for vaccinations among an important target group, making at least one-tenth test their vaccination status and half of those reporting a missing vaccination to consider getting vaccinated. We suggest extending this approach to preventive medical examinations for children. Targeting only parents who know that their vaccination status is unclear or incomplete could increase efficiency.

Keywords: Vaccines, Parents, Health promotion, primary prevention

PRESENTED BY: Jakob Schumacher (jakob.schumacher@web.de)

REFERENCE NUMBER: 3043

Parallel Session 20: Ebola Virus Outbreaks

MODERATOR: Tarik Derrough (ECDC, Expert VPD, Ebola Response operations)

Investigation of a cluster of three Ebola Virus Disease (EVD) cases among health care workers (HCW), N'Zerekore, Guinea, 2014

Coralie Giese (1,2), Hawa Bah (3), Lila Lucie Conde (4), Seny Mame Loua (4), Emmanuel Ronan Malano (5), William Perea (3), Boubacar Diallo (3), Kone Moussa (3), Thomas Mollet (6), Denis Coulombier (6)

1. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden
2. Health Protection Surveillance Centre, Dublin, Ireland
3. World Health Organization, Conakry, Guinea
4. Department of Health, N'zérékoré prefecture, Guinea
5. EVD response coordinator, N'zérékoré prefecture, Guinea
6. European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden

Background
Between August and December 2014, 7.6% of confirmed / probable EVD cases reported in N'zérékoré prefecture, Guinea were among HCWs; between 30/11/2014 and 5/12/2014, a cluster of three EVD cases were reported among Guinean HCWs, curtailing EVD response. We investigated their exposures to prevent further infections.

Methods
We collected information using notification forms, contact lists, the Red Cross (RC) activity calendar. We interviewed the RC team leader, hospital staff, the surviving case and treating physicians. We reviewed cases' activities and health status to identify the most likely exposure and the time when it could have occurred.

Results
The cluster included one ambulance driver who survived (case 1) and two RC volunteers involved in burials and transport of suspect patients who died (case 2 and 3). Case 1 and 2 breached infection prevention control (IPC) during an incident in the ambulance while transporting suspect cases on 17/11/2014. Case 2 worked while symptomatic and most likely infected case 3 when working together on 24 and 25/11/2014. RC did not monitor health of RC volunteers on a daily basis. Fear of stigmatisation may have hindered self-isolation. Community transmission, poor data quality, recall bias and prevarication complicated the investigation.

Conclusion
Breaks in ICPs, including during transport, and lack of monitoring may have exposed HCWs to EVD. To ensure continuity in response, we recommended incident management protocols for ambulance crews, training on risks of secondary EVD transmission, daily monitoring of HCW health status and addressing stigmatisation among HCWs. Stronger ongoing documentation of exposures could help with future investigations of HCWs infections.

Keywords: Ebola Virus Disease, Health Care Workers, outbreak, stigmatisation

PRESENTED BY: Coralie Giese (coraliegiese@hotmail.com)

REFERENCE NUMBER: 3126

Ebola virus disease outbreak in Nigeria; the response, gaps and lessons learned - October. 2014.

Abimbola Aman-Oloniyo (1), Saheed Gidado (1)

1. Nigeria Field Epidemiology and Laboratory Training Program

Background
Nigeria reported the first confirmed Ebola Virus Disease (EVD) on 20th July 2014, had 20 cases, 8 deaths (CFR 40%) and was declared Ebola-free on 20th October 2014. We reviewed the response, gaps and lessons learnt from EVD control in Nigeria.

Methods
We conducted a desk review of the EVD response between July and September, 2014 to identify gaps and proffer solutions for future outbreaks.

Results
The index case, an acutely ill traveler from Liberia, arrived Lagos July 20, 2014 with fever, vomiting, and diarrhea; was presumptuously treated by Healthcare Workers (HCWs) without adequate safety precautions. He was later confirmed EVD-positive and died July 25. Nineteen others were infected (18 confirmed and 1 probable) in Lagos and Rivers States. HCWs accounted for 12 (60%) of the cases (5 deaths (CFR:41.6%)); nosocomial and secondary infections occurred. Response was coordinated by EVD Emergency Operations Centre (EEOC) with 892 contacts traced for 21-days. Inadequate isolation facilities and dearth of HCWs at outset of outbreak. Mis-information resulted in mass drinking of and bathing with salt water by many Nigerians.

Conclusion
A gap in hospital infection control aided the spread of EVD; restricted movement of primary contacts may have stemmed the spread. The need for emergency preparedness and adequate management of information is emphasized. Improved routine hospital infection control practices are recommended.

Keywords: Ebola Virus Disease, health care workers, infection control, Nigeria.

PRESENTED BY: Abimbola Aman-Oloniyo (bimboaman@gmail.com)

REFERENCE NUMBER: 3180

Understanding the culture to stop Ebola: social and cultural factors behind community resistance and a super spreading event in the village of Fogna, Guinean Forest Region, February 2015.

Antonio Isidro Carrión Martín (1,2,3), Tarik Derrough (3,4), Patrice Honomou (5), Nestor Kolie (5), Boubacar Diallo (5), Kone Moussa (5), Guenael Rodier (5), Cécé Kpoghomou (6), Josep Jansa (3,4)

1. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden
2. Public Health England (PHE), London, United Kingdom
3. Global Outbreak Alert and Response Network (GOARN), World Health Organization (WHO), Conakry, Guinea.
4. European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden
5. World Health Organization, Conakry, Guinea
6. Ministry of Health of Guinea, Conakry, Guinea

Background

During the Ebola Virus Disease (EVD) epidemic in Guinea in 2014-2015, community resistance obstructed case investigation and response. We investigated a cluster of EVD in Fogna, Lola Préfecture, Guinean Forest Region in February 2015 to identify socio-cultural determinants related to community resistance and prevent further transmission.

Methods

We investigated the occurrence of events using observant participation, interviewed five key informants and conducted two focus groups discussions.

Results

Between 31/01/2015 and 02/02/2015, 21 EVD cases, (16 females (76%); age range: 16-70 years (median 37)) were reported in Fogna; sixteen were admitted, seventeen died, four of whom in the community (case-fatality : 81%); 148 contacts were identified. The index case was an elderly female, community and religious leader, who died of EVD on 19/01/2015. During her animist funeral ceremony, only women washed and prepared the body. The village-residents were initially resistant to interventions of the response team. Interviews and focus group discussions indicated that most of the symptomatic residents fled to the forest, fearing the Ebola Treatment Centre (ETC). There was the belief that people were killed in ETCs for organ trade. On 14/02/2015, four secondary cases who survived were accompanied back to the village to share their experience, educate and reassure the village-residents. Subsequently, two new cases were successfully identified among listed contacts on the day of their symptom onset.

Conclusion

Engaging EVD survivors from the same community improved community compliance leading to timely detection of cases and a more effective response. In resistant communities, understanding the socio-cultural context and community perceptions may improve community engagement and prevent Ebola Virus transmission.

Keywords: Ebola Virus Disease, Culture, Outbreak, Community

PRESENTED BY: Antonio Isidro Carrión Martín (isidro.carrion@phe.gov.uk)

REFERENCE NUMBER: 3013

Lessons to be learned from the epidemiological response to the Ebola Outbreak in West Africa 2014/15

Maya Holding (1,2), Caroline Coope (1,2), Chikwe Ihekweazu (3), James Stuart (2), Isabel Oliver (4)

1. Field Epidemiology Service, Public Health England, UK
2. University of Bristol, UK
3. EpiAfric,
4. Public Health England, Field Epidemiology Services, Bristol

Background

The 2014/15 West African outbreak is the largest and most complex outbreak of Ebola to date. A large international response has needed to bring the epidemic under control. There is a need to learn lessons from the epidemiological response to this outbreak to strengthen the response to future outbreaks of international significance. We aimed to identify priorities for future epidemiology training and deployment to assist with response to outbreaks.

Methods

Data was collected through an online anonymous questionnaire, sent to epidemiologists who had been deployed to West Africa, using a snowball sampling method. The questionnaire included questions on demographics, training and qualifications, role whilst in West Africa and information surrounding deployment, followed by open questions relating to participants experience while deployed. Data collection took place over a four week period.

Results

These results include the first 110 responses. Epidemiologists responded from 24 countries across 5 continents. Epidemiological qualifications varied with 76(68%) having completed an FETP. This was the first time 73 (65%) participants had supported an epidemiological mission abroad. Information on lessons learned was available for 76 (68%) of participants. Common needs identified included better understanding of organisational roles and responsibilities (27, 36%), cultural context (20,26%) and logistical information (11,14%) prior to deployment. Training needs identified included a variety of technical skills in particular contact tracing (11,14%) mapping (6,8%) and, PPE/IPC training (12,16%). 42 (54%) respondents highlighted communication, interpersonal skills and cultural awareness as the one key skill that epidemiologists deployed in future should have.

Conclusion

There was clear consistency in the responses from across the world, highlighting the importance of learning from this study to inform future field epidemiology training and response

Keywords: Ebolavirus, Outbreaks, Epidemiology, Epidemics, Evaluation

PRESENTED BY: Isabel Oliver (isabel.oliver@phe.gov.uk)

REFERENCE NUMBER: 3208

Parallel Session 21: Modelling

MODERATOR: Bruno Ciancio (ECDC, Head of section for Epidemiological methods)

Estimating true incidence of O157 and non-O157 Shiga Toxin-Producing Escherichia coli illness in Germany – based on notification data of Haemolytic Uremic Syndrome

Anna Kuehne (1), Martijn Bouwknegt (2), Arie Hendrik Havelaar (2,3), Andreas Gilsdorf (1), Klaus Stark (1), Dirk Werber (1,4)

1. Department for Infectious Disease Epidemiology, Robert Koch Institute (RKI), Berlin, Germany
2. Centre for Infectious Disease Control, National Institute for Public Health and the Environment (RIVM), Bilthoven, The Netherlands
3. Emerging Pathogens Institute and Animal Sciences Department, University of Florida, Gainesville,USA 4. State Office for Health and Social Affairs, Berlin, Germany

Background

Incidence of Shiga toxin-producing Escherichia coli (STEC)-illness is underestimated in surveillance data, particularly from serogroups other than O157 ("non-O157") because of their complex and disproportionally underutilized diagnosis. We estimated true incidence of STEC-illness and STEC-associated haemolytic uremic syndrome (HUS) in Germany to inform diagnostic and surveillance strategies.

Methods

Using German national HUS notification data (2008-2012, excl. 2011) as starting point, we modelled incidence of STEC-illness separately for O157 and non-O157 STEC (expressed as median annual incidence per 100,000 population), taking into account the serogroups' varying likelihood of causing bloody diarrhoea and HUS and the resulting difference in underestimation. Medline and Scopus were searched for peer-reviewed studies entailing this specific information for Germany. Uncertainty of input parameters was evaluated by stochastic simulations using @RISK version 6.1.1 (Palisade Corporation, Ithaca, NY).

Results

Five identified publications, German notification data and laboratory guidelines built the backbone of the simulation model. Median annual STEC-associated HUS incidence was estimated at 0.11 (95% CI 0.08-0.20), the median STEC-associated gastroenteritis (STEC-GE) incidence at 34.6 (95% CI 12-145). German notification data thus underestimated STEC-associated HUS and STEC-GE incidences by factors of 1.8 and 32.3, respectively. Non-O157 STEC accounted for 78% of all STEC-GE, 51% of all bloody STEC-associated diarrhoea and 32% of all STEC-associated HUS cases. Estimates were most sensitive to the proportion of HUS among laboratory-confirmed non-O157 STEC cases.

Conclusion

Non-O157 serogroups dominate incidence of STEC-GE and contribute significantly to STEC-associated HUS in Germany. This might apply to many other European counties considering surveillance data on HUS. Non-O157 STEC should be considered in parallel to STEC O157 when searching aetiology in patients with GE or HUS, and accounted for in modern surveillance systems for human STEC-illness.

Keywords: Shiga-Toxigenic, Escherichia coli ,Hemolytic-Uremic Syndrome ,Germany, Incidence, Disease, Notification, Surveillance

PRESENTED BY: Anna Kuehne (KuehneAn@rki.de)

REFERENCE NUMBER: 3133

Forecasting the incidence of human Puumala virus cases in South West Germany

S Brockmann (1), M Schwehm (2), Christiane Wagner-Wiening (3), G Kaendler (4), M Eichner (5)

1. Regional Public Health Office, Reutlingen
2. ExploSys, Leinfelden-Echterdingen
3. Baden-Württemberg State Health Office, Stuttgart
4. Baden-Württemberg Forest Research Institute (FVA), Department of Biometry and Computer Science, Freiburg
5. Department of Clinical Epidemiology and Applied Biometry, University of Tübingen

Background

Puumala virus (PUUV) is an endemic zoonosis in Germany. Since 2001, the State of Baden-Württemberg has been reporting the highest number of PUUV cases with a fluctuation from 22 (2006) to 1,694 (2012) cases per year. Aiming for an early warning tool to optimize public health response, we developed a predictive model for human PUUV cases in Baden-Württemberg.

Methods

Data on PUUV cases (onset of disease, site of infection) were extracted from the mandatory system. We used generalized linear models with Poisson distributed residuals with climate factors, beech mast-data and data on forest coverage with different types of trees as independent factors to explain reported PUUV cases for the time period 2006–2012. Model selection was based on the goodness of fit to the observed number of cases.

Results

The selected prediction model contains beech mast, beech tree and other broadleaf tree coverage, sunshine duration during September, mean temperature of August and September, and county, to explain the number of cases per county in the following year. This model qualitatively predicted 252 of 290 (86%) of the data points, given by a combination of county and year. The selected parameters are available from October and allow predicting PUUV cases of the following year.

Conclusion

A predicted PUUV outbreak allows for early information of the public and for planning observational and interventional studies. Results of such studies are urgently needed to target public health recommendations and interventions.

Keywords: Hanatvirus, Epidemiology, Modelling

PRESENTED BY: S Brockmann (s.brockmann@kreis-reutlingen.de)

REFERENCE NUMBER: 3109

Modelling the burden of hepatitis C infection among injecting drug users in Norway in 2013

Hinta Meijerink (1,2), Richard White (1), Astrid Løvlie (1), Hilde Kløvstad (1)

1. Norwegian Institute for Public Health, Oslo, Norway
2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden

Background

Hepatitis C viral (HCV) infection is recognised as a public health concern, leading to cirrhosis, hepatocellular carcinoma (HCC) and death. Lack of HCV incidence data in Norwegian high-risk groups impedes the ability to make informed decisions on prevention measures. In the absence of these data, we rely on modelling to estimate the incidence and burden of HCV infections.

Methods

We formulated a compartmental model for HCV infections in Norway among active and former injecting drug users (IDU). We based yearly transition rates on literature, the Norwegian Surveillance System for Communicable Diseases (MSIS) for genotype distribution, the death registry (DÅR) for mortality rates, and Norwegian Institute for Alcohol and Drug Research (SIRUS) for entry and exit rates among IDU. The model was fitted to absolute numbers using data from 2000 to 2013 from SIRUS, national patient registry (NPR), Norwegian cancer registry (NCR), liver transplant data and DÅR. This model enabled us to estimate the number (95%CI) of HCV infections, cirrhosis, HCC and death due to HCV infections in Norway in 2013.

Results

Among 8516 active and 30658 former IDU, 67% of active (5707; 5395-6176) and 57% of the former (17433; 17408-17451) IDU were predicted to have chronic HCV infection. In 2013, the model estimated 757 (410-1125) acquired HCV infections 20 (6.9-50) developed cirrhosis, 14 (11-18) HCC and 37 (34-42) died.

Conclusion

We predicted that over 700 people were newly infected with HCV in Norway in 2013. Implementation of early improved treatment has the potential to decrease the spread of HCV and prevent the development of cirrhosis and HCC. Therefore, we recommend the use of this model to assess the impact of improved HCV treatment on the burden of HCV.

Keywords: Hepatitis C, Disease Progression, Models, Biological, Substance Abuse, Intravenous, Public Health, Norway

PRESENTED BY: Hinta Meijerink (hinta.meijerink@fhi.no)

REFERENCE NUMBER: 3155

Screening for chronic hepatitis B and C among migrants: outcome and costs of different screening models

Abby M Falla (1,2), Irene Veldhuijzen (1,2), Maria K Rossi (3), Laura Kluzniak (3), Joan Cayla (4), Manuel Fernandez (4), Agnes Csohan (5), Jan Kunkel (6), Graham R Foster (6), Ardine de Wit (7), Jan Hendrik Richardus (1,2), Susan Hahne (7)

1. Division of Infectious Disease Control, Municipal Public Health Service Rotterdam-Rijnmond, Rotterdam, The Netherlands
2. Department of Public Health, Erasmus MC, University Medical Center Rotterdam, Rotterdam, The Netherlands
3. Public Health Directorate, NHS Grampian, Aberdeen, Scotland, UK
4. Epidemiology Service, Public Health Agency of Barcelona, Barcelona, Spain
5. Department of Epidemiology, National Center for Epidemiology, Budapest, Hungary
6. Hepatology Unit, Blizard Institute, Queen Mary University of London, London, UK
7. National Institute of Public Health and the Environment, Bilthoven, The Netherlands

Background

Chronic hepatitis B and C virus (HBV/HCV) infections are leading causes of liver cancer and cirrhosis. A significant burden of disease in most EU countries is found in migrants from endemic areas. In the EU-funded HEPscreen project we compared different screening models targeting migrants groups in the UK, Spain and Hungary between 2011-2014 to inform public health policy making.

Methods

Two outreach screening models in communities and workplaces, two primary care screening models (one opportunistic, the other invitation -based) and two extension models to migrant tuberculosis screening and existing antenatal screening were piloted. Diagnosed patients were referred to specialist care. Cost data were collected and costs per person screened calculated.

Results

Five of the six screening models were completed, screening 1,239 people for HBV and 1,203 for HCV. Uptake varied from 33% in the workplace outreach screening to 80% in the opportunistic screening. Drop out was seen in the community outreach where testing was not offered at the first point of contact. The highest HBsAg prevalence was detected among South-East Asian (12.9%) migrants. The highest anti-HCV prevalence was found in migrants from Central/South Asia (9.8%) and Eastern Europe (5.3%). Costs per person screened ranged from €67 (tuberculosis screening extension model) to €254 (community outreach model). The invitation-based model ceased prematurely due to a low uptake (2.3%).

Conclusion

Individuals at risk of chronic hepatitis infections can be effectively targeted for HBV/HCV testing through migrant-based screening models in health and community settings. Uptake in community-based outreach screening may be improved by offering testing at the first point of contact. The high prevalence found strengthens the rationale for implementing effective screening among migrant communities at risk of liver-related morbidity and mortality.

Keywords: chronic hepatitis B, chronic hepatitis C, screening, migrants

PRESENTED BY: Irene Veldhuijzen (irene.veldhuijzen@rivm.nl)

REFERENCE NUMBER: 3100

Poster Abstracts

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Moderated Poster Session A
Wednesday 11 November
15:00-16:10

Track 1: Antimicrobial Resistance

MODERATOR: Outi Lyytikäinen (ECDC, Advisory Forum, Finland)

Molecular epidemiology of plasmid-mediated AmpC beta-lactamase producing Klebsiella pneumoniae in Hungary, 2009-2013

Zoltan Kis (1,2), Ákos Tóth (1,2), Laura Jánvári (1), Tamás Tirczka (1), Judit Pászti (1), Ivelina Damjanova (1)

1. National Center for Epidemiology
2. ECDC, European Programme for Public Health Microbiology Training

Background
The first plasmid-mediated AmpC-producing K.pneumoniae (pAmpC-KP) isolate in Hungary was detected in December 2009 and during the next four years comprised 25% of all 3rd generation cephalosporin resistant KP isolates submitted to the Reference Laboratory at the National Center for Epidemiology (NCE). An investigation was conducted in order to outline the spatio-temporal distribution of pAmpC-KP isolates in Hungary.

Methods
Between November 2009 and December 2013, 312 K. pneumoniae clinical isolates producing acquired AmpC beta-lactamases were submitted to the NCE for further examination. Phenotypic investigations were performed by the ESBL combined disk test (MAST) and ESBL&AmpC ID test (MAST). The presence of genes coding for different β-lactamases (blaSHV, blaCTX-M, blaMOX, blaCMY, blaLAT, blaBIL, blaDHA, blaACC, blaMIR, blaACT, blaFOX) was investigated by PCR and sequencing. Molecular typing using pulsed field gel electrophoresis (PFGE) and multilocus sequence typing (MLST) was performed.

Results
All isolates showed resistance to 3rd generation cephalosprins, aminoglycosides and fluoroquinolones and 77% were non-susceptible to at least one carbapenem. By PCR all isolates were positive for blaDHA, whilst 90% were positive for both blaDHA and blaCTX-M. Sequence analysis of β-lactamase genes detected blaDHA-1 and blaCTX-M-15. PFGE revealed twelve pulsotypes; two KP053 (262/312) and KP070 (38/312) belonged to sequence type ST11 and comprised 96% of isolates. The blaDHA-1 and blaCTX-M-15 producing KP053 clone affected 234 patients and spread to 55 health care centers across Hungary during the four years.

Conclusion
This is the first documentation of the DHA-1 and CTX-M-15 co-producing KP epidemic clone in Hungary. The rapid countrywide spread of this multidrug-resistant 'high-risk' clone seriously endangers Hungarian health care facilities and warrants urgent strengthening of infection control practices and prudent use of carbapenems.

Keywords: plasmid-mediated AmpC-producing Klebsiella pneumoniae, antibiotic resistance, Hungary

PRESENTED BY: Zoltán Kis (kis.zoltan@oek.antsz.hu)
REFERENCE NUMBER: 2995

Attributable mortality of carbapenem-resistant Klebsiella pneumoniae: a prospective matched cohort study in Italy, 2012-2013

Tommi Kärki (1,2), Ana Hoxha (3), Cristina Giambi (1,2), Carmen Montano (1,2), Annamaria Sisto (4), ANTONINO BELLA (2), Fortunato D'Ancona (2)

1. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden
2. Istituto Superiore di Sanità (ISS), National Centre for Epidemiology Surveillance and Health Promotion (CNESPS), Rome, Italy
3. Università Cattolica del Sacro Cuore, Rome, Italy
4. Ospedale Bambino Gesù, Rome, Italy

Background
In Italy, infections of carbapenem-resistant Klebsiella pneumoniae (CRKP) have increased significantly since 2009, creating unprecedented problems in healthcare settings, limiting treatment options, and leading to increased morbidity and mortality. Our objective was to assess the effect of CRKP-infection on patient-mortality and estimate the attributable mortality from CRKP-infection.

Methods
We conducted a cohort study in ten Italian hospitals. We matched CRKP-patients with carbapenem-susceptible K.pneumoniae (CSKP)-patients by hospital, age and specimen-type, followed the patients for 30 days to determine their outcome, and compared the two matched groups using chi-squared test. We calculated the attributable mortality, excluding accidental reasons, for CRKP-infection within 30 days of K.pneumoniae isolation by subtracting the crude mortality of the CSKP-patients from the crude mortality of the CRKP-patients. We measured association between CRKP-infection and crude mortality using conditional Poisson regression, adjusting for simplified acute physiology score (SAPS) and invasive procedures, and calculated matched incidence rate ratios (mIRR) and 95% confidence intervals (CI).

Results
We included 49 pairs of CRKP/CSKP-patients. CRKP-patients had undergone invasive procedures more often (p=0.005) and tended to have more serious clinical conditions, measured by higher SAPS (p=0.088/0.099). The crude mortality of CRKP-patients was 61% and the attributable mortality of CRKP-infection 41%. CRKP-patients were three times more likely to die within 30 days than CSKP-patients; after adjustment for confounders the estimate did not change (adjusted mIRR: 3.0, 95% CI:1.3-7.1).

Conclusion
We show that CRKP-infection had a marked effect on patient-mortality, even after adjustment for other patient characteristics. We recommend prioritisation of control measures in hospitals where CRKP is found, including antimicrobial stewardship programmes, promotion of hand hygiene, contact precautions, isolation of CRKP-patients, minimizing device use, screening of high-risk patients, and staff and/or patient cohorting.

Keywords: Klebsiella pneumoniae, antibiotic resistance, carbapenems, mortality

PRESENTED BY: Tommi Kärki (tommi.karki@iss.it)
REFERENCE NUMBER: 2882

Prevalence of multidrug resistance, ESBL and AmpC in isolates of notified travel acquired salmonellosis in Norway 2005-2013

Margot Einöder-Moreno (1,2), Umaer Naseer (3,4), Astrid Louise Wester (3), Katrine Borgen (1), Karin Nygård (1)

1. Department of Infectious Disease Epidemiology, Norwegian Institute of Public Health, Oslo, Norway
2. European Program for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
3. National Reference Laboratory for Enteropathogenic Bacteria, Norwegian Institute of Public Health, Oslo, Norway
4. European Program for Public Health Microbiology Training (EUPHEM), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden

Background

Norway is a low-incidence country of salmonellosis with around 80% of cases travel acquired. Salmonellosis is mandatorily notifiable and all Salmonella isolates are tested for antimicrobial susceptibility. We describe the proportion of antimicrobial resistance among travel acquired Salmonella isolates to increase knowledge about importation of resistance through travelling.

Methods

We performed a cross-sectional study including all Salmonella notifications in Norway 2005-2013. We described cases by country of acquisition, antimicrobial resistance and serovars. Isolates non-susceptible to third generation cephalosporins were tested for presence of Extended Spectrum Beta-lactamase (ESBL) and AmpC genes. Multidrug-resistance (MDR) was defined as non-susceptibility to three or more antimicrobial classes (beta-lactams, fluoroquinolones, trimethoprim-sulfamethoxazole and chloramphenicol).

Results

We analysed 13,718 records. From 10,561 isolates (77%) travel acquired, 888 (8.4%) were MDR, 57 (0.54%) ESBL and 25 (0.24%) AmpC. The most frequent serovars were S. Enteritidis (5402, 51.2%) and S. Typhimurium (1028, (9.7%).The top three foreign countries of acquisition of Salmonella were: Thailand (1457, 13.8%), Turkey (1443, 13.7%) and Spain (1180, 11.2%). For Thailand, 168/1457 isolates (11.5%) were MDR, 23 (1.6%) ESBL and 14 (0.96%) AmpC. For Turkey, 48/1443 (3.3%) isolates were MDR, 5 (0.35%) ESBL and none AmpC. For Spain, 76/1180 (6.4%) isolates were MDR, 3 (0.25%) ESBL and one isolate AmpC. The most frequent serovars isolated from Thailand was S. Stanley 357 (24.5%), and S. Enteritidis from Turkey (1191, 82.5%) and from Spain (857, 72.6%).

Conclusion

Isolates acquired in Thailand showed the highest proportion of MDR, ESBL and AmpC from the top three countries of acquisition. We recommend strengthening advice on food and water hygiene measures in travellers to Thailand in order to lower salmonellosis and resistance importation.

Keywords: Salmonella, Antibacterial Drug Resistance, Travel, Multiple Antibacterial Drug Resistance

PRESENTED BY: Margot Einöder-Moreno (margot.einoder.moreno@fhi.no)

REFERENCE NUMBER: 3102

Molecular epidemiology of carbapenem resistant/ carbapenemase producing Enterobacteriaceae (CRE/ CPE) in valle d'Aosta region, northern Italy.

Roberto Novati (1), Maria Teresa Del Franco (2), Laura Paone (2), Chiara Galotto (1), Maria Bagattini (2), Claudio Giacomazzi (3), Piergiorgio Montanera (3), Maria Triassi (2), Raffaele Zarrilli (2)

1. Medical Direction, Aosta Regional Hospital, Italy
2. Department of Public Health, Federico II University, Naples, Italy
3. Microbiology, Aosta Regional Hospital, Italy

Background

Aims of the study were the molecular characterization of consecutive CRE/CPE isolates in valle d'Aosta region and the epidemiology of cases.

Methods

Sixty consecutive CRE/CPE samples were isolated from 52 patients from November 2013 to August 2014. Genotyping of microbial isolates was done by PFGE and Multi-locus sequencing typing (MLST), carbapenemases were identified by PCR and sequencing. Clinical charts of patients were analysed.

Results

The mean age of patients was 79,5 years. Twenty-one percent of patients came from the territory and 7,7% from ICU; 80% had at least one Hospital admission in the 12 months before CRE/CPE isolation; 51,9% had at least one ward transfer during admission. CRE/CPEs were isolated at admission in 6,5% of patients and meanly 28,8 days after admission in the others. Eighteen percent of patients were on carbapenem therapy at CRE/CPE isolation; six months crude mortality was 38,8%. Molecular characterization of CRE/CPE isolates assigned 25 K. pneumoniae isolates to PFGE types A1-A5 and sequencing type (ST)101, 17 K. pneumoniae isolates to PFGE type A and ST1789 (a single locus variant of ST101), 7 K. pneumoniae isolates to PFGE types B or C and ST512, and 5 E. coli isolates to PFGE type a and ST131. Molecular analysis of carbapenemase genes identified blaKPC-2 in ST101 and ST1789 K. pneumoniae isolates, blaKPC-3 in ST512 and ST405 K. pneumoniae isolates, blaVIM-1 in ST131 E.coli isolates.

Conclusion

We describe both high in-Hospital and Hospital and territory circulation of patients; our data show in a close setting as Valle d'Aosta region the spread of three epidemic clones of K. pneumoniae producing KPC-2 or KPC-3 carbapenemases, and one epidemic E. coli clone producing VIM-1 carbapenemase.

Keywords: carbapenemase, enterobacteriaceae, PFGE, klebsiella pneumoniae, escherichia coli

PRESENTED BY: Roberto Novati (novatirobe@gmail.com)

REFERENCE NUMBER: 2906

Antimicrobial use and urinary tract infections among Finnish home care clients, February-April, 2014

Triin Pärn (1,2), Matti Mäkelä (3), Outi Lyytikainen (1)

1. National Institute for Health and Welfare (THL), Department of Infectious Diseases, Helsinki, Finland
2. European Programme for Intervention Epidemiology Training (EPIET), Stockholm, Sweden
3. National Institute for Health and Welfare (THL), Department of Welfare, Helsinki, Finland

Background

Urinary tract infection (UTI) diagnosis among elderly is difficult, leading to unnecessary use of antimicrobials. A study among Finnish long-term care facility residents indicated a high prevalence of UTI (8%) and antimicrobial use (16%). The aging population has led to increased use of home care (HC). We estimated prevalence of UTI and antimicrobial use among HC clients in order to identify variations in antimicrobial use.

Methods

HC client was defined as a person ≥75 years receiving HC for ≥4 consecutive weeks. We included clients for whom the Resident Assessment Instrument (RAI) was completed during April–September 2014 from 15 municipalities meeting our reporting quality criteria. RAI data on UTI and antimicrobials was collected by nurses' interview. We estimated UTI prevalence in RAI and calculated the proportion of clients using antimicrobials and identified the main antimicrobials for treatment and prophylaxis.

Results

A total of 6887 clients were included (median age 85 years; 75% female). Among these, UTI prevalence was 4.5%. Of all clients, 5.9% (408/6887) used ≥1 antimicrobial, and 3.7% (252/6887) used antimicrobials for prophylaxis. Of the clients with a RAI-reported UTI (N=307), 24.8% had used antimicrobials. The most common antimicrobials for treatment were cephalexin (18,9%) and pivmecillinam (10,7%) and for prophylaxis methenamine (43,3%) and trimethoprim (40,1%).

Conclusion

The proportion of HC clients receiving antimicrobials for prophylaxis is concerning, suggesting there may be inappropriate use of UTI prophylaxis.

Keywords: Home care, urinary tract infections, antimicrobial use

PRESENTED BY: Triin Pärn (triin.parn@thl.fi)

REFERENCE NUMBER: 3192

Comparison of 2 strategies to reduce transmission of extended-spectrum betalactamase-producing Enterobacteriaceae (ESBL-E): Preliminary results from the European RGnosis study

Angela Rincón Carlavilla (1), Cristina Diaz-Agero Pérez (1), Nieves López Fresneña (1), Patricia López Pereira (1), Marta Hernández Garcia (1), R Cantón Moreno (1)

1. Hospital Universitario Ramón y Cajal, Madrid, Spain

Background

Approximately 30% of healthcare-associated infections are caused by Enterobacteriaceae. The prevalence of extended-spectrum beta-lactamase-producing Enterobacteriaceae species (ESBL-E) is increasing rapidly in Europe. However, isolation of ESBL-E carriers is not supported by clear evidence, and isolation measures are costly and associated with adverse effects. We are evaluating 2 strategies to reduce between-patient transmission of ESBL-E: standard precautions (SP) and contact isolation (CI).

Methods

A two-arm randomized crossover intervention study conducted in 4 European countries over two years (2014-2016). We compare outcomes obtained with SP in the respiratory and gastroenterology units with those obtained with CI in the neurosurgery and urology units. All patients are screened on admission, every 7 days, and on discharge. We determine the prevalence of ESBL-E carriage on admission and the density of incidence (DI) for ESBL-E acquisition during hospitalization.

Results

In the first study year of study (March 2014-February 2015), 6446 patients were screened: 52.42% in the SP arm and 47.58% in the CI arm. Rectal ESBL-E carriage prevalence at admission was 8.04% (gastroenterology 9.21%, urology 7.45%, neurosurgery 7.42% and respiratory 7.89%). The microorganisms most frequently isolated were E. coli (83.08%) and K. pneumonia (14.39%). The DI for nosocomial ESBL-E acquisition per 1000 days of hospitalization was 3.6 in the CI arm and 3.7 in the SP arm.

Conclusion

Nosocomial acquisition of ESBL-E did not differ between the SP and CI study arms. Prevalence of rectal ESBL-E carriage on admission is similar to other European hospitals. These preliminary results do not support isolation of patients with ESBL-E, what is against current recommendations.

Keywords: Enterobacteriaceae, ESBL-E acquisition, antimicrobial drug resistance, contact isolation, standard precautions

PRESENTED BY: Angela Rincón Carlavilla (angelarc@hotmail.com)

REFERENCE NUMBER: 3074

Track 2: Epidemiology and Microbiology Driving Public Health Policy

MODERATOR: Ines Steffens (ESCAIDE Scientific Committee, Eurosurveillance Editor in Chief)

Undocumented migrant women in Denmark have inadequate access to pregnancy screening and have a higher prevalence of Hepatitis B virus infection compared to documented migrants in Denmark

Annika Wendland (1,2), Boje Kvorning Ehmsen (3), Vibeke Lenskjold (3), Birgitte Schmidt Astrup (4), Marlene Mohr (5), Christopher Williams (2), Susan Cowan (1)

1. Statens Serum Institut, Copenhagen, Denmark
2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, Stockholm, Sweden
3. Røde Kors Sundhedsklinikken, Copenhagen, Denmark
4. ProVest Clinic, Fredericia, Denmark
5. Reden International, Copenhagen, Denmark

Background
Pregnant residents of Denmark are tested for current infections with Hepatitis B virus (HBV), HIV and syphilis through the Danish pregnancy screening programme to identify infections and initiate interventions to prevent mother-to-child transmission (MTCT). Documented migrants (DM) have access to this screening but undocumented migrants (UM) do not, relying on ad-hoc care from clinics run by non-governmental organisations (NGO). We investigated screening frequency in UM and compared the prevalence of infection in UM with DM.

Methods
We obtained individual-level information on HBV, HIV and syphilis testing frequency and results for pregnant UM women attending three NGO clinics between August 2011 and April 2014. We obtained aggregate data on prevalence of the three infections for DM from the Danish pregnancy screening program and birth register between January 2011-2014. Planned abortions were excluded from the study. We estimated screening frequency for HBV, HIV and syphilis in UM and compared prevalence of infections in UM and DM by calculating standardised prevalence ratios (SPR).

Results
The three clinics registered 219 pregnancies. Overall 43%, 58% and 60% of pregnant UM had a test result recorded for HBV, Syphilis and HIV respectively, compared to >99% in the general Danish population. The prevalence of HBV was higher in UM than DM (crude prevalence in UM 6.4%; SPR 2.4; 95% CI:1.1-5.3). Prevalence comparisons for HIV were not statistically significant. None of the pregnant UM tested positive for syphilis.

Conclusion
Pregnant UM have a poorer chance of being tested for HIV, HBV and syphilis than DM, despite having a higher prevalence of HBV. We recommend giving systematic access to routine pregnancy screening to all UM to prevent mother-to-child transmission and address this observed health-care inequity.

Keywords: Undocumented migrants, pregnancy screening, HIV, Hepatitis B, syphilis

PRESENTED BY: Annika Wendland (annikawendland@hotmail.com)

REFERENCE NUMBER: 2907

The emergence of enterovirus D68 (EV-D68) in England in autumn 2014: The necessity for reinforcing enterovirus respiratory screening.

Isidro Carrión Martín (1,2), Richard Pebody (2), Joanna Ellis (2), Kevin E Brown (2), , Maria Zambon (2), David James Allen (2)

1. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden
2. Public Health England (PHE), London, United Kingdom

Background
In autumn 2014, EV-D68 associated with severe respiratory disease and neurological presentation emerged in North America and in some European countries. We describe the epidemiology of EV-D68 in England, between October and December 2014.

Methods
In England, enterovirus cases presenting with acute neurological symptoms are reported to the Enterovirus Surveillance System (ESS). From September 2014, reports were extended to include enterovirus positive cases hospitalised with respiratory symptoms. We collected clinical information on all laboratory confirmed EV-D68 cases. In primary care, respiratory swabs from patients consulting with influenza-like-illness were tested for EV-D68 from September 2013 to January 2015. We further characterized EV-D68 strains by amplification and partial sequencing of the VP1 coding region.

Results
From October-December 2014, 36 EV-D68 cases were detected through ESS (age range: 0-71 years (median: 3); 55% male). 31 cases presented with respiratory and two with neurological symptoms (EV-D68 negative in cerebral spinal fluid); 18 were immunocompromised or had other underlying diseases. 29/36 (81%) cases were hospitalised; 12/29 (33%) were in ICU and one died. Seven were outpatients or only seen in emergency department. In primary care, EV-D68 positivity increased from 0.2% (4/1,074) (95%CI: 0.1-1.0) (September 2013-Janury 2014) to 0.8% (11/1359) (95%CI: 0.4-1.5) (September2014-January2015). EV-D68 strains genetically similar to those detected in 2014 in USA have been circulating in England since 2012 and were also detected in 2014/2015.

Conclusion
EV-D68 circulation in primary care in England increased after September 2014. In secondary care, EV-D68 presented mainly with severe respiratory symptoms, particularly in those with underlying diseases. We recommend reinforcing enterovirus surveillance through screening of respiratory samples of suspect cases to better understand the epidemiology of EV-D68 and to inform surveillance and laboratory-testing guidance.

Keywords: Enterovirus D68, Respiratory infections, Routinely screening, Surveillance,

PRESENTED BY: Antonio Isidro Carrión Martín (isidro.carrion@phe.gov.uk)

REFERENCE NUMBER: 3014

Environmental sources and pathways of verotoxigenic Escherichia coli (VTEC) infection in Ireland 2008-2013 - a geostatistical study

Coilín ÓhAiseadha (1), Jean O'Dwyer (2), Paul Hynds (3), Una Fallon (4)

1. Department of Public Health, HSE East, Ireland
2. Department of Environmental and Chemical Science, University of Limerick, Ireland
3. School of Engineering, Dublin Institute of Technology, Dublin, Ireland
4. Department of Public Health, HSE Midlands, Ireland

Background

Verotoxigenic Escherichia coli (VTEC) incidence rates in Ireland are among the highest in Europe, with 704 confirmed cases recorded in 2013 (crude incidence rate 12.1/100,000), and 30 developing haemolytic uraemic syndrome (HUS). Irish studies indicate that consumption of water from private (unregulated) wells are 4.3–4.9 times more likely to contract infection. This is of particular concern due to high groundwater reliance, with 13% of the Irish population using unregulated wells as primary source of drinking water. We explored spatial associations between VTEC infections in 2008–2013 and density of potential environmental pathogen sources.

Methods

A novel linked database was developed, comprising 989 primary VTEC cases notified during the 6-year period 2008–2013 and geo-referenced by Health Atlas Ireland. Each geo-referenced case was assigned to one of 18,488 Irish census enumeration areas and linked with private well usage per head of population and septic tank density (per km2) derived from the 2011 population census, and cattle and sheep densities derived from the 2010 agricultural survey.

Results

The most frequent VTEC serotype during the study period was O157 (n = 521, 52.7%). The calculated 6-year cumulative incidence rate for rural VTEC O157 (19/100,000) was approximately three times that of categorically urban areas (6.3/100,000) (p <0.001). Multivariate modelling indicates that private well usage (p <0.001) and cattle density (p = 0.007) are significant spatial predictors for VTEC O157 infection.

Conclusion

VTEC infection in Ireland is a predominantly rural hazard, closely associated with cattle density and private well usage. Findings may be used to minimise public exposure to VTEC through engagement with rural stakeholders to devise source protection strategies.

Keywords: Escherichia coli Infections epidemiology, Escherichia coli O157, Water Pollution prevention & control, Cattle Diseases transmission, Regression Analysis

PRESENTED BY: Coilín ÓhAiseadha (coilin.ohaiseadha@hse.ie)

REFERENCE NUMBER: 3162

Active versus Passive surveillance of Legionella in Hotels in Crete, January - December 2012

Maria Keramarou (1,2), Dimosthenis Chochlakis (2), Vassilios Sandalakis (2), Ioannis Goniotakis (1), Vassiliki Baltatzidi (1), Christos Panoulis (1), Nektarios Vasilios Voumvourakis (3), Paraskeui Voumvouraki (3), Emmanouil Perdikakis (3), Antonios Papadakis (4), Pamphilos Giasafakis (5), Sofia Kapaki (5), Stavroula Marakaki (5), Panayiotis Bobos (5), Evaggelia Panagiotaki (5), Antonia Pantelaki (5), Paraskevas Skoulas (5), Yannis Tselentis (1), Anna Psaroulaki (1)

1. Laboratory of Clinical Bacteriology, Parasitology, Zoonoses and Geographical Medicine, Medical School, University of Crete, Greece
2. Regional Public Health Laboratory of Crete, Greece
3. Public Health Authority, Regional Unit of Rethymnon, Crete, Greece
4. Public Health Authority, Regional Unit of Heraklion, Crete, Greece
5. Public Health Authority, Regional Unit of Chania, Crete, Greece

Background

More than 20% of Legionnaires' disease (LD) cases reported to ECDC annually are travel-associated; 83% of the cases are linked to hotel facilities. The Hellenic Public Health Authorities inspect hotel facilities, following notification of a confirmed human LD case. We conducted a pilot study to estimate the frequency of Legionella colonization in randomly inspected hotels (active surveillance scheme ASS) against the findings from the passive surveillance scheme (PSS), across the island of Crete

Methods

We collected 8-15 water samples from each facility which were cultured according to ISO 11731. Colonies were identified using MALDI TOF-MS. We compared water system temperature (WST), chlorine concentration (CC) and total plate count (TPC) using a x2, unpaired t-test and anova.

Results

47 samples (five hotels; PSS) and 477 samples (28 hotels; ASS) were tested. Both groups were equally colonized by Legionella (80% of samples). The proportion of samples colonized with L. pneumophila did not differ significantly between the two groups (p=0.616). L. pneumophila serogourp 1 was the predominant type (35%) detected in PSS hotels (p<0.001). ASS hotels were more likely to be colonized by Legionella species, other than L. pneumophila (p=0.002). TPC did not differ significantly between the two groups. WST of 85% of hot and 50% of cold samples, and CC levels (45%) were outside legislation, in both groups, but were not statistically different.

Conclusion

Study showed that the risk of colonization remains the same in all hotels. We recommend installment of a Water Safety Plan for each hotel and continuous monitoring of control measures at national level in order to combat legionella and reduce human cases.

Keywords: Legionella, hotels, active, surveillance, colonization, prevention

PRESENTED BY: Maria Keramarou (keramarou@gmail.com)

REFERENCE NUMBER: 3047

Long-term follow-up of contacts of two MERS-CoV positive returning travelers in the Netherlands, May 2014

Madelief Mollers (1,2), Marcel Jonges (1,3), Suzan Pas (1,3), Annemiek van der Eijk (1,3), Kees Dirksen (4), Casper Jansen (5), Luc Gelinck (5), Eliane Leyten (5), Ingrid Thurkow (6), Paul Groeneveld (7), Arianne van Gageldonk-Lafeber (1), Marion Koopmans (1,3), Aura Timen (1)

1. National Institute for Public Health and the Environment (RIVM), Bilthoven, The Netherlands
2. European Programme for Intervention Epidemiology Training (EPIET), European Center for Disease Prevention and Control (ECDC), Stockholm, Sweden
3. Erasmus MC, Rotterdam, The Netherlands
4. Public Health Service Haaglanden, The Hague, The Netherlands
5. Medical Centre Haaglanden, The Hague, The Netherlands
6. Public Health Service Ijsselland, Zwolle,The Netherlands
7. Ijsala Klinieken Zwolle, Zwolle, The Netherlands

Background
In 2014, Middle East Respiratory Syndrome coronavirus (MERS-CoV) was diagnosed in two Dutch residents returning from the Kingdom of Saudi Arabia. Contact monitoring among 78 unprotected (>15 minutes face-to-face) and 53 protected contacts (healthcare workers wearing adequate personal protection) was undertaken to identify possible secondary transmission. We assessed the psychological impact of this monitoring.

Methods
For 14 days, contacts measured their temperature daily and reported their symptoms. We performed RT-PCR on throat swabs collected on day 7 and 14 and antibody testing on serum collected on day 7 and 21. We assessed knowledge, perception, and the impact of monitoring via questionnaire. We measured psychological impact using the Impact of Event Scale-Revised (IES-R), a 22-item self-report that assesses distress, with a possible range of 0-88.

Results
Of 131 contacts, 106 (81%) provided paired throat swabs and 99 (76%) paired serum specimens, with unprotected contacts more likely to provide specimens. Eight developed respiratory symptoms, but none tested positive for MERS-CoV. Seventy-two contacts (55%) completed the questionnaire. 53% of contacts were afraid to contract MERS-CoV or to infect their families. IES-R scores were higher for unprotected than protected contacts (10.5 [95%CI 7.1-13.8] versus 3.3 [95%CI 1.1-5.6]).

Conclusion
Our study demonstrates a significant negative psychological impact in those people classed as contacts of a MERS-CoV case, which was greater in unprotected contacts. Laboratory testing did not show direct (in symptomatic contacts) or indirect evidence of infection in contacts. We recommend considering a tighter definition of contacts for MERS-CoV cases to reduce overall psychological impact of an incident, whilst still identifying secondary cases. Nevertheless, onset of symptoms in both protected and unprotected contacts should be the direct trigger for public health measures.

Keywords: MERS-CoV, contact investigation, psychological impact, IES-R

PRESENTED BY: Madelief Mollers (madelief.mollers@rivm.nl)

REFERENCE NUMBER: 2854

Disrupt Rift Valley fever (RVF) at the front line. The value of incorporating agricultural communities' knowledge to the early warning system of RVF in Sudan

Osama Ahmed Hassan Ahmed (1), Joacim Rocklöv (2), Clas Ahlm (3), Magnus Evander (1)

1. Department of Clinical Microbiology, Virology, Umeå University, Umeå; Sweden
2. Department of Public Health and Clinical Medicine, Epidemiology, Umeå University, Umeå; Sweden
3. Department of Clinical Microbiology, Infectious Diseases, Umeå University, Umeå; Sweden

Background
Rift Valley Fever (RVF) is a viral emerging zoonotic infectious disease that affects both animals and humans. It is caused by RVF virus (RVFV) and led to devastating outbreaks in Africa and Arabian Peninsula. From our analysis of the RVF outbreak in Sudan 2007 we could conclude that increased knowledge on RVF epidemiology is of utmost importance to enhance early warning-system and control strategies.

Methods
To accomplish this a cross-sectional, community-based survey was undertaken. A face to face interview with household heads was conducted in rural Sudan in March 2014 where high number of RVFV cases during the 2007 registered. A specially structured One Health questionnaire was developed to compile RVF determinants in environment, animals and humans at the same time. These includes socio-demographic characteristics, knowledge, attitude and practices.

Results
A total of 235 household heads, out of them 52% were females and 48% were males participated in this study. The majority of the participants' age group was ≥46 Years. A majority of respondents had heard of RVF, 56% are women and 44% are men. However, only 43% knew that RVF is a zoonosis with no difference between male and female. Only 7% mentioned mosquitoes as transmitting vectors but men were double knowledgeable than women. Over 50%, 63%, 65% and 72% revealed risky practices such as keep animals close to home, help animals to deliver without preventive measures, slaughter animals inside home and handling sick animals respectively.

Conclusion RVF outbreaks can be effectively managed with a bottom-up approach with a shared perception. The fact that this study was conducted in "high risk transmission areas" warrants further inquiry in other geographic regions with relatively low risk of RVF

Keywords: Rift Valley fever (RVF), Sudan, Farmer's Knowledge, Epidemiology, One Health Questionnaire, Early Warning System.

PRESENTED BY: Osama Ahmed Hassan Ahmed

REFERENCE NUMBER: 3083

Development of a national electronic reporting system for the enhanced surveillance of carbapenemase-producing Gram-negative bacteria in England

Rachel Freeman (1,2,3), Dean Ironmonger (4), William Welfare (5), Susan Hopkins (1), Russell Hope (1), Paul Cleary (4), Bharat Patel (6), Peter Hawkey (7,8), Neil Woodford (9), Alan P Johnson (1), Richard Puleston (4)

1. Centre for Infectious Disease Surveillance and Control (CIDSC), Public Health England (PHE), UK
2. Field Epidemiology Training Programme (FETP), UK
3. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden
4. Field Epidemiology Service, PHE, UK
5. Greater Manchester Public Health England Centre, PHE, UK
6. London Public Health Laboratory, PHE, UK
7. The Midlands Public Health Laboratory, PHE, UK
8. Institute of Microbiology and Infection, University of Birmingham, UK
9. Reference Microbiology Services, PHE, UK

Background

Carbapenem resistance poses a significant threat to healthcare provision globally. Accurate and timely data will play a crucial role in controlling the spread of resistance. We developed a surveillance system to describe and monitor changes in the epidemiology of infections and colonisation by carbapenemase-producing Gram-negative bacteria. Carbapenem resistance is complex, therefore effective surveillance of it is challenging. Our approach detailed here has attracted the interest of several other countries facing similar challenges.

Methods

A working group designed a surveillance system to capture enhanced surveillance data, providing functional specifications for the system developer. To ensure rapid development and minimise costs, we recommended the adaptation of an existing regional pilot system into a national surveillance system.

Results

The resulting surveillance system utilises web-based case data capture, integrated into an established national microbiology reference service for the characterisation of carbapenem-resistant Gram-negative bacteria. To account for variations in isolate referral and testing practices across England, the system design ensures that data can be recorded at all stages of the referral process. The system uses a two-stage data submission process: patient demographic data, laboratory details and healthcare setting are provided prospectively by the laboratory for each isolate submitted. Enhanced data on patient travel history, admission details and potential contact with carbapenemase-producing Gram-negative bacteria is provided retrospectively by hospital infection prevention and control teams. The surveillance system will be further enhanced through linkage with electronically-stored microbiology, administrative and mortality data. Reference microbiology results are made available to stakeholders via the system.

Conclusion

Our approach allowed for rapid system development, at minimal cost, and integrated the surveillance programme into existing practice. We anticipate this will improve acceptance and increase participation.

Keywords: carbapenems, drug resistance, Gram-negative bacteria, microbiology, surveillance

PRESENTED BY: Rachel Freeman (rachel.freeman@phe.gov.uk)

REFERENCE NUMBER: 3050

Track 3: Burden of Disease

MODERATOR: Edoardo Colzani (ECDC, Expert science-based prevention & guidance)

Estimation of incidence of symptomatic salmonella and campylobacter infections based on sero-incidence in 13 European countries

Alessandro Cassini (1), Kåre Mølbak (2), Hanne-Dorthe Emborg (2), Jacob Simonsen (2), Peter Teunis (3), Wilfrid van Pelt (3), Johanna Takkinen (1)

1. European Centre for Disease Prevention and Control, Sweden
2. Statens Serum Institute, Denmark
3. National Institute for Public Health and the Environment, The Netherlands

Background

In the surveillance of gastrointestinal diseases under-estimation of notified diseases is a widely recognised problem. Estimation of incidence of salmonellosis and campylobacteriosis is important for e.g. measuring the DALYs, the evaluation of intervention and prevention strategies and the description of European heterogeneous surveillance systems.

Methods

A sero-epidemiology study commissioned by the European Centre for Disease Prevention and Control (ECDC) and led by the Danish Statens Serum Institute estimated the incidence of Salmonella and Campylobacter infections between 2000 and 2012 in 13 MS for Salmonella and 11 MS for Campylobacter. The salmonellosis sero-incidence results of two EU MS were anchored to community based studies performed in the same MS thereby providing estimates of the incidence of symptomatic disease. This was used to estimate the relative incidence of symptomatic disease in other MS, assuming that the disease-to-infection rate is constant across countries. For campylobacteriosis, the sero-incidence results were anchored to one study.

Results

Compared to data notified to the European Surveillance System (TESSy) database, multipliers adjusting for under-notification of salmonellosis range between 1.2 in Sweden and Finland to 59.8 in Romania; the two sets of multipliers are comparable, corroborating the approach. Multipliers of campylobacteriosis range from 5.02 in Finland and 714.78 in Romania.

Conclusion

When estimating the incidence of salmonellosis and campylobacteriosis, this approach produces more realistic multipliers compared to previous, and provides further information on the sensitivity of surveillance systems in selected European countries. The MS included in the study represent different European geographical and epidemiological situations resulting in a robust picture of the epidemiology in the EU/EEA. Finally, the estimted incidence can be used to estimate the public health impact of these diseases.

Keywords: Burden of illness, Salmonella, Campylobacter, Seroepidemiologic Study, Incidence.

PRESENTED BY: Alessandro Cassini (alessandro.cassini@ecdc.europa.eu)

REFERENCE NUMBER: 3144

The health and economic burden of Cystic Echinococcosis in Italy: an expensive, neglected and preventable disease

Toni Piseddu (1), Diego Brundu (1), Gabriella Masu (1), Salvatore Ledda (1), Giovanna Masala (1)

1. Istituto Zooprofilattico Sperimentale della Sardegna Italian National Reference Centre for Echinococcosis (CeNRE), Italy

Background
Cystic echinococcosis (C.E.) is an important zoonotic parasitic infection. C.E represents a serious human health concern, causing important economic losses derived from the costs of medical treatment, morbidity, life impairment and fatalities in human cases. Moreover CE is endemic in several Italian Regions. The aim of this study is to conduct a detailed analysis of CE costs in Italy.

Methods
Between 2001 and 2012, a direct costs of 19,414 HDRs with CE-related primary diagnosis codes were analysed to quantify the economic burden of CE. The direct costs include the expenses for hospitalizations and medical and surgical treatments incurred by public and private hospitals. The direct costs were computed on an individual basis according to Italian Health Ministry guidelines. Moreover, we estimate the disability-adjusted life year (DALYs) for each patient.

Results
The Italian burden of CE is over 11,000 DALYs with a financial burden in excess of € 94 million. The majority of the direct costs are from the Island and South. National Annual disease burden averaged is 16,14 DALYs per million population with a peak of 52,30 DALYs in the Island.

Conclusion
In Italy, human CE is responsible for significant economic losses in the public health sector. In humans, costs associated with CE have been shown to have a great impact on affected individuals, their families, and the community as a whole. This study could be used as a tool to prioritize control measures for this largely preventable neglected disease. Currently, the implementation of CE control programmes is opportune in high incidence areas. It should be based on cross-sector approaches may be needed not only when addressing health issues but also for environmental and societal problem solving.

Keywords: DALYs, Cystic Echinococcosis, burden, Zoonosis.

PRESENTED BY: Toni Piseddu (tonipiseddu@gmail.com)
REFERENCE NUMBER: 3055

Reported measles cases during an epidemic in the Netherlands; just the tip of the iceberg

Tom Woudenberg (1), Frits Woonink (2), Karin Cox (2), Helma Ruijs (1), Rob van Binnendijk (1), Hester de Melker (1), Susan Hahne (1), Jacco Wallinga (1)

1. National Institute for Public Health and the Environment (RIVM), Bilthoven, The Netherlands
2. Department of infectious diseases, GGD Midden Nederland, Zeist, The Netherlands

Background
During an epidemic 2700 measles cases were reported in the Netherlands in 2013-2014. Measles is a notifiable disease, but not all measles cases will consult the GP, and not all consultations will be reported. We estimated the extent of underreporting and assessed determinants for reporting measles cases during the epidemic to improve understanding of the epidemiology and burden of disease of this epidemic.

Methods
A survey among all children under 15 years of age was conducted to identify measles cases in a municipality with vaccination coverage of 80%. Self-identified cases were matched with the cases reported to the Dutch national register system to estimate underreporting. A subset of the self-identified cases was followed up for laboratory confirmation (positive IgG-detection in oral fluid). Determinants of reporting were assessed by logistic regression analysis.

Results
Among 2078 responders (61% response rate), 307 (15%) indicated to have had measles during the epidemic, of which 122 were also tested for measles IgG antibodies. All, except for one, had positive measles IgG indicative for measles infection (positive predictive value [PPV] 99%). Of the 307 self-identified cases, 27 were matched to a case reported to the Dutch national register system; thus only 9% (95%CI 6%-12%) of the cases was reported. Cases with complications (OR=3.96, $p<0.01$), hospitalized cases (OR=14.0, $p<0.05$), GP consulting cases (OR=2.5, $p<0.1$), and cases occurring early in the epidemic (OR=4.2, $p<0.01$) were more likely to be reported.

Conclusion
Most measles infections remained unreported during the epidemic in the Netherlands. The PPV of self-reported measles was very high reflecting a high incidence. Cases occurring early in the epidemic, those consulting a GP, being hospitalized, and with complications were more likely to be reported.

Keywords: Measles, Disease Notification, Disease Outbreaks, Incidence

PRESENTED BY: Tom Woudenberg (tom.woudenberg@rivm.nl)
REFERENCE NUMBER: 3188

The cost analysis of uncomplicated chickenpox treatment in Slovakia

Viera Svihrova (1), Veronika Szaboova (1), Eva Malobicka (1), Jana Zibolenova (1), Henrieta Hudeckova (1)

1. Department of Public Health, Jessenius Faculty of medicine in Martin, Comenius University in Bratislava, Slovakia

Background

Chickenpox belongs to the most common infectious diseases globally. The aim of this work was to analyze direct and indirect costs for treatment of uncomplicated chickenpox in Slovakia in 2013.

Methods

Data of the infection incidence were obtained from Epidemiological information system of the Slovak Republic. Direct costs included costs for outpatient treatment: drug costs and the capitation payment in individual age groups according to the general practitioners. Indirect costs included: costs used to care a family member for year group from 1-14 years (for parent taking care of a sick child); wage compensation (calculated from minimum wage) from employer for employee within the first ten sick leave days (age group 19-62 years); and losses of gross domestic product during ten days (parents of children in the age group 1-14; employee in the age group 19-62 years).

Results

Around 18,000 cases are annually reported in Slovakia. Average direct costs per case of uncomplicated chickenpox represented EUR 12.27 which means an increase by more than 107 % compared to the year of 2007 (EUR 5.91). Loss of GDP was EUR 372. Total indirect costs reached EUR 421 per case which is more than 21 % growth as compared to the year of 2007 (EUR 349). Total costs reached EUR 433 per case and increase by more 22 % compared to the year of 2007 (EUR 354).

Conclusion

Treatment costs for chickenpox rise each year because of increasing mainly indirect costs. Indirect costs in Slovakia represent about 97 % of total costs, which is the highest proportion in comparison with other countries. This work was supported by the Slovak Research and Development Agency under the contract No. APVV-0096-12 (EPIBIOMAT).

Keywords: chickenpox, cost analysis, Slovakia

PRESENTED BY: Veronika Szaboova (szaboova.nikus@gmail.com)

REFERENCE NUMBER: 2870

Burden of retinopathy and associated risk factors amongst diabetic patients attending rural health facilities, Kancheepuram, India 2013

Tony Fredrick (1), Prabhdeep Kaur (1), Yuvaraj Jayaraman (1), Joseph David (1), Sudha Ramachandran (1)

1. National Institute Of Epidemiology, India

Background

In India, the prevalence of Diabetes and its microvascular complication diabetic retinopathy is increasing. Diabetic retinopathy is one of the main causes for avoidable blindness in the working age group. We investigated the independent associations between the stage of retinopathy and possible risk factors in self-reported diabetic patients attending rural health facilities in Kancheepuram, India.

Methods

We conducted cross-sectional survey among diabetic patients attending two rural public health facilities using convenient sampling. We did comprehensive eye examination, both by direct and indirect ophthalmoscopy following pupillary dilation and graded retinopathy using standard guidelines. We estimated systemic and ocular risk factors associated with retinopathy. Univariate and stepwise regression analyses were done to identify the independent risk factors associated with the presence and severity of diabetic retinopathy. We calculated adjusted odds ratio with 95% CI.

Results

We surveyed a total of 270 diabetic patients. The mean age of the study population was 54.5 (SD± 10) years and median duration of diabetes was 48 months. The prevalence of diabetic retinopathy was 30%. Factors associated with the presence of diabetic retinopathy were male gender, Family history of diabetes, duration, poor drug adherence, fasting and postprandial blood sugar levels, hypertension and nephropathy. Multivariate analysis of risk factors independently associated after adjustment of age and gender were, hypertension [AOR:3.8;95% CI: 1.8-7.7] , diabetes more than 5 years [AOR:5.3;95% CI: 2.6-10.9], poor drug adherence [AOR:1.8;95% CI: 1.2-3.0], and nephropathy [AOR:2.5;95% CI: 1.1-5.6].

Conclusion

Higher prevalence of diabetic retinopathy and associated risk factors were identified in the study population. We recommend periodic ophthalmic examinations for early detection of retinopathy, with counseling for strict adherence of drug intake, diet control and life style modification in the target population.

Keywords: Diabetic retinopathy, Risk factors, cross-sectional study.

PRESENTED BY: Tony Fredrick (tony_fredrick@yahoo.com)

REFERENCE NUMBER: 3062

Incidence of adult community acquired pneumonia in primary care in Spain. NEUMO-ES-RISK project

Irene Rivero (1,2), Jacobo Pardo (2), Pablo Aldaz (3,4), Diego Agustin Vargas (5,4), Enrique Mascarós (6,4), Esther Redondo (7,4), Jose Luis Diaz (8,4), Manuel Linares (9,4), María José Fierro (10,4), Angel Gil (11,4), Jesús Molina (12,4), Daniel Ocaña (13,4), Federico Martinón-Torres (1,2,4), on behalf of NEUMOEXPERTOS group (4)

1. Translational Pediatrics and Infectious Diseases Section Pediatrics Department, Hospital Clínico Universitario de Santiago de Compostela, Santiago de Compostela, Spain
2. Genetics Vaccines Infections and Pediatrics Research Group (GENVIP), Healthcare Research Institute of Santiago de Compostela, Santiago de Compostela, Spain
3. Specialist in Primary Care. Member of the preventive infectious disease group PAPPS-SEMFYC. Primary Health care Center San Juan. Pamplona. Spain
4. NEUMOEXPERTOS group is composed by: F. Martinón-Torres; P. Aldaz, D. Vargas, E. Mascarós, E. Redondo, JL. Díaz Maroto, M. Linares, MJ Fierro, A.Gil, J. Molina, D. Ocaña
5. Specialist Medical Area. Versatile unit hospitalization, Hospital for High Resolution El Toyo. Agencia Pública Sanitaria. Hospital de Poniente. Almería. Spain
6. Hospital Dr Peset Health Department. Primary Care Center Fuente de San Luís, Valencia, Spain
7. Specialist in Primary Care. Preventive and Public Health Activities Group SEMERDEN. International Heath Center. Madrid, Spain
8. Specialist in Primary Care. Primary Care Health Center Guadalajara, Spain
9. Specialist in Primary Care and Clinical Microbiology. Infectious Diseases Group SEMERGEN. Fundaciónio
10. Specialist in Primary Care. Primary Care Health Center El Olivillo. Cádiz. Spain
11. Professor of Preventive Medicine and Public Health at the Rey Juan Carlos University. Madrid. Spain
12. Primary Care Respiratory Group. Health Care Center Francia. Fuenlabrada. Madrid, Spain
13. Primary Care Respiratory Group. Health Care Center Algeciras, Spain

Background

Community-acquired pneumonia (CAP) is a major cause of morbidity and mortality in adults even in developed countries. The annual incidence of CAP in adults in Europe is between 1.07 and 1.2 per 1,000 person/year. The aim of this study is to assess the incidence of CAP in primary care adults in Spain.

Methods

Retrospective observational study in adults (›18 years-old) with CAP diagnosed and attended at primary care in Spain between 2009-2013, using the National Surveillance System of Primary Care Data (BiFAP).

Results

28.413 patient records were retrieved and analysed. Global incidence of CAP in adults was estimated at 4.63 per 1000 persons/year. CAP incidence increased progressively with age, ranging from a 1.98 at 18-20 years of age to 23.74 in patients above 90 years of age. According to gender, global CAP incidence was slightly higher in males (5.04) than females (4.26): CAP incidence from 18 to 65 years-old up was comparable between males (range: 2.18-5.75) and females (range: 1.47-5.21), whereas from 65 years of age, CAP incidence was noticeable higher in males (range: 7.06-36.93) than in females (range: 5.43-19.62).

Conclusion

Annual incidence of adult CAP in primary care in Spain is higher than that reported for Europe. CAP incidence is comparable between males and females up to 65 years of age, but clearly increases in males from that age.

Keywords: Community acquired pneumonia, vaccine-preventable diseases, Incidence, Primary care

PRESENTED BY: Irene Rivero (irina667@hotmail.com)

REFERENCE NUMBER: 3053

Estimating the relative proportion of community-acquired, healthcare-associated and hospital-acquired bloodstream infections in children in England from linked hospital and laboratory data

Katherine Henderson (1,2), Ruth Gilbert (2), Angie Wade (2), Berit Muller-Pebody(1)

1. Department of Healthcare-Associated Infection and Antimicrobial Resistance, Centre for Infectious Disease Surveillance and Control, Public Health England, London, UK
2. Population, Policy and Practice Program, UCL Institute of Child Health, London, UK

Background

Current national guidance for empiric antibiotic therapy of children with bloodstream infections (BSIs) is dependent on whether BSIs are community-acquired (CA) or hospital-acquired (HA). Recent changes in healthcare delivery have seen an emergence of patients from the community with healthcare-associated (HCA) BSIs who require different antibiotics compared to 'classic' CA-BSIs; attempts to differentiate these patients and update the guidance accordingly have concentrated on adults.

Methods

Four years (2007-2011) of national microbiology and hospital in-patient data were probabilistically linked for children (aged 1 month–5 years) with a positive bacterial blood specimen in England. Three statistical models were used to identify clinical and demographic risk factors to predict the upper and lower proportional range of CA-, HCA- and HA-BSIs.

Results

A total of 17,102 positive blood specimens were linked; of these, 73% were the index BSI cases for 10,587 children. The mean age was 1.8 years (median: 1.3 years). BSIs were isolated more frequently from boys (58%). The majority of bacterial pathogens (85%) occurred Enterococcus spp., Klebsiella spp.) widely regarded as HA. The predicted proportions for CA-, HCA- and HA-BSI were 21-69%, 13-60% and 18-25% respectively for children aged 1 month–1 year; 29-77%, 11-59% and 11-13% respectively for children aged 1-5 years.

Conclusion

HA-BSI in children accounted for less than a quarter of all BSI. Risk factors and causative organisms did not sufficiently differentiate between CA- and HCA-BSIs. The development of rapid bedside tests should be encouraged to identify invasive pathogens and guide antibiotic therapy.

Keywords: bacteremia, infection, child, epidemiology, England

PRESENTED BY: Katherine Henderson (katherine.henderson@phe.gov.uk)

REFERENCE NUMBER: 3139

Track 4: Vector-borne Diseases

MODERATOR: Kostas Danis (EPIET coordinator, France)

Re-emergence of urinary schistosomiasis in Europe? Investigation of a cluster of Schistosoma haematobium infections acquired in Southern Corsica in 2014.

Lauriane Ramalli (1), Harold Noël (1), Marc Ruello (1), Annie Macarry (2), Jérôme Boissier (3), Hélène Barré-Cardi (4), Judith Fillaux (5), Jean-Luc Termignon (6), Monique Debruyne (7), Georges Chyderiotis (8), Gérard-Antoine Denoyel (8), Tiphanie Succo (1), Marie-Claire Pathy (1), Guillaume Heuzé (1), Joseph Mattei (2), Alexis Armengaud (1), Antoine Théron (3), Antoine Berry (5)

1. French Institute for Public Health Surveillance, France
2. Regional Health Authority of Corsica, France
3. Functional and EvolutionaryParasitology Unit, UMR 5555 CNRS-UP, France
4. Environnemental agency of Corsica, France
5. Parasitology Unit of the hospital of Toulouse, France
6. Ministry of Health, France
7. Laboratory Cerba Pasteur, France
8. Laboratory Biomnis, France

Background
Schistosoma haematobium is a tropical parasite causing millions of silent infections worldwide with potential evolution toward severe urinary and reproductive diseases. Evidence of re-emergence in Europe has been detected. A cluster of cases of urinary schistosomiasis was reported in April 2014 among French and German tourists linked to exposure to the Cavu river, in Southern Corsica, between 2011 and 2013. The early response consisted in prohibiting bathing in the river, nationwide screening of all people exposed to the river and treating confirmed cases.

Methods
A surveillance system of autochthonous cases was implemented to identify the extent of the outbreak and identify potential sites of transmission in Corsica and other regions in France. Cases were defined as a French resident with serology positive for schistosomiasis or demonstration of schistosome eggs in urine and no history of contacts with fresh water in known endemic areas. Symptoms, place and time of exposure to fresh water were documented for each case. 20 streams were screened in Corsica for the intermediate snail host. Collected specimens were tested for infestation.

Results
In 2014, 37,000 French residents were screened for schistosomiasis instead of 5,000 to 7,000 the previous years. On March 2015, 110 autochthonous cases were reported, including 32 with a symptomatic infection. All bathed in the Cavu in 2013. Among non-Corsican resident patients (n=79), 63% reported bathing in the river in August 2013. Although 3,534 intermediate snail hosts were retrieved from the Cavu river, none were infested.

Conclusion
This cluster shows that environmental conditions are suitable for local transmission of S. haematobium in Corsica. Surveillance should be continued in France and considered in Mediterranean countries to detect new foci and guide necessary control measures.

Keywords: Schistosoma haematobium, Parasites, Disease Outbreaks, France

PRESENTED BY: Lauriane Ramalli (lauriane.ramalli@ars.sante.fr)

REFERENCE NUMBER: 3154

Awareness of existence of malaria diagnostic services and pattern of pre-hospital treatment, Makarfi, Nigeria

Olufemi Ajumobi (1,2), Godwin Ntadom (1), Patrick Nguku (2), Gabriele Poggensse(2)

1. National Malaria Elimination Programme
2. Nigeria Field Epidemiology and Laboratory Training Programme

Background
Malaria is the leading cause of childhood mortality in Nigeria. Artemisinin-based combination therapy (ACT) is the nationally recommended treatment of choice for uncomplicated malaria. Treatment has remained largely presumptive despite revision of the policy for parasitological diagnosis before commencement of treatment. We conducted a hospital-based cross-sectional study to determine factors associated with awareness of existence of malaria diagnostic services (MDS) among caregivers of febrile U5 (FU5) and pattern of pre-hospital treatment practices for FU5.

Methods
We interviewed consecutively selected caregivers of 295 FU5, attending Makarfi General Hospital, Kaduna state, Nigeria; from December 2010 to August 2011. We included all eligible FU5 without rash. Information on factors influencing awareness of MDS and pre-hospital treatment (PHT) was collected. We examined the Giemsa-stained blood smear of FU5 for malaria. Fifteen (5.1%) caregivers have ever heard about MDS.

Results
Eleven (3.7%) caregivers were ever offered MDS by physicians. Being formally educated (Prevalence Odds ratio (POR): 0.05, 95% Confidence Interval (CI): 0.01-0.20), living <5km from a health facility (POR: 4.21, CI: 1.39- 12.55), being a government staff (POR: 9.18, CI: 1.74- 39.93) and ever being offered MDS (POR: 35.09, CI 10.13-134.00) were positively associated with awareness of MDS. Overall, 201(67.9%) children had received any PHT, 121 children (41.0%) at patent medicine stores. Of the 31(10.5%) FU5 diagnosed with malaria and 264 (89.5%) without malaria diagnosis, 13 (41.9%) and 65 (24.6%) have had PHT with Chloroquine respectively.

Conclusion
Awareness of MDS remains low. Treatment of FU5 against malaria is predominantly inappropriate within the community despite widespread deployment of affordable ACTs. There is a need to sensitise caregivers and health staff on use of ACTs and adherence to confirmatory malaria diagnosis.

Keywords: malaria, awareness, diagnosis, Chloroquine, children, Nigeria

PRESENTED BY: Olufemi Ajumobi (femiajumobi@gmail.com)

REFERENCE NUMBER: 2860

The national hospital discharge diagnosis registry is the most suitable data source for surveillance of Lyme borreliosis in Sweden

Viktor Dahl (1,2), Karin Tegmark-Wisell (1), Anders Tegnell (1), Anders Wallensten(1)

1. The Public Health Agency of Sweden, Stockholm, Sweden
2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden

Background

Lyme borreliosis is not under surveillance in Sweden. To follow long-term trends in incidence and geographical spread of Lyme borreliosis in Sweden, the Public Health Agency of Sweden searched for suitable data sources. We identified neuroborreliosis as the manifestation to survey because this diagnosis, according to national guidelines, requires microbiological testing and is likely to be more specific. We compared two data sources: the national hospital discharge diagnosis registry and the hospital laboratory registers.

Methods

We extracted case data from the hospital discharge registry for 2012. We defined a case of Lyme neuroborreliosis as a patient discharged from a hospital, or visiting an outpatient clinic, with the following ICD-10 codes: A.69.2 (Borreliosis) and either G01.9 (Meningitis) and/or G63.0 (Polyneuropathy). In parallel we sent a questionnaire to all clinical microbiological laboratories asking for the number of neuroborreliosis cases in their registries, defined as someone with a positive cerebrospinal fluid/serum antibody index for Borrelia IgM and/or IgG during 2012. We then calculated incidence using the national census estimates as denominator.

Results

We found 501 cases of Lyme neuroborreliosis in the hospital discharge registry, corresponding to an incidence of 5.2/100,000. All 23 laboratories responded to the questionnaire. They reported 521 cases of Lyme neuroborreliosis, corresponding to an incidence of 5.5/100,000.

Conclusion

Both data sources gave similar estimations of Lyme neuroborreliosis incidence. The slight difference is probably due to different case definitions used for each data source and does not change the interpretation of the data. We recommend using the hospital discharge registry to follow long-term trends in incidence and geographical spread of Lyme neuroborreliosis in Sweden because data is easier to obtain compared to a yearly inventory among hospital laboratories.

Keywords: Borrelia, Lyme borreliosis, Lyme neuroborrelios, surveillance, Sweden, Europe

PRESENTED BY: Viktor Dahl (viktor.dahl@folkhalsomyndigheten.se)

REFERENCE NUMBER: 2962

Borrelia seroprevalence in Norway 2012-2013

Didrik Frimann Vestrheim (1,2), Ingeborg Aaberge (1), Audun Aase (1)

1. Department of Bacteriology and Immunology, Norwegian Institute of Public Health, Oslo, Norway
2. European Programme for Public Health Microbiology Training (EUPHEM), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden

Background

The incidence rate of Lyme borreliosis in Norway ranged between 5.0 and 7.3 cases per 100.000 population in the period 2004-2013, with the highest annual incidence in coastal areas in the south of Norway. In endemic areas, IgG antibodies can be detected in the healthy population, and a seroprevalence up to 18% has been measured in healthy adult blood donors in the southernmost part of Norway. We performed a cross-sectional study to estimate the prevalence of antibodies against Borrelia burgdorferi sensu lato in Norway by age-groups and geography to provide a nationwide reference of positive predictive values for diagnostic testing.

Methods

We used a convenience sample of 3057 residual sera from clinical chemistry laboratories in 10 of 19 counties in 2012-2013. IgG antibodies to Borrelia was identified using a commercially available ELISA assay (Enzygnost Lyme link VlsE, Siemens, Marburg, Germany). We defined seroprevalence as the percentage of positive specimens in the sample, and estimated seroprevalence with 95% confidence interval (CI) from a logistic regression model with random effects for county and a restricted cubic spline for the age term.

Results

The overall seroprevalence was 4.0% (95% CI: 2.4%-6.6%). By geography, age-standardised seroprevalence ranged from 1.8% (95% CI: 1.0%-3.0%) in northern Norway to 8.8% (95% CI: 5.4%-14.0%) in the southernmost county. The seroprevalence increased by age, finding a 6.3% (95% CI: 3.6%-10.7%) seroprevalence in the ≥ 50 years group, as compared to 1.8% (95% CI: 1.1%-2.9%) in children aged 2-4 years.

Conclusion

The overall seroprevalence is lower than what has previously been reported from Norway. The distribution varied by geography and increased by age. The results provide regional pre-test probabilities for positive test results.

Keywords: Borrelia, Lyme borreliosis, seroprevalence, cross-sectional study

PRESENTED BY: Didrik Frimann Vestrheim (didrik.frimann.vestrheim@fhi.no)

REFERENCE NUMBER: 2899

Nutritional and Anaemic Status associated with Asymptomatic Malaria in school aged children in Nkassomo, Centre region-Cameroon: Pilot study.

Clovis Hugues Seumen Tiogang (1)

1. Molecular Parasitology and Disease Vectors Research Laboratory, The Biotechnology Center, University Yaoundé I

Background
Undernutrition and anaemia among children remain a challenging public health problem in developing countries where malaria is endemic. The present study was designed to investigate the association between nutritional status, anaemia and malaria among children in Nkassomo (a village in the center region-Cameroon).

Methods
A cross- sectional survey was carried out in November 2014. Overall, 68 children aged 2-16 years were enrolled in the study. Anthropometric parameters were measured, Weight for age (WA) and Height for age (HA) z-scores were calculated to assess underweight and stunting respectively. Finger-prick blood samples were collected for haematocrit, malaria parasite determination and Plasmodial genomic DNA extraction from filter paper.

Results
38 children (55.88%) harbored malaria parasites. Plasmodium falciparum was the only species involved. 44(64.7%) [Median: 31%, 95%CI: 30.26-32.59] were anaemic; 24 (35.29%) had moderate anaemia and 20(29.41%) mild anemia. A significant association was found between malaria status and anaemia [OR: 3.04, 95%CI: 1.49-6.17; p=0.003]. However, there was no association between malaria status and the severity of anemia [OR: 0.71, 95%CI: 0.21-2.35; p=0.76]. Globally, 27 (39.7%) and 36 (52.9%) were underweight and stunted respectively. However, there was no statistically significant association between stunting and malaria status [OR: 1.31, 95%CI: 0.49-3.42; p=0.63] or underweight and malaria status [OR: 0.89, 95%CI: 0.33-2.38; p=0.9].

Conclusion
Malaria is highly prevalent in children in Nkassomo village, it is associated with anaemia but not with malnutrition.

Keywords: Nutritional status, anaemia, malaria,

PRESENTED BY: Clovis Hugues Seumen Tiogang (seumentio@gmail.com)

REFERENCE NUMBER: 3182

Mortality above emergency thresholds from malaria in Fizi Health Zone, South Kivu, Democratic Republic of Congo, December 2013-May 2014.

Annick Lenglet (1,2), Andrew-James Willis* (3,2), Cono Ariti (4), Alebela Selemani Alain (3), Alimasi Rashidi Patient (3), Jantina Mandelkow (3), Karla Bil (1)*

1. Médecins Sans Frontières, Operational Centre Amsterdam (OCA), The Netherlands
2. These authors contributed equally to this work
3. Médecins Sans Frontières OCA, South Kivu, Democratic Republic of Congo
4. London School of Hygiene and Tropical Medicine (LSHTM), UK

Background
Since 2010, malaria incidence in Fizi Health Zone (FHZ), eastern Democratic Republic of Congo (DRC) has been steadily increasing despite efforts to increase mosquito net ownership and improve access to rapid diagnosis and treatment. In May 2014, Médecins Sans Frontières conducted a retrospective mortality survey to estimate the mortality burden of malaria in the healthzone to re-evaluate our current prevention and treatment activities.

Methods
We implemented a two-stage randomised cluster survey (selected proportionate to population size) in FHZ, including all security-accessible villages. We aimed to include 6190 persons assuming: a crude mortality rate (CMR) of 0.9 deaths per 10,000 people per day (PPD), a precision of 0.4, a recall period of 130 days, a design effect (DEFF) of 4 and a 10% non-response rate. The CMR and mortality rate for children under 5 years (U5MR) (deaths PPD) were calculated. Death from fever was defined as the proxy for malaria deaths.

Results
We surveyed 1255 households with 7301 persons; mean age was 17.7 years and 51.6% of those surveyed were females. The CMR and U5MR were estimated at 2.8 deaths PPD (95%CI: 2.40-3.28) and 5.58 deaths PPD (95%CI: 4.6-6.8) respectively. Fever accounted for 133/276 deaths (48.2%). Forty-six households (3.7%) owned the global standard of nets to cover two persons sleeping per net.

Conclusion
Mortality rates in FHZ between December 2014 and May 2015 exceeded emergency thresholds. Malaria probably contributed to the majority of these deaths and remains a grave public health concern. Current prevention and treatment activities are failing to address this problem and alternative strategies for malaria control in this part of DRC must be identified in the short term to reduce morbidity and mortality in this population.

Keywords: malaria, mortality, two-stage cluster survey, Democratic Republic of Congo,

PRESENTED BY: Annick Lenglet (annick.lenglet@amsterdam.msf.org)

REFERENCE NUMBER: 3087

Rapid Q fever testing among humans led to a quick outbreak containment and cessation of sheep cell harvesting for live cell therapy in Rhineland-Palatinate, Germany, 2014

Maja George (1), Andreas Reich (2), Hermann Jehl (3), Florian Burckhardt (4)

1. Robert Koch Institute, Berlin, Germany
2. Department for Infectious Disease Epidemiology, Bavarian Health and Food Safety Authority (LGL), Oberschleißheim, Germany
3. Regional Health Department Bad Duerkheim, Germany
4. Landesuntersuchungsamt Rheinland-Pfalz, Germany

Background

On August 7th, the local health office (LHO) of Bad Dürkheim reported a possible Q fever outbreak after an increase of pneumonia cases among residents living close to a sheep flock. Pregnant ewes of this flock were used for life cell therapy (LCT), a form of alternative medicine lacking any medical evidence and consisting of injecting fetal sheep cell suspensions into humans at two local LCT facilities (LCTF). We investigated the outbreak to interrupt transmission and determine risks for LCT recipients.

Methods

LHO facilitated case finding by informing the public through a press release about the outbreak and offered free tests for pregnant women and persons at risk for chronic disease. Occupational physicians offered tests to LCTF staff. We defined cases as IGM-phase II positive in 2014 and distinguished residential (living within 1,5km of the flock) and occupational cases (potential occupational exposure during LCT preparation). Serum and vaginal swabs were tested for Coxiella burnettii (CB) from a sample of the flock.

Results

Thirteen (11 with Q fever compatible symptoms) residential and 17 (13 symptomatic) occupational cases were identified. The flock tested CB positive. A German LCT recipient who fell ill 3 days after receiving LCT was alerted through the newspaper coverage and subsequently tested CB positive.

Conclusion

The quick response of the LHO to test residential pneumonia patients prevented further cases. The flock was housed indoor, banned for LCT and vaccinated. The short incubation time of the LCT recipient is congruent with former reports of injectional Q fever and shows the potential for CB transmission through LCT. Local authorities ordered the LCTFs to inform all 2014 LCT recipients about their potential Q fever exposure and recommend medical consultation.

Keywords: Q fever, Life cell therapy, Germany, Rhineland-Palatinate, zoonoses

PRESENTED BY: Maja George (georgem@rki.de)

REFERENCE NUMBER: 3191

Track 5: Vaccine-preventable Diseases I

MODERATOR: Pawel Stefanoff (EPIET coordinator, Norway)

Increasing meningococcal group W disease in Scotland

Alison Smith-Palmer (1), J. Claire Cameron (1), Fiona Johnston (1), Genna Drennan (1), Andrew Smith (2,3), Kevin Scott (2), Barbara Denham (2), Alistair Brown (2), Diane Lindsay (2), Louise Thom (2), Roison Ure (2), Jim McMenamin (1)

1. Health Protection Scotland, Scotland
2. Scottish Haemophilus, Legionella, Meningococcus & Pneumococcus Reference Laboratory, Scotland
3. University of Glasgow , Scotland

Background

Increases in invasive meningococcal disease (IMD) due to N. meningitidis capsular group W (MenW) have been reported in several South American countries, and more recently in parts of Africa and Europe, including England, due to a single clone belonging to the ST-11 clonal complex (cc11)

Methods

Enhanced surveillance of IMD is conducted in Scotland, linking microbiological and epidemiological data

Results

Between 2009 and 2013, cases of MenW were relatively rare in Scotland ranging from one to four cases per annum (mean 2.2). This increased to five cases in 2014 and four cases in the first quarter of 2015. MenW accounted for 16% of all cases of IMD in the first quarter 2015, an early indication that the increase in MenW observed in a number of other countries is starting in Scotland. Of the nine cases of MenW in 2014 and first quarter of 2015, seven belonged to cc11, one to cc22 and for one there was insufficient sample to determine cc. Among these nine cases, there were two deaths, a case fatality ratio of 22%. Whilst the numbers are small it does reflect the pattern seen in England where case fatality rates are higher than for MenB.

Conclusion

In response to the increase in MenW in England, the UK advisory body on immunisation advised the need for an immunisation programme to vaccinate all UK adolescents aged 14-18 years with MenACWY as soon as practicable, in order to protect them and also to generate herd protection against MenW for the rest of the population. Planning is currently progressing to implement this programme in Scotland as soon as possible to stem the increase in MenW infection.

Keywords: meningococcal disease serogroup W, immunisation,

PRESENTED BY: Jim McMenamin (jim.mcmenamin@nhs.net)

REFERENCE NUMBER: 2913

Vaccine-preventable bacterial meningitis in Bulgaria, 2006-2014

Teodora Georgieva (1), Ivan Simeonovski (1), Radosveta Filipova (2), Mira Kojouharova (1)

1. National Centre of Infectious and Parasitic Diseases, Sofia, Bulgaria
2. Ministry of Health, Bulgaria

Background

Conjugated S. pneumoniae and H. influenzae (Hib) vaccines were introduced in the National immunization calendar of Bulgaria in 2010. Immunization against N. meningitidis is not mandatory, but recommended only for certain risk groups.The aim of this study is to analyze epidemiological characteristic of vaccine-preventable bacterial meningitis in Bulgaria during the period 2006-2014.

Methods

The age-specific annual data for registered bacterial meningitis, obtained from the National surveillance system were analyzed. Data for the prevaccination 2006-2010 period were compared with the data for the period 2011-2014, when infants were immunized with pneumococcal and Hib vaccines. Real-Time PCR was used for testing of bacterial isolates.

Results

The incidence of vaccine-preventable bacterial meningitis in the general population gradually decreased from 1.08/100,000 in the prevaccination period to 0.51/100,000 in 2014 (52.87% reduction), primarily due to the Hib meningitis reduction (94.74%). During 2006-2010, the incidence of meningococcal, Hib and pneumococcal meningitis in the most affected group of 0-4 years old children was on average 4.42, 3.18 and 1.87/100,000, respectively. Four years after, there were no cases of Hib and S. pneumonie meningitis in this age group. N. meningitidis, predominantly serogroup B (90.91% from all meningococcal isolates) was the only cause of bacterial meningitis in children under 4 years and the leading agent in 5-14 years old (1.46/100,000 and 0.61/100,000 incidence).

Conclusion

As a result of mandatory infant immunization, the incidence of pneumococcal and Hib meningitis decreased significantly. The sustainable use of both highly effective conjugated vaccines along with eventual introduction of serogroup B meningococcal vaccine would ensure an optimal control of the bacterial meningitis in children in Bulgaria.

Keywords: bacterial meningitis, conjugate vaccines

PRESENTED BY: Mira Kojouharova (tgeorgieva@ncipd.org)

REFERENCE NUMBER: 2928

Streptococcus pneumoniae serotype 3 causing Parapneumonic Pleural Effusions (PPE) in children immunized with 13-valent conjugated pneumococcal vaccine (PCV13)

Georgina Tzanakaki (1), Athanasia Xirogianni (1), Maria Tsolia (2), Nekarios Marmaras (1), Konstantinos Kesanopoulos (1), Emmanuel Roilides (3)

1. National Meningitis Reference Laboratory, National School of Public Health, Athens, Greece
2. 22nd Department of Paediatrics, University of Athens, "P. and A. Kyriakou Children's Hospital", Athens, Greece
3. 33rd Department of Paediatrics, Aristotle University, Hippokration Hospital, Thessaloniki, Greece

Background

Community –acquired pneumonia (CAP) due to S. pneumoniae in children is at times complicated by the development of parapneumonic plural effusion (PPE); the later often necessitates drainage and is associated with prolonged hospitalization. In 2010, PCV13 was introduced in Greece for immunization of infants and children against pneumococcal infections. The aim of the study was to investigate the S. pneumoniae serotypes associated with PPE in children for the time period 2012-2014.

Methods

During the study period (2012-2014), pleural fluid specimens from patients ≤14 years old with PPE were sent to the National Meningitis Reference Laboratory for molecular identification by the use of three multiplex PCR assays: one species-specific, for identification of S. pneumoniae, and two for serotype identification (1, 3, 4, 6B, 14, 18C, 19A, 19F, 23F). Patients' pneumococcal immunization history was recorded.

Results

In total 66 pleural fluid specimens were studied. Among 9 serotypes investigated, serotype 3 was identified in 47 specimens (71.2%). Among those cases, 48.9% (23/47) had been previously immunized with PCV13 according to the national immunization schedule. Notably, none of these patients had received ≥3 doses of PCV13.

Conclusion

Serotype 3 is currently the most frequent S. pneumoniae serotype causing PPE in Greece with almost 50% of children with PPE to be previously vaccinated with PCV13 according to the national immunization schedule. This finding warrants close monitoring and further investigation in order to evaluate the protection afforded by PCV13 against this serotype.

Keywords: s. pneumoniae, vaccine, serotypes

PRESENTED BY: Georgina Tzanakaki (gtzanakaki@esdy.edu.gr)

REFERENCE NUMBER: 2902

Assessing the impact of implementing 10-valent pneumococcal conjugate vaccine in childhood immunisation program on the incidence of invasive pneumococcal disease, Austria, 2005-2014

Yung-Ching Lin (1,2), Lukas Richter (1), Daniela Schmid (1)

1. Austrian Agency for Health and Food Safety (AGES), Vienna, Austria
2. The European Progamme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, Stockholm, Sweden

Background

Streptococcus pneumoniae infections can cause invasive pneumococcal diseases (IPD), including meningitis, septicemia, and pneumonia with bacteremia. Persons ‹5 years and ›65 years of age, especially among those with chronic diseases, are at highest risk. In January 2012, Austria implemented the 10-valent pneumococcal conjugate vaccine (PCV10) in national immunisation program with a 2+1-dose schedule for children ‹5 years of age. We aimed to assess the impact of the implementation of PCV10 vaccination on all-age IPD incidence.

Methods

We used the national surveillance data on IPD for all ages, including bacterial serotypes, from 2005–2014. We applied interrupted time-series analysis and defined study periods as pre-implementation (2005–2011), transition (2012) and implementation (2013–2014). We used negative binomial regression to estimate changes and their 95% confidence intervals (CI) in monthly incidences of total IPD, IPD with serotype(s) available (total ST-IPD), and IPD of serotypes covered by PCV10 (PCV10 ST-IPD), between pre-implementation and implementation periods.

Results

Compared with monthly incidence in 2005–2011, the monthly incidence of total IPD decreased by 2.2%/month (95% CI: 0. 5%–3.9%), monthly incidence of total ST-IPD decreased by 3%/month (95% CI: 1.3%–4.7%), and monthly incidence of PCV10 ST-IPD decreased by 3.1%/month (95% CI: 0.2%–5.8%) in 2013–2014.

Conclusion

The monthly incidence of total IPD, total ST-IPD, and PCV10 ST-IPD decreased significantly after implementing PCV10 in the childhood immunisation program in Austria. To assess the causal relationship between PCV10 and the reduction in IPD incidence, we recommend to survey PCV10 coverage among children ‹5 years of age and to assess the impacts on IPD incidences stratified by age groups and non-vaccine covered serotypes.

Keywords: Streptococcus pneumoniae, invasive pneumococcal disease, pneumococcal vaccines, interrupted time series, population surveillance, vaccine impact

PRESENTED BY: Yung-Ching Lin (yungching.lin@gmail.com)

REFERENCE NUMBER: 2868

Protective antibodies against measles, rubella and varicella among asylum seekers arriving in the Federal State of Lower Saxony, Germany, November 2014 to February 2015

Salla Toikkanen (1,2), Armin Baillot (1), Johannes Dreesman (1), Elke Mertens (1)

1. Governmental Institute of Public Health of Lower Saxony (Niedersächsisches Landesgesundheitsamt, NLGA), Hannover, Germany
2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden

Background

The number of asylum seekers arriving in Germany is increasing and cases of vaccine preventable diseases are reported in reception centres. In a measles outbreak linked to asylum seekers in Berlin, 1134 were infected since October 2014. Lower Saxony established screening for measles, rubella and varicella antibodies in 2014. We assessed the proportion of asylum seekers having protective antibodies in order to inform outbreak control and prevention strategies.

Methods

We included screening results for asylum seekers older than 11 years arriving in Lower Saxony between November 2014 and February 2015. We defined seropositives as having anti-rubella IgG antibody concentration ›20 IU/ml and/or presence of measles or varicella antibodies based on a qualitative test. We calculated the proportion of seropositives by region of origin with 95% Clopper-Pearson exact confidence intervals (CI). We defined a population appropriately protected if the proportion of seropositive exceeded 94% for measles and rubella and 91% for varicella. Z-score test was used to compare proportions with these thresholds.

Results

Median age of the 4958 tested persons (2279 males, 893 females, 1786 unknown) was 27 years. Of these, 45% originated from Southern Europe, 25% from Western Asia and 13% from Northern Africa. Overall seropositivity was 77.1% (95%CI 76.0-78.3%) for measles, 82.4% (81.3-83.4%) for rubella and 87.7% (86.8-88.6%) for varicella. Only Somalis were appropriately protected against measles (98.4% seropositive, 95%CI 94.4-99.8%), whereas Albanians had the lowest seropositivity (66.4%, 60.9-71.7%). For rubella, Western Balkan nationals, excluding Albanians, had the lowest proportion (73.3%, 71.2-75.2%). Varicella seropositvity was lowest among Sudanese (63.7%, 58.0-69.4%).

Conclusion

Asylum seekers form a heterogeneous population in terms of protective antibodies. Our findings provide information for prioritizing outbreak control interventions, as vaccinations, to poorly protected subgroups.

Keywords: Measles, Rubella, Chickenpox, Refugees, Disease Outbreaks

PRESENTED BY: Salla Toikkanen (salla.toikkanen@nlga.niedersachsen.de)

REFERENCE NUMBER: 3099

Development of a set of core competences for vaccine preventable diseases and immunization in Europe: Achievements and next steps

Ida Czumbel (1), Carmen Varela Santos (1)

1. European Centre for Disease Prevention and Control, Stockholm, Sweden

Background

ECDC successfully developed core competences for field epidemiology, public health microbiology and infection control/hospital hygiene but had not started with subject-matter specific competencies. We aimed at providing a competency framework for prevention and control of vaccine preventable diseases and immunization (VPD&I) in Europe.

Methods

A multidisciplinary group of volunteering experts of the VPD network reviewed and integrated a tentative set of domains and subdomains through a series of presentations and workshops. To conduct an explorative literature evidence mapping, we searched in Pubmed® and Embase® to identify relevant studies for competences in immunization, combining controlled vocabulary (MesH and Emtree terms) and natural vocabulary to represent the concepts. We restricted results to records published in English but did not restrict on date.

Results

Review of the articles showed scarcity in literature fitting the searching criteria, unspecified structure and varying terminology. The expert group listed five domains, including (1) the immune system and vaccines, (2) immunization programme management, (3) vaccine logistics management, (4) scientific and technical support and (5) communication and behaviour science and broke down these five domains into 18 subdomains consisting of 85 competences.

Conclusion

Systematic approach and expert input allowed framing a first set of core competence for prevention and control of VPD&I. ECDC will explore methods to facilitate endorsement, ownership and adaptation in the MS and will launch a Web-based survey among a larger group of stakeholders to get comments and suggestions.

Keywords: vaccine preventable diseases, immunization, public health, professional competence

PRESENTED BY: Ida Czumbel (ida.czumbel@ecdc.europa.eu)

REFERENCE NUMBER: 2969

Molecular Epidemiology of Measles Viruses in Italy, 2011-2014.

Melissa Baggieri (1), Antonella Marchi (1), Paola Bucci (1), Antonietta Filia (2), Antonino Bella (2), Del Manso Martina (2), Maria Chironna (3), Filippo Ansaldi (4), Antonella Amendola (5), Tiziana Lazzarotto (6), Loredana Nicoletti (1), Fabio Magurano (1)

1. Laboratorio di Riferimento Nazionale per la sorveglianza Morbillo-Rosolia, Dipartimento di Malattie Infettive, Parassitarie ed Immunomediate, Istituto Superiore di Sanità, Rome, Italy
2. Centro Nazionale di Epidemiologia, Sorveglianza e Promozione della Salute, Istituto Superiore di Sanità, Rome, Italy
3. Dipartimento di Scienze Biomediche ed Oncologia Umana, Sezione di Igiene e medicina preventiva, Policlinico di Bari, Bari, Italy
4. DiSSal, University of Genoa and IRCCS, Genoa, Italy
5. Dipartimento di Scienze Biomediche per la Salute Università degli Studi di Milano, Milan, Italy
6. Laboratorio di Riferimento Regionale per la sorveglianza Morbillo-Rosolia, UO di Microbiologia, Laboratorio di Virologia Policlinico S. Orsola Malpighi, Bologna, Italy

Background

The Italian National Reference Laboratory for Measles and Rubella (NRL) is part of the WHO European Regional Network of Measles and Rubella Reference Laboratories with the goal of the measles elimination in Europe by 2015. This study describes the molecular characterization of measles virus (MV) strains identified in Italy during the years 2011-2014, as part of the laboratory measles surveillance activity. Clinical samples were collected from patients with suspected measles infection. Molecular tests were performed for MV detection and positive samples were sequenced and phylogenetically analysed.

Methods

Molecular detection was performed by real time PCR. A traditional RT-PCR was performed on positives (500/638) for sequencing reactions. Sequences were compared aligning the fragment coding for the carboxyl terminus of the nucleoprotein (450 nucleotides) with those of reference strains.

Results

Between 2011 and 2014, a total of 862 samples positive for MV were sequenced and phylogenetically analysed. Phylogenetic analysis showed a steady circulation of genotype D8. Genotype D4 was endemic during 2011 - 2012, and was identified until June 2013. Several cases associated to genotype B3 were identified in 2011 and 2013. Then, B3 became endemic during 2014 when it co-circulated with D8. Sporadic cases belonged to genotypes D9 and H1 during all the reviewed period.

Conclusion

Positive measles samples were genotyped to identify MV strains circulating in Italy. Genetic characterization is an essential component of laboratory-based surveillance. It provides a means to study transmission pathways of the virus and find origins and routes of MV wild-type circulation. Knowledge of currently circulating MV genotypes in Italy will help in monitoring the success of the measles elimination programme and will contribute to evaluate the effectiveness of future vaccination campaigns.

Keywords: Measles virus, Molecular epidemiology, Genotype, Phylogenetic analysis

PRESENTED BY: Fabio Magurano (fabio.magurano@iss.it)

REFERENCE NUMBER: 3197

Track 6: Influenza

MODERATOR: Pasi Penttinen (ECDC, Head of Disease Programme, Influenza and Respiratory Viruses)

Comparison of European influenza data from sentinel and non-sentinel surveillance systems, seasons 2008/09-2013/14

Cornelia Adlhoch (1), Joana Gomes Dias (1), Eeva Broberg (1), René Snacken (1), Julien Beauté (1), Phillip Zucs (1)

1. European Centre for Disease Prevention and Control, Stockholm, Sweden

Background

Surveillance of influenza virus strains in EU Member States, Iceland and Norway is based on networks of systematically selected population-representative primary care providers (sentinel sites) and a variety of other data sources (non-sentinel). Specimens from sentinel sites for laboratory testing are systematically collected from a representative sample of outpatients with influenza-like illness or acute respiratory infection, while sampling of specimens reported in the non-sentinel systems follows no particular algorithm. This study compared the reported data from sentinel and non-sentinel surveillance systems regarding influenza activity estimates and the distribution of virus types/subtypes to assess their value in monitoring the influenza season.

Methods

Weekly data on influenza detections reported from the sentinel and non-sentinel systems were extracted and described by country and season (2008/09—2013/14). A positivity rate of ≥10% was considered as an indicator of epidemic seasonal influenza activity. Spearman's rank correlation coefficient was calculated to compare weekly proportions of influenza types and subtypes reported in the sentinel and non-sentinel systems.

Results

After the 2009 A(H1N1) pandemic, the number of weekly specimens tested increased, especially in the non-sentinel systems. Compared to the sentinel systems, the non-sentinel positivity rate was lower (21-47% versus 45-61%), crossing the 10% threshold 2-6 weeks later and for a shorter duration (mean 14.7 versus 21.7 weeks). The non-sentinel system subtyped a lower proportion of viruses (37-88% versus 75-96%). The weekly proportions of virus types as well as of subtypes showed low correlation values between sentinel and non-sentinel surveillance.

Conclusion

The non-sentinel system showed a lower amplitude for seasonal influenza activity and provided less subtype information. Non-sentinel influenza surveillance adds data, but of limited value compared to the systematically collected data in the sentinel system.

Keywords: influenza, surveillance, sentinel, non-sentinel, Europe

PRESENTED BY: Cornelia Adlhoch (cornelia.adlhoch@ecdc.europa.eu)

REFERENCE NUMBER: 2930

Temporal patterns of influenza A and B in the Northern hemisphere (including Europe) compared to the Southern hemisphere and the tropics: what are the lessons for influenza vaccination?

Saverio Caini (1), Francois Schellevis (1), John Paget (1)

1. Netherlands Institute for Health Services Research (NIVEL), Utrecht, The Netherlands.

Background

Determining the optimal time to vaccinate is important for influenza vaccination programmes, particularly in the tropics where influenza activity is less predictable. We compared the temporal characteristics of influenza epidemics and discuss their implications for vaccination programmes worldwide.

Methods

We analyzed the surveillance data of 30 countries, including six European countries (England, Italy, Kazakhstan, Portugal, Turkey and Ukraine), the US, China and Brazil, between 2000 and 2014 from the Global Influenza B Study database. Seasonal peaks of influenza were identified from the weekly proportion of influenza cases. The duration of seasonal activity was assessed using the maximum proportion of cases during three consecutive months and the minimum number of months with ≥80% of cases in the season.

Results

A total of 212 influenza seasons (48 in Europe) and 571,907 cases were included in the analysis. In temperate countries (Northern and Southern hemispheres), most cases occurred during a short period in winter (2-4 months; mainly in January-February in Europe), the timing of epidemics did not differ by virus type, and the current timing of influenza vaccination campaigns seemed appropriate. In tropical countries, the seasonal influenza activity lasted longer (3-10 months), the peaks of influenza A and B coincided less frequently, and the temporal characteristics of influenza epidemics were more heterogeneous, with distinct seasonal epidemics observed only in some countries.

Conclusion

In conclusion, contrary to Europe and other countries of the Northern and Southern hemispheres, a harmonized approach for influenza vaccination timing is probably not effective in the tropics. Recommendations on when to vaccinate in the tropics should be based on an analysis of surveillance data collected locally, highlighting the need for high-quality influenza surveillance systems in these countries.

Keywords: Influenza, timing of epidemics, duration of epidemics, vaccination, surveillance, tropics

PRESENTED BY: Saverio Caini (s.caini@nivel.nl)

REFERENCE NUMBER: 2919

Neuraminidase inhibitor susceptibility profile of Greek seasonal influenza viruses during post pandemic seasons (2010 - 2014)

Kyriaki Tryfinopoulou (1,2), Athanassios Kossyvakis (3), Vasiliki Pogka (3), Antonios Kalliaropoulos (3), Afroditi Moutousi (3), Sotirios Tsiodras (4), Petros Karakitsos (5), Andreas Mentis (3)

1. European Public Health Microbiology Training programme (EUPHEM), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
2. Antimicrobial Resistance and HAI Laboratory, National School of Public Health-CPHL-HSDCP, Greece
3. National Influenza Reference Laboratory of Southern Greece, Hellenic Pasteur Institute
4. Department of Internal Medicine
5. Department of Cytopathology

Background
Neuraminidase inhibitors (NAIs) are currently the only effective class of anti-influenza drugs. The potential emergence of NAI-resistant influenza viruses and their efficient broad transmission necessitates extensive antiviral susceptibility vigilance. This study aimed to determine the susceptibility to NAIs of A and B influenza viruses circulated in Greece during post-pandemic (2010 - 2014) seasons.

Methods
In total 269 representative [152 A(H1N1)pdm09, 82 A(H3N2) and 35 B] influenza strains isolated in Greece were studied. The fluorescence-based 50% inhibitory concentration (IC50) phenotypic method was used to determine susceptibility to NAIs, according to WHO criteria proposed for NAI susceptibility. Sequencing of NA gene was used to reveal resistance-associated mutations. HA-gene sequencing was performed in parallel.

Results
No A(H3N2) or B viruses were found NAI-resistant using both genetic and phenotypic testing. All influenza type A and B viruses were susceptible to zanamivir. Oseltamivir resistance was only observed in five A(H1N1) pdm09 viruses isolated from immunocompromised patients during oseltamivir treatment and the NA H275Y amino acid substitution was confirmed. None of the NA permissive substitutions (V241I, T289M, N369K and N386K) were confirmed in oseltamivir-resistant A(H1N1) pdm09 viruses. However, V241I, N369K and N386K were detected in A(H1N1)pdm09 strains isolated since 2011, all phylogenetically distinct from the vaccine strain when compared at the HA gene level. Emergence of D93G NA mutant H3N2 viruses (4 strains in 2012 and all strains in 2013 and 2014) coincided with the extensive HA variation of H3N2 viruses.

Conclusion
This study demonstrated no reduction in NAIs susceptibility or increased frequency of resistant variants for any strain or subtype. However, considering the public health impact of emergence of highly transmissible NAIs resistant influenza viruses in a pandemic situation, monitoring of NAI resistance is essential.

Keywords: Influenza, Neuraminidase-Inhibitors resistance, mutations

PRESENTED BY: Kyriaki Tryfinopoulou (k.tryfinopoulou@otenet.gr)
REFERENCE NUMBER: 2976

Monitoring influenza activity: Use of healthcare staff sickness absence rates as a novel measure of influenza surveillance

Naomh Gallagher (1), Jillian Johnson (1)

1. Health Protection, Public Health Agency, Belfast, Northern Ireland

Background
Influenza is a major cause of morbidity and mortality, and there are a number of indicators that are traditionally used to measure the burden of flu. Novel methods, such as Google trends and emergency department attendances, have been used in recent times to complement traditional surveillance. This study examines the correlation between staff sickness absence rates and routine flu indicators to assess possible utilisation of absence rates as a novel surveillance indicator.

Methods
Electronic staff sickness absence data were collated from eleven healthcare organisations in NI over a 24 month period (April 2013 – March 2015). Organisations contributed an average of 16 month's data, dependent on introduction of the electronic human resources system, and total staff time included was 79.8m hours. Pearson's correlation coefficients were calculated to measure the association between monthly rates of sickness absence recorded as a respiratory condition or influenza, and GP consultations for influenza-like-illness (ILI) and acute respiratory infection (ARI) per 100,000 population and influenza laboratory positivity proportions.

Results
There were approximately 280,000 hours of respiratory absence and 78,000 hours of influenza absence over the time period. The mean absence rates across all organisations were 0.348% and 0.096% respectively. Significant positive correlation was found between respiratory absence and all three traditional indicators, and between flu absence and ARI consultations (Table 1). Table 1: Pearson's correlation coefficient values ILIARILaboratory PositivityRespiratory Absence 0.6471*0.6023*0.6339* P Value0.0010.0020.001Flu Absence0.51470.5941*0.4253 P Value0.0100.0020.043* Statistically significant

Conclusion
Higher rates of respiratory and influenza sickness absence are positively associated with higher rates of flu activity, and should be considered as a novel addition to traditional surveillance methods.

Keywords: Influenza, health care sector, influenza vaccine, absenteeism, respiratory

PRESENTED BY: Naomh Gallagher (naomh.gallagher@hscni.net)
REFERENCE NUMBER: 3116

Genetic variability of influenza virus and vaccine effectiveness

Raquel Guiomar (1), Pedro Pechirra (1), Inês Costa (1), Paula Cristovão (1), Ana Paula Rodrigues (2), Baltazar Nunes (2), Ausenda Machado (2)

1. National Influenza Reference Laboratory, National Institute of Health Dr Ricardo Jorge
2. Department of Epidemiology, National Institute of Health Dr Ricardo Jorge

Background
Since 2008, EuroEVA estimates the influenza vaccine effectiveness (VE) for each influenza season in primary care in Portugal. A higher VE is expected when circulating viruses are similar to the vaccine strains.

Methods
VE was estimated using the test negative design. Genetic characterization was performed by sequence analysis of HA1subunit of haemaglutinin gene, antigenic characterization by hemaglutination inhibition assay.

Results
Since 2010 A(H1)pdm09 was the most frequent in 2010/11 (55.7%) and 2013/2014 (59.7%). The influenza A(H3) was predominant in 2011/2012 (97.7%). Influenza B virus co-circulated in 2010/2011 (42.7%) and 2012/2013 (49.5%) with A(H1)pdm09, and was dominant in 2014/2015 (66.0%). The VE for A(H1)pdm09 was 33.7% (CI50%: -254.9%; 87.6%) in 2010/2011 and 43.7% (CI95%: -51.6%; 79.1%) in 2012/2013. For A(H3) the VE was approximately 49% in 2011/2012 and 5.9% in 2014/2015. Influenza B VE was 75,1% (CI95%: -98,3%-96,9%), 92.5% (CI95%: 39.2%-99.1%) and 80.0% in 2010/11, 2012/13 and 2014/15, respectively. For both subtypes of influenza A the acquisition of substitutions in antigenic sites that correlates with higher differences comparing with vaccine strains was observed.

Conclusion
Overall, VE for A(H1)pdm09 did not reflect the genetic variability of circulating strains, although for A(H3) a dramatically reduction in VE was observed in last season when drift virus dissimilar to the vaccine strain circulated. For influenza B, the VE was always higher comparing with influenza A, even when the circulating lineage is different from the vaccine selected virus. This fact is in line with cross-immunity between different influenza B strains. The antigenic and genetic characteristics of circulating viruses are an important clue for VE interpretations however there are other individual immunological factors that should be considered, such as the role of cellular immunity.

Keywords: effectiveness, influenza, vacine, genetic, antigenic

PRESENTED BY: Ana Paula Rodrigues (ana.rodrigues@insa.min-saude.pt)
REFERENCE NUMBER: 3168

Influenza Sentinel Surveillance in Nigeria, 2008-2012: A Secondary data analysis

Abimbola Aman-Oloniyo (1), Adebayo Adedeji (2), Endie Waziri (1), Ibrahim Dalhatu (3), Akin Oyemakinde (2)

1. Nigeria Field Epidemiology and Laboratory Training Programme, Abuja, Nigeria
2. Federal Ministry of Health, Epidemiology Division, Abuja, Nigeria
3. Centers for Disease Control and Prevention, Nigeria Office, Abuja, Nigeria

Background
The epizootics of avian Influenza among poultry between 2006 and 2008 and the confirmation of one human case in Nigeria in 2007, highlighted the need to establish an Influenza Sentinel Surveillance (ISS) system to determine influenza trends and characterize associated influenza types and subtypes in the human population. ISS commenced in Nigeria 2008.. A national influenza reference laboratory (NIRL) and one ISS site each was established in 4 of the 6 geo-political zones. Our objective was to determine the distribution and influenza types and subtypes detected.

Methods
We obtained and analysed the 2008 – 2012 data on results of specimens collected from patients with influenza-like illness (ILI) at the outpatient departments and severe acute respiratory infection (SARI) at in-patient wards from the ISS sites using Epi info 3.5.4.

Results
A total of 8254 patients were reported; about 52.5% were males and mean age was 9.7 (+/- 16.0) years; children aged 0-4 years constituted the highest number 5447.6 (66%). Of all specimens collected, 6547 (80.1%) and 1587 (19.4%) were from patients with ILI and SARI, respectively. Only 472 (5.7%) of all samples were positive for influenza type A and 243 (3.0%) for influenza type B. Influenza occurred all year round; influenza A peaked during epidemiological weeks 1-15 and 32-44; Influenza B peaked in weeks 35-49. Subtypes of influenza A and proportional occurrence observed between 2008 and 2012 were A/H1 (3.2%), A/H3 (50.2%), novel A (H1N1) (43%) and A/unsubtyped (0.2%).

Conclusion
The information from ISS sites is useful in characterizing seasonal human influenza (sub) types. Both seasonal and pandemic influenza occurred in Nigeria between 2008 and 2012. Children aged 0-4 years have been most vulnerable.

Keywords: Influenza, sub types, Nigeria, sentinel surveillance

PRESENTED BY: Abimbola Aman-Oloniyo (bimboaman@gmail.com)
REFERENCE NUMBER: 2889

Track 7: Surveillance I

MODERATOR: Alicia Barrasa (EPIET coordinator, Spain)

Evaluation of the surveillance of haemolytic uremic syndrome in France: need to involve regional health authorities

Laure Fonteneau (1,2), Lisa King (1), Mathias Bruyand (1), Henriette de Valk (1)

1. French Institute for public health surveillance, France
2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden

Background
Since 1996, surveillance of shigatoxin-producing Escherichia coli (STEC) infections in France was based on surveillance of haemolytic uremic syndrome (HUS) through a network of voluntary pediatric nephrology departments. The surveillance, managed at national level, aims at detecting, controlling and preventing cases and outbreaks, and monitoring trends in disease occurrence. We evaluated the system in order to identify strengths and weaknesses and formulate recommendations.

Methods
To assess timeliness, we calculated the median delay between diagnosis and notification. To assess data quality, we checked the completeness of variables allowing identification of clusters, laboratory confirmation and ascertainment of exposures. To assess representativeness we calculated the number of reporting departments by regions. To evaluate usefulness, we assessed the numbers of notified HUS cases, the number of detected and investigated clusters (≥ 2 STEC infections with epidemiological link) and the number of investigations which triggered control measures, in view of the system objectives.

Results
During 2011-2013, 31 nephrology departments covering all the French regions participated in the network, 459 HUS cases were notified, and 50 clusters were detected and investigated. In 4 clusters, the investigations incriminated a common source and guided the implementation of control measures. The completeness was 51% for exposure variables and above 80% for others variables. The median delay between diagnosis and notification was shortened from 13 days in 2003 to 3 days in 2013.

Conclusion
The HUS surveillance system collected high-quality data, allowed the timely detection of HUS cases, and the implementation of control measures. Human resources at national level were insufficient to systematically explore at risk exposures. We recommend involving the regional health authorities to routinely document the risk factors for each case.

Keywords: Evaluation, Surveillance, Shiga-Toxigenic Escherichia Coli, Haemolytic Uremic Syndrome, France

PRESENTED BY: Laure Fonteneau (l.fonteneau@invs.sante.fr)

REFERENCE NUMBER: 3031

Evaluation of post-discharge surveillance of surgical site infections in Finland, 1999-2013: Can register linkage improve completeness of reporting?

Jozica Skufca (1,2), Jukka Ollgren (1), Dinah Arifulla (1), Teemu Möttönen (1), Outi Lyytikainen (1)

1. Department of Infectious Diseases, National Institute for Health and Welfare (THL), Helsinki, Finland
2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden

Background
Due to increasingly shorter hospital stays, post-discharge surveillance (PDS) of surgical site infections (SSIs) is vital for estimating SSI incidence. Hospitals participating in the Finnish Hospital Infection Programme (SIRO) include three methods to detect SSIs after hospital discharge: post-discharge questionnaire, follow-up visits and readmissions to the hospital. However, some cases may be missed. We evaluated whether the National Hospital Discharge Register (HILMO) can be used to validate and increase the completeness of SSI surveillance data and sensitivity to detect SSI on readmission.

Methods
We included all surgical procedures under surveillance in SIRO hospitals during 1999-2013 and identified the overlapping hospitalizations from HILMO by using the national identity number and hospital codes. We assessed the overall percentage of SSIs detected by PDS and percentage detected on readmission. We completed the missing hospital discharge dates from HILMO, which allowed us to ascertain the percentage of SSIs occurring after discharge. We compared the number of SSIs identified on readmission with the number of readmitted patients with the ICD infection code (T81.4) in HILMO.

Results
In total, 185,351 surgical procedures and 4,757 (2.6%) SSIs were identified in 19 hospitals, of which 3,288 (69%) were detected by PDS, including 1,708 (36%) on readmission. 177,108 (96%) surgical procedures matched with hospitalizations in HILMO, allowing to complete 177,069 (96%) hospital discharge dates and to confirm 3,337 (70%) post-discharge SSIs in SIRO. In total, 2,442 readmissions coded as T81.4 were identified in HILMO, including 640 overlapping with SIRO.

Conclusion
HILMO can be used to validate and complete SSI data in SIRO and for additional case finding. Number of post-discharge SSIs on readmissions detected by only one of the systems indicates that their combination will increase sensitivity.

Keywords: surgical site infections, surveillance, post-discharge, readmission, register

PRESENTED BY: Jozica Skufca (josie.skufca@gmail.com)

REFERENCE NUMBER: 2880

Resurgence of scarlet fever in England, 2014

Theresa Lamagni (1), Rebecca Guy (1), Katherine Henderson (1), Victoria Chalker (1), Ali Al-Shahib (1), Anthony Underwood (1), Alex J Elliot (1), Juliana M Coelho (1), Meera Chand (1), Vanessa Saliba (1), Gillian Smith (1), Mary Ramsay (1), Alan P Johnson (1)

1. Public Health England, UK

Background
Following a prolonged period of low incidence of scarlet fever, a remarkable upsurge in disease incidence occurred in Spring 2014 in the UK. Investigations were initiated to assess possible reasons for, and the impact of, the increase.

Methods
Notifications of clinical scarlet fever and outbreaks were analysed. Cases were linked to hospital admissions to identify severe outcomes. GP sentinel surveillance was used to estimate the total number of consultations. A sentinel sampling scheme collected a representative number of group A streptococcal throat isolates from clinical cases for emm typing and genomic sequencing.

Results
A total of 14,398 scarlet fever notifications were made across England in 2014, more than triple the number of cases in 2013 (4436). Elevated levels were reported across the country with incidence peaking just before Easter. The age distribution of cases ranged from <1y to 90y with 87% of cases <10y and peak incidence in 4y olds. GP surveillance data estimated a total of 26,500 consultations in 2014 compared to 13,200 in 2013. A total of 81 outbreaks of scarlet fever were reported in a variety of community settings. Analysis of linked hospital records identified 1280 admissions of which 125 specified management of scarlet fever. No attributable deaths were identified. Assessment of 430 throat isolates from cases identified a diverse range of emm types with emm3 most common (43%). Genomic sequencing analysis of 336 isolates identified multiple lineages.

Conclusion
The UK has noted the highest number of scarlet fever cases in 45 years and is the latest in a series of countries reporting resurgence in disease. Further understanding of the drivers behind the rise is essential to guide future prevention strategies.

Keywords: scarlet fever, Streptococcus pyogenes, epidemics, Epidemiological monitoring, Disease outbreaks, England

PRESENTED BY: Theresa Lamagni (theresa.lamagni@phe.gov.uk)

REFERENCE NUMBER: 3061

Two thirds of all notifications in the German surveillance system are notified until the next day

Jakob Schumacher (1), Drik Schumacher (1), Maelle Salmon (1), Michaela Diercke (1), Hermann Claus (1), Andreas Gilsdorf (1)

1. Robert Koch Institute, Department for infectious disease epidemiology, Seestraße 10, 13353 Berlin, Germany

Background
Late notification of infectious diseases delays public health actions. In Germany, the infection protection act specifies which infectious diseases have to be notified by physicians and laboratories to the local public health authorities (LPHA). On 29/03/2013 an amendment changed the obligation to "notify within 24h" to "notifications must arrive within 24h". We compared the timeliness of notifications from physicians and laboratories and examined the impact of the amendment.

Methods
We defined notification delay as the period between diagnosis date and the notification's first arrival at the LPHA. We selected notifications from 29/03/2012 until 28/03/2014, that were forwarded to the national level, of time-critical (as appraised by the study group) and common diseases (>100 cases in the time period). We calculated the proportion of notifications arriving at the LPHA until the day after diagnosis, and median and mean aggregated notification delays before and since 29/03/2013.

Results
Delay could be calculated for 8,479/40,003 (21%) physicians' notifications and 442,562/679,557 (65%) laboratories' notifications. Overall, 49% of physicians' notification and 69% of laboratories' notifications arrived until the day after diagnosis. Before the revision of the law the median notification delay of physicians was 2 days (mean 6.0) and 1 day (mean 4.3) afterwards, for laboratories 1 day (mean 1.7) before and 1 day (mean 1.5) afterwards

Conclusion
Laboratories notify diseases faster than physicians. Since the 29/03/2013 revision, the notification delay for physicians has decreased. This might be attributable to the amendment, to changes in LPHA recording practice or to changes in recording software. About one third of all cases are not notified until the next day. An electronic system for notification could improve the timeliness of notifications in the German surveillance system.

Keywords: Disease, Outbreaks, Mumps, immunisation, Measles-Mumps-Rubella vaccine

PRESENTED BY: Jakob Schumacher (jakob.schumacher@web.de)

REFERENCE NUMBER: 3044

Increased number of campylobacter detections in blood samples in Sweden from June to October in 2014 - artefact or true increase?

Heli Harvala (1,2), Elsie Castro (1), Mia Brytting (1), Karin Tegmark-Wisell (1), Cecilia Jernberg (1), Anders Wallensten (1)

1. Public Health Agency of Sweden, Solna, Sweden
2. European Programme for Public Health Microbiology Training (EUPHEM), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden

Background

Data on campylobacteremia is limited globally, and its clinical significance is poorly understood. It is thought to be a rare entity occurring mostly in immunocompromised patients. The incidence of campylobacteremia has varied between 0.1% and 0.4% of the total incidence of Campylobacter infections in the UK, Denmark and Finland. We performed a detailed retrospective investigation on all reported Campylobacter infections in Sweden as an increase in the number of campylobacteremia was first noted in October 2014.

Methods

Due to mandatory reporting, all Campylobacter infections diagnosed in Sweden (population of 9.64 million people) are reported to the SmiNet2 database maintained by the Public Health Agency of Sweden. Data on Campylobacter infections reported in 2010-2014 was collected and analyzed. An on-line questionnaire regarding the laboratory methods used was submitted to all 28 laboratories.

Results

Between 2010 and 2014, 39,832 Campylobacter infections were noted in Sweden and 133 were bacteremia cases. Interestingly, the number of campylobacteremia cases increased from five cases in 2010 to 83 in 2014. The incidence of campylobacteremia increased from 0.15% of the total incidence of Campylobacter infections between 2010 and 2013 to 1% in 2014 (OR 6.6, 95%CI 4.6-9.5, p<0.0001). Cases of campylobacteremia were reported throughout Sweden, and in all age groups. Whereas no changes in denominators or reporting were identified, the increase co-insided with the change in blood cultivation material by a commercial company.

Conclusion

The incidence of campylobacteremia increased significantly in Sweden in 2014, most likely due to increased sensitivity of blood cultivation. It is unknown whether campylobacteremia was associated with the specific campylobacter type(s) and hence typing of Campylobacter-positive blood isolates needs to be considered.

Keywords: Campylobacter, bacteremia, typing, reporting, blood culture

PRESENTED BY: Heli Harvala (heli.simmonds@hotmail.com)

REFERENCE NUMBER: 2949

Comparison of sporadic cases of invasive meningococcal disease (IMD) with cases in clusters, Germany, 2005-2013

Emilie Johanna Peron (1,2), Johannes Elias (3), Ulrich Vogel (3), Heike Claus (3), Wiebke Hellenbrand (2)

1. European Programme for Interventional Epidemiology Training (EPIET), ECDC Stockholm, Sweden
2. Department for Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany
3. University of Wuerzburg, Institute for hygiene and Microbiology and National Reference Laboratory for Meningococci, Wuerzburg, Germany

Background

Although pharyngeal carriage of Neisseria meningitidis is common, ensuing invasive meningococcal disease (IMD) is rare and mostly sporadic, but clusters may occur. We compared sporadic cases and cases in clusters identified by two different approaches to gain insight into transmission patterns.

Methods

Cases of IMD notified in Germany from 2005-2013 were matched to reference laboratory typing data. Epidemiological clusters (EC) were defined as two or more cases with documented known direct or indirect contact. Spatiotemporal clusters (STC) included cases without known direct or indirect contact, but with identical finetype (based on serogroup and antigen sequence typing of variable regions of outer membrane proteins PorA and FetA) and significantly clustered in space and time, shown using SaTScanTM. We compared age, sex, serogroup, and seasonality of sporadic cases (SC) and cases in clusters using Kolmogorov-Smirnov and Chi-square tests.

Results

Of 4,184 IMD cases, 3,816 (91.2%) were sporadic, 304 (7.3%) in 111 STC and 64 (1.5%) in 29 EC. In EC, 84% of cases were 1-24 years old versus 57% in SC and 64% in STC (p≤0.04). There were more males in EC (64%) than STC and SC (53%, p=0.2). The proportion of serogroups B and C was similar in SC, STC and EC (70% and 23% overall). Cases within EC had identical finetypes (when available).The proportion of cases in the first annual quarter was 45.1% in STC, 43.7% in EC and 35.3% among SC (p=0.001).

Conclusion

Clusters occurred rarely, and mainly as STC, reflecting predominantly asymptomatic community transmission chains. Results suggest a higher risk of transmission to close contacts in childhood and young adulthood. More clusters occurred in winter months, when IMD incidence, and thus force of infection, is highest.

Keywords: Invasive meningococcal disease, surveillance, cluster, Germany

PRESENTED BY: Emilie Johanna Peron (emilie.peron@free.fr)

REFERENCE NUMBER: 3120

Evaluation of the enterovirus laboratory surveillance system in Denmark, 2010 to 2013

Orla Condell (1,2), Sofie Elisabeth Midgley (1), Peter Henrik Andersen (3), Thea Kølsen Fischer (1,4)

1. Department of Microbiological Diagnostics and Virology, Statens Serum Institut, Copenhagen, Denmark
2. European Program for Public Health Microbiology Training (EUPHEM), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden
3. Department of Infectious Diseases Epidemiology, Statens Serum Institut, Copenhagen, Denmark
4. Center for Global Health and Department of Infectious Diseases, Clinical Institute, University of Southern Denmark

Background

Renewed spread of poliovirus poses a global threat. Closest to Europe the current armed conflict in Syria has left many children unvaccinated. The refugee influx to European countries calls for increased awareness to detect and respond to poliovirus-transmission in a timely manner. This study aims to evaluate the EV laboratory surveillance system in Denmark based on cultivation, typing and sequencing of clinical samples, in order to generate recommendations for system strengthening.

Methods

A national EV-database (EV-DK) was generated combining data from the national EV-laboratory database with the Danish Microbiology Database. EV-DK was analysed for completeness of submission of EV-positive-specimens for characterization from primary diagnostic laboratories to the National WHO Poliovirus Reference Laboratory (NRL). The timeliness of specimen collection, laboratory results and reporting of clinical information was assessed. Stakeholder-interviews were conducted to map the laboratory-data reporting structure for Denmark.

Results

Of 23,720 specimens screened, 2,202 were EV-positive. Submission of CSF and stool specimens from primary diagnostic laboratories to the NRL was 79.5% complete (845/1,063), and varied by the laboratory (p-value ‹0.001) and patient age (p-value ‹0.001). EV sub-types were successfully determined in 68.5% (979/1,430) of cases, and clinical information available for 63.1% (903/1,430). Primary diagnostic results were available after a median of 1.4 days, typing results after 17 days, and detailed clinical information after a median of 33 days.

Conclusion

The large number of samples tested for EV demonstrated the continued monitoring of EV-circulation in Denmark. The system could be improved in several ways: increasing participation of primary diagnostic laboratories and improved laboratory typing-methodology to reduce the number of non-typeable EV (representativeness) and applying electronic reporting of clinical information (timeliness). National guidelines will be updated to address these issues.

Keywords: Surveillance objectives, Evaluation, Enterovirus, Denmark

PRESENTED BY: Orla Condell (ORCO@ssi.dk)

REFERENCE NUMBER: 2933

Track 8: Outbreaks I

MODERATOR: Christian Winter (EPIET coordinator, Germany)

Outbreak of acute hepatitis B virus infection associated with exposure to acupuncture, British Columbia, 2014

Shirley Rempel (1,2), Michelle Murti (2), Geoffrey Ramler (2), Christina Fung (2), Jasdeep Virk (2), Susan Loadman (1), Mel Krajden (3), Jane Buxton (3), Anton Andonov (4), Marcus Lem (2)

1. Canadian Field Epidemiology Program, Public Health Agency of Canada, Surrey, British Columbia, Canada
2. Fraser Health Authority, Surrey, British Columbia, Canada
3. British Columbia Centre for Disease Control, Vancouver, British Columbia, Canada
4. National Microbiology Laboratory, Public Health Agency of Canada, Winnipeg, Manitoba, Canada

Background

Two cases of acute hepatitis B virus (HBV) infection were reported to the Fraser Health Authority (FH), British Columbia between July and September, 2014. Both cases had received acupuncture services from the same provider within four months of symptom onset. Objectives of the outbreak investigation were to confirm acupuncture as the suspected source of transmission, identify those at risk, determine if there were additional cases and prevent further spread.

Methods

The outbreak investigation included genotyping of HBV from the identified cases, inspection of the acupuncturist's infection prevention and control practices, and chart review of known clients.

Results

Both cases had HBV genotype D1 with an identical fingerprint which was highly suggestive of a common source of infection. Case investigations revealed that both clients had visited the clinic on the same day in May 2014 and denied other recent risk exposures. Inspection of the acupuncturist's practice revealed high-risk re-use and inappropriate storage of disposable needles. The practitioner tested negative for HBV. FH ordered cessation of clinic practice until infection control measures were remediated. A public service announcement and mailed notifications to 1516 clients with address information, recommended that all clients be tested for HBV, HIV and hepatitis C. One new case of chronic HBV was reported to FH in a former client, but with unrelated genotype.

Conclusion

Based on the epidemiologic investigation and the similarity of the molecular HBV genotypic profile, contaminated acupuncture needles likely resulted in at least two cases of acute HBV infection. Single use needles are the practice standard based on previously identified HBV transmissions from re-usable needles in acupuncture. This is the first reported transmission of HBV from improper reuse of disposable needles.

Keywords: Acupuncture, Medicine, Chinese Traditional, Hepatitis B Virus, Blood-Borne Pathogens

PRESENTED BY: Shirley Rempel (shirley.rempel@fraserhealth.ca)

REFERENCE NUMBER: 2973

Cluster of two cases of botulism due to Clostridium baratii type F in France, November 2014

Christine Castor (1), Christelle Mazuet (2), Melanie Saint-leger (3), Sabine Vygen (1,4), Juliette Coutureau (1), Patrick Rolland (1), Nathalie Jourdan-Da Silva (5), Michel-Robert Popoff (2)

1. French Institute of Public Health, Department of Coordination of Alerts and Regions, Regional office in Aquitaine, Bordeaux, France
2. National Reference Centre (NRC) for anaerobic bacteria and botulism, Institut Pasteur, Paris, France
3. Perigueux Hospital Centre, Intensive care unit, Périgueux, France
4. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
5. French Institute of Public Health, Department of Infectious Disease, Saint-Maurice, France

Background

On 12 November 2014, two cases of botulism were notified in France by the same hospital. Epidemiological and microbiological investigations were conducted to confirm the outbreak and to determine the source of exposure.

Methods

Microbiological confirmation and toxin identification were undertaken by the national reference centre (NRC) for botulism. Both cases were hospitalised in intensive care and could not be interviewed. Epidemiological investigations were performed with family members.

Results

The NRC confirmed the diagnosis of botulism due to Clostridium baratii type F for both cases. One had extremely high toxin serum levels and remained paralysed for two weeks. No predisposing factors for intestinal or wound botulism were identified for either case. Both cases had participated in a meal together with six other family members on 9 November 2014 and had had lunch together on 6 November but eaten different meals. They live in different towns and had not met on any other occasion during the two weeks before symptom onset. The food list of the family meal included mainly industrially processed food; no food classically at risk of botulism was identified. The only common exposure not shared with any other person was a same bottle of alcopop. However, all analyses of leftover food remained negative.

Conclusion

These are the first two cases in France of botulism due to Clostridium baratii type F, which is unusual worldwide. For most cases documented in the literature, the source of contamination is not reported. Our Investigations generated the hypothesis of a common exposure during the family meal with a highly contaminated source, which remained undetected. Continuous mandatory notification of botulism cases will help identify other toxin F cases and direct future investigations.

Keywords: botulism, Clostridium baratii, neurotoxin F, foodborne outbreak, epidemiology

PRESENTED BY: Christine Castor (christine.castor@ars.sante.fr)

REFERENCE NUMBER: 3030

An outbreak investigation of Cryptosporidiosis in Dorset, England, in April-May 2013 and follow up of intervention: a case-control study strengthened epidemiological evidence

Benedetto Simone (1), Naomi Boxall (1), Sanch Kanagarajah (1), Linda Booth (2), Sooria Balasegaram (1)

1. Field Epidemiology Services, South East and London, Public Health England, UK
2. Wessex Public Health England Centre, UK

Background

We investigated an outbreak of cryptosporidiosis in Dorset, England, in April/May 2013. Descriptive analysis suggested a water source (A) supplying Water Company X, serving the area with most cases. Additionally, low oocyst levels had been detected in Source A. Our objective was to measure the association between illness and exposure to Source A, accounting for demographic and behavioural confounders.

Methods

We defined study cases as adult residents in the area served by Company X with microbiologically-confirmed cryptosporidiosis. We compared each case with three controls, selected from the same area via sequential digit dialling, in terms of demographic characteristics, foods eaten, water imbibed from different sources and contact with animals in 10 days prior to symptom onset. We fitted the variables associated with the occurrence of illness ($p<0.20$) in a logistic regression model, provided adjusted odds ratios and 95% confidence intervals (aOR;CI). We continued case surveillance after a water treatment system was installed.

Results

We included 15 cases and 53 controls and found an association between illness and residence in households supplied by Source A (aOR=25.8; CI:2.2-306.2), age (aOR=0.9; CI:0.9-1.0) and animal faeces contact (aOR=8.5; CI:1.7-43.8). Univariable analysis showed 10% increased odds of illness per additional glass of unboiled water imbibed from Water Source A ($p=0.036$) but this was not demonstrated in multivariable analysis. Since February 2014 to present, cases from Source A have declined.

Conclusion

Our case-control study confirmed the association between cryptosporidiosis and the water source and excluded confounding by other factors investigated. We recommend using case-control studies to investigate similar outbreaks to strengthen epidemiological evidence. The findings contributed to a review of water treatment and the installation of an ultra-violet treatment system in February 2014.

Keywords: Cryptosporidiosis, Disease Outbreaks, Case-Control Studies, commumicable-disease control

PRESENTED BY: Sooria Balasegaram (sooria.balasegaram@phe.gov.uk)

REFERENCE NUMBER: 3079

Investigation of a national outbreak of VTEC Escherichia coli O157 using online consumer panel control methods - Great Britain, October 2014

Chantil Sinclair (1,2), John Paul Harris (1), Bob Adak (1)

1. Public Health England, UK
2. UK Field Epidemiology Training Programme

Background
In October 2014, Public Health England (PHE) identified a cluster of Escherichia coli O157 PT8 (VTEC) which shared a Multiple Locus Variable-number Tandem Repeat Analysis (MLVA) profile. Due to increased cluster detection it has become necessary to find less resource-intensive investigation methods. During 2013, an online consumer panel, which rewards members for completing surveys, was trialled as a novel recruitment method. It was found to be comparable to traditional methods. The aims of this investigation were to identify the vehicle of infection using online survey methods.

Methods
We conducted a case-control study, recruiting two controls per case. Cases were identified as Great British residents, aged 18 or over, with the outbreak MLVA strain. Multivariable logistic regression was carried out to calculate adjusted odds ratios (aOR) and 95% confidence intervals (95%CI). A consumer survey panel randomly recruited controls by emailing members an online survey link. PHE contacted cases first by phone and then email. We excluded participants with history of travel within seven days of symptom onset.

Results
We recruited 36 (75%) of 48 contactable cases and 96 controls over five days; only several hours were needed to prepare data for analysis. Cases had greater odds of consumption of pre-packed salad (aOR 13; 95%CI 4.2-42). Additionally, they were more likely to have purchased salad (aOR 28; 95%CI 5.0-157) or potatoes (aOR 3.3; 95%CI 1.0-10) from a specific retailer.

Conclusion
This study demonstrates a strong epidemiological link between consumption of pre-packed salad and disease. The use of consumer panel controls in conjunction with online surveys was less resource intensive than traditional data collection methods. Therefore we recommend this as a plausible method for use in future outbreak investigations.

Keywords: case-control studies, disease outbreaks, Escherichia coli O157, Gastrointestinal Diseases, Public Health

PRESENTED BY: Chantil Sinclair (chantil.sinclair@phe.gov.uk)

REFERENCE NUMBER: 2903

A rapid communication protocol for sharing infectious disease risk alerts with cross-border partners in the Euregions of Germany, Belgium and the Netherlands

Henriëtte ter Waarbeek (1), Chakib Kara-Zaïtri (2), Verena Bochat (3), Christian Hoebe (1), Robert Hamilton (4)

1. Dpt. of Infectious Disease Control, Public Health Service South Limburg, Geleen, Netherlands, and Dept of Microbiology, Maastricht University, Maastricht, The Netherlands
2. Faculty of Engineering and Informatics, University of Bradford, Bradford, England
3. Public Health Service Aachen, Aachen, Germany
4. inFact. Shipley. England

Background
Recent international outbreaks have exposed several gaps in the timeliness and accuracy of data exchanged between cross-border partners due to disparate un-integrated national surveillance systems and inconsistent notification protocols. There is an urgent need for a simple but effective communication protocol for alerting cross-border partners of any public health risks, and exchanging key information required for harmonising the control of infectious disease despite varying legislation.

Methods
This paper presents the results of a two-year research programme in the Euregion Maas-Rhine focused on developing a practical and effective communication protocol for cross-border partners to transmit and receive concise essential notifications of current concerns. Two outcomes have been realised via extensive Delphi workshops involving communicable diseases consultants from the Euregion and have been tested successfully in a cross-border hepatitis A simulation exercise and evaluated as part of daily work.

Results
Five clearly defined and agreed Cross-border Risk Alert Levels (CBRAL) like Richter Scales, immediately conveying the risk level associated with a given notification. The CBRALs take into consideration disease spread, management, cross-border impact and response actions. An agreed simple Cross-border Risk Notification Template (CBRNT), which conveys at a glance the given risk level coded by the CBRAL and a basic description of the notified case/outbreak (disease) or exposure (agent) with associated minimal data sets. The CBRNT also includes quick check boxes indicating actual cross-border connections (contacts, context, residency and media/public interest), crossborder response (cross-border cooperation or special awareness required) and the likely spread across the border.

Conclusion
The professionals found the communication protocol easy to use, effective and practical (email friendly). The CBRNT has also been rolled-out in a cross-border software tool.

Keywords: Infectious Disease, Cross-border, Risk, Risk Alert Level, Risk Notification, Simulation

PRESENTED BY: Chakib Kara-Zaïtri

REFERENCE NUMBER: 3011

Late Breaker: Mumps - A large outbreak in a vaccinated population

Hannah Austin (1), Kirsty Morrison (1), Lorna Willocks (1), Kate Templeton (2)

1. NHS Lothian Department of Public Health and Health Policy, Edinburgh, UK
2. NHS Lothian Department of Laboratory Medicine, Royal Infirmary Edinburgh, Edinburgh, UK

Background
The incidence of mumps has fallen in the UK since the introduction of MMR vaccine. Previous outbreaks in Scotland (2004-2009) were predominantly in young adults who had not received two doses of MMR vaccine[1]. We report a widespread outbreak of mumps affecting the young adult population of Lothian in Scotland. We aim to investigate the immunisation status of those affected, illustrate the consequence of this on clinical presentation and describe the challenges in managing this outbreak. [1] Health Protection Scotland: http://www.hps.scot.nhs.uk/immvax/mumps.aspx

Methods
Enhanced surveillance of notified cases was carried out, including: collection of epidemiological data for all cases; review of electronic records and telephone calls to GPs to collect MMR status; review of hospital and general practice records to collect detail of clinical presentation.

Results
341 cases were notified between week 40 2014 and week 31 2015. 78.9% of cases were aged between 18 and 27 and 42.0% were known to be university students. MMR status was collected for 278 cases. Of these 172 (61.9%) had received full vaccination with 2 MMRs. Over 70 patient files were reviewed indicating a predominantly mild pattern of illness. A complication was reported in only 5 cases, none of whom had received 2 MMR vaccinations.

Conclusion
We describe an outbreak of mumps in which a large proportion of cases were fully vaccinated and suffered a mild pattern of illness. Our experience shows that the mild pattern of disease and high pre-existing levels of immunisation impacted on the management of the outbreak: interventions targeting MMR uptake were largely unsuccessful. The implications of this on future immunisation policy and public health practice are significant.

Keywords: Disease Outbreaks Mumps Immunization Measles-Mumps-Rubella-Vaccine

PRESENTED BY: Hannah Austin (hannahaustin@nhs.net)

Moderated Poster Session B
Thursday 12 November
15:30-16:40

Track 9: Intervention Studies in Public Health

MODERATOR: Arnold Bosman (ECDC, Head of Section, Public health training)

Communicating About Pandemic Flu: Not All Facts are Equally Influential

Angela Fagerlin (1,2), Aaron Scherer (1), Megan Knaus (1), Enny Das (3), Brian Zikmund-Fisher (1)

1. University of Michigan
2. VA Ann Arbor
3. Radboud University

Background
The public's perception of the risks associated with a flu epidemic could be influenced by numerous factors and can affect communication strategies: whether the number of confirmed cases is described precisely or vaguely, reported speed of spread, the severity of the average case of influenza, or the severity of the most severe cases of influenza.

Methods
2762 Dutch participants completed an Internet survey after reading a scenario designed to look like a newspaper article about an ongoing influenza epidemic in the Netherlands. Participants were randomized to 1 of 16 cells which reflected our 2 (presentation of confirmed cases: gist, verbatim) X 2 (reported speed of spread: slow, quick) X 2 (severity of average case: moderate, severe) x 2 (severity of worse case: moderate, severe) between-subjects design. Participants answered items measuring knowledge, risk perceptions, and behavioral intentions after reading the scenario.

Results
The speed of spread and severity of the average case manipulations produced a number of significant differences across our measures. Specifically, these factors showed a significant impact on knowledge (spread: $t=15.3$, $p<0.001$; severity: $F=19.25$, $p<0.001$), risk perceptions (spread: $t's=0.11-3.71$;$p's<0.01$; severity: $F's=3.15-16.85$, $p's<0.05$) and behavioral intentions (spread: ns, severity $F=5.35$; $p<0.005$). There were no consistent differences across measures based on whether participants received risk information presented in gist vs. verbatim language. Similarly, the severity of the most severe case did not influence responses to any of our measures.

Conclusion
They way risk information is communicated about an influenza epidemic can influence how at risk people feel and their motivation to vaccinate. Participants are more influenced by learning about the average case than the most severe case and by how quickly the virus is spreading through their country.

Keywords: risk communication, patient education

PRESENTED BY: Angela Fagerlin (fagerlin@umich.edu)

REFERENCE NUMBER: 3211

The opening of a district Ebola Management Centre reduced delays of healthcare and the number of dead on arrival, Tonkolili district, Sierra Leone, 2014-15

Georgios Theocharopoulos (1,2,3), Konstandinos Danis (1,2,3), Jane Greig (3), Alexandra Hoffmann (2,3,4,5), Henriette de Valk (1), Jenn Duncombe (3), Kamalini Lokuge (3,6), Ivan Gayton (3), Rob Broeder (3), Ronald Kremer (3), Grazia Caleo (3)

1. Institut de Veille Sanitaire (InVS), Département des Maladies Infectieuses, St. Maurice, France
2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, Stockholm, Sweden
3. Médecins Sans Frontières (UK/OCA)
4. State Office for Health and Social Affairs, Berlin, Germany
5. Postgraduate Training for Applied Epidemiology (PAE), Robert Koch Institute, Germany
6. National Centre for Epidemiology and Population Health, Research School of Population Health, Australian National University

Background

During August-December 2014, Ebola patients from Tonkolili district were referred to distant Médecins Sans Frontières (MSF), Ebola Management Centers (EMCs) in Bo and Kailahun districts. In December 2014, MSF opened an EMC in Tonkolili district (district EMC). We aimed to determine whether the opening of the district EMC reduced delays of care and identify factors associated with fatality.

Methods

Cases were residents of Tonkolili district with Ebola positive PCR tests, referred to the MSF EMCs, during 12/09/2014-23/2/2015. We calculated case-fatality and adjusted Risk Ratios (aRR) using Poisson regression.

Results

Of the 251 Ebola cases, 211 (84%) were admitted to the distant EMCs and 40 (16%) in the district EMC. Of those, 114 (45%) died. Dead on arrival (n=10) presented only in the distant EMCs. The mean time from symptom onset to admission ranged from 7 days (SD=4.6) in distant EMCs to 3.7 days (SD= 2.8) in the district EMC (p<0.001). Cases were 2.3 (95%CI 1.5-3.5) times more likely to have delayed admission (>3days after symptom onset) in the distant compared with the district EMCs, but were less likely (aRR=0.78: 95%CI 0.62-0.98) to have a high viral load. Case fatality decreased with decreasing viral load at admission (aRR 0.88; 95%CI 0.85-0.91) and was higher among cases presenting with vomiting (aRR 1.5: 95%Ci 1.0-2.1).

Conclusion

The opening of a district EMC resulted in earlier admission of cases and in reduction of the number of dead on arrival. Viral load and vomiting at admission predicted fatality. Community deaths were not included, leading to an underestimate of case-fatality. Health actors should consider the location of EMCs to ensure equitable access to healthcare for all during Ebola outbreaks.

Keywords: Access, Health Care, Ebola, Mortality

PRESENTED BY: Georgios Theocharopoulos (g.theocharopoulos@invs.sante.fr)

REFERENCE NUMBER: 3149

A surveillance evaluation shows under-reporting of bloodstream infections in adult critical care units, Northern Ireland, 2011-2014

Lynsey Patterson (1), Gerry McIlvenny (2), Lourda Geoghegan (2)

1. UK Field Epidemiology Training Programme
2. Public Health Agency, Northern Ireland

Background

In 2011, surveillance of healthcare associated infections in critical care units (CCU) was implemented in Northern Ireland using a European protocol. Information on bloodstream infections (BSI) including catheter-related BSI (CR-BSI), a quality of care indicator, is collected using a clinical information system 'WardWatcher' which combines human and catheter isolate information. The aims are to monitor trends in nosocomial infections and facilitate comparisons between units. We aimed to evaluate completeness of the system and adherence to protocols.

Methods

We defined a BSI as a positive blood culture sampled from day 3 of admission onwards; and a CR-BSI as a BSI and culture-positive catheter in a patient with signs and symptoms of systemic infection. We quantified reporting completeness comparing BSI from: 1) WardWatcher and; 2) CoSurv (regional human isolate database) linking datasets using a national unique number, date of birth and CCU identifier, and calculated CR-BSI/BSI proportion. We assessed adherence to protocols through a survey of all microbiologists and intensivists.

Results

51 BSIs (19 CR-BSI (37.2%)), were reported through WardWatcher and an additional 266 reported through Co-Surv. The CR-BSI/BSI proportion was 19/317 (6%). 4/5 microbiologists and 8/10 intensivists responded to the survey. All microbiologists but only 1/8 intensivists adhered to European case definitions.

Conclusion

There is significant underreporting of BSI in WardWatcher and possible under-reporting of CR-BSI, which as a measure of care quality should be captured. There is evidence of variation in the application of surveillance case definitions. We propose training to improve compliance with the protocol and on-going monitoring of reporting completeness.

Keywords: Evaluation, surveillance, Hospital Infections, Critical Care

PRESENTED BY: Lynsey Patterson (lynsey.patterson@hscni.net)

REFERENCE NUMBER: 2912

Risk factors associated with outbreak of methanol poisoning in Southern Districts of Ondo State, Nigeria. May 2015

Adefisoye Adewole (1), Elizabeth Adedire (1), Oluwapemi Fadahunsi (1), Patrick Nguku (1)

1. NFELTP

Background
On the 13th of April three people from Irele LGA, Ondo State Nigeria were reported having symptoms of headache, blurring of vision, respiratory symptom and loss of consciousness/death all resulting to death within 24-72 hours of onset. The State ministry of health was alerted for the investigation of the outbreak. We investigated the outbreak to characterize the outbreak in terms of time place and person, identify the causative agent, source and mode of transmission and to identify the possible risk factors responsible for the outbreak.

Methods
We conducted a community based case control study. We defined a case as any person presenting with headache, blurring of vision and/or blindness, and/or respiratory distress with or without loss of consciousness within 24-48 hours of onset of symptoms beginning from 12th of April 2015 in Ode-Irele LGA Ondo State We were able to interview 19 cases and 57 controls (1case to 3 un-matched controls) using a semi-structured interviewer administered questionnaire. Data were analyzed using Epi-info statistical software.

Results
A total of 39 cases were line-listed with 29 deaths with the case fatality rate of 74.4%. Mean age was 40.4±12.5 years. Almost all the cases were males 38 (97.4%) and mostly farmers 16 (57.1%). 32 (94.1%) claimed to have consumed local gin prior to development of symptoms. Risk factors for the outbreak were consumption of local gin [OR=17.2, CI=4.6-84.0] and alcohol consumption [OR=24.2, CI=4.0-555.6]. Laboratory findings revealed methanol toxicity in both blood and urine samples as well as toxicology result of the local gin sample.

Conclusion
Local gin contaminated with methanol was the major risk factor for the occurrence of the outbreak.

Keywords: Methanol poisoning, Alcohol and Local gin

PRESENTED BY: Adefisoye Adewole (chatwithoba@yahoo.com)
REFERENCE NUMBER: 2982

Assessment of JC virus in Portuguese wastewaters: Impact on Public Health

Filipa Rodrigues (1), Daniel Goncalves (1), Cristina Luxo (2), Ana Matos (2)

1. Faculty of Pharmacy, University of Coimbra, Coimbra, Portugal
2. Research Centre on Chemical Processes Engineering and Forest Products (CIEPQF); Faculty of Pharmacy, University of Coimbra, Coimbra, Portugal

Background
Despite the increasing number of global population with access to an improved drinking-water source and to a better-quality sanitation, waterborne and water-related diseases still represent a major human health risk with massive socio-economic repercussions. The frequent detection of viruses in effluent sewage treatment facilities has been reported in different countries, which has led to the hypothesis that additional indicators of human contamination, apart from the bacteriological common used indicators may be needed to assure the microbiological quality of water. In this order, we aimed to create the first national profile of the ubiquitous human JC virus (JCV) in Portuguese wastewaters and to evaluate its removal efficiency by Wastewater Treatment Plants (WWTP).

Methods
Influent (WWI) and effluent (WWE) wastewater samples from fifteen different Portuguese Wastewater Treatment Plants were collected during winter time. After ultracentrifugation and nucleic acid extraction, they were evaluated by qPCR for the presence of JCV.

Results
Only one of the 15 WWTP evaluated did not present JCV detectable in both influent and effluent samples. Respecting the others 14 WWTP, JCV genome was detected in all the influent samples, and in 9 (64%) of the 14 effluent samples.

Conclusion
This was the first epidemiologic study regarding the presence of JCV in waters made in Portugal. The results demonstrate that JCV is frequent in Portuguese wastewaters, and 64% of WWTP were not able to efficiently eliminate this virus. For that reason, viral surveillance of water quality reveals itself crucial with the purpose of identifying possible sources of contamination and prevent the widespread dispersion of certain potentially pathogenic agents.

Keywords: JC Virus, waste water, Real-Time Polymerase Chain Reaction, surveillance

PRESENTED BY: Daniel Gonçalves (leinad_goncalves@hotmail.com)
REFERENCE NUMBER: 2972

Reduced usage of health services, but low mortality during the Ebola epidemic in Freetown, Sierra Leone, May 2014 - February 2015

Sabine Vygen (1,2,3), Amanda Tiffany (1,4,5), Monica Rull (5), Allexandre Ventura (5), Anja Wolz (5), Klaudia Porten (6)

1. Both authors have contributed equally
2. European Program for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Sweden
3. French Institute of Public Health Surveillance, Alerts and Regions Coordination Department, Regional office in Aquitaine, Bordeaux, France
4. Epicentre,Geneva, Switzerland
5. Médecins sans Frontières, Geneva, Switzerland
6. Epicentre,Paris, France

Background

The impact of Ebola on mortality and health seeking behavior in Sierra Leone was unknown. We conducted a household-based survey to describe health seeking behavior and estimate mortality in Western Area (capital region) between May 25, 2014 and February 16, 2015.

Methods

Using two stage cluster sampling methodology, we selected 30 geographical sectors with probability proportional to population size, and sampled 30 households per sector. We conducted face-to-face interviews. The questionnaire covered household size, places and causes of death and health seeking behavior. We defined an Ebola related death as any death reported by the deceased's family as being due to Ebola. We compared attendance at healthcare facilities when symptomatic before and during the epidemic (before May 2014 and during the past month before the interview in February 2015), using the chi-square test. We calculated overall and Ebola specific mortality rates.

Results

Before the Ebola epidemic, 75% (671/893) of respondents indicated attendance at healthcare facility when symptomatic compared to 58% (50/86) in February 2015 (p=0.006). Reported self-medication increased from 8% (75/893) prior to the epidemic to 23% (20/86) during the epidemic. Ninety-six deaths were reported in 898 households, 39 due to Ebola. The overall and Ebola-specific mortality rates were 0.52 (95%CI: 0.29-0.76) and 0.19 (95%CI: 0.01-0.38) per 10,000 inhabitants per day, respectively.

Conclusion

The overall mortality rate in this survey was similar to rates usually described in low-income countries outside crisis situations. However, Ebola related mortality represented 41% of overall mortality. The reduced usage of health services might explain some of the non-Ebola related deaths. Reasons for this reduced usage need to be explored in further studies, in order to address those in the near future.

Keywords: Ebola, mortality, health seeking behavior

PRESENTED BY: Sabine Vygen (s.vygen@yahoo.de)

REFERENCE NUMBER: 2866

Track 10: HIV-STI

MODERATOR: Derval Igoe (EPIET supervisor, Ireland)

HIV self-testing in Spain: a potential and innovative option for men-who-have-sex-with-men who were never tested for HIV

Konstantinos Koutentakis (1,2), María Elena Rosales Statkus (1,3), Mónica Ruiz García (1,3), Sonia Fernández Balbuena (3,4), Juan Hoyos Miller (3), Cristian Gil (5), Luís de la Fuente (1,3), María-José Belza (3,4)

1. Centro Nacional de Epidemiología, Instituto de Salud Carlos III (ISCIII), Madrid, Spain
2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden
3. CIBERESP
4. Escuela Nacional de Sanidad, Instituto de Salud Carlos III (ISCIII), Madrid, Spain
5. Unidad Docente de Medicina Preventiva y Salud Pública de la Comunidad de Madrid, Spain
6. Hospital Universitario Gregorio Marañón, Madrid, Spain

Background

Spain has not yet authorized the sale of HIV self-test kits. In order to assess the impact of such an innovative strategy on HIV control, we surveyed men who have had sex with men (MSM) and we selected those who had never tested for HIV to analyze their interest in self-testing and the characteristics of potential users.

Methods

From September 2012 to April 2013 we posted a questionnaire on several gay websites. We collected information about social and demographic characteristics, HIV testing history, risk behaviours, reasons for not testing and intention to test if a self-test had been authorized. We calculated adjusted Prevalence Ratios (PRs) using Poisson regression, and 95% confidence intervals (CI) for factors associated with intention to self-test.

Results

We collected information on 2,818 individuals with no previous HIV testing. Out of 2,589 who gave information about self-testing, 54% lived in a large city (≥100,000), 92% were Spanish and 47% had university education. Eighty four percent respondents stated that they would have used a self-test if it had been available in pharmacies. Intention to self-test was associated with age ≥30 years (PR=1.04; 95% CI:1.01–1.08), planning to test for HIV in the upcoming year (PR=1.14; 95% CI:1.10–1.17), having anal sex in the past year (PR=1.18; 95% CI:1.04–1.33), reporting fear for testing (PR=1.10; 95% CI:1.03–1.17) and facing barriers to healthcare access (PR=1.22; 95% CI:1.18–1.27).

Conclusion

Our results suggest that if a HIV self-test becomes authorized in Spain, it will be welcome by MSM who have never tested for HIV, reaching people with fears or barriers to access health care that otherwise would probably not be tested. [Financial support: MSSSI EC11-279]

Keywords: Self-testing, HIV Infections, Early Diagnosis, Homosexuals

PRESENTED BY: Konstantinos Koutentakis (koutendakis@gmail.com)

REFERENCE NUMBER: 3123

Do migrants and Germans differ regarding initation of HIV treatment in Germany?

Nadine Zeitlmann (1,2,3), Christian Kollan (3), Barbara Gunsenheimer-Bartmeyer (3), Claudia Santos-Hövener (3), Matthias an der Heiden (3)

1. Postgraduate Training for Applied Epidemiology (PAE), Robert Koch Institute, Berlin Germany
2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden
3. Department for Infectious Disease Epidemiology, Robert Koch Institute (RKI), Berlin, Germany

Background

HIV infected patients benefit most when antiretroviral treatment (ART) is initiated prior to clinical AIDS and CD4 cell count ‹350 cells/ul. In Germany 33% of newly-diagnosed people with HIV originate from another country, but information on migrants' clinical status at treatment initiation is lacking. Our study aims to analyse clinical differences between HIV-positive migrants and Germans at ART-initiation.

Methods

We analysed data from the German ClinSurvHIV-study, a national multi-centre observational cohort, between 01/01/1999 and 31/07/2013 and included treatment-naïve patients with information on ART-initiation and country of origin. Migration was defined by country of origin. We compared trends for CD4 count and occurrence of AIDS (CDC Stage C) at ART-initiation between migrants from sub-Saharan Africa (SSA), Central Europe (CE), South East Asia (SEA) and Germans using age and sex-adjusted multivariable regressions.

Results

Altogether, 8,786 patients commenced ART, of which 2,317 were migrants (SSA: 43%, CE: 16%, SEA: 10%).

The proportion of patients initiating ART with AIDS decreased in all groups by 5.5% (95%CI: 4.3-6.6) per year. Consistently over time, this proportion was higher in SSA- (Odds Ratio (OR): 1.2, 95%-confidence interval (CI): 1.0-1.5) and SEA-migrants (OR: 2.2, 95%CI: 1.6-2.9).

Mean CD4 count at ART-initiation in 38 year old males increased significantly by 231 to 331 cells/ul over the study period in Germans, 174 to 347 in CE and 190 to 266 in SSA-migrants (p-values:≤0.001); no significant increase (188 to 186) was seen in SEA-migrants.

Conclusion

Migrants initiate ART at a more advanced stage of HIV-infection suggesting need for better access to HIV-testing and care for SSA- and SEA-migrant communities in Germany.

Keywords: HIV-treatment, migrants, CD4, AIDS, sub-Saharan Africa, South-East Asia

PRESENTED BY: Nadine Zeitlmann (nadine.zeitlmann@gmail.com)

REFERENCE NUMBER: 3210

Pre-vaccination age and cytology standardised key human papillomavirus (HPV) infection prevalence estimates, Slovenia, 2010

Veronika Učakar (1), Irena Klavs (1), Mario Poljak (2)

1. Communicable Diseases Centre, National Institute of Public Health, Ljubljana, Slovenia
2. Institute of Microbiology and Immunology, Faculty of Medicine, University of Ljubljana, Ljubljana, Slovenia

Background

Objective was to estimate age and cytology-standardized prevalence for current and lifetime HPV infection among Slovenian women screened within the National Cervical Cancer Screening Programme (NCCSP) before the introduction of school-based vaccination against HPV in 2009 to assess the potential impact of vaccination programme.

Methods

A cross-sectional study was conducted in a convenience sample of 20-64 years old women screened within the NCCSP in 2010. Cervical smear specimens were tested for infection with selected HPV types (12 high-risk HPV types according to International Agency for Research on Cancer (IARC) and 25 other HPV types) and blood specimens for antibodies to selected HPV types (11 high-risk HPV types according to IARC and 4 other HPV types). We used a direct method of standardization and standard population, women screened within NCCPS in 2010.

Results

Of 4,602 women invited, 98.6% participated. Cervical smear for HPV DNA testing was obtained from 99.5% and a blood specimen from 73.2% participants. Age and cytology standardised cervical infection prevalence estimates together with 95% confidence intervals (CI) with at least one of the 12 high-risk HPV were 11.0% (8.4-13.7) and 12.0% (10.6-13.4). Age and cytology standardised seropositivity estimates together with 95% CI for at least one of the 11 high-risk HPV types were 57.5% (51-9-63.2) and 59.3% (57.1-61.7), for HPV 16 23.6% (18.9-28.3) and 25.3% (23.1-27.6), and for at least one of the four vaccine HPV types (HPV 6, HPV11, HPV16 and HPV18) 39.2% (33.7-44.7) and 40.9% (38.4-43.2).

Conclusion

School based vaccination against HPV has the potential to reduce substantially the very high pre-vaccination HPV infection occurrence among Slovenian women. The results provide baseline data for monitoring the impact of vaccination program.

Keywords: HPV, prevalence, survey, Slovenia

PRESENTED BY: Veronika Učakar (veronika.ucakar@nijz.si)

REFERENCE NUMBER: 3086

Strong and ongoing increase of syphilis in MSM in Germany

Klaus Jansen (1), Viviane Bremer (1)

1. Robert Koch-Institut, Berlin, Germany

Background
In Germany, the number of syphilis cases doubled 2001-04 to over 3,000/year and remained mainly stable until 2009. Between 2010 and 2013, the number increased between 11% and 22%. We analysed syphilis surveillance data to assess characteristics of this rise.

Methods
Since 2001, laboratories are required to notify syphilis diagnoses anonymously, physicians complement clinical information. Potential double notifications are identified. We analysed syphilis cases by year of diagnosis, age, sex, area of residence and transmission category.

Results
In 2014 5,722 cases were reported, corresponding to a 14% rise compared to 2013. Incidence was 7.1 per 100,000 inhabitants, with highest incidences in large cities as Berlin (31.0), Cologne (31.9) and Munich (27.2), especially in Berlin inner city areas (61.3-86.2/100,000 inhabitants). Notified cases increased in 13/16 federal states in 2014, and increased in Germany in a linear manner by 669 cases/year since 2010 (R2=0.9994).Men accounted for 94% of cases in 2014. The likely mode of transmission was available for 74% of cases; of these, 84% were men who have sex with men (MSM), in 16% heterosexual persons. The proportion of MSM aged 40 years or above was stable since 2008 with 49%. Stage of infection was reported in 74% of cases in 2014. Of these, 35% were diagnosed as primary, 27% as secondary and 35% as latent syphilis, similar to previous years.

Conclusion
Syphilis cases continue to increase strongly since 2010, mainly attributable to MSM in large German cities, also in higher age groups. Due to high proportions of cases diagnosed in later stages, early diagnosis and treatment, but also consistent condom use, are important to minimise the risk of syphilis and subsequently potential HIV-transmission.

Keywords: syphilis, surveillance, MSM, Germany, increase

PRESENTED BY: Klaus Jansen (jansenk@rki.de)

REFERENCE NUMBER: 3018

Factors associated with recent HIV infection among newly diagnosed STI clinic attendees in the Netherlands in 2014

Saara Parkkali (1,2), Yolanda van Weert (1), Birgit van Benthem (1), Maarten Koot (3), Eline op de Coul (1)

1. Unit of Epidemiology and Surveillance, National Institute for Public Health and Environment (RIVM), Centre for Infectious Disease Control, the Netherlands
2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
3. Sanquin Blood Supply, Virus Diagnostic Services, Amsterdam, Tthe Netherlands

Background
During 2014, we enhanced HIV surveillance in Dutch STI clinics to differentiate recent from established infections. Identification of recent infections (RI) enables calculating HIV incidence, identification of transmission risk groups, monitoring of HIV trends, and assessment of the impact of preventive interventions. We identified factors associated with RI and compared results with a previous pilot study among men who have sex with men (MSM) in Amsterdam and Rotterdam.

Methods
We collected leftover specimens from persons attending STI clinics who were newly diagnosed with HIV and tested them with the Architect-immunoassay for antibody avidity. RI was defined as avidity index (AI) ≤ 0.80. AI results were linked with epidemiological information from HIV/STI surveillance data. We identified factors associated with RI in MSM using multivariable logistic regression.

Results
In 2014, 323 STI clinic attendees were newly diagnosed with HIV: 278 MSM, 25 heterosexual men, and 20 women. 179/323 (55%) had a specimen available for AI testing. RIs were more frequent among MSM (39%, 60/153) than heterosexuals (11%, 3/26). Factors independently associated with RI in MSM were: diagnosis with an STI within the previous 2 years (aOR 12.5, 95%CI 4.1-38.4) and Dutch ethnicity (aOR 4.3, 95%CI 1.4-13.2). The percentage of RIs among MSM in this study was higher compared to a previous pilot in 2009-2011.

Conclusion
Specimens were only available for about half of HIV infected STI clinic attendees, which limits the representativeness of our results. MSM more frequently had a RI than heterosexuals. Among MSM, previous STIs and Dutch ethnicity were associated with RI. We recommend targeting interventions to these groups, and to continue testing for recent infections at the STI clinics.

Keywords: HIV, surveillance, MSM, The Netherlands

PRESENTED BY: Saara Parkkali (saara.parkkali@gmail.com)

REFERENCE NUMBER: 3029

Trends and determinants for resistance of Neisseria gonorrhoeae in the Netherlands.

Sanne Hofstraat (1), A. van Dam (2), Marianne van der Sande (1,3), Birgit van Benthem (1)

1. Centre for Infectious Disease Control, National Institute for Public Health and the Environment, Bilthoven, The Netherlands
2. Public Health Laboratory, Amsterdam, The Netherlands
3. Julius Center for Public Health and Primary Care, Utrecht, The Netherlands

Background
We analysed the Gonococcal Resistance to Antimicrobials Surveillance (GRAS) in the Netherlands to identify trends and determinants of decreased ceftriaxone, azithromycin and cefotaxime susceptibility.

Methods
Currently, GRAS includes almost 80% of STI centres in the Netherlands. From each patient with a positive gonorrhoea culture, the minimum inhibitory concentration (MIC) for several antibiotics was determined using E-tests. Time trends were assessed by x2 test and geometric means. Determinants for decreased susceptibility for ceftriaxone (MIC>0.016mg/L) and resistance for cefotaxime (MIC>0.125mg/L) and azithromycin (MIC>0.5mg/L) were assessed using stratified logistic regression.

Results
Between 2007 and 2014, 10,321 isolates were tested for Neisseria gonorrhoea susceptibility. Hitherto, resistance to ceftriaxone (current first-line treatment) was not found. In 2014, 3.1% of isolates were resistant for cefotaxime and for azithromycin 7.7% resistance was measured. Testing for trends, isolates showed significant increase in MIC over time for cefotaxime (p<.0001) and azithromycin (p<.0001). The multivariable model for ceftriaxone susceptibility in men who have sex with men (MSM) showed that isolates collected from non-Dutch MSM, MSM that are clients of commercial sex workers (CSW) or from MSM with an oral gonorrhoea infection were significantly less susceptible to ceftriaxone. Among heterosexual males, being over 30 was associated with decreased ceftriaxone susceptibility whilst having a co-infection with chlamydia and being Non-Dutch were protective factors. In women, determinants associated with decreased susceptibility to ceftriaxone were being a CSW, being over 30 and having an anorectal or oral gonorrhoea infection.

Conclusion
In conclusion, a trend over time of decreased susceptibility to ceftriaxone has not been identified in the Netherlands between 2007 and 2014. However, determinants associated with reduced susceptibility for the current treatment were detected and can be used for focused intervention strategies.

Keywords: Sexually Transmitted Diseases, Neisseria gonorroeae, Gonorrhoea, Microbial Drug Resistance

PRESENTED BY: Sanne Hofstraat (sanne.hofstraat@rivm.nl)
REFERENCE NUMBER: 2926

Track 11: Vaccine-preventable Diseases II

MODERATOR: Androulla Efstratiou (EUPHEM coordinator, UK)

Knowledge and attitudes towards HPV vaccination among mothers of teenage girls – a web based survey after HPV vaccine introduction in Finland

Pauliina Leivo (1,2), Veikko Launis (2), Hanna Nohynek (1)

1. National Institute for Health and Welfare THL Helsinki Finland
2. University of Turku, Finland

Background
Human papilloma virus (HPV) vaccine was introduced school-based into Finnish national immunization programme (NIP) in November 2013. An open tender was won by GSK´s CervarixR. Negative media attention accompanied the introduction campaign, which was targeted to girls 11-15 year of age and designed by THL in consultation with extensive stakeholder network and professionals in social marketing. During first year, HPV vaccine coverage for 1.dose was 70% with large geographic variation (40-85%). Maternal knowledge/attitudes were studied to understand reasons for noncompliance and make changes to NIP HPV communications.

Methods
Primary school principals in cities Espoo and Oulu were approached asking to send via school emailing system an invitation to mothers of girls attending 6-9th grade, eligible for HPV vaccination, to partipate in study. A web based semistructured survey with knowledge test and total 25 questions was devised for filling in during early fall 2014.

Results
9/17 Espoo schools and 13/22 Oulu schools sent emails to mothers. Total 685 mothers participate: 44% from Espoo, 56% from Oulu. 2/3 respondents thought of having received sufficient information on HPV vaccine, although only 1/3 knew HPV infection was prerequisite for cervical cancer. For stratified uni/multivariate analyses, respondents were divided into groups based on willingness to have child vaccinated with HPVV (positive, yes-504 vs. critical, no-172); and among those positive, willingness to pay should vaccine not be available for free (232 vs.272). Opinions expressed could be classified into different categories of biased views: lack of information, status quo, negligence, false balance. Religion did not explain differences observed.

Conclusion
1/4 mothers was critical of HPV vaccination for multitude of reasons. Several subgroups with different attitudes were identified posing challenges to planning HPVV communication strategies.

Keywords: HPV vaccination, knowledge and attitudes, vaccine hesitancy

PRESENTED BY: Hanna Nohynek (hanna.nohynek@thl.fi)
REFERENCE NUMBER: 3207

Measles in London and the South East of England in 2014- can the fall in cases be sustained?

Amanda Wright (1), Maria Saavedra-Campos (1), Sooria Balasegaram (1)

1. Field Epidemiology Services, Public Health England, UK

Background
In 2013, changes in the health economy including immunisation services delivery and a MMR catch up campaign in England implied concerns regarding measles immunity. This study describes the epidemiology of measles in London and South East (SE) England in 2014 to elicit changes in epidemiology to direct public health action.

Methods
All laboratory confirmed and clinically probable measles cases resident in London and South East of England with date of onset in 2014 were analysed and compared with cases from 2010-2013. Cases were extracted from the national case management system , described and analysed using STATA 13. Numbers were also compared to mumps cases to assess any changes in notification patterns or testing.

Results
There were 72 confirmed measles cases in 2014 (0.42 per 100000); the lowest in the period. Cases fell steadily from the peak in 2011 of 808 cases (4.2 per 100 000) , to 548 (3.3 per 100000) in 2012 and 201 (1.5 per 100000) in 2013.The proportion of confirmed cases (65%) in 2014 was consistent with the previous years and mumps cases in 2014 remained similar or higher. Measles cases with foreign travel were a higher proportion (19%) than in previous years, conversely the number of outbreaks fell to 3, compared to an average of 20 , excluding the peak year 2011. In London, 27% of cases were prevaccination (under 1 years old), compared to a median of 8.1 % for the years 2010-2013.

Conclusion
Measles cases have declined tenfold from 2011 to 2014. There was reduced circulating measles and community transmission in 2014. However, there is still scope to improve vaccination rates which remain below 95% coverage.

Keywords: Measles, MMR vaccine, infectious disease transmission, epidemiology

PRESENTED BY: Sooria Balasegaram (sooria.balasegaram@phe.gov.uk)
REFERENCE NUMBER: 3186

Measles outbreak in Zagreb, Croatia

Mirjana Lana Kosanovic Licina (1), Ojdana Bastaic (1), Daniela Vojvodic (1)

1. Teaching Institute of Public Health "Dr. Andrija Stampar", Zagreb, Croatia

Background
Following an almost six-year period with zero indigenous measles cases notified in Zagreb, and less than 10 measles cases in Croatia respectively, the disease has been reintroduced at the beginning of December 2014. Since then we have registered 122 measles cases among citizens of Zagreb.

Methods
We analysed the data from epidemiological investigation upon notification from Infectious Disease Clinic, collected on the official form which contains demographic data, vaccination status, clinical signs and hospitalization. We also collected additional information (gathered on the field) –probable source and origin of infection (clusters).

Results
Within the period from December to 2014 April 2015, 122 measles cases were notified in Zagreb. Of these 67 (55%) cases were laboratory confirmed (PCR and/ or ELISA). Majority of the measles cases were unvaccinated (93%). The most affected age group are patients older than 20 years and younger or equal to 4 years. In the beginning of epidemic, measles cases were found mainly in Roma population (85), but within last 4 weeks of epidemic, cases are noted among non Roma population. 31 cases were hospitalized, in 17 patients, measles were complicated mostly with pneumonia. As a result of two circular letters to paediatricians, general practitioners and adolescent health specialists, 444 persons were vaccinated.

Conclusion
Despite the achieved high vaccination coverage (≥95%), Zagreb faced with measles epidemic driven by non-vaccinated persons. We identified pockets of susceptible persons living in Zagreb (migrating Roma population) and identified the need of tailored programme in order to increase vaccine uptake in that community. It's also clear that we have promote vaccination against measles, rubella and parotitis and to maintain high vaccination coverages as the only effective measure against future epidemics.

Keywords:Croatia, disease outbreaks, measles, vaccination

PRESENTED BY: Mirjana Lana Kosanovic Licina (mirjanalana.kosanoviclicina@stampar.hr)
REFERENCE NUMBER: 3117

Age groups susceptible to mumps infection remain: the results of the 2013-2014 mumps seroprevalence study, Belgium.

Amber Litzroth (1), Toon Braeye (1), Jean-Marc Collard (2,3), Magali Wautier (4), Martine Sabbe (1), Vera Verburgh (4), Tinne Lernout (1,5), Sophie Quoilin (1), Steven Van Gucht (4), Heidi Theeten (5), Kris Huygen (2), Veronik Hutse (4)

1. Operational directorate public health and surveillance, Service of epidemiology of infectious diseases, Scientific institute of public health, Brussels, Belgium
2. Operational directorate communicable and infectious diseases, Service of immunology, Scientific institute of public health, Brussels, Belgium
3. Unit of experimental bacteriology, Pasteur institute, Antananarivo, Madagascar
4. Operational directorate communicable and infectious diseases, Service of viral diseases, Scientific institute of public health, Brussels, Belgium
5. Centre for the evaluation of vaccinations, University of Antwerp, Antwerp, Belgium.

Background
In 1985, Belgium implemented vaccination against measles, mumps and rubella (MMR) at one year of age. In 1995, a second doses was added at 10-12 years. In 2011-2012, outbreaks occurred in Belgium, mainly among young adults who received two doses of MMR vaccine. This study aimed at identifying susceptible age cohorts and risk factors for seronegativity in order to inform policies.

Methods
Voluntarily participating laboratories collected residual sera. The Belgian National Reference Centre for mumps tested for mumps-specific IgG. We used seronegativity as a proxy for susceptibility to mumps infection. We estimated prevalence of seronegativity per region, sex, age and MMR vaccine target group. We performed log-binomial regression to evaluate the effect of age, sex, number of MMR doses and region upon prevalence of seronegativity.

Results
We collected 3252 specimens. We estimated 12% of the Belgian population to be seronegative for mumps IgG, 16% equivocal and 72% seropositive. Prevalence of seronegativity did not differ between region or sex. After the first MMR vaccination, prevalence of seronegativity dropped, but never below 20%. After the second, it dropped to 4%, but increased again with age in those 12-28 years. In those not targeted by MMR vaccination, the prevalence of seronegativity was significantly lower than in those targeted by MMR vaccination.

Conclusion
In Belgium, vulnerable groups for mumps infection remain, mainly 1-9 year olds and those with increasing age after the target moment of the second dose. Our results suggest waning immunity in ages targeted with the second MMR dose, previous suboptimal coverage with this dose or a combination of both factors. We recommend close monitoring of mumps seroprevalence and mumps clinical disease as waning immunity could lead to future outbreaks.

Keywords: Belgium, mumps, seroepidemiologic studies, vaccination.

PRESENTED BY: Amber Litzroth (amber.litzroth@wiv-isp.be)
REFERENCE NUMBER: 3093

Nasopharyngeal Carriage of Streptococcus pneumoniae in children under 5 years of age before introduction of pneumococcal vaccine (PCV 10) in urban and rural Sindh

Muhammad Imran Nisar (1), Fyezah Jehan (1), Tauseef Akhund (1), Sadia Shakoor (1), Anita Zaidi (1)

1. Aga Khan University

Background
Pneumococcal Vaccine -10 (PCV 10) was included in the Expanded Program of immunization (EPI) in Sindh, Pakistan in February 2013. PCV 10 is given as a three dose schedule at 6, 10 and 14 weeks of life with no catch-up currently offered. We undertook this study immediately before the introduction of PCV 10 to establish baseline pneumococcal carriage in naso-pharynx of children 3-12 months of age and 1 to 5 years of age in an urban community and children 3-12 months of age in a rural community in Sindh.

Methods
Baseline questionnaires were filled and nasopharyngeal specimens were collected from a random sample of children. Samples were processed in a central laboratory in Karachi using CDC standardized sequential multiplex PCR assay. Serotypes were then categorized into vaccine type and non-vaccine type.

Results
A total of 670 children were enrolled. Culture positivity rate for pneumococcus was 76 % and 80 % in the infant group in Karachi and Matiari respectively and 80% for children 1 to 5 years of age in Karachi. Prevalence of PCV 10 serotypes in infants was 30% and 23 % in Karachi and Matiari. In the older age group in Karachi, prevalence was 24%. Most common serotypes were 6A, 6B, 23F, 19A and 18C

Conclusion
This survey establishes the pre PCV 10 introduction vaccine and non-vaccine serotype carriage rate in children in a rural and urban community in Sindh. Annually planned surveys in the same communities will inform change in carriage rate after the introduction and uptake of PCV 10 in these communities

Keywords: Nasopharyngeal carriage, Nasopharyngeal colonization, Pneumococcal conjugate vaccine, Pneumococcus

PRESENTED BY: Muhammad Imran Nisar (imran.nisar@aku.edu)
REFERENCE NUMBER: 2865

A comparative study of statistic-based techniques for detecting changes in influenza-like illness activity, Greece, influenza seasons 2010-2015

Christina Parpoula (1), Angeliki Lambrou (1), Kassiani Golfinopoulou (1), Lambrini Veneti (1), Maria Pantelikizi (1), Maria Potamiti-Komi (1), Eirini Terzaki (1), Theano Georgakopoulou (1), Agoritsa Baka (1), christos Hadjichristodoulou (1,2)

1. Hellenic Center for Disease Control and Prevention, Athens, Greece
2. Faculty of Medicine, University of Thessaly, Larissa, Greece

Background

Detecting changes in influenza-like illness (ILI) activity requires surveillance time series data and advanced statistical outbreak detection methods, since the length of outbreaks varies. The aim here was to determine the signaled start and end weeks for the past five seasonal influenza outbreaks, and also to establish an optimal empirical epidemic threshold.

Methods

Weekly ILI rate data were collected through the sentinel surveillance network, between October 4, 2010 and April 26, 2015, and were used for the analysis. A retrospective analysis of the past four influenza seasons was performed. Restructuring and reorganization of the sentinel network, for the 2014-2015 period, required a separate short-term analysis based on a model fit to the minimum of one season historical data, in order to accommodate changes in the process. In this case, the change of baseline activity is not immediately clear. Therefore, statistical analysis methods of regression and statistical process control (SPC) were implemented and compared.

Results

Retrospective analysis through regression and SPC yielded similar results for the signaled start (sw) and end weeks (ew) (i.e., sw03-ew09/2011, sw05-ew13/2012, sw05-ew12/2013 and sw03-ew13/201 for the four past influenza seasons, respectively), whereas differences were observed for short-term analysis (i.e., sw04-ew06/2015 and sw01-ew11/2015 for regression and SPC, respectively). The results for the epidemic threshold through retrospective analysis were 28.79 and 27.97 for regression and SPC, respectively. Corresponding results through short-term analysis were 157.59 and 134.51 for regression and SPC, respectively.

Conclusion

SPC modelling compares favorably to regression modelling for its ability to perform well both for long and short-term data, and for detecting alert signals earlier. This comparative study revealed an effective way to identify the pattern that best matches the recent influenza activity.

Keywords: Influenza, Outbreaks, Quality Control, Regression, Sentinel, Surveillance

PRESENTED BY: Christina Parpoula (parpoula@keelpno.gr)

REFERENCE NUMBER: 3065

Necrotizing soft tissue infection caused by nontypeable Haemophilus influenzae in an adult

Carmela Stigliano (1), Enea Gino Di Domenico (2), Luigi Toma (2), Maria Teresa Gallo (2), Grazia Prignano (2), Lorella Pelagalli (1), Fabrizio Ensoli (2)

1. Intensive Care Medicine, National Cancer Institute
2. Department of Clinical Pathology and Microbiology, San Gallicano Dermatology Institute, Rome, Italy.

Background

Haemophilus influenzae is a Gram-negative bacterium that exists as ubiquitous human-specific commensal or as a pathogen. Before the introduction of the conjugate vaccine H. influenzae type b (Hib) accounted for more than 95% of cases of invasive disease among children, and it was the leading cause of bacterial meningitis and other bacterial diseases among children under five. Despite in developed countries invasive type b disease has been virtually eliminated, in the post-vaccine era another form of invasive H. Influenzae, no longer supported by the capsulated strain of type b, is spreading. The new strains of nontypeable H. influenzae (NTHi), showed a mortality rate of 12.7% among the population older than 65 years of age. The incidence of the invasive form NTHi has increased since 1996 shifting from a childhood disease, to an adult disease. NTHi is clinically indistinguishable from Hib however those patients infected with NTHi have a higher frequency of underlying disorders.

Methods

From respiratory secretions of an adult patient an invasive NTHi strain was recoveredand and cultured on chocolate agar. Identification and biotyping was carried out by standard biochemical tests, and confirmed by 16S rRNA sequencing (ABI PRISM 3130xl Genetic Analyzer).

Results

In this report, we describe the case of a 58-year old woman with a necrotizing soft tissue infection caused by an invasive NTHi.

Conclusion

Our findings highlights the role of the new strains of NTHi as a cause of severe invasive disease in adults emphasizing the importance of a constant surveillance of NTHis in the post Hib-vaccine era.

Keywords: Haemophilus influenzae, nontypeable H. influenzae, Necrotizing soft tissue infection, Hib-vaccine.

PRESENTED BY: Luigi Toma (toma@ifo.it)

REFERENCE NUMBER: 3209

Track 12: TB and other Respiratory Viruses (excluding Influenza)

MODERATOR: Helen Maguire (Former EPIET coordinator, UK)

Trends in mean age of tuberculosis (TB) cases: performance of an indicator for monitoring the progress in TB control in the EU/EEA, 2004 - 2013

Vahur Hollo (1), Csaba Ködmön (1), Joana Gomes Dias (1), Julien Beauté (1), Marieke J. van der Werf (1)

1. European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden

Background
Trends in mean age of TB cases is an epidemiological indicator used for monitoring progress towards TB elimination in the EU/EEA. Increasing mean age is assumed to reflect decreasing recent transmission, suggesting effectiveness of a TB programme. The objective of this study was to assess the performance of this indicator by comparing it to the trend in notification rate.

Methods
We retrieved TB surveillance data from EU/EEA Member States with more than 20 cases per yearand continuous annual reporting from the European Surveillance System (TESSy) for the period 2004-2013. To adjust for changes in population structure, population-weighted country-specific mean ages and age-standardised notification rates were calculated. Trends for both indicators were analysed using linear regression analysis. Congruence of trends was defined as trends in mean age and notification rate pointing in opposite directions.

Results
Data from 26 countries were included. Population-weighted mean age was 46 (range 28-62) years in 2004 and 44 (range 31-58) in 2013. Annual average change of mean age was below one year. Increasing trends in mean age were observed in seven countries including three with statistically significant trends. Decreasing trends in notification rates were observed in 22 countries including 19 with statistically significant trends. Trends were congruent in nine countries including three for which both trends were statistically significant.

Conclusion
Trends in mean age of TB cases showed little agreement with trends in notification rates. The assumption that increasing mean age is associated with decreasing transmission should be further validated. Trends may show better agreement when analysed separately for native and foreign-born TB cases. However, population data for foreign-born were not available for the 10 year period.

Keywords: Tuberculosis, epidemiological monitoring, Europe, surveillance

PRESENTED BY: Vahur Hollo (vahur.hollo@ecdc.europa.eu)

REFERENCE NUMBER: 3072

Analysis of Quarterly Tuberculosis data from the Lagos State Tuberculosis Control Program 2009 -2012- Nigeria

Abimbola Aman-Oloniyo (1), Hussein Abdur-razaq (2), Gabriele Poggensse (1)

1. Nigeria Field Epidemiology and Laboratory Training Program
2. Lagos State Ministry of Health

Background
Tuberculosis (TB) is a communicable disease caused by members of the Mycobacterium Tuberculosis complex. Nigeria ranks 3rd among 22 worst TB affected countries. Lagos, the State with highest population density, carries 8.4% TB burden and is consistently responsible for 11% of registered TB cases; its Directly Observed Treatment Shortcourse (DOTS) centers increased from 11 in 2003 to 270 in 2013. We conducted a secondary analysis of Lagos State quarterly TB reports for 2009 to 2012.

Methods
We obtained and analyzed January 2009 – December 2012 data from Lagos State TB control program. Denominators for rate calculations were based on extrapolations of 2006 census data. We assessed incidence, prevalence, type, quarterly case notification of TB and HIV detection among TB cases.

Results
There was a decline in TB incidence rate from 44/100000 population in 2009 to 37/100,000 in 2010 with subsequent increase to 41/100,000 in 2012. The quarterly incidence and prevalence rates ranged from 32/100,000 to 48.5/ 100,000 and from 69.2/100,000 to 99.6/100,000 respectively. Between 21% - 31% (average 26%) suspected cases were found to be positive by microscopy during the period. Age group of 15 – 44 years and more males (6179 (58.8%)) were affected; the difference in annual rate of positivity between sexes was not statistically significant (p= 0.514). The rate of positivity for HIV among new and all TB cases (except new) was 14% and 24% respectively.

Conclusion
Rate of TB notification is increasing since year 2010. Targeted measures should be taken to address TB spread among the age group 15 – 44 years. Index of suspicion at DOTS centers should be monitored so true TB suspects will be tested by microscopy (to minimize resources wastage).

Keywords: Tuberculosis, HIV, Nigeria, Lagos.

PRESENTED BY: Abimbola Aman-Oloniyo (bimboaman@gmail.com)

REFERENCE NUMBER: 2891

Screening for tuberculosis among refugees and asylum seekers, Finland, 2013

Pirre Räisänen (1,2), Hanna Soini (1), Pirjo Turtiainen (1), Jorma Kuuluvainen (3), Mari Helenius (3), Petri Ruutu (1), Pekka Nuorti (1,2), Outi Lyytikainen (1)

1. National Institute for Health and Welfare, Finland
2. University of Tampere, Finland
3. The Finnish Immigration Service, Finland

Background

The incidence of tuberculosis (TB) in Finland is low. Currently, the majority of reported TB cases are among older Finns, but foreign-born cases are increasing; 86/260 (33%) in 2014. According to national guidelines, all refugees and asylum seekers arriving in Finland from countries with high TB incidence (≥ 50/100 000/pop/yr) should be screened for active TB within two weeks of arrival. The screening includes a chest x-ray examination and an interview. We evaluated the implementation of the screening guidelines at Finnish reception centres in 2013.

Methods

An electronic questionnaire was sent to each hospital district (n=11) which housed a reception centre (n=26). Information was collected on the number of persons arriving at each centre, country of origin, number of chest x-ray examinations performed, and number of persons referred to Respiratory diseases unit for clinical evaluation of possible TB.

Results

A total of 4599 persons seeking international protection arrived at the reception centres in 2013; 3422 (74%) came from high TB incidence countries, most often from Iraq, Russia, Somalia, Nigeria, Afghanistan, and Syria. 2752 (80%) individuals participated in screening: 1735 (63%) were examined by both chest x-ray and interview, whereas 1017 (37%) had chest x-ray only. On average, the examinations were performed within two weeks of arrival (range 0-4 weeks). Based on chest x-ray results, 32 (1%) persons were further referred to clinical evaluation.

Conclusion

Although a substantial proportion of refugees and asylum seekers were screened, only a few TB cases were diagnosed. Screening has a crucial role in controlling TB but other actions are needed as well. Early detection of TB requires increased awareness both among immigrants and physicians, together with appropriate communication tools.

Keywords: tuberculosis, screening, immigrants, asylum seekers, refugees

PRESENTED BY: Hanna Soini (hanna.soini@thl.fi)

REFERENCE NUMBER: 2892

Tuberculosis in Turkey- and Russia-born patients notified in Germany: drug resistance less prevalent than in patients notified in Turkey (2005-2010) and Russia (2010-2011)

Anne Lallemand (1,2), Walter Haas (1), Barbara Hauer (1), Lena Fiebig (1)

1. Robert Koch Institute, Berlin, Germany
2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden

Background

For tuberculosis (TB) patients born abroad (nearly 50% of cases, most frequently from Turkey and Russia (2005-2011)), German treatment recommendations advise using birth country drug resistance information when drug susceptibility testing (DST) results are not available. We aimed to determine whether the prevalence of drug resistance is similar in Turkey- and Russia- born patients notified in Germany and in patients notified in Turkey or Russia.

Methods

We used (a) German national TB notification data (b) Turkish Ministry of Health TB reports and (c) Russian federal annual TB reports. We compared Turkey- and Russia-born TB patients notified in Germany in terms of prevalence of Isoniazid (H), Rifampicin (R) and/or multidrug resistance (MDR) with notifications in Turkey (2005-2010) and Russia (2010-2011).

Results

In Turkey, of 27,756 TB cases with DST results, 13.2 % were resistant to H, 6.7% to R and 5.1% were MDR versus 6.1 % (71/1,168), 0.7 % (8/1,167) and 0.5% (6/1,161) among the Turkey-born notified in Germany (all three P<0.0001). In Russia, of 202,162 culture-confirmed TB cases, the prevalence of MDR was 32.2% versus 13.8% (28/203) among the Russia-born notified in Germany (P<0.0001).

Conclusion

The prevalence of drug resistance among TB patients born in Turkey or Russia notified in Germany was lower than that of cases notified in their country of birth. Our results suggest to also consider the German notification data to inform patient management in Germany for patients born abroad, when DST results are not yet available. We thus recommend to present the German DST data by country of birth. As our results are influenced by changing drug resistance rates over time, we also suggest to collect information on date of migration.

Keywords: Tuberculosis, Drug Resistance, Prevalence, Epidemiology, Immigrants

PRESENTED BY: Anne Lallemand (lallemanda@rki.de)

REFERENCE NUMBER: 3025

Nationwide Anti-tuberculosis Drug Resistance Survey (DRS) -The Republic of Azerbaijan 2012-2013

Sharafat Ismayilova (1), Irada Akhundova (1)

1. Ministry of Health Republic of Azerbaijan

Background
Azerbaijan is a high tuberculosis (TB) priority country in the WHO European Region where 22% of new and 56% of retreated TB cases is multi drug resistant (MDR). The goal of this survey was to assess the prevalence and risk factors for MDR-TB and make recommendations to reduce the burden of MDR-TB in Azerbaijan.

Methods
A cross-sectional survey was conducted between October 2012 and April 2013. Study included 549 new and 240 retreated patients › 15 years of age. The latter included cases which had deteriorated after improvement, treatment failures, non-standard regimens and patients arbitrarily interrupt treatment. Diagnostic procedures included sputum microscopy, culture identification, drug susceptibility testing to first (Rifampicin, Isoniazid, Ethambutol, Streptomycin) and second-line (Ethionamide, Ofloxacilin, Para-AminosalicylicAcid, Cycloserine, Amicacin, Capreomycin) drugs.

Results
231 (42%) of new and 146 (61%) of retreated patients were resistant to ›1 drugs; 72 (13%) of new and 66 (28%) of retreated cases were resistant to RMP and INH. Amongst MDR-TB cases, 27 (38%) of new and 31 (47%) of retreated cases had pre-XDR/XDRTB (resistant to RMP, INH, FQS, and injectable drugs). In those with treatment failure, 38 (51%) had MDR/XDR-TB which was fifteen times higher than found in relapse cases (RR=15.2, 95%CI: 6.0-39). A history of imprisonment was significantly associated with new cases of MDR/XDR-TB (RR=3.4, 95%CI:1.1-10.4). Retreated patients also had high risk for MDR/XDR (RR=2.7 95%CI: 1.0-7.0).

Conclusion
Azerbaijan remains a high MDR-TB burden country. Risk factors including retreatment, treatment failure, and imprisonment contribute to MDR/XDR TB problem. We recommend standard interventions including psychosocial support to improve adherence to treatment and mandatory TB drug resistance testing.

Keywords: Azerbaijan, TB situation

PRESENTED BY: Sharafat Ismayilova (sharafat.ismayilova@gmail.com)
REFERENCE NUMBER: 3070

Detection of human Coronaviruses using multiplex real-time reverse-transcription polymerase chain reaction during virological surveillance of influenza, Finland October 2013-September 2014

Francesca Latronico (1,2), Niina Ikonen (1), Soile Blomqvist (1), Outi Lyytikainen (1), Carita Savolainen-Kopra (1)

1. National Institute for Health and Welfare (THL), Helsinki, Finland
2. European Programme for Public Health Microbiology Training (EUPHEM), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden

Background
More than one third of respiratory specimens collected under the Finnish influenza surveillance during October 2013-September 2014 were negative for all tested viral pathogens (influenza A, influenza B, respiratory syncytial virus, adenovirus, rhinovirus) included in the diagnostic panel used at the National Influenza Centre laboratory (NIC). Our objectives were to enhance laboratory diagnosis and identification of uncharacterized cases of respiratory illness under surveillance and to estimate the occurrence of human coronavirus (HCoVs) in respiratory infections in Finland.

Methods
We tested 581 respiratory specimens collected in garrisons, healthcare centers (HCC) and intensive care units (ICU) for the laboratory-based influenza surveillance during 30.9.2013 - 28.9.2014 to detect four HCoV species (HKU1, 229E, NL63, and OC43) using a multiplex real-time reverse-transcription polymerase chain reaction (RT-qPCR). We analysed distribution across seasons, place of origin, and age groups.

Results
HCoVs were detected in 41 (7.1%; median age: 19 years, range: 16-74; 88% male) of 581 specimens. Six persons were co-infected with two HCoVs and 22 with at least one other respiratory virus included in the diagnostic panel. HKU1 was most frequently detected (26/41), followed by 229E (13/41), NL63 (5/41), and OC43 (3/41). HCoVs were detected during January-April and peaked in February (25/41) simultaneously with high influenza activity. Among persons with HCoV positive finding, 31 were from garrisons, 6 from HCC and 4 were from ICU. No other respiratory virus was detected in the four specimens from ICU.

Conclusion
HCoVs circulate frequently together with the other respiratory viruses in Finland especially during winter and may sometimes be responsible of severe illness. The inclusion of HCoVs RT-qPCR in the diagnostic panel at NIC will enhance the etiological diagnosis of respiratory viral infections under surveillance.

Keywords: surveillance, viral infection, respiratory virus, human coronavirus

PRESENTED BY: Francesca Latronico (francesca.latronico@thl.fi)
REFERENCE NUMBER: 3021

Prevalence of enterovirus D68 in 17 European countries during the North-American outbreak in 2014

Eeva Broberg (1), Randy Poelman (2), Hubert G.M. Niesters (2), Bruno Lina (3)

1. European Centre for Disease Prevention and Control, Stockholm, Sweden
2. The University of Groningen, The Netherlands
3. Centre de Biologie Est des Hospices Civils de Lyon; Université de Lyon, France

Background
During August- September 2014, clusters of enterovirus-D68 (EV-D68) infection emerged in the USA and Canada. Fourteen cases died. The European Centre for Disease Prevention and Control (ECDC) asked European countries to strengthen enterovirus screening of respiratory samples and typing of isolates, especially in cases with severe respiratory symptoms, in order to be prepared for detecting an EV-D68 outbreak in Europe and to assess the prevalence of this virus in Europe.

Methods
The European Society for Clinical Virology and ECDC invited all European hospital-based and/or clinical laboratory public health laboratories and National Microbiology Focal Points to screen for EV-D68 in respiratory specimens collected between 1 July and 1 December. We performed descriptive analysis of the clinical variables and phylogenetic analysis based on VP1-sequences.

Results
Forty-two laboratories from 17 European countries set-up specific EV-D68 detection assays and analysed 17 248 specimens yielding 389 EV-D68 positive samples (2.3%) in 14 countries (range 0 and 25%). These infections were mainly detected in children below 5 years of age presenting with wheezing and in immunocompromised adults. The majority of the viruses (83%) were from clade B and genetically very similar to the ones causing the North American epidemic. Only four cases were severe including three acute flaccid paralyses and one fatal case.

Conclusion
Through adapted virus detection and typing tools, the participating European laboratories showed that EV-D68 circulated in Europe during summer and fall 2014. There were less severe cases than in the USA. This study emphasizes the need for preparedness for a wider diagnostic portfolio than that for the classical influenza and respiratory syncytial viruses for virological surveillance of emerging respiratory pathogens and assessing of their disease burden.

Keywords: Disease outbreaks, Enterovirus, Enterovirus infection, Laboratories

PRESENTED BY: Eeva Broberg (eeva.broberg@ecdc.europa.eu)
REFERENCE NUMBER: 2905

Track 13: Food and Waterborne Diseases and Zoonoses I

MODERATOR: Ettore Severi (ECDC, Expert Outbreak Response)

Waterborne outbreak of shigellosis in Georgia, 2014

Maka Tsilosani (1,2), Marina Lashkarashvili (1,2), Naile Malakmadze (3), Thomas H. Rush (2,4), Mariam Geleishvili (2,4), Jon E. Tongren (2,4)

1. National Center For Disease Control and Public Health of Georgia
2. Field Epidemiology and Laboratory Training Program
3. Northrop Grumman Corporation
4. US Centers for Disease Control and Prevention, South Caucasus Office

Background
Three severe cases of diarrhea of unknown etiology from the village of Tolebi were hospitalized in December 2014. Concurrently, many diarrhea cases were reported. The goal of investigation was to confirm the outbreak, identify the source to prevent spread of the disease

Methods
A case-control study was conducted using a standardized questionnaire. Cases were identified as persons having diarrhea (3 and more stools a day) and living in Tolebi. Controls were residents of Tolebi who had no symptoms and were either healthy family members or neighbors of the case. Stool samples were obtained for laboratory culture confirmation. Water samples from centralized water supply were tested for coliforms and fecal coliforms. Statistical analysis was conducted in EpiInfo.

Results
From total of 338 persons interviewed 169 were cases and 169 controls. Attack rate was 33.8%. 62% of cases used central water compared to 38% controls (OR=19 (95% CI: 8.0-46)) and 10% of cases – well water compared to 90% of controls (OR=0.08 (95% CI: 0.02-0.2)). 9% of cases drank bottled water compared to 91% of controls (OR=0.09 (95% CI: 0.01-0.4)). With those using central water, 91% of controls and 9% of cases boiled central water before drinking (OR=0.06 (95% CI: 0.001- 0.4) showing protection. Laboratory testing identified Shigella from 11(65%) cases out of 17 tested. Water testing showed high coliforms and E.coli. Investigation identified two damaged central water tanks allowing for fecal contamination. Chlorination had not been done for several years.

Conclusion
Our investigation implicated the central water supply as a possible source of this outbreak. No cases were reported after the centralized water supply was repaired and chlorinated. Regular maintenance of tanks and water chlorination were recommended.

Keywords: shigella, outbreak, waterborne

PRESENTED BY: Maka Tsilosani (makatsilosani@gmail.com)
REFERENCE NUMBER: 2960

Hepatitis E transmissions via blood products: an underreported source of infection in Germany

Christiane Wagner-Wiening (1,2), Dorothee Lohr (1,2), Juergen Wenzel (3), Elisabeth Aichinger (1), Guenter Pfaff (1)

1. Baden Wuerttemberg State Health Office, Stuttgart, Germany
2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Pre-vention and Control, (ECDC), Stockholm, Sweden
3. Institute of Clinical Microbiology and Hygiene, Regensburg University Medical Center, Regensburg, Germany

Background

In December 2013, two cases of Hepatitis E (HE) associated with blood transfusion in Baden-Wuerttemberg, South West Germany were reported. We investigated to identify additional cases and raise awareness of public health officers and physicians on HE especially in blood transfusion patients and blood donors.

Methods

Public health authorities interviewed all reported HE cases in Baden-Wuerttemberg in 2013 using a questionnaire on risk factors, related to blood product reception and information on blood donation. We defined blood recipient cases and blood donor cases as those with reported clinically apparent HE and/or HE-IgM and –IgG antibodies or HEV-RNA, 2-12 weeks after blood transfusion or within three months after blood donation, respectively. Following nested real time-PCR, the HEV nucleotide sequence of a 242 bp fragment of the ORF1 region was amplified and sequenced.

Results

Of all 44 HE cases notified in 2013, one did not meet the case-definition and was discarded. Three cases of HE in blood donors and two in blood recipients were identified. The same two genotypes (3C and 3F) were identified among two pairs of infected donors and recipients. One infected donor had informed the blood transfusion service and his blood products had been withdrawn. The exact source could not be identified in one case of chronic HE who reported renal transplantation in 2009.

Conclusion

Those blood product-associated HE cases were the first described in Germany. Transmission of HEV via blood products should be considered during the routine investigation of notified HE cases. The National Advisory Committee on Blood and public health authorities in Germany need to reassess whether HE screening of blood donors is required.

Keywords: Hepatitis E, blood transfusion, blood donor, blood recipient, chronic HE

PRESENTED BY: Christiane Wagner-Wiening (christiane.wagner-wiening@rps.bwl.de)

REFERENCE NUMBER: 2885

Human Salmonella Dublin infections in Denmark from 1993-2014: No spatial relation between cases and cattle farms

Silvia Funke (1,2), Janus CH Rasmussen (2), Steen Ethelberg (2)

1. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
2. Statens Serum Institut, Denmark

Background

Geo epidemiological study shows no spatial relation between geographic areas with high densities of cattle farms and Salmonella Dublin incidence. Salmonella Dublin is specifically adapted to cattle but can infect humans leading to severe disease with a higher case fatality than other Salmonella serotypes. In Denmark, 30 human cases are reported each year. The Danish programme to eradicate Salmonella Dublin in cattle initiated in 2002 led to marked decreases in the burden of infection in cattle. The main transmission route from cattle to human has not been conclusively described, direct transmission has been hypothesized. We investigated a potential geographical association between cases and cattle farms.

Methods

We included all cases confirmed by the reference library in 1993-2014, excluding those with a travel history before diagnosis. We calculated cumulative incidences stratified by municipality, using national statistics as denominator. Using spatial autocorrelation analysis, we calculated the Moran's Index (MI) to identify the geographical pattern of cases based on municipality level. We geocoded the residential addresses of cases, 20, 000 randomly selected controls and cattle farms registered in the Danish husbandry register. We calculated the proximity of cases and controls to the closest cattle farm.

Results

We included 526 cases in our analysis. The municipality with the highest cumulative incidence (29.2 per 100,000 inhabitants) was in the greater Copenhagen area, an area with a low density of cattle farms. The MI of 0.004 indicates random distribution of cases. The proximity analysis showed no difference in the distance from cattle farms to addresses of cases or controls.

Conclusion

We did not find a geographical pattern of municipalities with high cumulative incidences of human Salmonella Dublin infections. Our study shows that residency close to cattle farms is not associated with human Salmonella Dublin infections.

Keywords: Salmonella, incidence, cattle, spatial analysis

PRESENTED BY: Silvia Funke (sifu@ssi.dk)

REFERENCE NUMBER: 2909

Animal contact and distance to infected goat farms not associated with Q fever infection 7 years after the first outbreak in a small village in the Netherlands, 2007-2014

Sandra van Dam (1,2,3), Gabriella Morroy (1), Peter Schneeberger (4), Ben Bom (2), Wim Hoek van der (2)

1. Department of Infectious Disease Control, Municipal Health Service Hart voor Brabant, 's-Hertogenbosch, The Netherlands
2. National Institute for Public Health and the Environment (RIVM), Bilthoven, The Netherlands
3. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
4. Department of Medical Microbiology, Jeroen Bosch Hospital, 's-Hertogenbosch, The Netherlands

Background
The large Q fever outbreak in the Netherlands started in Herpen, a small village in the south. In 2007, 44 cases were notified and living close to an infected goat farm increased the chance of infection. Between 2008-2010, another 33 cases were notified. The aim of the study was to assess the occurrence of Q fever infections and risk factors for seroconversion after the first outbreak.

Methods
We followed up 287 inhabitants aged ≥18 years for whom serological results were available for both 2007 and 2014. Participants seropositive in 2007 (n=83) were excluded. Seroconversion was defined as lack of antibodies against Coxiella burnetii in 2007 and detection of IgG phase I and/or II titre ≥1:64 by indirect immunofluorescence assay in 2014. We identified risk factors for seroconversion, including contact with a wide range of animals, by calculating risk ratios. Distance from the home address to known infected goat farms within a radius of eight kilometres were compared with the Wilcoxon ranksum test.

Results
Of the 204 seronegative participants in 2007, 36 (18%) seroconverted. Mean age of the seroconverters was 58 years (SD 11) and 27 (75%) were male. Seroconversion was not associated with intensive contacts with small ruminants, farm animals, companion animals, work related exposure to animals or the living distance to one of the four infected goat farms in the area.

Conclusion
We did not find determinants for seroconversion based on known risk factors for Coxiella burnetii infection. We assume that due to environmental contamination after the first outbreak, there was a more diffuse pattern of exposure in combination with travel and outdoor activities of humans living in the area. This needs to be further investigated.

Keywords: Q fever, Coxiella burnetii, Animals, Goats, Risk Factors

PRESENTED BY: Sandra van Dam (s.van.dam@ggdhvb.nl)

REFERENCE NUMBER: 2944

Risk factors for Q fever infection and illness, South West Germany, 2014

Christiane Wagner-Wiening (1,2), Elke Göhring-Zwacka (1,3), Silke Fischer (1,3), Guenter Pfaff (1), Christoph Bauer (4)

1. Baden Wuerttemberg State Health Office, Stuttgart, Germany
2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Pre-vention and Control, (ECDC), Stockholm, Sweden
3. National Consulting Laboratory for Q fever, Stuttgart, Germany
4. Local Health Office Heidenheim County, Baden-Württemberg, Germany

Background
On 04/07/2014, the Health Department of Baden-Württemberg was informed of a Q fever outbreak associated with a farmers` market where sheep had lambed some days earlier. Microbiological investigation confirmed Q fever infection in human and sheep. We investigated this outbreak to identify risk factors for infection and illness.

Methods
We conducted a retrospective cohort study among visitors of the farmers' market. We recruited participants through a press release, by reviewing mandatory notifications and via stimulated reporting by local physicians. Participants were offered a serological test and interviewed using a mail-in questionnaire collecting information on demographics, clinical characteristics and exposures. A case was defined as visitor of the market on 13th of June with Phase2-IgM-antibodies diagnosed between 15th June and 30th September of 2014. Relative risk (RR) and 95% confidence intervals (CI) were calculated using Poisson regression.

Results
Among 385 respondents, we identified 228 cases (attack rate=59%), of which 46 asymptomatic. The incubation period ranged from 2 to 32 days (median: 17). Median age was 50 years (range: 1-88), and 55% were female. Reported duration of symptoms was 1 to 35 days (median: 8). Among symptomatic cases 55 had pneumonia and 50 had underlying diseases. In multivariable analysis, underlying diseases (RR=1.7; 95% CI:1.5-2.0), age <48 years (RR=1.4; 95% CI:1.2-1.7), visiting the sheep flock (RR=1.6: 95% CI:1.3-1.9) and having touched sheep (RR=1.3: 95% CI:1.1-1.6) were significantly associated with infection. Being a symptomatic case was associated with underlying diseases (RR=1.4: 95% CI: 1.2-1.5) and smoking (RR=1.6: 95% CI: 1.2-1.9).

Conclusion
To prevent further outbreaks we strongly recommend strengthening Q fever-monitoring in sheep especially located in places frequented by the public. Health authorities should consider vaccination of sheep as preventive measure.

Keywords: Qfever outbreak, cohort study, underlying diseases, sheep

PRESENTED BY: Christiane Wagner-Wiening (christiane.wagner-wiening@rps.bwl.de)

REFERENCE NUMBER: 2886

Evaluation of the surveillance system of National Laboratory-based Surveillance Network for Enteric Pathogens (UEPLA), Turkey, 2007-2012.

Mine Yenice (1), Belkis Levent (2), Revasiye Gulesen (2), Fehminaz Temel (1)

1. EWRS and FETP Department, Public Health Institution of Turkey, Turkey
2. National Enteric Pathogens Reference Laboratory, Public Health Institution of Turkey, Turkey

Background

Laboratory-based Surveillance Network for Enteric Pathogens (UEPLA) established in 2007 to strengthen notifiable diseases surveillance systems. Laboratory-notifiable Salmonella spp., Shigella spp., Campylobacter spp. and VTEC were given priority to be included in UEPLA; for having common diagnostic tests, potential for outbreaks, and antimicrobial resistance (AMR); and easily diagnosed.

Methods

UEPLA is a sentinel surveillance covers 34 laboratories country-wide. Those participants are public health, university, public hospital and private laboratories. Participants send their data via software that was initiated at the beginning of 2014. Isolates are sent to National Reference Laboratory for Enteric Pathogens to perform confirmatory and AMR tests. Reference Laboratory confirms, determines subtypes/serogroups and AMR of isolates and reports feedback to participants.

Results

For each year; the most common isolated microorganism was Salmonella spp. and serotype of Enteritidis. Salmonella spp. had highest percentage of resistance to nalidixic acide (NA). Combined resistance percentages to three or more antimicrobial groups (multidrug resistance) had rising trend in 2007-2012. The most frequently isolated Shigella serogroup was S.sonnei and S.flexneri. For each year, for Shigella spp. and serogroup flexneri; the highest percentage of resistance was to Streptomycin. Resistance of Shigella spp. to one antimicrobial group had decreasing trend in 2007-2012, contrary to multidrug resistance. In 2007-2012, dominant isolated Campylobacter species was C.jejuni, and Campylobacter spp. had high AMR levels to NA and ciprofloxacin. Multidrug resistance had a rising trend especially in 2012.

Conclusion

Monitoring the quality and accuracy, completeness and timeliness of the data from all laboratories are important problems. UEPLA software is needed to be improved for analysis. System should generate monthly surveillance indicator and summary reports, and produce maps.

Keywords: Surveillance, Salmonella, Shigella, Campylobacter, Antimicrobial Drug Resistance

PRESENTED BY: Mine Yenice (kayamine70@yahoo.com)

REFERENCE NUMBER: 3049

Food and water-borne outbreaks: Compliance with Portuguese guidelines of the food and water-borne outbreaks in Northern Health Region of Portugal, 2009-2014

Ana Mendes (1), Isabel Andrade (2), Rocha Nogueira (2), Maria Neto (2)

1. Public Health Unit of Braga, Braga, Portugal
2. Regional Public Health Department – Northern Region Health Administration, Oporto, Portugal

Background

The World Health Organization estimates that food and water-borne diseases are responsible for 2 million deaths worldwide. In 2013, 5196 foodborne outbreaks (1.19/100 000 inhabitants) were reported to European Centre for Disease Control and Prevention, of which 18 were reported by Portugal (0.17/100 000 inhabitants, classified as strong evidence). Our goal was to assess the guidelines compliance in the Northern Health Region in order to suggest improvements to the surveillance system for food and water-borne outbreaks in Portugal.

Methods

We established criteria, based on the Portuguese guidelines for food and water-borne outbreaks. We analyzed all the food and water-borne outbreaks that the Regional Public Health Department (RPHD) was informed between 2009 and 2014. We investigate food and water-borne outbreaks regarding three aspects: communication, epidemiological investigations and activities performed by the RPHD.

Results

In total, 138 food and water-borne outbreaks were known by the RPHD. The number of outbreaks varied from 27 (2009) to 19 (2014). We found that 24.6% complied with communication criteria, 0.7% complied with epidemiological investigation criteria and 0% in accordance with criteria established for activities performed by the RPHD.

Conclusion

We concluded that, in Northern region, food and water-borne outbreaks investigation does not follow national recommendations. To improve the epidemiological investigation of food and water-borne outbreaks, we propose the disclosure of a food and water-borne outbreaks research protocol to the local level. Additionally, we propose the inclusion of the food and water-borne outbreak notification and epidemiological inquire, in the electronic platform which supports the National Epidemiological Surveillance System (SINAVE). This will allow improvements in the compliance with the recommendations and the definition of alerts to Health Authorities.

Keywords: Surveillance, foodborne, outbreaks, Portugal

PRESENTED BY: Ana Mendes (anaisamendesc@gmail.com)

REFERENCE NUMBER: 3108

Track 14: Surveillance II

MODERATOR: Sam Bracebridge (UK FETP coordinator, UK)

Genetic diversity of Salmonella Enteritidis isolates found within clusters indentified using traditional outbreak detection methods

Alison Waldram (1,2,3), Philip Ashton (4), Richard Elson (5), Andre Charlett (6), Tim Dallman (5)

1. Field Epidemiology Service Liverpool, Public Health England, UK
2. Field Epidemiology Training Programme (FETP), Public Health England, UK
3. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden
4. Gastrointestinal Bacterial Reference Unit, Centre for Infectious Disease Surveillance and Control, Public Health England, UK
5. Gastrointestinal, Emerging and Zoonotic Infections Department, Centre for Infectious Disease Surveillance and Control, Public Health England, UK
6. Statistics, Modelling and Economics Department, Centre for Infectious Disease Surveillance and Control, Public Health England, UK

Background

In England and Wales (E&W), public health investigation is frequently instigated when laboratory reports exceed a threshold identified by a detection algorithm applied weekly to all reported organism phage types. In April 2014, whole genome sequencing (WGS) was implemented for all Salmonella isolates in E&W. The aim of our study was to determine the accuracy of the algorithm exceedance system in detecting outbreaks.

Methods

We included all Salmonella Enteritidis isolates within exceedances during a 48 week period (31 March 2014-1 March 2015). We described the genetic diversity of the isolates within each exceedance, quantified by Simpson's Index of Diversity, and visualised on phylogenetic trees. We compared the number of isolates within the exceedances against the numbers of genetically similar isolates grouped by WGS.

Results

There were 382 isolates reported in 30 exceedances of Salmonella Enteritidis. WGS found 23 clusters within the exceedance isolates (median: four isolates per cluster, range: 2-177) and 38 sporadic isolates (no matching WGS profiles). Isolates within each phage type exceedance were genetically diverse (median Index of Diversity: 0.62).

Conclusion

WGS has potential to provide a more reliable approach to the identification of strain specific clusters. Failure to attribute all exceedance cases to the causal exposure in outbreak investigations may be explained by the cases not being part of the real cluster due to the genetic diversity within phenotype exceedances. We recommend field investigation of WGS clusters to assess causal exposures and the development of algorithms using WGS to routinely identify potential outbreaks.

Keywords: Salmonella, Sequence Analysis, DNA, Surveillance, Disease Outbreaks

PRESENTED BY: Alison Waldram (alison.waldram@phe.gov.uk)

REFERENCE NUMBER: 2884

Evaluating the impact of the application of standardized tools for generating and investigating aberrant events to syndromic data in Canadian public health agencies

Laura Rivera (1), Ye Li (1,2), Rachel Savage (2), Natasha Crowcroft (1,2,3), Laura Rosella (1,2,4), Wendy Lou (2), Ian Johnson (1,2,5)

1. Public Health Ontario, Toronto, Canada
2. Dalla Lana School of Public Health, University of Toronto, Toronto, Canada
3. Department of Laboratory Medicine and Pathobiology, University of Toronto, Toronto, Canada
4. Institute of Clinical Evaluative Sciences, Toronto, Canada
5. Department of Family Medicine, Queen's University, Kingston, Canada

Background

In Ontario, Canada, many local public health departments use emergency department (ED) visits and/or school absenteeism (SA) data to conduct syndromic surveillance. However, the way the data are used varies widely among agencies. This study evaluated whether the provision of a standardized aberration detection algorithm and response protocol for investigating alerts led to improved ability of syndromic surveillance systems to detect communicable disease phenomena.

Methods

Fifteen syndromic surveillance-using local public health departments in Ontario were recruited and assigned to the study intervention or control group. The intervention consisted of (1) alerts from a standard CUSUM algorithm in addition to any routine alerting systems, and (2) a standard protocol to guide the investigation of all aberrant events. Control agencies continued with their usual investigation practices. Documentation of the number and nature of alerts, and any resulting public health action were recorded in logbooks and compared for intervention and control groups.

Results

Preliminary analysis spanning October 2013 to August 2014 encompassed information on 1,109 ED (intervention, n=550; control, n=559) and 523 SA alerts (intervention, n=386; control, n=137). Two health agencies used their syndromic surveillance system to detect the onset of the influenza season, with one agency in the intervention group and one agency in the control group. No other outbreaks were detected using these data sources. The most commonly reported public health response among all agencies was "watchful waiting", indicated for 382/1,109 (34%) ED alerts and 36/523 (7%) SA alerts.

Conclusion

The relatively small proportion of aberrant events that led to a public health action raises questions about the added value of syndromic surveillance to communicable disease monitoring and control.

Keywords: Surveillance, Mixed-methods, Evaluation, Outbreaks

PRESENTED BY: Natasha Crowcroft (natasha.crowcroft@oahpp.ca)

REFERENCE NUMBER: 2981

The impact of field epidemiology and laboratory trainings on surveillance data of human and animal brucellosis cases into the Electronic Integrated Disease Surveillance System (EIDSS), Azerbaijan 2013 - 2014

Natig Javadov (1), Marika Geleishvili (2), Thomas H. Rush (2), Jon E. Tongren (2)

1. Baku Veterinary Office, Baku, Azerbaijan
2. Centers for Disease Control and Prevention, Tbilisi, Georgia

Background

In 2011, Azerbaijan implemented the Electronic Integrated Disease Surveillance System (EIDSS) in medicine and veterinary, which integrates clinical, laboratory and epidemiological data. In February 2014, South Caucasus Field Epidemiology and Laboratory Training (SC/FELTP) graduates conducted epidemiology (epi) training at various levels of the Azeri health system to improve brucellosis reporting, case investigations, and control response. Evidence-based decision from well-trained epi is important in reducing the burden of brucellosis in animals and humans, which is endemic in Azerbaijan (sero-prevalence in sheep 246/100,000), (human incidence=3.1/100,000).

Methods

We conducted a retrospective cohort study of the EIDSS database (pre/post 11 months) SC/FELTP epi trainings. The SC/FELTP training included 10 (15%) of 65 districts. Assessment of surveillance data was measured with multiple surveillance evaluation indicators between epi trained and non-epi trained (control) groups. These include notification (days from initial diagnosis), entry (days from notification), case investigation (days from notification), and epi link/risk factors.

Results

Notification and entry improved significantly in the epi training group versus the control (96% vs. 75%, RR=1.3; 95% CI 1.2-1.4), (98% vs. 66%, RR=1.5; 95%CI 1.3 - 1.7) respectively. Timeliness of case investigation also improved but was not significant (96% vs. 91%,RR=1.1; 95% CI 1.0-1.1). Public health response also improved significantly in identifying epi links and risk factors to confirmed cases (82% vs. 35%, RR=2.4; 95% CI 1.8 – 3.1).

Conclusion

Improvements in surveillance evaluation indictors of the data entered demonstrates effectiveness of SC/FELTP epi trainings. The study also showed better epi links and identification of risk factors to confirm cases which improved response and mitigate the burden of brucellosis. We recommend scaling up the SC/FELTP epi trainings in other districts of Azerbaijan and continue to evaluate their efficacy.

Keywords: brucellosis, epi trainings SC/FELTP, EIDSS and Azerbaijan

PRESENTED BY: Natig Javadov (nar1917@mail.ru)

REFERENCE NUMBER: 2979

Evaluation of the reinforced Integrated Disease Surveillance and Response strategy using short message service data transmission in two southern regions of Madagascar, 2014-5

Rado Randriamiarana (1,2), Harena Rasamoelina (3), Harimahefa Razafimandimby (3), Grégoire Raminosoa (2), Nikaria Vonjitsara (2), Arthur Lamina Rakotonjanabelo (4), Ariane Halm (3), Loïc Flachet (3)

1. Indian Ocean Field Epidemiology Training Programme, Indian Ocean Commission, Mauritius
2. Epidemiological Surveillance Department, Ministry of Health, Madagascar
3. Health Surveillance Unit, Indian Ocean Commission, Mauritius
4. Disease Prevention and Control Cluster, World Health Organization, Madagascar

Background

The Integrated Disease Surveillance and Response (IDSR) strategy was introduced in Madagascar in 2006. Information was collected by Health structures (HS) on paper forms and transfered to central level by post or email. The completeness of data reporting was 20%. From 2011, data are transmitted through SMS in two southern regions using one telephone provider. We evaluated the system to determine its performance before changing or expanding it.

Methods

We randomly selected 80 HS and interviewed their representatives face-to-face (42) or by telephone (38). We evaluated knowledge of surveillance activities and selected case definitions, number of SMS with erroneous or missing information among the last ten transferred SMS, proportion of weekly reports received in the last four weeks and of the last four health alerts notified within 48 hours, and mobile network coverage.

Results

Seventy-four percent of 80 interviewed HS representatives didn't know their terms of reference, 83% the malaria case definition and 32 % that of dengue. Ninety percent (37/41) of visited HS had five or more errors and 47% had missing data in the last ten SMS. The average time needed for weekly data compilation was 24 minutes in the South region and 47 in the Southeast. Of 320 expected SMS 232 (73%) were received, 136 (34%) of them on time. Out of 38 alerts detected, four were notified on time. Nine percent (7/80) of HS had no telephone network with the current provider.

Conclusion

SMS transfer has improved IDSR data completeness, but timeliness and data quality remain a problem. Healthcare staff needs training on guidelines and case definitions. From 2015, data will be collected and managed electronically to reduce errors and improve the system's performance.

Keywords: Madagascar, surveillance, evaluation, IDSR, attributes, SMS

PRESENTED BY: Ariane Halm (ariane.halm@coi-ioc.org)

REFERENCE NUMBER: 3069

Evidence for an increase in recent transmission of hepatitis C amongst people who inject drugs in Wales.

Laia Fina Homar (1), Daniel Thomas (1), Noel Craine (1), Josie Smith (1), Sion Lingard (1), Malorie Perry (1), Andrew Malone (1), Claire Midgley (1), Christopher Williams (1)

1. Public Health Wales, UK

Background
In 2010 Public Health Wales launched a surveillance scheme for blood borne virus infections amongst clients of substance misuse services. Following an outbreak of acute, genetically similar hepatitis C (HCV) infection in one area of South Wales, we analysed surveillance data from across Wales to examine whether the increase in prevalence of HCV was confined to one area or was more widespread.

Methods
We analysed 2538 forms collected from injecting drug using clients with a recorded HCV result between 2011 and 2014.

Results
Amongst injecting clients aged under 25 (n=201), the HCV positivity increased from 7.5% in 2012 to 20.0% in 2014 (Fisher's exact p=0.08). Those who reported injecting stimulants (including crack, amphetamines or mephedrone) appeared to be at increased risk for HCV (RR=2.7, 95%CI: 1.1-6.4, chi2 p=0.02). Those injecting only steroids had a lower risk when compared to other drug injection (RR=0.2, 95%CI: 0.02-1.4, chi2 p=0.06). The proportion of clients reporting injecting for 2 years or less (n=408) that were HCV positive increased from 8.8% in 2012 to 18.2% in 2014 (Fisher's exact p=0.09).

Conclusion
The prevalence of HCV infection appears to be increasing in Wales amongst young people who inject drugs and in recent initiates, suggesting a wider increase in recent transmission. The reasons for this increase may include changing patterns in drug use, with anecdotal reports of an increase in mephedrone injection. In response we have extended the surveillance system and continued efforts are needed to improve diagnosis and to strengthen local needle-exchange programmes to reduce further transmission.

Keywords: Hepatitis C, intravenous drug use, Surveillance, Wales

PRESENTED BY: Laia Fina Homar (laia.fina@wales.nhs.uk)

REFERENCE NUMBER: 3146

The perceived contribution of syndromic data to communicable disease action in Ontario, Canada: a qualitative study

Laura Rivera (1), Ye Li (1,2), Rachel Savage (2), Natasha Crowcroft (1,2,3), Laura Rosella (1,2,4), Wendy Lou (1,2), Ian Johnson (1,2,5)

1. Public Health Ontario, Toronto, Canada
2. Dalla Lana School of Public Health, University of Toronto, Toronto, Canada
3. Department of Laboratory Medicine and Pathobiology, University of Toronto, Toronto, Canada
4. Institute of Clinical Evaluative Sciences, Toronto, Canada
5. Department of Family Medicine, Queen's University, Kingston, Canada

Background
The practice of incorporating syndromic data into routine communicable disease surveillance is growing in Ontario; however, there is skepticism regarding whether these data add value to traditional surveillance systems. This study assessed perceptions of local public health epidemiologists of the extent to which emergency department visit and school absenteeism syndromic surveillance data inform tangible public health action related to communicable disease control.

Methods
Semi-structured interviews were conducted with communicable disease epidemiologists at fifteen syndromic surveillance-using local public health agencies in Ontario, Canada. Interviews assessed whether respondents considered their syndromic surveillance systems to have played a primary or secondary role in informing decisions to take communicable disease-related actions. Qualitative data were coded inductively and thematic analysis was performed to synthesize commonly occurring concepts.

Results
Collectively, respondents provided insight into the varying degrees to which epidemiologists use syndromic surveillance as a basis for action. Those who considered syndromic surveillance as a primary source to base action mentioned the benefits of having a real-time information stream to monitor the current level of communicable disease activity in their community and provide "situational awareness", as well the ability to strengthen relationships with community institutions such as local hospitals. However, many respondents did not consider it a primary information source, noting factors such as the large volume of alerts, difficulty ascribing public health significance to individual aberrations, and the need to corroborate aberrant event findings with other information sources (such as laboratory-confirmed data).

Conclusion
These results indicate that despite widespread adoption of syndromic surveillance in local public health practice, communicable disease epidemiologists perceive varying purposes for these systems.

Keywords: surveillance, outbreaks, qualitative evaluation

PRESENTED BY: Natasha Crowcroft (natasha.crowcroft@oahpp.ca)

REFERENCE NUMBER: 2980

Evaluation of the Norwegian surveillance system for pertussis, 1996-2014

Margot Einöder-Moreno (1,2), Didrik Frimann Vestrheim (1,3), Hanne Nøkleby (1), Katrine Borgen (1)

1. Division of Infectious Disease Control, Norwegian Institute of Public Health, Oslo, Norway
2. European Program for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
3. European Program for Public Health Microbiology Training (EUPHEM), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden

Background
In the last decade Norway has reported the highest incidence of pertussis in Europe, despite vaccination coverage above 90%. The vaccination program objective is to prevent severe disease in children under two years of age. We evaluated Norway's surveillance for pertussis in terms of data completeness, to assess the reliability of the data used for estimating the incidence and impact of preventive measures.

Methods
We used all records of notified pertussis cases in the Norwegian Surveillance System for Communicable Diseases from 1996-2014. Cases are defined as pertussis-compatible symptoms with epidemiological link, or laboratory diagnosis. We assessed completeness of the variables: symptoms, laboratory diagnosis, epidemiological link, onset date, hospitalization, and disease outcome by calculating the proportion of complete values overall and in children under two years of age.

Results
Of 68,130 pertussis records analysed, 21,204 (31.1%) had complete symptoms information and 44,111 (64.8%) complete laboratory information. The system does not have a variable for epidemiological link. Onset date was complete in 24,170 (35.5%) records, hospitalization in 35,209 (51.7%) and disease outcome in 23,358 (34.3%). Of 2,222 records of children under two years, 1122 (50.5%) had complete symptoms and 1837 (82.7%) complete laboratory information, 1412 (63.6%) had complete onset date, 2166 (97.5%) hospitalization and 1468 (66.1%) disease outcome.

Conclusion
Low completeness of symptoms, laboratory diagnosis and epidemiological link reduce the accuracy of the system for assessing incidence. Low completeness of hospitalization and disease outcome limits the ability to verify the severity of the cases notified, hampering the evaluation of the effectiveness of the immunization program in preventing severe disease among those under two years. We recommend active collection of clinical information in children under two years to improve completeness.

Keywords: Whooping Cough, Bordetella pertussis, Evaluation Studies, Public Health Surveillance

PRESENTED BY: Margot Einöder-Moreno (margot.einoder.moreno@fhi.no)

REFERENCE NUMBER: 3107

Track 15: Outbreaks II

MODERATOR: Ioannis Karagiannis (UK FETP coordinator, UK)

A large community outbreak of Legionnaires' disease in Portugal: the use of geospatial analysis to identify wet cooling systems, October to December 2014.

Tara Shivaji (1,2), Luís Serra (1), Cátia Sousa Pinto (1), Paulo J Nogueira (1)

1. Directorate-General of Health, Lisbon Portugal
2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden

Background
On 7 November 2014, a hospital laboratory informed the Directorate-General of Health of 17 Legionnaires' disease cases admitted overnight. A multidisciplinary taskforce identified 403 cases and 49 potential sources. Legionella sp was isolated from cooling towers of four industries. NE winds were recorded during the estimated exposure period. To help identify the source, we tested the hypothesis that risk of Legionnaires' disease was inversely related to distance from the towers and influenced by direction.

Methods
We georeferenced cases' residences and locations of cooling systems using Google Earth. We used QGIS to define a 10km buffer centered on each of the four systems. We compared observed to expected cases. We calculated expected cases by applying overall attack rates to 2011 census data for the buffer. Using Stones' Test (ST), we tested observed-to-expected ratios for decline in risk, with distance up to 10km in the northeast, northwest, southeast and southwest.

Results
The study areas included 328 cases that we could georeference. Factory 1 demonstrated clustering in NW (ST 1.93 p=0.01), NE (ST 5.00 p=0.01) and SW (ST 157.06 p<0.001). Factory 2 demonstrated clustering the NE (ST 4.18 p=0.009) and SW (ST 117.17 p<0.001). Factory 3 and 4 demonstrated clustering in the SW only (ST 126.63 p<0.001; ST 66.14 p<0.001 respectively).

Conclusion
The southwesterly clustering from all four industries indicates that all of them contributed to this outbreak. This is probably explained by cross-contamination and a predominant NE wind. Exposure was probably underestimated by excluding non-residents and displacement within the study area. All four industries were shut down and disinfected. Source proximity studies should consider incorporating direction into the analysis.

Keywords: Legionnaires' Disease, Outbreak, Geospatial analysis

PRESENTED BY: Tara Shivaji (tarashivaji@dgs.pt)

REFERENCE NUMBER: 2953

A mixed viral gastroenteritis outbreak caused by Rotavirus and Norovirus in a Karen temporary shelter, Suan Phueng District, Ratchaburi Province, Thailand February - March 2013

Nirandorn Yimchoho (1,2), Orathai Suwannachairob (2), Piplat Piyapongdecha (3), Rome Buathong (2)

1. Field Epidemiology and Management Training Programme (FEMT), Bureau of Epidemiology, Ministry of Public Health, Thailand
2. Bureau of Epidemiology, Ministry of Public Health, Thailand
3. Suan Phueng District Health Offices, Ratchaburi Provincial Health Offices, Ministry of Public Health, Thailand

Background

Viral diarrhea is common in crowded living condition and can rapidly cause wide spread outbreaks. On February 2013, an increasing incidence rate of acute watery diarrhea was detected in a Karen temporary shelter at Thai-Myanmar border in Suan Phueng District, Ratchaburi Province. An outbreak investigation was initiated to determine the etiology and source of infection and to recommend specific control measures.

Methods

We reviewed medical records and interviewed cases and conducted active case finding in the shelter. An environmental survey was carried out and 11 samples of water supplied in the shelter were collected for virological study. Additionally, 11 stool and rectal swab samples were collectedfrom cases and sent for RT-PCR and PAGE studies.

Results

The shelter supported 7,426 Karen population who lived in 4 zones. Totally, 111 cases were identified with an overall attack rate 1.5%. The median age was 3 years (11 days – 65 years) with the highest attack rate in infants(13.63%). The most common clinical presentation was watery diarrhea(93%), followed by fever(72%) and vomiting(70%), respectively. Forty percent of cases were admitted. Of 5 fresh stool samples and 6 rectal swabs tested, Rotavirus and Norovirus were found positive in 7(64%) and 2(18%) of samples, respectively. But none were negative for enteropathogenic bacteria. The epidemic curve demonstrated a continuous common source. Natural water supply before treatment process was contaminated by Rotavirus.

Conclusion

An outbreak of mixed viral gastroenteritis caused by Rotavirus and Norovirus was confirmed in the shelter. Contamination of viruses in water reservoir resulted in the common source outbreak. Hyperchlorination was recommended during outbreak and intensive health education to improve personal hygiene and sanitation.

Keywords: Outbreak, Acute gastroenteritis, Norovirus, Rotavirus, Temporary shelter, Thailand

PRESENTED BY: Nirandorn Yimchoho (u4908118@gmail.com)

REFERENCE NUMBER: 3005

Salmonella Enteritidis outbreak among day care center employees in Budapest

Zoltán Kis (1,2), Ágnes Fehér (1), Zsuzsanna Samrák (3), Agnes Csohan (1), Ivelina Damjanova (1)

1. National Center for Epidemiology
2. ECDC, European Programme for Public Health Microbiology Training
3. Budapest Capital Policy Administration Services of Public Health, Hungary

Background

The Public Health Office of Budapest (PHO) was informed on 8 October 2014 of gastrointestinal illnesses amongst employees from five Day Care Centers' (DCCs) in Budapest. The DCCs have one common central kitchen producing food for adults and toddlers. The same day the PHO commenced an outbreak investigation to assess the extent, identify the mode and the vehicle of transmission, initiate the appropriate recommendations and control measures.

Methods

Cases were defined as a person who worked in any of the DCCs and developed any of the following symptoms: diarrhea, vomiting, fever, abdominal cramps between 6 and 8 October 2014. All interviewed symptomatic people were asked to provide a stool sample. On 9 October, the National Food Chain Safety Office (NFCSO) inspected the DCCs and the remaining food. In our cohort study we calculated the overall and food-specific attack rates (AR) and risk ratios (RR) using univariate analyses.

Results

Amongst the 87 exposed persons, 64 (73.6%) participated in the study and 39 cases were identified (AR=61.1%), 84.6% were female. Those who ate Vargabéles cake were 2.6 times more likely to be ill (33/42) than those who did not (2/18) (RR = 2.6; 95%CI 1.5–4.5). Thirty-three of 34 stool specimens were culture positive for Salmonella Enteritidis (Phage Type 8, PT8). Amongst food remaining and ingredients investigated by NFCSO, the Vargabéles cake was positive for Salmonella Enteritidis PT8. The investigation also revealed that the baking time and storage of the Vargabéles cake was inadequate.

Conclusion

Inadequate cake preparation was the most likely cause of the outbreak. Thorough cleaning of the kitchen was recommended along with firm recommendations to educate the kitchen staff to adhere to the food safety regulations.

Keywords: Infectious Disease Outbreak, Salmonella, Food-borne Disease, Hungary

PRESENTED BY: Zoltán Kis (kis.zoltan@oek.antsz.hu)

Outbreak of Sindbis virus infection in northern Sweden associated with chronic arthralgia

Åsa Gylfe (1), Oscar Forsman (1), Joakim Berqvist (2), Göran Bucht (2), Åsa Ribers (3), Solveig Wållberg-Jonsson (3), Clas Ahlm (1), Magnus Evander (1)

1. Department of Clinical Microbiology, Umeå University, Umeå, Sweden
2. Swedish Defense Research Agency, Umeå, Sweden
3. Department of Public Health and Clinical Medicine, Umeå University, Umeå, Sweden

Background

The mosquito-borne Sindbis virus (SINV) has birds as amplifying hosts. The infection, named Ockelbo disease in Sweden, is characterized by fever, exanthema and arthritis-like symptoms that may persist for years. At the end of August 2013, an unexpected outbreak of Ockelbo disease appeared in Sweden, north of the endemic region.

Methods

SINV IgM and IgG were analyzed by immunofluorescence and viral RNA by SINV specific qRT-PCR. Patients answered a web-based questionnaire and were examined 6-8 months after acute infection for rheumatologic symptoms and laboratory parameters. Mosquitoes were captured from a hot-spot region and analyzed by qRT-PCR for SINV RNA and DNA barcoding for mosquito typing.

Results

46 of 107 patients with Ockelbo disease symptoms were positive for SINV IgM and 34 for SINV IgG. Patients were between 7- and -85 years of age (median 53), 17 men, 29 women. Acute disease symptoms were rash (95%), arthritis (97%), fever (53%). Patients were followed regarding prolonged and chronic symptoms and 39% had chronic arthralgia 6-8 months after infection. 1,800 mosquitoes were captured and the SINV associated with the outbreak was isolated from mosquitoes. The weather was unusually warm just before and during the outbreak, favoring conditions for a prolonged mosquito season and stay of migrating birds.

Conclusion

This is the first time a large outbreak of Ockelbo disease has been documented in northern Sweden. The outbreak raises questions regarding the origin of the virus and future surveillance strategies. Although not a life-threating disease, the outbreak resulted in human suffering, sick leave, concern in the society and, in several cases, a prolonged arthritis.

Keywords: Sindbis virus, Ockelbo disease, Arthritis, Arthralgia, Mosquito, Outbreak

PRESENTED BY: Clas Ahlm (magnus.evander@umu.se)

REFERENCE NUMBER: 3094

Cluster of Ebola cases associated with funeral preparations in Freetown, 2015

Anna Kuehne (1,2), Chris Lane (2,3), Jeffrey Gilbert (2), MarkAlain Dery (2,4), James Bangura (5), Charles Kembei (5), Christina Frank (2,6), Ifeolu John David (2), Bintu Jabbie (2), Eilish Cleary (2)

1. Postgraduate Training for Applied Epidemiology (PAE), Robert Koch Institute, Berlin, Germany affiliated to the European Programme for Intervention Epidemiology Training (EPIET), ECDC, Stockholm, Sweden
2. WHO, Freetown, Sierra Leone
3. Centre for Infectious Disease Surveillance and Control, Public Health England, UK
4. Tulane University School of Medicine, New Orleans, USA
5. Western Area Ebola Response Team, Ministry of Health and Sanitation, Freetown, Sierra Leone
6. Department for Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany

Background

From March 2014 to April 2015, Sierra Leone reported more than 8,500 cases of Ebola virus disease (EVD) including 3,490 deaths. On 26/02/2015 Western Area Emergency Response Centre in Freetown received an alert about a death of an herbalist and initiated case investigation to confirm EVD-aetiology and identify source and contacts.

Methods

We defined a confirmed EVD case as anyone with laboratory diagnosis by polymerase-chain-reaction. We identified and traced contacts to minimize further transmission.

Results

The herbalist's exposure stemmed from treating Ebola patients. He died 25/02/2015 and was confirmed positive post-mortem. The preparation of his body for the burial resulted in a cluster of 13 cases (31% female, median age 28 years, case-fatality-ratio 62%): The index case, 10 secondary and two tertiary cases. Nine known contacts of the herbalist were traced, all developed symptoms between 06/03/2015 and 12/03/2015 and were confirmed positive. Another herbalist also had attended the body preparation of the index case but evaded line-listing. He died 17/03/2015, his body was prepared for burial, following delayed alert and laboratory confirmation. Eight known contacts of the second herbalist were traced. One developed symptoms 28/03/2015 and was confirmed positive. Again one additional contact evaded line-listing, fell ill 24/03/2015 and presented at a health-centre where he was confirmed positive. No additional cases ensued.

Conclusion

In this cluster linked to unsafe funeral preparations, the transmission of Ebola virus was a consequence of late alerts of deaths and evasions from contact tracing. Secondary cases among those appropriately contact-traced were identified early, enabling prevention of further transmission. To stop the outbreak, we recommend involvement of the community and education of herbalists, who play an important role in healthcare provision and burials.

Keywords: Ebola Hemorrhagic Fever, Sierra Leone, Contact tracing, Disease Outbreaks, Population Surveillance, Traditional Medicine

PRESENTED BY: Anna Kuehne (KuehneAn@rki.de)

REFERENCE NUMBER: 3160

Post-Ebola Measles Outbreak in Lola, Guinea

Jonathan Evan Suk (1,2), Adela Paez Jimenez (2,3), Vladimir Prikazsky (1,2)

1. European Centre for Disease Prevention and Control, Stockholm, Sweden
2. WHO Global Outbreak Alert and Response Network
3. Mediterranean Programme for Intervention Epidemiology Training (MediPIET)

Background
In Guinea, healthcare consultations have declined due to Ebola. This could lead to significant underreporting of infectious disease. The prefecture of Lola had active Ebola transmission between September 2014 and February 2015, and experienced an outbreak of Measles beginning January, 2015.

Methods
Data on population, healthcare consultations, and routine surveillance were provided by the Direction Prefectorale de la Sante of Lola, Guinea. Measles surveillance was reinforced by a WHO GOARN team. Teams were also dispatched to health centres to validate data.

Results
Outbreak data was most comprehensive in the sub-prefecture N'Zoo. This was used as a proxy to estimate the number of children 0-5 years old potentially affected by the outbreak in Lola. Healthcare consultations declined by 27% in Lola the period commencing with the onset of Ebola, from 0.22 visitations per capita per year to 0.16. Field investigations identified a total of 596 cases that had presented at local health centres between weeks 1-17, 2015. Of these, 525 (88%) were among children between 0-5 years old, representing an attack rate of 1.47% among this age cohort. The sub-prefecture of N'Zoo accounts for 8.6% of Lola's population, but 37% of all measles cases identified (219/596), with an attack rate among children 0-5 years of 6.1%. Extrapolating this rate to all of Lola yields an estimate of 2198 cases among children 0-5 years.

Conclusion
There are many limitations to outbreak investigation in Guinea, including infrequent healthcare consultations and highly variable levels of reporting. Given the assumption that data from N'Zoo is a realistic proxy, measles outbreak data in Lola is substantially underestimated. Strengthening surveillance and enhancing outbreak response will be important priorities in Lola in the aftermath of Ebola.

Keywords: Ebola, Measles, Infectious Disease Outbreaks, Epidemiology, Guinea

PRESENTED BY: Jonathan Evan Suk (jonathan.suk@ecdc.europa.eu)
REFERENCE NUMBER: 2965

Late breaker: Worrying emergence of severe malaria in non-endemic area: Case of the hospital of Fianarantsoa, from October 2014 to May 2015, Madagascar

Mireille Randria (1,2,3), Laurence Randrianasolo (2), Lea Randriamampionona (2), Patrice Piola (2)

1. Indian Ocean Field Epidemiology Training Program, Indian Ocean Commission, Mauritius
2. Epidemiology Unit, Pasteur Institute of Madagascar, Madagascar
3. Health Watch and Epidemiological Surveillance Department, Ministry of Health, Madagascar

Background
October From 2014 to May 2015, 219 cases of severe malaria were reported by the Hospital of Fianarantsoa, in a non-endemic area of Madagascar. We described the cases and described potential risk factors for this emergence.

Methods
A severe malaria case is a hospital patient with fever, positive Rapid Diagnostic Test (RDT) and/or positive Microscopy and a sign of severity (WHO). A doubling of malaria cases over two successive weeks is an alert. An alert is issued in case of one autochthonous case in non-endemic areas. We collected information on cases from health facility registers and analysed those for whom information were complete. We conducted geographic, climatic and environmental investigations.

Results
Over eight months, we detected eight alerts for doubling cases and investigated 107 cases. The M/F sex ratio was 1.6. Of all cases, 48.6% were adults >25 years old. Of all cases, 77.6% were imported cases and 22.4% autochthonous. Case fatality was 0.7%. Among children

Conclusion
Importation of cases is likely due to the proximity to endemic areas. High humidity and rice cultivation create favourable conditions for vectors. A more prevalent use of impregnated bednets by women is consistent with the M/F sex ratio. Autochthonous malaria alerts in non-endemic areas, more prevalent in children (a non-immune group), may suggest the emergence of new transmission area.Climate change could further facilitate the emergence and extension of malaria-endemic areas in the central highlands. Reinforced surveillance and vector control are crucial for dealing with this alarming emergence and preventing epidemics.

Keywords: Malaria, emergence, non-endemic, Madagascar

PRESENTED BY: Mireille Randria (randria.mireille@gmail.com)

Track 16: Public Health Microbiology and Molecular Epidemiology

MODERATOR: Johanna Takkinen (ECDC, Head of Disease Programme FWD and Plenary session C speaker)

Sero- and molecular epidemiology survey on Coxiella burnetii in Cyprus, 2005-2013.

Dimosthenis Chochlakis (1,2), Ioannis Ioannou (3), Ioannis Goniotakis (2), Maria Keramarou (1,2), Sofia Kokkini (4), Elena Grigoriou (3), Yannis Tselentis (2), Anna Psaroulaki (2)

1. Regional Laboratory of Public Health of Crete, University of Crete, School of Medicine,Heraklion, Crete, Greece
2. Laboratory of Clinical Bacteriology, Parasitology, Zoonoses and Geographical Medicine, University of Crete, Heraklion, Crete, Greece
3. Veterinary Services, Nicosia, Cyprus
4. Unit of Intensive care, University Hospital of Heraklion, Crete, Greece

Background
Infection of animals by Coxiella burnetii may be associated with late abortions, stillbirth, delivery of weak offspring and infertility, while human infection can be acute or chronic (usually endocarditis). We tried to estimate the prevalence of the pathogen in human and animal population, record regions with abortions in animals due to C. burnetii and endemic areas using GIS, in Cyprus.

Methods
The study took place in two phases, (1st: 2005-2006; 2nd: 2006-2013). During the 1st phase, samples were drawn from a representative sample of ruminants and from human population (farm owners and people with no animal contact). Sera were tested against IgG phase II antibodies by IFA. During the 2nd phase, samples from animals with abortions were tested by Real-time PCR.

Results
The overall seroprevalence (goats: 292/347, 84.1%; sheep: 273/337, 81%; bovines: 135/338, 40%; 98 farming units from all prefectures) was 68.5%. A positive correlation was recorded between altitude of farms and seropositivity, but not between seropositivity and annual mean temperature. Eighty five (85/127; 67%) of the farm owners and 63% (78/124) of the control group revealed antibodies. Odds ratio for humans, regarding occupation, gender, age against seropositivity did not reveal any statistical significance. Of the 90 fetuses and 120 placentas collected (98 sheep; 82 goats), C. burnetii was detected in 41.8% (41/98) of the sheep and 52.4% (43/82) of the goats. Farms with unsatisfactory biosecurity levels were almost two times more likely to suffer from abortions. Seropositive areas coincided with those where abortions were recorded.

Conclusion
Q fever is endemic in Cyprus. The control of the pathogen needs to be multifactorial extending to all parameters and links of the transmission chain of the pathogen.

Keywords: Q fever, surveillance, IFA, Real-time PCR, Cyprus

PRESENTED BY: Maria Keramarou (keramarou@gmail.com)
REFERENCE NUMBER: 3038

Should sequencing of the haemagglutinin gene or the hypervariable region be part of outbreak investigations in the measles elimination end-game?

Heli Harvala (1,2), Åsa Wiman (1), Katherina Zakikhany (1), Anders Wallensten (1), Hélène Englund (1), Mia Brytting (1)

1. Public Health Agency of Swede, Solna, Sweden
2. European Programme for Public Health Microbiology Training (EUPHEM), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden

Background
Through measles elimination activities, the genetic diversity within circulating measles virus (MeV) strains has decreased. Therefore it has become increasingly difficult to differentiate MeVs relating to different outbreaks based only on N-gene sequencing, which is used for genotyping (24 types, A-H). We aimed to identify further genomic regions that could provide better molecular resolution between epidemiologically linked and unlinked MeV variants in Sweden.

Methods
The variability across the MeV genome was studied via pairwise distance mapping. The haemagglutinin (H)-gene and hypervariable region between the fusion and matrix genes (HVR; identified as the most variable region) were amplified and sequenced from 52 MeV-positive samples genotyped at the Public Health Agency in 2013-2014. Phylogenetic clustering of MeVs based on N-gene, H-gene and HVR was compared with epidemiological data including date and place of diagnosis, and probable source of infection.

Results
We identified 27 MeVs as genotype B3 and 25 as D8; two B3-clusters matched with epidemiological data, whereas third cluster (all sequences identical) contained epidemiologically unrelated viruses from four outbreaks. Similarly one of four D8-cluster was inconsistent with epidemiological data, comprising viruses from five outbreaks. Phylogeny of H-gene and HVR of B3 viruses identified five clusters and three single cases, consistent with the epidemiological data. Clustering of D8 viruses based on the H-gene was unclear, whereas HVR phylogeny mirrored epidemiological data.

Conclusion
By extending the sequencing repertoire to include H-gene and/or HVR, a more detailed picture of MeV circulation with more defined links between outbreaks and transmission chains in Sweden was obtained. Further identification and better genetic characterisation of MeVs internationally is essential in identifying sources and routes of MeV spread within Europe and beyond during the measles elimination end-game.

Keywords: measles virus, genotyping, elimination, H-gene, hypervariable region, outbreak

PRESENTED BY: Heli Harvala (heli.simmonds@hotmail.com)
REFERENCE NUMBER: 2952

Evaluation of the standardised S. Typhimurium multiple locus variable number of tandem repeats analysis (MLVA) as a tool for investigating S. Chester outbreaks

Natacha Milhano (1,2), Inger Løbersli (1), Lin Thorstensen Brandal (1), Ulf Dahle (1)

1. Folkehelseinstituttet, Oslo, Norway
2. European Programme for Public Health Microbiology Training (EUPHEM), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden

Background

Salmonella Chester is rarely reported as a causative agent of foodborne outbreaks. However, since August 2014 an unexpected number of Salmonella Chester cases have been notified from several European countries, the majority travel-related to Morocco. This serovar is usually examined using the pulse-field gel electrophoresis (PFGE). Since S. Chester belongs to the same group as S. Typhimurium we aimed to investigate whether it could be typed using the standard MLVA used for S. Typhimurium, and therefore serve as a useful tool in outbreak investigations.

Methods

Sixteen isolates of S. Chester from 15 individuals hospitalised in Norway from 2012 to 2014 were analysed with S. Typhimurium MLVA. This technique is based on PCR amplification of five variable number of tandem repeats (VNTR) loci and identification of fragment sizes by capillary electrophoresis, each of which is assigned an allele number.

Results

Seven MLVA profiles were obtained, one included a cluster of seven cases that traveled to Mediterranean countries. The six remaining profiles were from individuals with different travel destinations to other global regions. The MLVA amplification profile was incomplete, as only two of five loci amplified, using S. Typhimurium specific primers, for all isolates tested.

Conclusion

The standard S. Typhimurium MLVA allowed for a degree of discrimination between S. Chester strains, identifying a geographical cluster, albeit the resolution was low due to incomplete profiles. As MLVA is a more timely and comparable method than the PFGE currently in use, MLVA development by identification of VNTRs unique to S. Chester should be pursued allowing investigation of future outbreaks. The current S. Typhimurium MLVA may serve as a guideline for identifying appropriate S. Chester VNTRs.

Keywords: Outbreak, Salmonella Chester, MLVA, travel.

PRESENTED BY: Natacha Milhano (nami@fhi.no)

REFERENCE NUMBER: 2893

Circulation of enteroviruses and human parechoviruses in children aged up to 5 years with influenza-like illness in Northern Italy during the 5 previous winter seasons.

Laura Bubba (1), Laura Pellegrinelli (1), Marianna Martinelli (1), Talya Raphael (2), Mathilde Laureti (2), Sandro Binda (1), Elena Pariani (1)

1. Department of Biomedical Sciences for Health, University of Milan, Milan, Italy.
2. Department of Health Sciences, University Paris Diderot, Paris VII, Paris, France

Background

Influenza-like illness (ILI) is a cause of child morbidity during the winter. Predominantly caused by influenzavirus, it can also be caused by different respiratory viruses, such as enterovirus (EV) and human parechovirus (HPeV). Aim: to describe the circulation of influenzaviruses, HPeV, EV and EV-D68 in children aged up to 5 years during the five previous winter seasons (2010/11-2014/15) in Lombardy (Northern Italy).

Methods

Throat swabs were collected from 392 children (0-5 years; 45.4% females, median age: 3 years ; IQR: 4 years) with ILI in the framework of the Italian influenza surveillance network InfluNet. RNA was extracted from each sample (Invitek), and amplified for detection of influenzavirus type A/B and EV/HPeV with two one-step multiplex real-time RT-PCRs. EV-positive samples were tested for EV-D68 with a one-step real-time RT-PCR.

Results

Of the 392 samples, 46.9% (184/392) were influenzavirus-positive (75% type A), 9.4% were EV-positive and 3.8% were HPeV-positive. EV-D68 was not detected. Among the 208 influenzavirus-negative samples, 11.5% and 3.8% were positive for EV and HPeV, respectively. HPeV-positive children were younger (mean age: 21 months) than both EV-positive (mean: 34 months, p=0.002) and influenzavirus-positive children (mean: 39 months, p<0.001). HPeV was identified in 1.6% (in 2010/11) to 5% (in 2014/15) of samples. EV was similarly detected (9.7% to 11.3%) except in 2012/13 (4.3%). Co-infections were detected in 10.9% (20/184) of cases: 7.1% (13/184) were influenzavirus/EV-positive and 3.9% were influenzavirus/HPeV-positive. None were EV/HPeV.

Conclusion

Almost half (47%) of ILI cases in our study were influenzavirus-positive, as expected. No EV-D68 was identified. Of the remaining influenzavirus-negative cases, 15% were positive for EV or HPeV, highlighting the importance of monitoring the circulation of these viruses, generally not included among common investigated pathogens.

Keywords: Influenzavirus, enterovirus, parechovirus, influenza-like illness,enterovirus-D68

PRESENTED BY: Laura Bubba (laura.bubba@unimi.it)

REFERENCE NUMBER: 3092

Hepatitis E virus in wastewaters from Portugal - preliminary results of an across country study

Daniel Goncalves (1), Joao Pereira-Vaz (2), Filipa Rodrigues (1), Ana Donato (3), Cristina Luxo (4), Ana Matos (4)

1. Faculty of Pharmacy University of Coimbra, Coimbra, Portugal
2. Virology laboratory - Hospital and University Center of Coimbra, Coimbra, Portugal
3. Clinical laboratory- Faculty of Pharmacy, University of Coimbra, Coimbra, Portugal
4. Research Centre on Chemical Processes Engineering and Forest Products (CIEPQF); Faculty of Pharmacy- University of Coimbra, Coimbra, Portugal

Background
Hepatitis E virus (HEV) belongs to Hepevirus genus from Hepeviridae family, is a non-enveloped small icosahedral virus with a (+)ssRNA genome. There are four genotypes (1-4) of the virus, genotype 1 and 2 are associated with exclusive infection on humans, while genotype 3 and 4 can infect pigs and other mammalians. The main way of transmission of HEV is faecal-oral, although genotypes 3 and 4 may cause outbreaks of infection through their zoonotic potential. The main objective of the present study was to evaluate the presence of HEV in Portuguese wastewaters, in order to evaluate the risk for public health caused by waterborne HEV.

Methods
Influent (WWI) and effluent (WWE) wastewater samples from fifteen different Portuguese Wastewater Treatment Plants (WWTP) were collected for analysis. All samples were submitted to nucleic-acid extraction followed by qRT-PCR, aiming the detection of HEV genome.

Results
Two (13.3%) out of the 15 influent WWTP samples revealed the presence of HEV-RNA. The viral genome was undetectable in all effluent samples.

Conclusion
This study, even preliminarily, points to the presence of HEV in wastewaters of geographically unrelated areas from Portugal. The detection of viral genome in influent samples, along with its not detection in respective effluent sample could further point to an effective treatment process at the WWTP, regarding viral remove. Nevertheless, to discard the effect of different viral loads in samples, quantification assays are needed in order to understand the effectiveness of the treatment. This is the first study of its kind in Portugal, but the number of samples needs to be raised, as well as the seasons of sample collection, allowing the evaluation of HEV spread in wastewaters of Portugal.

Keywords: hepatitis E, virus, wastewater, viral outbreaks, zoonotic infection

PRESENTED BY: Daniel Gonçalves (leinad_goncalves@hotmail.com)
REFERENCE NUMBER: 2963

Invasive Group A Streptococcal Infections in Norway 2011-2014: A Change in Epidemiology

Umaer Naseer (1,2), Martin Steinbakk (1), Hans Blystad (1), Dominique A. Caugant (1)

1. Division of Infectious Disease Control, Norwegian Institute of Public Health, Oslo, Norway
2. European Programme for Public Health Microbiology Training (EUPHEM), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden

Background
Strain emm1 of Streptococcus pyogenes, group A streptococci (GAS) was responsible for severe disease in the 1980s. In Nordic countries emm28 replaced emm1; in Norway 19% of the isolates were emm28 and 14% emm1 in 2006-2007. Recently an increase in GAS infections and resurgence of emm1 was reported from Sweden. In this study we investigate the epidemiology of invasive GAS (iGAS) infections and the association of emm-types with clinical presentations in Norway, 2010-2014.

Methods
We collected data from 2010-2014 on antimicrobial susceptibility, multi-locus sequence-type and emm-type of iGAS isolates from the National Reference Laboratory, and linked it to demographic and clinical presentation data from the Norwegian Surveillance System for Communicable Diseases. We calculated the age and sex distribution, major emm- and sequence-types (ST), and prevalence ratios (PR) with 95% confidence intervals (CI) on the association of emm-types with clinical presentations.

Results
We analysed 756 isolates, incidence 3.4 per 100 000 (2014), median age 59 years (range: ‹1-102), male 56%. Most common presentation was sepsis (43%) followed by necrotizing fasciitis (9%). Emm1 was the most prevalent strain in all years (33% in 2014), and 15% of the isolates were emm28 (2014). All isolates were susceptible to penicillin and ‹4% resistant to erythromycin. No significant association was seen between emm-type and the most frequent clinical presentations. Exposure to emm12 had a PR of 3.55 (95%CI; 1.45-8.66) for osteomyelitis or arthritis.

Conclusion
This study documents a re-emergence of emm1 in Norway. The clinical presentation of iGAS infections has not changed and no significant association was observed between emm-type and clinical presentation. We recommend research into the epidemiology of non-invasive GAS infections, for better understanding of GAS strains circulating in Norway.

Keywords: Streptococcus pyogenes, Retrospective study, Epidemiology, emm-type, MLST

PRESENTED BY: Umaer Naseer (mohammed.umaer.naseer@fhi.no)
REFERENCE NUMBER: 2947

Capabilities and capacities of European Union public health microbiology system - results of the first European Laboratory Capability (EULabCap) survey 2013

Laura Espinosa (1), Katrin Leitmeyer (1), Amanda J. Ozin-Hofsaess (1), Marc Struelens (1)

1. Microbiology Coordination Section, Office of the Chief Scientist, European Centre for Disease Prevention and Control, Solna, Sweden

Background
Little is known about European laboratory capability (ability to perform a function) and capacity (ability to deliver a quantified level of service outputs over a defined time period). ECDC and the European Union/ European Economic Area National Microbiology Focal Points (NMFPs) developed the EULabCAP to assess public health microbiology capabilities and capacities for surveillance and epidemic preparedness within the EU.

Methods
In 2014 we collected information on 2013 activities and outputs for thirty EU/EEA countries using sixty indicators aligned to EU policy targets and standards that covered twelve targets within three public health microbiology system dimensions (primary diagnostics, national reference laboratory [NRL], surveillance and response support). We calculated stratified aggregated indices for targets, adjusting values on a total scale of 0-10 and using median and interquartile range (IQR) for comparison.

Results
100% countries responded and 94% completely. The highest capability targets (median≥8) were for primary antimicrobial susceptibility testing, for NRL diagnostics and for EU network participation. The lowest capability targets (median≤6) were for regulation, guidance and use of primary diagnostics; for NRL molecular surveillance; and for response support. 83% of thirty countries reported capability within the country for diagnostic confirmation and pathogen identification for more than 35 out of 53 pathogens under Decision 2119/98/EC.

Conclusion
The capability and capacity varies between countries and across system dimensions in the EU/EEA. In the context of EU legislation on serious cross-border threats to health it is of note that laboratory-based surveillance and EU network participation had high scoring capability and capacity whereas response support showed operational limitations. ECDC and NMFPs will use the annual EULabCap monitoring system to evaluate the impact of national public health microbiology policies and EU support activities.

Keywords: Microbiology, European Union, survey, quality control

PRESENTED BY: Laura Espinosa (laura.espinosa@ecdc.europa.eu)
REFERENCE NUMBER: 2978

Moderated Poster Session C
Friday 13 November
15:00-16:10

Track 17: Vaccine Coverage, Effectiveness and Safety

MODERATOR: Thea Kølsen Fischer (ESCAIDE SC, ECDC National Microbiology Focal Point, Denmark)

Timely monitoring of teenagers vaccination coverage using reimbursement data in France

Laure Fonteneau (1,2), Marine Ragot (1), Marie-Anne Botrel (1), Jean-Paul Guthmann (1), Isabelle Parent du Châtelet (1), Daniel Lévy-Bruhl (1)

1. French institute for public health surveillance, France
2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden

Background
School surveys serve to monitor vaccination coverage (VC) among teenagers in France, but are done every six years. In order to rapidly identify problems with VC we have explored the feasibility of using vaccine reimbursement data to estimate VC. We used the example of two vaccines, conjugate meningococcal C (MenC) and human papillomavirus (HPV), which are recommended to teenagers and young adults aged

Methods
The National Health Insurance Information System (SNIIR-AM) contains individual data on health spending reimbursement for 99% of the population. We used the Permanent Sample of Beneficiaries, which is a representative sample of the SNIIR-AM. It includes about 600.000 individuals and is updated monthly. VC was defined as the proportion of teenagers who received the complete vaccination series at a given age. We estimated HPV VC among 16 years old and MenC VC among 10-14, 15-19, 20-24 years old. We monitored annual VC during 2011-2014.

Results
MenC VC among those aged 10-14, 15-19, 20-24 years was 14.9%, 8.6%, 1.7%, respectively, in 2011 and 25.9%, 16.4%, 8.2%, respectively, in 2014. HPV VC was 26.5% in 2011 and 18.6% in 2014.

Conclusion
Reimbursement data allowed timely VC estimations among teenagers. It timely detected the low but steadily increasing MenC VC and decreasing in HPV VC. It does not allow to estimate VC at small geographical level. We have therefore recently started to use the comprehensive SNIIR-AM database to estimate local MenC VC. Those data will be provided to local decision-makers. We recommend using vaccine reimbursement data twice a year to closely monitor national and local VC among teenagers, to guide actions of sensitization and catch-up in areas of low VC

Keywords: Vaccination Coverage, Reimbursement data. Teenagers. France. Meningitis C. HPV

PRESENTED BY: Laure Fonteneau (l.fonteneau@invs.sante.fr)
REFERENCE NUMBER: 3119

Seasonal influenza vaccine effectiveness in Finland, a nationwide cohort study comparing the seasons 2012-13, 2013-14 and 2014-15

Ulrike Baum (1), Hanna Nohynek (1), Jonas Sundman (1), Jukka Jokinen (1), Terhi Kilpi (1)

1. National Institute for Health and Welfare, Finland

Background

In Finnish National Vaccination Programme (NVP), seasonal influenza vaccination (SIV) is recommended to children aged 6 to 35 months (hereafter referred to as children) since 2007 and since 2002 to adults 65 years of age and older (hereafter referred to as elderly). Last 3 seasons' vaccination coverage has been constant. In 2014-15, 16.5% of children and 37.5% of elderly received SIV. It is essential to evaluate SIV effectiveness (SIVE) for assessing NVP's performance and developing preventive policies.

Methods

Population and vaccination data were provided by Finnish Population Register and National Vaccination Register, which covers 75% (2014-15) to 90% (2012-13, 2013-14) of Finnish population. Influenza like illness (ILI) cases were retrieved from Primary Healthcare Register. Registers were linked via personal identification code assigned to all Finnish residents (5.45mi). SIVE was calculated using number of vaccinated and unvaccinated cases, as well as person-time the population was vaccinated and unvaccinated.

Results

In 2012-13, 268 (15 vaccinated) children and 328 (95) elderly were diagnosed with ILI demonstrating SIVE of 59.91% (95%CI: 32.51%-76.19%) in children and 29.35% (10.31%-44.35%) in elderly. In 2013-14, 192 (14) children and 189 (57) elderly were diagnosed with ILI demonstrating SIVE of 54.11% (20.94%-73.37%) in children and 37.17% (14.28%-53.95%) in elderly. In 2014-15, 158 (12) and 493 (188) ILI cases were observed in children and in elderly yielding preliminary SIVE of 57.89% (24.14%-76.62%) and -2.64% (-23.10%-14.41%).

Conclusion

SIV was more effective in children than in elderly. Although case numbers vary between seasons and despite mismatch of vaccine antigens and circulating viruses in 2014-15, SIVE in children seems constant. Analyzing SIVE using national register data is possible, and important when formulating policies and messages to better protect population against influenza.

Keywords: Coverage, Effectiveness, Immunisation, Influenza, Vaccination

PRESENTED BY: Ulrike Baum (ulrike.baum@thl.fi)

REFERENCE NUMBER: 2964

A comparative study of transport media for upper respiratory tract carriage of Streptococcus pneumoniae in Norway.

Natacha Milhano (1,2), Anneke Steens (1), Didrik Frimann Vestrheim (1,2), Ingeborg Aaberge (1)

1. Folkehelseinstituttet, Oslo, Norway
2. European Programme for Public Health Microbiology Training (EUPHEM), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden

Background

Monitoring of Streptococcus pneumoniae in carriage and surveillance of pneumococcal has been paramount to evaluate the impact of pneumococcal conjugate vaccine introduction into childhood immunisation programmes. Since 2006, three pneumococcal carriage studies have been performed in Norway, using serum broth for transport of nasopharyngeal swabs. This method has been sensitive for detection of carriage of multiple serotypes by latex agglutination from incubated broths. However, the method differs from the standard method for carriage studies recommended by WHO, in which specimens are transported and stored in a medium containing skimmed milk, tryptone, glucose, and glycerin (STGG). In order to adhere to this recommendation and still be able to compare retrospective and prospective Norwegian carriage studies, we compared pneumococcal recovery in both media.

Methods

Recovery of serotypes 19F, 4 and 3 of Streptococcus pneumoniae was compared between incubation in each transport media, serum broth and STGG, by counting colony forming units (CFU), by latex agglutination for detection of capsular polysaccharide and by quantification of pneumococcal DNA by real-time PCR targeting the autolysin gene (lytA).

Results

For the serotypes tested the results for DNA quantification were comparable ($p>0.05$, F-test) between both media, however small differences in CFU counts were observed. All serotypes were detected by the pneumococcal latex agglutination test in both transport media, according to DNA quantification detection limits.

Conclusion

We found STGG to be as sensitive as the serum broth for detecting S. pneumoniae, however a limitation to this study is that few serotypes were tested. Based on these results, previous Norwegian pneumococcal carriage studies can be compared to similar studies performed in other countries, and also to future Norwegian ones using the transport medium recommended by WHO.

Keywords: Streptococcus pneumoniae, transport media, real-time PCR, colony forming units, latex agglutination

PRESENTED BY: Natacha Milhano (nami@fhi.no)

REFERENCE NUMBER: 2895

Timeliness and completeness of post-exposure vaccinations in homes for asylum seekers during a large measles outbreak in Berlin, 2014/2015

Alexandra Hoffmann (1,2,3), Daniel Sagebiel (1), Kathrin Hentschel (1), Dirk Werber (1)

1. State Office for Health and Social Affairs, Berlin, Germany
2. Postgraduate Training for Applied Epidemiology (PAE), Robert Koch-Institute, Berlin, Germany
3. European Programme for Intervention Epidemiology Training (EPIET), ECDC, Sweden

Background

The German national committee for vaccinations recommends performing post-exposure vaccinations within 72 hours after contact to a measles case in institutional settings. The first cases in a large measles outbreak in Berlin 2014/2015 occurred among asylum seekers. To control the outbreak, local public health authorities (LHA) performed post-exposure vaccinations in asylum-seeker homes. This study aimed to assess timeliness and completeness of this intervention.

Methods

We used data of the mandatory notification system, supplemented by data collected from LHAs. We computed median time and interquartile range (IQR) between symptom onset of the first measles case in an asylum seeker home and its date of notification, respectively, and the post-exposure intervention. Furthermore, we assessed the proportion of asylum seekers reached by the post-exposure intervention.

Results

In the first ten weeks of the outbreak (calendar week 41-50 2014), 38/48 (79%) cases were asylum seekers. Until February 2015, cases had been notified in 32 asylum seeker homes. In 18 homes with available data on dates and persons registered, median time from symptom onset to notification and post-exposure intervention was four (IQR: 3-8) and 7.5(IQR: 6-10) days respectively; median time from notification to post-exposure intervention was two days (IQR: 0-6). In eight homes where the post-exposure intervention targeted all asylum seekers, 1133/2390 (47%) were reached; in four homes no interventions were performed due to lack of resources, in three homes only vulnerable subgroups (e.g. children, husbands of pregnant women) were considered.

Conclusion

Post-exposure vaccinations in asylum-seeker homes were incomplete and not possible to perform within the first 72 hours due to inherent delay between symptom onset and notification. Asylum seekers should be offered measles vaccinations at their first contact with public authorities.

Keywords: Measles, Vaccination, Disease Outbreaks, Berlin, Germany, Refugees

PRESENTED BY: Alexandra Hoffmann (alexandra.hoffmann@lageso.berlin.de)

REFERENCE NUMBER: 2911

Effect of vaccination on complications and transmission of measles during a large epidemic, the Netherlands, 2013-2014

Sandra van Dam (1,2,3), Tom Woudenberg (2), Hester de Melker (2), Jacco Wallinga (2), Susan Hahne (2)

1. Department of Infectious Disease Control, Municipal Health Service Hart voor Brabant, 's-Hertogenbosch, The Netherlands
2. National Institute for Public Health and the Environment (RIVM), Bilthoven, The Netherlands
3. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden

Background

In 2013-2014, the Netherlands experienced a large outbreak of measles, with 2,700 notified cases. Measles vaccination has been part of the national immunisation programme since 1976. The outbreak provided an opportunity to study the effect of MMR vaccination on occurrence of measles complications and transmission.

Methods

For measles cases notified 25/05/2013-12/03/2014, we extracted information from national surveillance on vaccination status, complications (encephalitis, pneumonia, otitis media) and most likely source(s) of infection. We excluded cases with unknown vaccination status and those not eligible for vaccination. A case was defined as having transmitted measles when it was listed as a likely source for at least one other case. We estimated the age-adjusted effect of vaccination on the outcomes complications and transmission with logistic regression.

Results

Of 2,674 reported cases, 2,533 (94.7%) were unvaccinated, 125 (4.7%) were vaccinated once and 16 (0.6%) were vaccinated twice. Of all cases 329 (13%) reported at least one complication, most often pneumonia (6%). Of unvaccinated cases, 316 (13%) had at least one complication, compared to 12 (9%) vaccinated cases [OR 0.5 (CI 95% 0.3-1)]. None of the twice-vaccinated cases had complications. In total 203 cases were indicated as a likely source, 194 (8%) of these were unvaccinated and seven (5%) vaccinated [OR 0.7 (CI 95% 0.3-1.5)]. None of the twice-vaccinated cases was indicated as a likely source.

Conclusion

Our findings suggest a protective effect of vaccination on the occurrence of complications and transmission and support the WHO recommendation of a two-dose MMR vaccination schedule. However, vaccinated people tend to cluster and might have less contact with unvaccinated people, which influences transmission. Hence, further research is needed during larger outbreaks or with surveillance data.

Keywords: Disease Outbreaks, Measles, Measles-Mumps-Rubella Vaccine, Vaccination, Infectious Disease Transmission

PRESENTED BY: Sandra van Dam (s.van.dam@ggdhvb.nl)

REFERENCE NUMBER: 2974

Vaccine effectiveness of an early MMR-vaccination among 6-14 month-old infants during an epidemic in the Netherlands: an observational cohort study.

Tom Woudenberg (1), Nicoline van der Maas (1), Mirjam Knol (1), Rob van Binnendijk (1), Susan Hahne (1)

1. National Institute for Public Health and the Environment (RIVM), Bilthoven, The Netherlands

Background

In the Netherlands, a measles epidemic with 2700 reported cases occurred in 2013-2014. Routinely, the first MMR is given at 14 months, but during the epidemic, MMR-vaccination was offered to 6-14 months-old infants in municipalities with MMR-vaccination coverage below 90%. We studied the vaccine effectiveness (VE) of this early MMR-vaccination.

Methods

A prospective cohort study was performed including all infants of 6-14 months of age in 29 municipalities targeted. Six weeks after the invitation for the early MMR-vaccination, parents were asked to fill in a questionnaire and to report suspected measles in their infant by mail during the follow-up period. In case of suspected measles, parents received a saliva test kit for detection of measles specific IgM antibodies. The crude and adjusted VE against laboratory-confirmed and self-reported measles was estimated using Cox regression, whereby VE=1-hazard ratio.

Results

Of 1304 participating infants, 1008 (77.3%) were vaccinated, with 27 and 38 self-reported measles cases reported in vaccinated and unvaccinated infants, respectively. Of the self-reported cases who were tested, 3 and 11 infants showed positive measles IgM in vaccinated and unvaccinated infants. The unadjusted VE against laboratory confirmed and self-reported measles was 93% (95%CI 74%-98%) and 74% (55%-85%), respectively. When adjusting for age, gender, sibling vaccination status, religion and day-care centre attendance, the VE against laboratory-confirmed and self-reported measles was 65% (-116%-94%) and 52% (8.5%-75%). Mainly sibling vaccination status decreased VE.

Conclusion

MMR-vaccination of infants aged 6-14 months protected against measles, albeit with a relatively lower VE. The adjusted VE was considerably lower than the crude VE probably because of the difference in exposure between mostly unvaccinated orthodox Protestants and vaccine-accepting population. This latter group is probably largely protected through herd-immunity.

Keywords: Measles-Mumps-Rubella Vaccine, Infants, Prevention & control, Intervention Studies

PRESENTED BY: Tom Woudenberg (tom.woudenberg@rivm.nl)

REFERENCE NUMBER: 3200

Future pandemics and vaccination: public opinion and attitudes across three European countries.

Domino Determann (1,2), Esther W. de Bekker-Grob (1), Jeff French (3), Helene Voeten (4), Jan Hendrik Richardus (4), Enny Das (5), Ida Korfage (1)

1. Department of Public Health, Erasmus MC University Medical Center Rotterdam, Rotterdam, The Netherlands
2. Centre for Prevention and Health Services Research, National Institute for Public Health and the Environment (RIVM), Bilthoven, The Netherlands
3. Strategic Social Marketing Ltd, Liphook, The Netherlands
4. Rotterdam-Rijnmond Municipal Public Health Service, Rotterdam, The Netherlands
5. Centre for Language studies, Radboud University, Nijmegen, The Netherlands

Background

Understanding public opinion and attitudes regarding pandemic vaccination is crucial for successful outbreak management and effective communication at the European level.

Methods

We explored national differences by conducting focus group discussions (N=6) in the Netherlands, Poland and Sweden. Discussions were structured using concepts from behavioural models.

Results

Thematic analysis showed that participants would base their vaccination decision on trade-offs between perceived benefits and barriers of the vaccine also taking into account the seriousness of the new outbreak. Except for those having chronic diseases, participants expected a low infection risk, resulting in a low willingness to get vaccinated. Information about the health status of cases was considered important, since this might change perceived susceptibility. Participants displayed concerns about vaccine safety, due to limited time to produce and test vaccines in the acute situation of a new pandemic. Swedish participants mentioned their tendency of doing the right thing and following the rules, as well as to get vaccinated because of solidarity with other citizens and social influences. This appeared much less prominent for the Dutch and Polish participants. However, Swedish participants indicated that negative experiences during the Influenza A/H1N1 2009 pandemic decreases their acceptance of future vaccinations. Polish participants lacked trust in their national (public) health system and government, and were therefore sceptical about the availability and quality of vaccines in Poland.

Conclusion

Although participants overall expressed similar considerations, important differences between countries stand out, such as previous vaccination experiences, the degree of adherence to social norms, and the degree of trust in health authorities. Our findings highlight the importance of transparent communication about testing and production of vaccines, and the need to adapt preparedness strategies to the local situation.

Keywords: Vaccination, Pandemics, Public health, Europe, Emergency Preparedness

PRESENTED BY: Domino Determann (d.determann@erasmusmc.nl)

REFERENCE NUMBER: 3010

Track 18: Food and Waterborne Diseases and Zoonoses II

MODERATOR: Loredana Ingrosso (EUPHEM coordinator, Italy)

Epidemiology of Campylobacter jejuni infections in Sweden between 2011 and 2012- are infections caused by C. jejuni ST-677 clonal complex more severe than others?

Heli Harvala (1,2), Thomas Rosendal (3), Mia Brytting (1), Anders Wallensten (1), Ann Lindberg (3)

1. Public Health Agency of Swede, Solna, Sweden
2. European Programme for Public Health Microbiology Training (EUPHEM), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
3. National Veterinary Institute of Sweden, Uppsala, Sweden

Background
Campylobacter jejuni is among the most frequent causes of bacterial gastroenteritis in Europe. A total of 44 C. jejuni clonal complexes (CC) have been described; ST-21 and ST-45 have been identified as the most frequent CC in all human studies so far. Furthermore, ST-22 has been associated with Guillen-Barré syndrome and ST-677 was recently linked to severe systemic infections. We investigated the burden of C. jejuni infections, and whether C. jejuni ST-677 CC is associated with more severe disease also in Sweden.

Methods
A total of 1013 C. jejuni isolates obtained from Swedish Microbiology Laboratories between November 2011 and October 2012 were included in this retrospective cohort study. All samples were typed. Clinical data including hospitalisation dates and diagnosis codes was obtained from the registry of hospitalizations.

Results
A total of 401 individuals were hospitalized due to C. jejuni infection; those with underlying health issues were 3-times more likely to become hospitalized than those without (RR 3.19, 95%CI 2.8-3.6, p<0.0001). The four most common CC identified during the study period included ST-21 (42%; 426 from 1013 typed isolates), ST-45 (17%), ST-677 (10%) and ST-48 (9.4%). Individuals infected with ST-45 CC were older than individuals infected with other CCs (55 vs 46 years), more often hospitalized (49% vs 38%) and were hospitalized for a longer period of time (4 vs 3.7 days).

Conclusion
The clonal complex ST-677 was not associated with the increased hospitalization or a longer hospital stay in our study based on univariable analysis. However, the role of ST-677 and other C. jejuni infections in those with underlying health issues is generally underestimated and requires further thoughts including possible targeted interventions.

Keywords: Campylobacter, ST-677, clonal complex, severity, hospitalization

PRESENTED BY: Heli Harvala (heli.simmonds@hotmail.com)
REFERENCE NUMBER: 2950

Investigation of shellfish-associated hepatitis A outbreak-Taiwan,2014

Ying shih Su (1), Hao Yuan Cheng (1), Yi chun Lo (1), Wan chin Chen (1)

1. Centers for Disease Control Ministry of Health and Welfare, Taiwan

Background
A higher than usual cases with hepatitis A virus (HAV) infection was notified in October 2014. Viruses from 10 patients were shown to be genotype IA with the same sequence. We conducted an investigation to identify the possible food vehicles and traced back the source.

Methods
A confirmed case of hepatitis A is defined as a symptomatic person positive for HAV IgM with onset of symptoms. Since March 2014, the confirmed locally acquired HAV cases were questioned on hundreds of possible food items exposed in the 15–50 days before illness onset. In addition, fecal or serum specimens from HAV cases were genotyped and alalyzed. We defined outbreak cases as HAV cases with symptom onset after October 1, 2014 and an identical HAV sequence. We compared their food exposure to non-outbreak cases. Bivariate analyses were used to determine associated food. We conducted traced back investigation and food testing for HAV.

Results
From October 1– November 30 2014, of 39 locally- acquired HAV cases, 10 were identified as outbreak cases. The median age was 33 years, and 7 were male. All the outbreak cases consumed shellfish (OR: 45.5; 95% CI: 2.43-848.9), and 7 ate raw oysters (OR: 5.30; 95% CI: 1.15-24.4). The traceback investigation found 8 cases had consumed bivalves from Farm A during late September. Inspection showed the tunnel for seawater drained to bivalves beds had connection to the sewerage outlet. HAV testing of 45 shellfish and 15 water samplings from Farm A were all negative.

Conclusion
Consumption of shellfish or raw oysters was associated with the HAV outbreak. We recommend efforts to prevent contamination in breeding farms and issue public advisories to cook shellfish well.

Keywords: Hepatitis A, Outbreak

PRESENTED BY: Ying shih Su (siho818@cdc.gov.tw)
REFERENCE NUMBER: 3205

An oyster-associated norovirus outbreak following a corporate banquet - France, January 2015

Cécile Durand (1), Nelly Fournet (2), Sandrine Camberlin-Defrocourt (3), Damien Mouly (1)

1. French institute for public health surveillance (InVS), regional office Midi-Pyrénées, Toulouse, France
2. French institute for public health surveillance (InVS), Infectious diseases department, Saint-Maurice, France
3. Regional Health Agency Midi-Pyrénées (ARS Midi-Pyrénées), Toulouse, France

Background

The presence of gastroenteritis outbreaks associated with norovirus-contaminated shellfish is a public health concern in Europe. An outbreak of acute gastroenteritis occurred among 650 participants following a corporate dinner on January 9, 2015. Epidemiological and microbiological investigations were conducted to describe the outbreak, identify the etiological agent, investigate the source of infection and take control measures.

Methods

A case-control study was conducted among all participants using an anonymous web-based questionnaire from January 16 to 19. A case was defined as occurrence of vomiting or diarrhea in a dinner attendee from January 9. Multivariate logistic regression was used to measure the association between the gastrointestinal signs and food items by odds-ratios (OR) with their 95% confidence intervals (95%CI). A dose-response relationship was studied. Trace-back investigations of suspected oysters were performed. Stool samples from cases and suspected oysters were analyzed for bacterial and viral pathogens.

Results

Among 216 (33%) participants who completed the questionnaire, there were 99 cases (attack rate among respondents= 46%). Median incubation was 38 hours and 98% of cases occurred during the first 60h after the dinner. Main clinical signs were abdominal pain (87%), nausea (84%), diarrhea (68%), headache (62%) and vomiting (57%). Oyster consumption was associated with gastrointestinal illness: OR=31.1 (95%CI 11.8-82.4; p<10-3). The OR increased with the number of oysters consumed: 1–3 oysters: OR=28.2 (95%CI 8.6–92.7); 4–6: OR=37.1 (95%CI 11.1–124.6); ≥ 7: OR=61.7 (95%CI 14.3-265.3). Norovirus was detected in both stool and oysters samples.

Conclusion

These investigations quickly suggested a strong causal link between the presence of gastrointestinal signs and contaminated oyster consumption, leading to removal of the implicated product from the market.

Keywords: Foodborne diseases, norovirus, gastroenteritis, ostreidae, outbreaks

PRESENTED BY: Cécile Durand (cecile.durand@ars.sante.fr)

REFERENCE NUMBER: 2910

High seroprevalence of Hepatitis E virus in swine workers in Norway, 2013.

Heidi Lange (1,2), Joakim Øverbø (3), Susanne G. Dudman (3), Line Vold (1)

1. Department of Infectious Disease Epidemiology, Norwegian Institute of Public Health, Oslo, Norway
2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, Stockholm, Sweden
3. Department of Virology, Norwegian Institute of Public Health, Oslo, Norway

Background

Recent studies have shown Hepatitis E virus (HEV) has been endemic in swine in Norway since at least 1994, but the prevalence of HEV in humans is unknown. We performed a cross-sectional study to estimate the seroprevalence of HEV in Norway among swine workers, veterinarians and blood donors, investigate the zoonotic link between humans and swine, and to raise awareness about HEV.

Methods

We used convenience sampling to select swine workers and veterinarians attending two national vocational conferences and blood donors from different hospitals. We gathered information on demographics and work experience using a standardized questionnaire. We collected blood specimens and tested them for HEV IgG antibodies using an ELISA test. We calculated seroprevalence by age group and work experience and Prevalence Ratios (PR) with 95% confidence intervals (95%CI).

Results

Overall, 1442 blood specimens were analyzed. The seroprevalence of HEV was 30% (21/79) in swine workers compared to 13% (21/163) in veterinarians and 14 % (162/1200) in blood donors (PR=2.4; 95% CI 1.4-4.0 and PR=2.3; 95% CI 1.6-3.2, respectively). Swine workers aged >50 years and veterinarians working with swine were twice as likely to be HEV seropositive veterinarians working with swine were twice as likely to be HEV seropositive compared with swine workers <=50 years and veterinarians who did not work with swine (PR=2.3; 95 %CI 1.1- 4.8 and PR=2.3; 95%CI 1.04 -5.0, respectively).

Conclusion

The high seroprevalence of HEV in swine workers, especially among those >50 years, and among veterinarians working with swine support the evidence from other European countries that swine are a reservoir for HEV. Swine workers and veterinarians need to become aware of the risk of zoonotic transmission of HEV in order to take appropriate precautions.

Keywords: Hepatitis E, swine, zoonoses, seroepidemiologic studies, blood donors, veterinarians

PRESENTED BY: Heidi Lange (heidi.lange@fhi.no)

REFERENCE NUMBER: 2945

Case-Control Study of Risk Factors for Animal Anthrax in Georgia: Preliminary Findings, 2013-2014

Giorgi Maghlakelidze (1), Zviad Asanishvili (1,2), Tsira Napetvaridze (1,2), Mariam Geleishvili (3), Edd Maes (3), Rita Traxler (4), Sangeeta Rao (5), Debby Reynolds (5), Mo Salman (5), Sean Shadomy (4)

1. South Caucasus Field Epidemiology and Laboratory Training Program
2. National Food Agency, Ministry of Agriculture of Georgia
3. SC/FELTP, US CDC GDD Georgia
4. US Centers for Disease Control and Prevention, USA
5. Colorado State University, USA

Background

Anthrax is endemic in Georgia. From 2010 to 2012, there were 36 animal and 110 human cases reported in Georgia which were three- and five-fold increase, respectively. Responsibility for livestock vaccination shifted from government to livestock owners in 2007. Animal vaccination decreased by 95% from 2007 through 2010. We investigated possible risk factors for livestock anthrax in Georgia.

Methods

Cases were defined as a livestock animal with compatible clinical signs/death, positive anthrax culture or PCR, and onset/death from 06/01/2013 through 05/31/2015. Four controls per case were randomly selected: two from the same village and two from villages 3-10 km away. An unmatched case-control design was used to detect a 20%-25% difference in exposure to a potential risk factor between cases and controls for a sample size of 40 to 60 cases. Data on exposures and potential risk factors within a one-month period before onset/death were collected from animal owners/caretakers using a standardized questionnaire. Descriptive and univariate analyses were conducted in EpiInfo7.

Results

During the first study year, 30 cases and 114 controls were enrolled. Differences in feeding from the rest of the herd (OR=19.1; CI 95% 2.23-164.04.), and sudden death of another animal in herd (OR=13.7; CI 95% 1.51-125.20) were significantly associated with higher risk of anthrax in cattle. Vaccination against anthrax (OR=0.03; CI 95% 0.004-0.25) or any other disease (OR=0.12; CI 95% 0.037-0.41) during the lifetime was associated with a lower likelihood of anthrax.

Conclusion

The study revealed certain risk-factors for animal anthrax in Georgia including feeding management and sudden death of other animals in herd. A protective effect of vaccination against anthrax or any vaccination was confirmed. We recommend further investigation of zoonotic diseases in Georgia.

Keywords: Anthrax, case-control, risk-factors, Georgia.

PRESENTED BY: Giorgi Maghlakelidze (giom@hotmail.com)

REFERENCE NUMBER: 3170

A study to identify knowledge, attitudes, and practices (KAP) about rabies following an education campaign in Gakh-Gabala, Azerbaijan, 2014

Eldar Hasanov (1), Thomas H. Rush (2), Marika Geleishvili (3), Jon E. Tongren (3), Edmond Maes (4)

1. Veterinary Department city Baku, resident SC FELTP Georgian office
2. CDC SC FELTP Georgian office
3. CDC SC FELTP Georgian office
4. CDC Atlanta, USA

Background

Rabies is a zoonotic disease causing public health problems worldwide. From 2009–2014, the Republican Veterinary Laboratory of Azerbaijan registered 163 animals rabies, 71 (44%) were reported from the northeast region (Gkah-Gabala). In 2013, an awareness campaign was conducted to educate on rabies symptoms and prevention via posters, leaflets (school distribution and medical facilities and SMS sent to randomly select local phone numbers. To evaluate campaign's effectiveness, a KAP study was conducted in the region (two districts with the campaign compared to two without.

Methods

Cluster cross-sectional study was conducted in July 2014. Sample size was calculated for each district for 95% confidence level at 600. 96 clusters of 7 households were included using probability proportional to size (PPS) methodology. Standardized questionnaire was applied; data were analyzed in EpiInfo7.

Results

Among the 672 study participants 337 (50%) were from the districts with the educational campaign, 456 (68%) were men. No differences were found in knowledge of rabies and visiting doctor following dog bite. The educational campaign group had better knowledge of no cure with symptom onset (PRR=1.3 95% CI 1.1-1.5) and vaccination schedule PRR=1.3 (95% CI 1.1-1.4). Education campaign group vaccinated their dogs and cats 1.4 times more: RR-14 (95% CI 1.1-1.7). No difference was found between rabies sources identified by the two groups.

Conclusion

The study revealed the educated group knew preventive measures better, were aware about the annual vaccination of domestic animals and increased vaccination of their animals. The Ministry will continue the education campaign but improve effective dissemination and messaging through mass - media.

Keywords: rabies, cluster method, respondent, Risk Ratio (RR)

PRESENTED BY: Eldar Hasanov (eldar_gasanov@rambler.ru)

REFERENCE NUMBER: 3023

Household and behavioral risk factors for human plague in Madagascar, 2012-3

Harimahefa Razafimandimby (1,2,3), Mino Rajerison (3), Patrice Piola (3), Armand Rafalimanantsoa (1,2,3), Maherisoa Ratsitorahina (3), Christophe Rogier (3)

1. Direction de la veille sanitaire et de la surveillance épidémiologique
2. Programme FETP-OI
3. Institut Pasteur de Madagascar

Background
Plague is endemic in Madagascar where small isolated outbreaks occur every year. We adopted a standardized methodology for the investigation of outbreak in eight districts from April 2012 to June 2013 in order to identify risk factors and to guide preventive measures.

Methods
For case finding in villages, we defined a suspected case as a person with symptoms compatible with plague (fever and swollen painful lymph nodes for bubonic plague or pneumonia for pneumonic plague). We used Yersinia pestis F1 specific antigen detection test, serology and culture for biological confirmation. People without symptoms but with positive serology were considered as asymptomatic cases. We conducted a case-control study including confirmed, suspected and asymptomatic cases. For each household with a case, we randomly selected three households free of cases and included all individuals as controls. We administered a questionnaire to collect individual and household exposures. We computed crude and adjusted-OR and 95%CI using a GEE population-averaged model.

Results
We included a total of 98 cases and 421 controls. The preliminary results presented below relate to an investigation site (29 cases and 163 controls). Among cases, sex ratio was 1.1 and median age was 31 years. Cases were older (>19y) than controls (OR=1.8 CI[1.0-3.2]). Households with a case were more likely to have a dog (adjusted-OR=3.1 CI[0.9-10.9]) and more likely to be overcrowded (adjusted-OR =12.2 CI[1.8-83.8]).

Conclusion
Overcrowding at the household level could reflect favourable micro-epidemiological conditions for plague transmission. The association between plague and the presence of a dog in the household has already been documented. Dogs could bring fleas into the houses. Final results which are being finalized will bring information to improve our knowledge of the disease.

Keywords: plague, risk factors, case-control studies, Madagascar

PRESENTED BY: Harimahefa Razafimandimby (harimahefa.razafimandimby@coi-ioc.org)

REFERENCE NUMBER: 3187

Track 19: Novel Methodological Approaches

MODERATOR: Julien Beaute (ECDC, Acting group leader, Surveillance)

Improvement of surveillance indicators after implementation of electronic reporting in Azerbaijan, 2010-2013

Zlata Rasulzade (1), Naile Malakmadze (2), Edd Maes (3)

1. South Caucasus FELTP, Republican Anti-Plague Station, MoH, Azerbaijan
2. Northrop Grumman, Atlanta, USA
3. Center for Diseases Control, Atlanta, USA

Background
Electronic Integrated Diseases Surveillance System (EIDSS) was implemented in Azerbaijan in 2010. Surveillance indicators were not used previously for system evaluations. Our goal is to assess of progress of surveillance indicators since implementation of electronic reporting.

Methods
We compared indicators (timeliness of notification, data entry and case investigation) obtained from EIDSS on Brucellosis, Pulmonary TB and Salmonellae infections for 2010-2013. Selection of those diseases was stipulated by differences in reporting flow and data entry into EIDSS.

Results
Probable and confirmed case definitions were included into analyses (N =12996). Timeliness of urgent notification (notified within 24 hours after diagnosis) of Brucellosis increased in 2013 by 17.1% compared to previous years but below the threshold (74.6%). Timeliness of notification (within 48 hours) of pulmonary TB and Salmonellae infections increased in 2013 by 0.2 and 0.7% compared to previous years but below the threshold (69.7% and 61.7% correspondingly). Timeliness of case investigation for all three diseases (within 48 hours after notification) increased in 2013 by 3-4% compared to previous years but above the threshold (92-96% for three diseases). Proportion of collected samples for brucellosis was 97.5%, for pulmonary TB – 95.2% and for Salmonellae infections – 64.7% in 2013.Timeliness of data entry into EIDSS for Brucellosis increased in 2013 by 50% compared to previous years, for two other diseases by 2-4%, but mean of days decreased in 2013 (3.3, 8.7 and 5.3 correspondingly).

Conclusion
Timeliness of notification is poor for all three diseases. In order to improve notification it is necessary to provide direct access to EIDSS for healthcare providers. Systematic assessment of surveillance indicators and planning of surveillance system improvements based on them was recommended.

Keywords: electronic reporting, notification, surveillance indicators, Azerbaijan

PRESENTED BY: Zlata Rasulzade (zlata.eidss@gmail.com)

REFERENCE NUMBER: 3156

Monitoring gender ratio of gastrointestinal infection laboratory reports as a mechanism for identifying possible increases among men who have sex with men, England, 2003-2013

Piers Mook (1), Sanch Kanagarajah (1), Daniel Gardiner (1), Marko Kerac (1,2), Gwenda Hughes (1), Nigel Field (1,3), Noel McCarthy (1,4), Ian Simms (1), Chris Lane (1), Bob Adak (1), Paul Crook (1)

1. Public Health England, UK
2. London School of Hygiene and Tropical Medicine, UK
3. University College London, UK
4. University of Warwick, UK

Background

Since 2011, an increase in Shigella flexneri has been observed in men due to faecal-oral transmission associated with sexual contact between men who have sex with men (MSM). Sexual history is not routinely collected for cases of gastrointestinal infections. We used gender ratio to detect greater than expected numbers of gastrointestinal infections in MSM.

Methods

We examined annual male to female ratios of laboratory confirmed patient-episodes from those aged 16-65 years with no known history of travel for eight gastrointestinal pathogens (Campylobacter, Cryptosporidium, Giardia, Hepatitis A, Norovirus, Salmonella, Shigella, and VTEC) in England between 2003 and 2013. Chi-squared tests for linear trend were conducted and a male to female ratio of more than two was considered suggestive of an excess. Sub-analyses by age and high-risk areas (London, Brighton and Manchester) were conducted.

Results

An increased linear trend and excess of male episodes was observed for Shigella ($p<0.001$; m:f ratio of 2.0 and 2.5 in 2012 and 2013, respectively) but not the other gastrointestinal infections. Consistent with MSM-mediated transmission, the excess of male Shigella episodes was most pronounced among those aged 25-49 years (ratios of 2.4 and 2.9) and those in high-risk areas (ratios of 2.9 and 4.0); no excess was observed among children.

Conclusion

This method identified the recent outbreak of Shigella among MSM. Utility of this approach to detect excess episodes among MSM is likely to be pathogen specific and dependent on several factors including Ro. Optimisation and routine application might alert public health authorities to some future gastrointestinal infection outbreaks in MSM.

Keywords: Gastrointestinal Diseases, Public Health Surveillance, Sexual Behaviour, Epidemiologic Methods

PRESENTED BY: Daniel Gardiner (daniel.gardiner@phe.gov.uk)

REFERENCE NUMBER: 3121

Dishing the dirt: Self-reported data on domestic hygiene in sporadic salmonellosis cases and their controls - describing, evaluating and correcting a social desirability bias (SDB)

Jeanette Kluba (1), Dagmar Ziehm (1), Sophie Rettenbacher-Riefler (1), Matthias Pulz (1), Johannes Dreesman (1)

1. Governmental Institute of Public Health of Lower Saxony, Germany

Background

Food safety precautions in domestic kitchens are considered an important means of reducing the incidence of sporadic food-borne infections. Assessments of hygienic behaviour using questionnaires can however be biased by social desirability. In a matched case-control study on sporadic salmonellosis between 2011 and 2013 in Lower Saxony, Germany, cases reported hygienic behaviour more frequently than controls, although questions were phrased very carefully to minimize social desirability bias (SDB). We analysed potential predictors of SDB and applied two different correction methods.

Methods

285 cases and 447 controls returned questionnaires about six different routine hygiene practices expected to prevent salmonella infections ("hygiene questions"). To reveal discrepancies between performed and reported behaviour, four additional questions addressed unrealistic hygiene practices ("SDB-questions"). In the first correction approach, we partitioned cases and controls via k-means calculation into clusters depending on their answers to the SDB-questions, excluded the cluster where bias was supposed and re-analysed the hygiene questions data from the remaining clusters. In the second approach, the overall hygiene questions' score of cases was adjusted, using a correction factor derived from their answers to SDB-questions.

Results

Associations between reported hygienic behaviour and sociodemographic characteristics were not observed. After rejecting the biased cluster, the association between salmonellosis and hand washing before food preparation was no longer significant. Applying the correction factor reversed the previously found higher overall answering score of cases (OR=1.3; 95% CI: 1.1-1.4), now indicating lower hygiene in salmonellosis cases than controls (OR=0.8; 95% CI: 0.7-0.9).

Conclusion

We present two approaches to handle and correct SDB during the analytical stage of a study, which could be applied in similar investigations where SDB cannot be ruled out completely in advance.

Keywords: zoonosis, gastrointestinal infections, cluster analysis, case-control study, risk factor

PRESENTED BY: Sophie Rettenbacher-Riefler (Sophie.Rettenbacher-Riefler@nlga.niedersachsen.de)

REFERENCE NUMBER: 2920

A rapid response to the Ebola outbreak in England: innovative web and mobile technologies for new and (re) emerging diseases

Chakib Kara-Zaïtri (1), Martin Schweiger (2), Robert Hamilton (3)

1. University of Bradford, UK
2. Dept. of Infectious Disease Control. Public Health England, Leeds, UK
3. inFact, Shipley, UK

Background
On August 8, 2014, WHO declared a public health emergency of international concern about the rapidly emerging outbreak of Ebola virus in West Africa. Since then, an unprecedented large-scale national response to monitor 4000 exposed humanitarian workers returning to England from single or multiple trips to affected areas began.

Methods
The work presented was facilitated via the rapid development and implementation of an Ebola software plugin onto HPZone, a secure web-based application for infectious disease control used by all Health Protection Teams in England. The plugin focused on the rapid development and deployment of continuously evolving workflows required for cases, contacts and exposed persons, and their registration and close monitoring.

Results
The plugin provided two key outcomes:The provision of a one-stop data gateway for creating new, and managing existing exposed person episodes when returning at different locations in England and recording time-bound types of contact with associated risk categories. The gateway, also imports returning health workers data automatically from port health authorities, and provides an effective facility for exporting accurate national contact and exposed person data for further analysis and mapping.The development of a mobile application which automatically sends and receives SMS messages to/from targeted exposed people who are reminded to log their temperature twice daily directly into HPZone for 21 days. It also issues alerts when the temperature recorded is outside specified threshold values or when no message is received before a given time, and provides visual monitoring reports.

Conclusion
The new functionality provided by the plugin has well served health protection professionals with their particular urgent needs and led the way for using similar technologies for new and (re)emerging infections beyond Ebola.

Keywords: Infectious Disease Control, Ebola, Surveillance, Web technology, Mobile technology, SMS

PRESENTED BY: Chakib Kara-Zaïtri (c.karazaitri@bradford.ac.uk)

REFERENCE NUMBER: 3009

Best practices in cost-effective risk-based animal health surveillance: RISKSUR document for guidance integrates new design and evaluation tools.

Anoek Backx (1), Jorge Pinto Ferreira (2), Paolo Calistri (3), Caryl Lockhart (1), Julio Pinto (1)

1. Food and Agricultural Organization of the United Nations (FAO), Rome, Italy
2. Safe food solutions (SAFOSO), Liebefeld, Switzerland
3. Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise (IZSAM), Teramo, Italy

Background
The EU-FP RISKSUR consortium developed novel tools and methods for facing challenges in animal health surveillance (AHS). Those challenges included decreased financial means for surveillance and linking animal with human health surveillance. After reviewing AHS systems, the consortium developed a surveillance design framework and an economic evaluation tool to support the design and practice of cost-effective and, when appropriate, risk-based AHS. Four AHS objectives were addressed: freedom-from-disease, prevalence, detection of cases/new incursions. Since no comprehensive guidance for designing and implementing risk-based surveillance systems existed at the time, the consortium developed a Best Practices Document (BPD) that we present here.

Methods
Systematic reviews of guidelines for surveillance design plus expert consultations provided the basis for the BDP. Then the consortium held a one-day best-practice workshop, where 41 European AHS-related professionals identified gaps and needs. Finally, it established an editorial board to outline the work and mobilise epidemiological and economic contributors and internal and external reviewers. Contributions were by AHS objective.

Results
Each BPD chapter focuses on a particular step of cost-effective risk-based AHS: planning, design, implementation and evaluation. BPD provides best-practice examples and works out epidemiological and economical Backgroundfor risk-based surveillance for the four objectives. Each chapter contains references to key documents and experts, and a toolbox referring to methods and tools.

Conclusion
The BPD is the result of bundling thorough systematic reviews with epidemiological, economic expertise, and links with specifically developed tools for design and evaluation of risk-based surveillance systems. Further external review is in progress as are considerations to adapt it into an easily updatable online format. RISKSUR partner FAO proceeds to see how risk-based surveillance and the BPD can be translated to developing countries.

Keywords: risk-based, surveillance, cost-effectiveness, best practices, design, evaluation,

PRESENTED BY: Arianne Comin

REFERENCE NUMBER: 3138

Cost-effective analysis of childhood rotavirus vaccination in Sweden using a dynamic model

Ellen Wolff (1), Tobias Fasth (1), Ann Lindstrand (1), Olof Lindgren (1)

1. Public Health Agency of Sweden

Background
Rotavirus is the primary cause of gastroenteritis among children in Sweden. About 50,000 children under the age of five are assumed to be suffering from rotavirus gastroenteritis annually, of which about 2,000 are hospitalized. This has both a direct and indirect effect on the economy, and the burden of disease has been shown to be greatly reduced in countries that have introduced rotavirus vaccination. The aim of the study was to conduct a health economic evaluation of rotavirus vaccination to assess potential cost effectiveness.

Methods
We developed a dynamic compartmental model that simulated the course of rotavirus in the population while including seasonality and herd immunity. The main outcome was the number of children 0-5 years old with mild or severe gastroenteritis due to rotavirus. In the health economic analysis of costs and health effects, we compared a situation without vaccination with a scenario where 95 percent of children 0-2 years had been vaccinated. Costs included those incurred during treatment of hospitalized cases, production loss from parents, and acquisition of vaccine. Health effects were measured in quality-adjusted life years. The time horizon was set at six years, and effects and costs were discounted with 3 % annually.

Results
Preliminary results indicate that vaccination will reduce the number of mild cases from 44,000 to 10,000 annually, and the number of hospitalized cases from 2,100 to 300. In terms of cost-effectiveness, the intervention is dominant from a societal perspective, i.e. have a better health effect at a lower cost. This is mostly due to less production losses among parents.

Conclusion
The main benefit from vaccination, however, is the reduction of the burden of disease of rotavirus among young children.

Keywords: Rotavirus, vaccination, dynamic modelling, cost effectiveness, health economic evaluation

PRESENTED BY: Ellen Wolff (ellen.wolff@folkhalsomyndigheten.se)

REFERENCE NUMBER: 2898

Late Breaker: One year of sentinel surveillance of malaria and severe acute respiratory hospitalisations and deaths in Madagascar, September 2014 - August 2015

Mireille Randria (1,2,3), Laurence Randrianasolo (2), Lea Randriamampionona (2), Patrice Piola (2)

1. Indian Ocean Field Epidemiology Training Program, Indian Ocean Commission, Mauritius
2. Epidemiology Unit, Pasteur Institute of Madagascar, Madagascar
3. Health Watch and Epidemiological Surveillance Department, Ministry of Health, Madagascar

Background
The sentinel hospital surveillance system of the Pasteur Institute of Madagascar focuses on severe malaria and severe acute respiratory infections (SARI), two leading mortality causes in Africa. Its objectives are early detection of epidemics and monitoring of trends in malaria and SARI mortality. We describe the results of the first year.

Methods
All hospitalised febrile patients attending one of 18 sentinel hospitals (CH) are subject to a malaria confirmation test. A severe malaria case is a patient with fever, positive test and a severe malaria sign (WHO criteria). A patient with fever and cough over less than 10 days is a SARI case. Suspected pandemic influenza SARI cases (based on WHO criteria) are sampled (naso-pharyngeal swab) for virus identification. A doubling of malaria cases over two successive weeks is an alert. In non-endemic areas, this is an autochthonous case. Data on hospitalizations and deaths are collected and transferred weekly via a web interface.

Results
Over 12 months ending on 31/08/2015, 29,157 patients were admitted of whom 36.3% had fever. Of these, 48.6% were tested for malaria, with 12.9% testing positive. Two percent (222/10,588) were SARI cases. Malaria fatality was 3.6% (60/1670) and 8.3% (60/725) of deaths were attributed to malaria. There were no SARI patient deaths and no pandemic influenza strain identification. We detected 56 malaria threshold exceedances at 13 sites, and 25 autochthonous malaria cases all in Fianarantsoa, a non-endemic area. Timeliness (number reports received on time/total expected) was 47.0% (364/777).

Conclusion
The sentinel surveillance system is useful. It allowed detection of and response to malaria outbreaks as well as virological evaluation of samples. Targeted supervision and training is needed to improve timeliness of data transmission.

Keywords: Malaria, SARI, surveillance, sentinel, Madagascar

PRESENTED BY: Mireille Randria (randria.mireille@gmail.com)

Track 20: Public Health Issues in Mass Gatherings

MODERATOR: Kostas Danis (EPIET coordinator, France)

Use of emergency medical services data during the 2015 Pan Am and Parapan Am Games in Toronto, Canada.

Amanda Shane (1,2), Effie Gournis (2,3), Chris Olynyk (4), Anne Arthur (3), Leslie Shulman (3)

1. Canadian Field Epidemiology Program, Public Health Agency of Canada
2. Toronto Public Health, Toronto, Canada
3. Dalla Lana School of Public Health, University of Toronto, Toronto, Canada
4. Toronto Paramedic Services, Toronto, Canada

Background
Monitoring infectious diseases and injuries during mass gatherings can prevent or mitigate adverse health impacts. During planning for the 2015 Pan Am and Parapan Am Games (P/PAG), Toronto Public Health (TPH) identified that its existing surveillance systems lack timely data related to location where health events occur (unrelated to client address). This information is important for mass events where visitors and residents congregate at event venues. This study describes a timely and sensitive data solution implemented for use during the P/PAG to enhance monitoring of the spatial distribution of health events.

Methods
A literature review confirmed that emergency medical services (EMS) dispatch data is a source of geospatial information reflecting where illness/injury occurred. TPH invited the Toronto Paramedic Service to partner in piloting the use of EMS data during the P/PAG. The U.S. Centers for Disease Control and Prevention's framework for surveillance evaluation was used to guide decision-making related to the system's design.

Results
TPH established a data-sharing agreement with Toronto Paramedic Services to access their existing EMS database during the P/PAG. Each call is assigned geographic information and a disease syndrome. The data are monitored through an aberration detection algorithm which identifies spatial and temporal clusters and can assure high levels of sensitivity for important syndromes.

Conclusion
As contact with EMS is one of the first interactions with the health system, these data can provide timely information for detecting events of public health interest. Use of EMS data during the P/PAG can complement traditional surveillance sources for health events where location of illness matters. A post-event evaluation will inform other jurisdictions on the utility of EMS data during mass gathering events.

Keywords: Public Health Surveillance, Emergency Medical Services, Disease Outbreaks, Evaluation Studies as Topic, Anniversaries and Special Events, Ontario

PRESENTED BY: Amanda Shane (amanda.shane@phac-aspc.gc.ca)

REFERENCE NUMBER: 3204

EXPO Milan 2015: a risk assessment of infectious diseases to guide the implementation of event based surveillance

Flavia Riccardo (1,2), Alessandra Piatti (3), DEL MANSO MARTINA (2), Maria Grazia Caporali (2), Christian Napoli (2), Anan Judina Bastiampillai (4), Eugenia Gabrielli (4), Maria Gramegna (3), Silvia Declich (2)

1. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden
2. Istituto Superiore di Sanità, Rome, Italy
3. General Directorate of Health, Lombardy Region, Milan, Italy
4. Scuola di Specializzazione in Igiene e Medicina Preventiva, Università degli studi di Milano

Background
EXPO-Milan, between May and October 2015, will involve 147 countries and over 20 million expected participants. Italian health authorities enhanced indicator based surveillance (IBS) for infectious diseases and planned an event based monitoring system (EBS). We assessed the risk of infectious disease transmission during the EXPO-Milan, to provide information for the implementation of EBS.

Methods
We revised the London Olympics list of priority infectious diseases and the list of potential public health emergencies of international concern reported by countries to WHO in 2014-15. We then added endemic/emerging diseases in Italy. We listed and described all the IBS systems in place that monitored each disease, nationally and regionally. For each disease, an expert-panel categorized, on a nine-point scale from very low to very high, the probability of its occurrence and assessed the potential public health impact in case of outbreaks, importation and exportation of cases.

Results
We included 40 infectious diseases, also including agents with potential for intentional release. All conditions assessed were found to be already monitored by both statutory and enhanced IBS. We classified the risk of: i) importation/transmission/exportation of measles and food-waterborne infections as medium/high, ii) legionella and West-Nile-virus-disease transmission as medium, and iii) active transmission of meningococcal meningitis and of introduction of Chickungunya and Zika viruses as low. We concluded that EBS could contribute to: i) the monitoring of acute, rather than chronic, infectious diseases and ii) the identification of epidemiological links between cases (occurring locally, in other parts of Italy or internationally) and participation to EXPO-Milan.

Conclusion
Our assessment helped define the role of EBS in EXPO-Milan enhanced surveillance. We recommend conducting a collaborative risk assessment before establishing EBS for future mass gatherings.

Keywords: Public Health Surveillance/methods, Travel, Crowding, Risk Assessment/methods

PRESENTED BY: Flavia Riccardo (flavia.riccardo@iss.it)

REFERENCE NUMBER: 3024

An outbreak of gastroenteritis following an international conference in Brussels, January 2015

Cristina Valencia (1,2), Javiera Rebolledo (2), Sophie Quolin (2), Toon Braeye (2), Jean-Marie Tremerie (3)

1. European Programme for Interventional Epidemiology Training (EPIET), ECDC Stockholm, Sweden
2. Wetenschappelijk Instituut Volkgezondheid/Institute scientifique de santé publique, Brussels, Belgium
3. Health Inspection Agency Brussels, Belgium

Background

In February 2015, organizers of an international conference in Brussels on 27-29 January reported an outbreak of gastroenteritis among its 130 attendees. We investigated the outbreak to estimate its magnitude and implement control measures.

Methods

On 10/02/2015 we emailed a standard questionnaire to all attendees to gather demographic, clinical and exposure information and laboratory results. We defined cases as attendees with vomiting, nausea, abdominal pain or diarrhea between 27/01-02/02/2015. We interviewed food handlers and tested leftovers of the sandwiches served. Faecal specimens of five cases were tested for enteric pathogens. We computed relative risks with 95% confidence intervals (CIs).

Results

Of 107 attendees who responded, 57 were cases (AR=53%). Disease onset was between 6 hours after consuming lunch on 27 January and noon on 29 January, 54 cases occurred6-24 hours after the second lunch. 52 cases (91%) reported nausea, 41 (72%) abdominal pain, 38 (66%) vomiting and 27 (47%) diarrhoea. All participants attended both lunches. Participants who consumed salmon sandwiches were three times more likely to become ill (RR= 2.98 95%CI: 1.6-5.5). One stool specimen was positive for Salmonella spp. Leftovers of de-frosted salmon used for sandwiches during the first lunch were re-frozen then thawed for the second lunch. No food handlers reported ill. No salmon sandwich was available for testing. None of the other sandwiches tested positive for enteric pathogens.

Conclusion

Salmon sandwiches were the probable vehicle in this large point-source outbreak. De-freezing and re-freezing salmon leftovers may have contributed to increased pathogen concentration. Food Health authorities need to reinforce compliance with established recommendations and the education of food-handlers on proper handling and storage of leftovers

Keywords: Gastroenteritis, Outbreak, International-Conference, Food-handling, Salmon

PRESENTED BY: Cristina Valencia (cristina.valencia@wiv-isp.be)

REFERENCE NUMBER: 3150

An investigation of food-born Salmonella enteritidis outbreak following a public gathering at a restaurant-Semei city, East Kazakhstan Region, July 5-7, 2014

Nazym Tleumbetova (1,2), Nazira Kerimbekova (3,2)

1. State Republican Veterinary Referent Center, Kazakhstan Ministry of Agriculture
2. FELTP in Central Asia
3. Almaty City Policlinic, Kazakhstan Ministry of Health

Background

On July 6, 2014, six individuals with gastrointestinal manifestations were hospitalized in Semei city in Kazakhstan. All ate at a wedding dinner in a restaurant on July 4, 2014. We conducted a retrospective cohort study to determine the etiology and the factors contributing to disease occurrence to provide appropriate preventive recommendations

Methods

The study cohort was 103 guests who attended the dinner on July 4. A case-guest was a cohort member who had ≥2 episodes of diarrhea during July 5-7. Cases (n=63) were identified through surveillance and active search. We interviewed all guests for ingested foods at the dinner. The restaurant was inspected, and food-leftover samples and stool specimens from case-guests were lab-tested. Attack rates and relative risks (RR) comparing those who ate and did not eat specific foods were calculated. We used logistic regression to study the adjusted odds ratios for food-disease associations

Results

The disease median incubation period was 18 hours (range 10-72 hours). Of the 14 food-items served at the dinner, dastan salad (egg, sausage, mayonnaise, fresh herbs) had the highest attack rates (95%) and RR (5.6). In multivariate analysis, only the dastan salad was associated with disease (OR=94.9, 95% CI 20.2-446.2). Salmonella enteritidis was isolated from 30 case-guests and the dastan salad. We found out that the salad was prepared on July 3, and probably kept at room temperature overnight. We also noticed signs of other poor food safety practices in the restaurant's kitchen

Conclusion

Poor food practices led to this Salmonella enteritidis outbreak, with an ingredient of dastan salad as the source for disease. The restaurant was temporarily closed and the owners were requested to ensure safe food practices there

Keywords: cohort study, foodborne outbreak, salmonella enteritidis, Semei city, Kazakhstan

PRESENTED BY: Serik Suleimenov & Rashidam Yussopova (idu9@cdc.gov)

REFERENCE NUMBER: 2991

Asymptomatic carriers of EHEC in Sweden

Anna Pääjärvi (1), Camilla Sundborger (1), Ingela Hedenström (1), Cecilia Jernberg (1)

1. Public Health Agency of Sweden

Background

Infection with EHEC can be everything from asymptomatic to severe. It can even lead to death in rare cases. The outcome of infection depends on an array of factors, like the immune status of the subject, infectious dose and the pathogenic potential of the bacterium itself. Data on characteristics of EHEC isolates comes foremost from patients who had to seek medical care. Reference laboratories often only receive a limited number of EHEC isolates from asymptomatic individuals, eg from contact tracing investigations.

Methods

Randomly selected healthy individuals, 18-72 years of age, from nine regions in Sweden were recruited to the study during 2013. The subjects were asked to fill in a short questionnaire on travel history, antibiotic treatment, animal contacts and general food habits. Fecal samples were sent in from the participants to the Public Health Agency of Sweden for EHEC analysis.

Results

In total, 1081 healthy volunteers were recruited to the study. 12 subjects (1.1%) were tested positive for EHEC by real time-PCR. From seven of the PCR positive samples an isolate could be retrieved and characterized. For three additional PCR-positive samples the vtx gene subtype was characterized. The most common subtype was vtx2b which was identified in eight subjects. Only one of the EHEC positive samples were also positive for the intimin gene eae.

Conclusion

Severe diseases like HUS (Haemolytic Uraemic Syndrome) are often associated with vtx2a. In this study the most common type of verotoxin gene in asymptomatic individuals is vtx2b. Screening of healthy individuals is an important piece in the puzzle to link severity of disease outcome to virulence profiles of EHEC.

Keywords: EHEC, vtx genes, molecular typing, asymptomatic carriage

PRESENTED BY: Anna Pääjärvi (anna.paajarvi @folkhalsomyndigheten.se)

REFERENCE NUMBER: 3195

A serosurvey for Campylobacter, Yersinia, Brucella, Trichinella and hepatitis E virus among migrant and non-migrant populations in Berlin and Brandenburg (Germany)

Ides Boone (1), Sabrina Janssen (2), Anne Stephan (1), Jens-Andre Hammerl (1), Verena Moos (2), Kristina Allers (2), Thomas Schneider (2), Sascha Al Dahouk (1)

1. Department of Biological Safety, Federal Institute for Risk Assessment, Germany
2. Medical Department I, Charité - University Medicine Berlin, Campus Benjamin Franklin, Berlin, Germany

Background

Although migrants represent 27% of Berlin inhabitants, data is lacking on subpopulation-specific prevalence of food-borne zoonoses. We aimed to estimate the seroprevalence of Campylobacter, Yersinia, Brucella, Trichinella and hepatitis E virus (HEV) and to identify potential risk factors for seropositivity in migrants and non-migrants living in Berlin/Brandenburg.

Methods

We used a cross-sectional survey to determine IgG-antibodies in participants without migration background, and in subpopulations with a Turkish, Russian or Vietnamese background. Using a convenience sample, we included healthy participants, aged ≥ 18 years, presenting to the participating hospitals, health care centres and migrant associations. We conducted face-to-face interviews with a language-adapted questionnaire covering demographics, travel history, alimentation, animal contacts and medical history. Multiple logistic regression was used to examine potential risk factors.

Results

Between 02/2014-04/2015, we included 562 participants in the study (370 of German, 114 of Turkish, 56 of Vietnamese and 22 of Russian origin). Yersinia seropositivity was twice as high in Germans (57%) than in Vietnamese and Turks (30%). Campylobacter seropositivity ranged between 15 and 26%. HEV seroprevalence was higher among Vietnamese (34%) and Germans (24%), compared to Turks (11%). No seropositive Trichinella or Brucella-samples were found. HEV seroprevalence increased with age, within each subpopulation. Yersinia-seropositivity was associated with raw pork consumption (aOR 2.1, 95%CI 1.4-3.2).

Conclusion

In contrast to the low number of cases, Yersinia and HEV seropositivity was high, suggesting underdiagnosis of mild or asymptomatic infections. Although yersiniosis is often associated with the consumption of raw/undercooked pork, a high seroprevalence was also detected in the Turkish subpopulation, known to eat pork rarely. Hence other transmission routes may play a role. To prevent zoonoses, risk factors among subpopulations including migrants should be further investigated.

Keywords: Yersinia, Campylobacter, Brucella, hepatitis E, Trichinella, migrants

PRESENTED BY: Ides Boone (idesbald.boone@bfr.bund.de)

REFERENCE NUMBER: 3114

Track 21: International Health

MODERATOR: Marion Muehlen (ECDC, acting Head of EPIET)

Hepatitis A in Lebanon - a three-fold increase in incidence after the start of the Syrian civil war in 2011

Nadeen Haddad (1,2), Viktor Dahl (3,4, 5), Gabriele Riedner (5), Zeina Farah (1), Sahar Chokor (1), Nada Ghosn (1)

1. Ministry of Public Health-Lebanon, Epidemiological Surveillance Program
2. Mediterranean Programme for Intervention Epidemiology Training
3. The Public Health Agency of Sweden
4. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden
5. WHO Country Office, Lebanon

Background

The Lebanese Ministry of Public Health observed an increased number of reported cases of hepatitis A in 2014 after the influx of over one million Syrian refugees to Lebanon following the start of the Syrian civil war in 2011. Prevalence of IgG antibodies against hepatitis A virus in 2011 was 11% among Lebanese 1-5 years old and 50% among same-aged Syrian children. Hepatitis A vaccine is not included in the Lebanese childhood vaccination program. We investigated the increase in reported hepatitis A cases in order to recommend interventions.

Methods

Yearly incidence for hepatitis A in Lebanon were calculated since 1995 using national surveillance data. A suspected case was defined by clinical symptoms and biochemical markers. Additional negative laboratory results for hepatitis B and C defined a probable case. Confirmed cases had positive IgM antibodies for hepatitis A. Analysis included suspected, probable and confirmed cases. Denominators came from official Lebanese population surveys and UN agencies working with refugees in Lebanon.

Results

Hepatitis A incidence increased from 6.3/100,000 in 1995 to 10/100,000 in 2011, and tripled to 34/100,000 in 2014 for the combined Lebanese population and Syrian refugees. In 2014, hepatitis A incidence among Lebanese population was 24/100,000, a more than two-fold increase compared to 2011, and 74/100,000 among the Syrian refugees.

Conclusion

The increase in reported hepatitis A incidence is likely due to the arrival of Syrian refugees. It can be explained by a combination of additional cases from the Syrian refugee population, with a higher level of virus circulating, and an increase among the Lebanese population. We recommended to include hepatitis A vaccination in the childhood vaccination programme for the Lebanese and Syrian refugee population free of charge.

Keywords: hepatitis A, Lebanon, Syria, refugees, vaccination

PRESENTED BY: Viktor Dahl (viktor.dahl@folkhalsomyndigheten.se)

REFERENCE NUMBER: 3194

Three years of regional field epidemiology training programme in the Indian Ocean

Ariane Halm (1), Sainda Mohamed (2), Saindou Ben Ali Mbaé (3), Armand Eugène Randrianarivo-Solofoniaina (4), Maherisoa Ratsitorahina (4), Ram Nundlall (5), Shahina Aboobakar (5), Jastin Bibi (6), Laurent Filleul (7), Patrice Piola (8), Thomas Seyler (9), Richard Lepec (1), Loïc Flachet (1)

1. Health Surveillance Unit, Indian Ocean Commission, Mauritius
2. Surveillance Unit, World Health Organisation, Union of the Comoros
3. National Epidemiological Surveillance Unit, Ministry of Health, Union of the Comoros
4. Epidemiological Surveillance Department, Ministry of Health, Madagascar
5. Communicable Diseases Control Unit, Ministry of Health and Quality of Life, Maurice
6. Disease Surveillance and Response Unit, Ministry of Health, Seychelles
7. French Regional Epidemiology Unit (CIRE), La Réunion
8. Epidemiology Unit, Pasteur Institute, Madagascar
9. Epidemiology Department, EpiConcept, France

Background

Following the 2005-6 chikungunya outbreak, a project to strengthen regional public health preparedness was implemented in the Indian Ocean. It is coordinated by the Health Alert Unit of the Indian Ocean Commission (IOC), an intergovernmental organisation comprising the culturally, economically and socially highly diverse Comoros, Madagascar, Mauritius, Réunion (France) and Seychelles. A Field Epidemiology Training Programme (FETP-OI) was started in 2011 to develop a pool of well-trained intervention epidemiologists.

Methods

The FETP-OI consists of two years of supervised, learning-by-doing, on the job training at national sites involved in disease surveillance and response, including two three-month work placements at the Pasteur Institute in Madagascar and the French regional epidemiology unit (CIRE) in la Réunion, and up to three training courses per year. The training objectives include epidemiological surveillance, outbreak investigations, and studies, scientific communication and transfer of competences. A scientific seminar allows for exchanges about methods and results.

Results

In its first 3.5 years, two cohorts of in total 15 fellows from four countries followed the FETP-OI. The third cohort is currently being recruited. The fellows have led 43 projects in routine management (56%), set up (23%), evaluation (12%) or planning (9 %) of epidemiological surveillance. Thirty-two outbreak alerts were investigated, of which 53% in Madagascar. Fellows were involved in 15 specific studies (disease burden; evaluation of disease risk factors or clinical case definitions; foodborne, malaria, dengue or plague outbreaks; and post-elimination malaria laboratory confirmation).

Conclusion

The FETP-OI has created a regional force of intervention consisting of field epidemiologists and trained supervisors using the same technical language and epidemiological methods. Technically and financially sustainable FETP-OI work projects help addressing the public health priorities of the IOC member states.

Keywords FETP, regional surveillance, epidemiology training

PRESENTED BY: Ariane Halm (ariane.halm@coi-ioc.org)

REFERENCE NUMBER: 3066

Common mild side-effects of Artesunate/Amodiaquine (ASAQ) do not affect adherence to malaria chemoprevention during mass drug administration, Monrovia, 2014

Anna Kuehne (1,2,3), Amanda Tiffany (4), Kostas Danis (2,5), Michel Janssens (6), Estrella Lasry (7), Chibuzo Okonta (8), Victor Koko (9), Kwabena Larbi (9), Alfred Pah (9), Klaudia Porten (3)

1. Postgraduate Training for Applied Epidemiology (PAE), Robert Koch Institute, Berlin, Germany
2. European Programme for Intervention Epidemiology Training (EPIET), ECDC, Stockholm, Sweden
3. Epicentre, Paris, France
4. Epicentre, Geneva, Switzerland
5. Institut de Veille Sanitaire, Paris, France
6. Médecins Sans Frontières, Operational Centre Paris, Monrovia Project, Monrovia, Liberia
7. Médecins Sans Frontières, Operational Centre Paris, Tropical Medicine, New York, USA
8. Médecins Sans Frontières, Operational Centre Paris, Desk Urgence, Paris, France
9. Liberian National Malaria Control Programme, Ministry of Health and Social Welfare, Monrovia, Liberia

Background

In Monrovia, 2014, Médecins Sans Frontières implemented community-based mass drug administration (MDA) of a 3-day-course of Artesunate/Amodiaquine (ASAQ) malaria chemoprevention to reduce admissions for fever to Ebola-treatment-centres and malaria-associated morbidity and mortality. Since ASAQ had never been used as chemoprevention in large-scale-MDAs, we examined the influence of frequent but mild side-effects on adherence.

Methods

We included every 200th household in the distribution area (approximate population 550,000) in a cohort to monitor two rounds of ASAQ-MDA (one month apart). During follow-up telephone calls, trained surveyors collected information from every household member (HM) on age, sex, initiation of chemoprevention, adherence and possible side-effects using a standardized questionnaire one week after each round. Among HMs identifiable in both rounds, we calculated proportions of side-effects and related treatment interruptions in round 1 (r1). We used poisson regression to calculate incidence ratio (IR) of initiating chemoprevention during the second round (r2) of MDA, taking into account the cluster effect of sampling all members of a household on adherence.

Results

Of 643 HMs initiating ASAQ-chemoprevention during r1, 10% reported drowsiness, 10% dizziness, 2% fever, 1% nausea, 1% headache, 1% vomiting and 0.6% skin reactions (overall proportion of side-effects: 17%). 2% HMs interrupted ASAQ due to side-effects during r1. In multivariable analysis, initiation of chemoprevention in r2 did not significantly differ by gender (female: IR 0.97, 95%-CI 0.77-1.22), years of age (IR 1.00, 95%-CI 0.99-1.01) or experience of any side-effect during r1 (IR 1.00, 95%-CI 0.6;1.64).

Conclusion

During this intervention, ASAQ-chemoprevention caused mild side-effects that did not influence adherence in multiple rounds of MDA. We recommend future studies during or after ASAQ-MDA to document symptoms and their cause better through clinical assessment or laboratory tests.

Keywords: Malaria, Chemoprevention, Side-effects, Adherence, Liberia, Ebola

PRESENTED BY: Anna Kuehne (KuehneAn@rki.de)

REFERENCE NUMBER: 3110

Have a nice trip but be careful! Food and waterborne diseases and sexually transmitted infections among Swedish international travellers 2009-2013, Sweden

Viktor Dahl (1,2), Anders Wallensten (1)

1. The Public Health Agency of Sweden, Stockholm, Sweden
2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden

Background

We studied food and water-borne diseases (FWDs) and sexually transmitted infections (STIs) contracted abroad and notified in Sweden between 2009 and 2013 per country of acquisition in order to enable evidence based advice to Swedish travellers on risks of contracting infections abroad.

Methods

We used the Swedish database of notifiable infectious diseases to estimate number of FWDs (Campylobacteriosis, Salmonellosis, Giardiasis, Shigellosis, EHEC, Entamoeba histolytica, Yersinosis, hepatitis A, Paratyphoid fever, Typhoid fever, hepatitis E , Listeriosis, Cholera) and STIs (Chlamydia, Gonorrhea and acute hepatitis B) acquired abroad 2009-2013. Duration of trips in days was obtained from a commercial database that collects travel data from a randomly selected proportion of the Swedish population. We calculated frequency of infections per country for the five year period and, for the five countries with the highest frequency, incidence/million travel days.

Results

Overall for the five year period, 61 FWDs and 17 STIs/million travel days were reported. Thailand had the highest frequency of FWDs (7697, incidence 191/million travel days) followed by Turkey (3681, incidence 155/million travel days), Spain (2928, incidence 36/million travel days), India (2564, incidence 388/million travel days) and Egypt (1689, incidence 248/million travel days). Thailand also had the highest frequency of STIs 1388, incidence 34/million travel days) followed by Spain (967, incidence 12/million travel days), Norway (737, incidence 26/million travel days), Turkey (544, incidence 23/million travel days) and Greece (465, incidence 18/million travel days).

Conclusion

This study provides evidence for travel medicine practitioners to base their recommendations on. Extra focus should be on giving advice on how to minimize risks to those travelling to countries with a high frequency of infections, such as Thailand, or with a high incidence, such as India.

Keywords: travel, communicable diseases, sexually transmitted diseases, food-borne disease, water

PRESENTED BY: Viktor Dahl (viktor.dahl@folkhalsomyndigheten.se)

REFERENCE NUMBER: 3052

Association between quality indicator of antibiotic consumption and antimicrobial resistance

Marta Vargas-Gomes (1,2), Carla Torre (1), Jose Guerreiro (1), Paulo J Nogueira (2), Cristina Furtado (2)

1. Centre for Health, Evaluation & Research (CEFAR), National Association of Pharmacies, Lisboa, Portugal
2. Faculty of Medicine, Institute of Preventive Medicine and Public Health, University of Lisbon, Portugal

Background

Antimicrobial resistance (AR) is a worrisome problem and several studies have associated AR with antibiotic consumption (AC). European Surveillance of Antimicrobial Consumption Network (ESAC-net) has developed several quality indicators and among them the ratio of broad to narrow-spectrum antibiotics (RBN) that provides a quick evaluation of AC quality.This study aimed to explore the correlation between RBN and the rates of AR in Portugal, 2004-2013.

Methods

Ecological study. Annual outpatient systemic AC in Portugal, between 2004-2013, was retrieved from CEFAR Pharmacy Sales Information System, a representative nationwide sell-out database for ambulatory care. The outcome measure selected was the RBN of the consumption between broad {J01[CR+DC+DD+(F-FA01)]} and narrow-spectrum antibiotics [J01(CE+DB+FA01)]. Annual AR percentage was retrieved from The European Surveillance System (TESSy), 2004-2013. Selected bacteria comprised those collected by European Antimicrobial Resistance Surveillance Network and resistant to antibiotics available at ambulatory level in Portugal (Streptococcus pneumoniae, Staphylococcus aureus, Pseudomonas aeruginosa, Klebsiella pneumonia, Escherichia coli and Enterococcus spp.). Linear correlations were assessed using parametric (Pearson) and non-parametric (Spearman) methods, with a minimum of 8 observations.Statistical analysis were performed using SAS Enterprise Guidev4.1 with a significance level of 5%.

Results

Correlations were observed between the ratio and Klebsiella pneumoniae resistant to 3rd-generation cephalosporin (r=0.98; p<0.0001) and to fluoroquinolones (r=0.90; p=0.0020), Enterococcus faecalis (r=0.83; p=0.0029) resistant to aminopenicilins, Staphylococcus aureus resistant to Methicillin (r=0.71; p=0.0217) and Escherichia coli resistant to 3rd-generation cephalosporins (r=0.65; p=0.0425).

Conclusion

An association between RBN and some AR in Portugal is suggested. The RBN should play an important role when analysing AC, once it might reduce AR. Specific recommendations should consider this quality indicator to improve AC and, probably, AR.

Keywords: Antimicrobial resistance, Portugal, Quality Indicators, Correlation

PRESENTED BY: Paulo Noguiera (paulo.nogueira@dgs.pt)

REFERENCE NUMBER: 3172

Characteristics of diphtheria cases, Haiti, 2009-2014

Hugguens Lacoste (1), Jean Charles Phaimyr (2,3), Patrick Dely (4,3)

1. FETP-HAITI
2. Center for Diseases Control and Prevention, Atlanta, United State
3. Field Epidemiology Training Program of Haiti, Haiti
4. Direction of Epidemiology Laboratory and Research, Port-au-Prince, Haiti

Background

Diphtheria is caused by Corynebacterium diphtheria, being phased out in many countries, remains endemic in some regions including Haiti. Through the sentinel surveillance system (SSS) of Haiti, cases and deaths are reported without a systematic analysis to characterize this disease in the country. This study is to analyze the SSS data to describe the disease person, time and place.

Methods

A retrospective descriptive study has made. The 2009 to 2014 databases owned by the SSS were compiled. The analysis was performed on Epi Info 7 calculating certain measures of central tendency, dispersion and frequency. The results are presented in tables and graphs.

Results

98 suspected cases were reported which 38(38.7%) confirmed. Of these, 19 (50%) were reported in 2009 with a predominance during the 37th epidemiological week: seven (36.8 %). 14 (37%) in 2010; 2 (5%) in 2011; 0 (0%) in 2012 and 2013; 3 (8%) in 2014. 28(73.6 %) of 38 had unknown vaccination status , 24(63.1%) were female , ratio F / H : 2: 1, the mean age was 9 years (1-42 years), predominant age group 5-9 years, 23 (60.5%) were from the health department of the West and an overall case fatality rate of 36.8%.

Conclusion

The analysis shows a significant reduction in reported cases from 2009 to 2014 with predominance in females, the age group 5-9 years and the health department of the West were predominant. Lack of completeness is the identified limitation. Improve the completeness and increase the children vaccination coverage to reduce the incidence of diphtheria in Haiti.

Keywords: Diphtheria, cases, characteristics, Haiti

PRESENTED BY: Hugguens Lacoste (hug1787@yahoo.fr)

REFERENCE NUMBER: 3202

Track 22: Outbreaks III

MODERATOR: Birgitta de Jong (ECDC, group leader EU preparedness & FWD expert)

A point source Clostridium perfringens outbreak related to food delivered by a catering company in Copenhagen, November 2014

Silvia Funke (1,2), Luise Muller (2), Sarah Mikkelsen (3), Kirsten Andersen (3), Steen Ethelberg (2)

1. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
2. Statens Serum Institut, Denmark
3. Danish Veterinary and Food Administration, Denmark

Background
On 14 November 2014, a local caterer informed us about an ongoing gastroenteritis outbreak among employees of companies supplied by the caterer. We investigated the outbreak to identify the source of infection and to prevent further spread.

Methods
We conducted a cohort study using an electronic questionnaire among employees at companies receiving food from the catering company. For the analysis, we defined cases as persons who became ill with either diarrhoea, vomiting, stomach pain and/or nausea between 12 am on 13/11 and 12 pm on 14/11. We calculated relative risks (RR) with 95% confidence intervals (CI) using univariate analysis. Stool specimens of symptomatic cases and two food items were tested for common bacterial and viral agents of gastroenteritis.

Results
The study population consisted of 690 persons from 69 different companies, of whom 382 were cases (attack rate=55.4%). Eighty-two percent of the cases had onset of symptoms between 4 pm on 13/11 and 3 am on 14/11. Food consumption on 13/11 was significantly associated with illness (RR=9.8, 95% CI 3.3-29.4). Persons who ate a turkey dish were more likely to develop symptoms (RR=19.5, 95% CI 7.4-50.9). No other food items were associated with illness. The leftover turkey dish tested positive for Clostridium perfringens (›106 CFU/g). In addition, 11 out of 15 cases tested positive for Clostridium perfringens.

Conclusion
Our epidemiological investigation suggested that the consumption of the turkey dish caused the outbreak. Based on the microbiological analyses we identified Clostridium perfringens as the causative agent. Communicating and reinforcing guidelines for food handling, including cooling procedures, to catering companies would help to prevent similar outbreaks with spore forming, toxin-producing bacteria.

Keywords: Outbreak, Clostridium perfringens, gastroenteritis, food handling

PRESENTED BY: Silvia Funke (sifu@ssi.dk)

REFERENCE NUMBER: 2908

Chikungunya Outbreak with Concurrent Dengue Virus Co-Infection, AlfonsoXIII, Quezon,Palawan,May28 to August 15, 2014.

Sheryl Racelis (1,2), Enrique Tayag (2), Vikki Carr Delos Reyes (1,2), Nemia Sucaldito (1,2)

1. Field Epidemiology Training Program, Epidemiology Bureau, Department Health, Philippines
2. Department of Health, Philippines

Background
The Epidemiology Bureau received report of increasing cases presentinwith feverand joint pains. FETP was sent to conduct epidemiologicinvestigation to verify existence of an outbreak, to identify the source andmode oftransmission and to recommend control and preventive measures.

Methods
Unmatched case control study was done. Suspect case is previously well individual who developed fever and joint pains with any of the following: rashes, muscle pain, headache and body malaise. Confirmed case was a suspect case positive for either Chikungunya IgM by ELISA and/or Chikungunya virus with PCR. Blood samples were tested for Chikungunya IgM and PCR and Dengue IgM. Environmental and entomological surveys were also conducted

Results
323 suspect cases with age ranging from 1 to 83 year old, median age of 34 and most of the cases were females (60%). 57% cases were positive for Chikungunya with either ELISA or PCR, three were positive for both Chickungunya and Dengue virus. Three were positive for Dengue IgM alone. Cases were more likely to those who have household members with the disease (OR 7.3, 95% CI 3.51-15.37), not wearing long sleeves (OR 3.99, 95% CI 1.89-8.42), do not spay insecticide (OR 4.09, 95% CI 1.04-16.09), and house not well lighted (OR 1.65, 95% CI 1.35-7.60), The house index is 71% with Aedes aegypti as the most common vector.

Conclusion
There was a Chikungunya outbreak in Alfonso XIII, Quezon, Palawan with some cases having coinfection with dengue. The presence of numerous breeding sites led to high dense population of mosquitoes which resulted to higher transmission rate. A municipal ordinance was created declaring a municipal wide holiday for the cleanup drive and ordered a regular entomological survey.

Keywords: Chikungunya virus, Dengue virus, case-control studies, PCR, ELISA

PRESENTED BY: Sheryl Racelis (sherylqracelis@gmail.com)

REFERENCE NUMBER: 3215

Investigation of a possible outbreak of staphylococcal food poisoning, Bucharest 2014

Ani Ioana Cotar (1,2), Alina Zaharia (3), Elena Carmina Dragulescu (1), Adriana Pistol (3), Florin Popovici (4), Irina Codita (1)

1. Cantacuzino National Institute of Research-Development in Microbiology and Immunology, Bucharest, Romania
2. The European Programme for Public Health Microbiology Training (EUPHEM), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
3. National Centre for Communicable Diseases Surveillance and Control, National Institute of Public Health, Bucharest, Romania
4. National Institute of Public Health, Bucharest, Romania

Background

On 28th July 2014 we were informed about a possible food poisoning outbreak after a christening party on 26th July 2014, and started an investigation to identify the source of outbreak.

Methods

We performed a retrospective cohort study to identify the food item/s as possible vehicle/s of the outbreak. A case was defined as any person who attended and ate at the party in a Bucharest restaurant on 26th July 2014, having following symptoms: vomiting, diarrhoea, nausea, fever, headache, chills, abdominal cramps within the next 48 hours. We performed univariable analysis and calculated risk ratios (RR), and 95% confidence intervals (CI). Faecal specimens from patients and kitchen employees and swabs from throat, nose, hands of restaurant employees and kitchen surfaces were tested for foodborne pathogens. Toxigenicity testing of Staphylococcus aureus isolates was performed by PCR and their genetic relatedness was established by Pulsed Field Gel Electrophoresis (PFGE).

Results

Of 44 participants 32 responded to the questionnaire, 18 met the case definition. Univariable analysis couldn't point to a specific food item related to the onset of illness, but the clinical manifestation, incubation period, duration of illness and laboratory results suggested as the most plausible hypothesis a staphylococcal food poisoning. Environmental samples from the kitchen surfaces and clinical samples from the kitchen employees, were positive for enterotoxin-producing Staphylococcus aureus harbouring the enterotoxin D and had PFGE profiles which were indistinguishable.

Conclusion

Molecular analysis results suggested a staphylococcal food poisoning even if the univariable analysis could identify a specific food item related to the onset of illness in cases. We recommended training the food handlers in the hygienic preparation and serving of food and the implementation of infection control measures.

Keywords: foodborne outbreak, enterotoxin-producing Staphylococcus aureus, staphylococcal food poisoning, molecular typing

PRESENTED BY: Ani Ioana Cotar (aniioana@gmail.com)

REFERENCE NUMBER: 2997

A large outbreak of cryptosporidiosis among school children in Thuringia, Germany, November 2014

Joana Haussig (1,2,3), Emilie Peron (2,3), Katrin Lapp (4), Dagmar Rimek (4), Heike Pickert (5), Egbert Tannich (6), Peter Renner (7), Bettina Rosner (3), Sabine Schroeder (4)

1. Postgraduate Training for Applied Epidemiology (PAE), Robert Koch Institute, Berlin, Germany
2. European Programme for Intervention Epidemiology Training (EPIET), ECDC, Sweden
3. Robert Koch Institute, Berlin, Germany
4. Thuringian State Authority for Consumer Protection, Bad Langensalza, Germany
5. Local Health Office, Saale-Holzland-Kreis, Stadtroda, Germany
6. Bernhard Nocht Institute for Tropical Medicine, Hamburg, Germany
7. Federal Environmental Agency (UBA), Bad Elster, Germany

Background

In November 2014, four schools in one Thuringian county, all supplied by the same caterer, notified outbreaks of cryptosporidiosis. We investigated to identify the source and implement control measures.

Methods

We defined suspect cases as persons living in or visiting Saale-Holzland County with gastroenteritis of <3 days duration between 01/10/2014 and 31/12/2014, probable cases had diarrhoea for at least 3 days and confirmed cases a laboratory-diagnosed Cryptosporidium infection. We contacted physicians in the district and laboratories to search for additional cases. Stool samples of cases, the caterer's staff and water of the district's public swimming-pool were tested for Cryptosporidium. One isolate was sequenced. We cohorted students from three affected schools; they completed a self-administered questionnaire with their parents. We queried consumption of food at the school canteen, swimming-pool visits and contact to animals prior to symptom onset.

Results

We identified 108 suspect, 59 probable and 18 confirmed cases among students and three confirmed cases among relatives. Median age of cases was 10 years (range 3- 57), 93 (48%) were female. Confirmed cases' symptoms started on 10/11/2014 and peaked on 12/11/2015. The last case was among a relative, with symptom onset on 28/11/2014. DNA sequencing identified Cryptosporidium parvum (genotype: IIaA17G1R1). Staff's samples and the swimming-pool water tested negative for Cryptosporidium. All confirmed student cases had eaten at the school canteen in the week prior to symptom onset. We found no associations between any analysed exposure and illness.

Conclusion

This large point-source outbreak of cryptosporidiosis was possibly foodborne. Genotype analysis suggests a zoonotic origin. Although large outbreaks of cryptosporidiosis are rarely notified in Germany, medical practitioners and public health authorities should consider testing for Cryptosporidium in gastroenteritis outbreaks.

Keywords: Cryptosporidium, Infectious Disease Outbreaks, Schools, Germany

PRESENTED BY: Joana Haussig (haussigj@rki.de)

REFERENCE NUMBER: 3151

An outbreak of Salmonella Typhimurium associated with snakes and feeder rodents from a small network of breeders

Sujani Sivanantharajah (1), Joanne Tataryn (1), Ryan N. Walton (2), Christina Lee (2), Yvonne Whitfield (2), Isabelle Picard (3), Núria Chapinal (4), Colette Gaulin (5), Eleni Galanis (4), Linda Vrbova (1)

1. Centre for Food-borne, Environmental & Zoonotic Infectious Diseases, Public Health Agency of Canada, Canada
2. Public Health Ontario, Ontario, Canada
3. Ministère de l'Agriculture, des Pêcheries et de l'Alimentation du Canada, Canada
4. British Columbia Centre for Disease Control, Canada
5. Ministère de la Santé et des Services sociaux, Canada

Background
An increase of Salmonella Typhimurium with the same PFGE pattern was observed across Canada between June 2013 and May 2014. The PFGE pattern was previously associated with exposure to snakes and feeder rodents. A collaborative investigation was initiated in May 2014 to confirm the source of the outbreak and determine whether there was a common feeder rodent supplier.

Methods
Cases were defined as residents or visitors to Canada with the outbreak strain reported between January and August 2014. Cases were interviewed with a standardized questionnaire. Expected exposure levels were obtained from a population-based survey.

Results
Twenty-seven cases from three provinces were identified with a median age of 15 (range: 0-79) years; 50% were female. Reptile and rodent exposures were significantly higher among cases compared to expected: reptiles 76% (expected: 3%, p<0.0001); any rodents 80% (4%, p<0.0001); feeder rodents 88% (2%, p<0.001). Eighty-eight percent of cases with reptile exposure reported snake exposure. Eight of 11 cases exposed to feeder rodents with available traceback information were linked to three Ontario rodent farms; two of the farms were established from the same breeding stock. Awareness of the association between Salmonella and rodents was low amongst cases (38%).

Conclusion
The likely source of this protracted outbreak was contact with feeder rodents, snakes, and/or their environments. Cases were traced back to a small network of local breeders. A gap in awareness of the association between Salmonella and rodents was identified. To reduce risks of Salmonella infections, public health partners are working with industry to produce point of sale educational materials.

Keywords: Outbreak, Salmonella, Zoonoses, Reptiles, Snakes, Rodentia

PRESENTED BY: Melissa Phypers (melissa.phypers@phac-aspc.gc.ca)

REFERENCE NUMBER: 2875

An outbreak of Verocytotoxigenic Escherichia coli O55 (VTEC O55) in a nursery in England, October - December 2014

Sabrina Weiss (1,2), Amy Mikhail (1), Sooria Balasegaram (1), Noel McCarthy (1), Hikaru Bolt (1), Girija Dabke (1), Marie Chattaway (1), Gauri Godbole (1), Tim Dallman (1), Claire Jenkins (1), Chas Rawlings (1), Noeleen McFarland (1)

1. Public Health England (PHE), London, UK
2. European Program for Public Health Microbiology Training (EUPHEM), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden

Background
Whilst investigating an outbreak of verocytotoxigenic Escherichia coli serotype O55 ongoing since July 2014 in the South of England, the local Health Protection Team was informed about three new cases in November in children and staff attending the same nursery. We investigated to describe transmission in the nursery and to implement control measures.

Methods
Stool specimens and/or sera were collected from children and staff attending the nursery and screened for the presence of VTEC O55 bacteria by culture and PCR or for the presence of antibodies to VTEC O55 lipopolysaccharides by immunoblot, respectively. Nursery-associated cases were defined as laboratory confirmed cases of VTEC O55 that had attended or visited the affected nursery or were a family contact. Staff and parents were interviewed regarding risk factors. VTEC O55 positive cultures were analysed by whole genome sequencing to determine the degree of genetic identity between isolates from different cases.

Results
There were 12 nursery-associated cases, including nine children, one staff member and two parents; no other common risk factors were identified. Five cases were identified after screening 99 people at the nursery. Six cases were symptomatic; of these three were hospitalised. Phylogenetic analysis showed that isolates from the nursery cases were identical or differed by a single nucleotide polymorphism (SNP) and comprised a distinct subcluster differing by three SNPs from non-nursery cases in the wider outbreak.

Conclusion
The nursery subcluster was likely to have arisen by person to person transmission, including asymptomatic cases. Although ten people were infected in this setting, there were no new cases after control measures implemented, including voluntary closure of the nursery, deep cleaning and exclusion of cases from the nursery until they achieved microbiological clearance.

Keywords: Shiga-Toxigenic Escherichia coli, Hemolytic-Uremic Syndrome, Nurseries, Disease Outbreaks, Epidemiology, Single Nucleotide Polymorphism

PRESENTED BY: Sabrina Weiss (sabrina.weiss@phe.gov.uk)

REFERENCE NUMBER: 3015

Outbreak of methanol poisoning in Semi Urban Community, Ondo State, Southwest, Nigeria, April-May 2015.

Maureen Anyanwu (1), Elizabeth Adedire (2), Michael Oguntoye (3), Patrick Nguku (1), Abisola Oladimeji (1), Adefisoye Adewole (1), Femi Akinyode (1), Kayode Ojo (1)

1. Oyo Ministry of Health/NFELTP
2. Ladoke Akintola University Teaching Hospital, Ogbomoso, Osun State, Nigeria
3. Nigeria Field and Laboratory Training Programme, Abuja

Background

Patients of methanol poisoning often need intensive care and can result to high mortality. Methanol poisoning with an outbreak potential is uncommon in Nigeria. In April, 2015, we investigated a reported outbreak of methanol poisoning in Ode-Irele, Ondo State. We identified the source(s) and determined risk factors for methanol poisoning in the area.

Methods

We obtained social demographic data of suspected cases. We conducted an active case search in the community and health facilities using a semi-structured, interviewer administered questionnaire, using a case definition as any person from Ode-Irele, presenting with headache, blurring of vision, and any of blindness, respiratory distress, loss of consciousness, sudden death, with onset of symptoms occurring 24-48 hours prior to 12th April, 2015. Detailed history of chronology of symptoms was elicited and hospital records were also reviewed. We sent samples of urine and informally-produced spirit drinks for laboratory analysis.

Results

Of the 39 cases line-listed, 38 (97.4%) were males, with 29 deaths (CFR 74.4%). Most frequently reported symptoms were blindness 29 (82.9%), blurring of vision 28 (82.3%), headache 17 (54.8%). Almost all of the cases were males with majority being farmers and thirty two (94.1%) of the case-patients claimed to have consumed informally-produced spirit drinks, prior to onset of symptoms.Analysed samples of urine and informally produced spirit drinks also revealed methanol concentrations of ›10mg% and ›0.018g/l respectively, above the tolerable limit.

Conclusion

Ode Irele community experienced an outbreak of methanol poisoning with high fatality. The outbreak was contained through intensive case management and community mobilization. Community health education sessions were held and trainings on lifestyle modification conducted.

Keywords: Methanol, Outbreak, Ondo state, Nigeria.

PRESENTED BY: Maureen Anyanwu (maureenanyanwu23@yahoo.com)

REFERENCE NUMBER: 3213

Track 23: Healthcare Associated Infections

MODERATOR: Diamantis Plachouras (ECDC, expert AMR and HAI)

Health care infection of *Ralstonia mannitolilytica* in an oncologic day ward; characterization of a new pathogen for vulnerable patients.

Claudia Lucarelli (1,2), Luigi Toma (3), Grazia Prignano (3), Maria Fortunati (3), Patrizio Pezzotti (1), Aurora García-Fernández (1), Enea Gino Di Domenico (3), Domenico Bracco (3), Annalisa Pantosti (1), Loredana Ingrosso (1)

1. Istituto Superiore di Sanità, Rome, Italy
2. European Program for Public Health Microbiology Training (EUPHEM), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden
3. Istituto Nazionale Tumori Regina Elena – Istituto Dermatologico San Gallicano, Rome, Italy

Background

Ralstonia spp, an environmental microorganism, has been occasionally associated to healthcare infection. 22 cases of *Ralstonia mannitolilytica* infections in an oncology hospital in Rome-Italy prompted microbiological and epidemiological investigation.

Methods

Oncology outpatients attending a day ward from September 2013 to June 2014 had positive blood and/or central venous catheter (CVC) culture for *Ralstonia spp*. We analysed medical records, procedures and environmental samples. *Ralstonia spp*. was identified by 16S rRNA sequencing, typed by Pulsed Field Gel Electrophoresis (PFGE) with *SpeI*, biofilm production was evaluated by the BioFilm Ring Test; resistance to carbapenemes was investigated by phenotypic and molecular methods.

Results

The patients were 13 males and 9 females, age range 30-84 (median 66), had different malignancies and therapy and were symptomatic with chills and/or fever. *Ralstonia mannitolilytica* was isolated from blood/CVC (n=12), blood (n=6) or CVC tips (n=4). All isolates had indistinguishable PFGE profile, were weak biofilm producers, showed resistance to carbapenems but were negative for carbapenemase genes. All patients had had CVC- flushed with saline before receiving chemotherapy or to keep the venous access pervious. After the first 4 cases the multiple-dose saline bottles were replaced with single-dose vials and were unavailable for microbiological tests; environmental samples were negative for *Ralstonia mannitolilytica*.

Conclusion

Although the culprit is still unidentified, CVC colonization following washing with contaminated saline solution likely caused clonal outbreak of *Ralstonia mannitolilytica* in oncology patients. This mostly environmental pathogen may represent a new threat to vulnerable patients due to unexpected way of transmission and unusual carbapenem resistance. We recommend attention to previously unforeseen sources of infection and suggest whenever possible use of single dose solutions.

Keywords: health care, infection, Ralstonia, antibiotic resistance, oncology, outbreak

PRESENTED BY: Claudia Lucarelli (claudia.lucarelli@iss.it)

REFERENCE NUMBER: 2937

Device-associated infection in a Medical Intensive Care Unit in Spain: 5 years of surveillance.

Cristina Díaz-Agero Pérez (1), Ángela Rincón Carlavilla (1), Nieves Lopez Fresneña (1), A Rincón Carlavilla (1), Jesús María Aranaz Andrés (1)

1. Hospital Universitario Ramón y Cajal, Madrid, Spain

Background

Device-related infections in critical care patients are associated with a high morbidity and mortality rate. Estimating quality healthcare indicators in an intensive care unit (ICU) is a starting point for implementing healthcare quality improvement measures.

Methods

Infection surveillance study at the medical ICU of Ramón y Cajal Hospital (Madrid, Spain). All patients referred to the medical ICU for more than 48 hours from January 1 2009 through 31 December 2014 were included. The criteria used to define healthcare-associated infection (HAI) are those established by the Centers for Disease Control and Prevention (CDC) and the National Healthcare Safety Network (NHSN).

Results

1,861 patients were included. 6.18% developed a device-associated infection attributable to their stay in the ICU. The average length of stay (LOS) was 8.78 days (±5.8). 2.04% of the patients developed a ventilator-associated pneumonia (VAP), with a VAP rate of 4.84 per 1,000 ventilator-days. 2.96% of the patients developed a catheter-associated urinary tract infection (CAUTI) with a CAUTI rate of 4.01 per 1,000 catheter-days. The cumulative incidence of central line-associated bloodstream infection (CLABSI) was 1.18% with a CLABSI rate of 1.52 per 1,000 central line-days.

Conclusion

Our results are similar to those of other studies using the same methodology. An HAI surveillance system is a key factor for implementing a healthcare quality improvement system. The obtained indicators act as alarm signals to identify deviations of the habitual sanitary practice. They allow intra comparison over time and with other similar hospitals, the monitorization of infection control measures, and therefore the effective improvement of healthcare quality and patient safety.

Keywords: Healthcare associated infections, Surveillance, Intensive Care Units, Quality Indicators, Patient Safety

PRESENTED BY: Nieves López Fresneña (nieves.lopez@salud.madrid.org)

REFERENCE NUMBER: 3075

Validation of a computer algorithm for hospital-acquired Clostridium difficile infections in Denmark

Manon CHAINE (1), Sophie Gubbels (1), Marianne Voldstedlund (1), Jens Nielsen (1), Bente Olesen (2), Jens Otto Jarløv (2), Henrik Carl Schønheyder(3,4), Jørgen Engberg (5), . The HAIBA stakeholder group (6), Kåre Mølbak (1)

1. Statens Serum Institut – Epidemiology department
2. Department of Clinical Microbiology, Herlev Hospital, Herlev, Denmark
3. Department of Clinical Microbiology, Aalborg University Hospital, Aalborg, Denmark
4. Department of Clinical Medicine, Aalborg University, Aalborg, Denmark
5. Department of Clinical Microbiology, Zealand Region, Slagelse, Denmark
6. Representatives from the Capital Region of Denmark, Region Zealand, Region of Southern Denmark, Central Denmark Region, North Denmark Region

Background

The Hospital-Acquired Infection Database (HAIBA) is a real time and automatic surveillance system for hospital-acquired infections in Denmark including Clostridium difficile infections (CDI). This study aimed to validate the algorithm implemented in HAIBA to select positive results for toxigenic Clostridium difficile (CD) against data from four large Departments of Clinical Microbiology (DCMs). These DCMs perform CDI diagnostics in their respective catchment populations.

Methods

For the algorithm, all CD positive results by either cultures or PCR were extracted from the Danish Microbiology Database (MiBa). Results specifying non-toxigenic CD were excluded. For comparison we obtained all results positive for toxigenic CD in 2013 from three DCMs (Aalborg and Capital Region (Herlev and Rigshopitalet)) and results for half a year only from one DCM (Region Zealand). We assessed the completeness of positive results for CD in HAIBA using the capture re-capture method. For Aalborg and Region Zealand, we linked the extracts on sample identifier and for the Capital Region on the civil registration number (CPR).

Results

Data from HAIBA covered 99.7% (1157) of the results from Aalborg; three were not found in HAIBA. We found 27 results only in HAIBA. HAIBA found 98.6% (492) of the results from Region Zealand and eight additional results. Seven results were not found in HAIBA. Lastly, 99.5% (2291) unique CPRs overlapped between HAIBA and Capital Region with 66 CPRs only found in HAIBA. Eleven CPRs were only found in the Capital Region.

Conclusion

We showed that the algorithm to select toxigenic CD covered the data from the participating DCMs with a high sensitivity. This study was important to show the validity of data for CD that we presented at www.HAIBA.dk.

Keywords: hospital, infection control, Clostridium difficile, surveillance

PRESENTED BY: Manon Chaine (manc@ssi.dk)

REFERENCE NUMBER: 3051

Evolution of the infection control/hospital hygiene capacity and training needs in Europe

Silvio Brusaferro (1), Luca Arnoldo (1), Giovanni Cattani (1), Elisa Fabbro (1), Barry Cookson (2), Rose Gallagher (3), Philippe Hartemann (4), Jette Holt (5), Smilja Kalenic (6), Walter Popp (7), Gaetano Privitera (8), Carl Suetens (9), Carmen Varela Santos (9)

1. Department of Medical and Biological Sciences, University of Udine, Udine, Italy
2. Division of Infection and Immunity, University College London, UK
3. Nurse Advisor Infection Prevention and Control, Royal College of Nursing, London, UK
4. Service d'Hygiène Hospitalière C.H.U. de Nancy & DESP-SERES, Faculté de Médecine, Vandoeuvre-Nancy, France
5. National Center for Infection Control, Statens Serum Institut, Copenhagen, Denmark
6. Department of Medical Microbiology, University of Zagreb, Zagreb, Croatia
7. Hospital Hygiene, University Clinics Essen, Hufelandstr. 55, 45147 Essen, Germany
8. Dipartimento di Ricerca Traslazionale e delle Nuove Tecnologie in Medicina e Chirurgia, Pisa, Italy
9. European Centre for Disease Prevention and Control, Stockholm, Sweden

Background

Since 2009, several official European Union (EU) documents, including the recent Council conclusions on patient safety and quality of care, have recommended improving training in infection control and hospital hygiene (IC/HH) in Europe. The project "Training in Infection Control in Europe-Implementation Strategy" (TRICE-IS) was commissioned by ECDC to explore any improvement in IC/HH training in Europe since a similar survey in 2010.

Methods

In October 2014, a 45-item questionnaire, based on the 2010 TRICE survey, was sent to designated Member State Experts (MSEs) of 30 EU/European Economic Area countries. In 36.7% of countries, the MSE was the same as in 2010. In February 2015, the project team interacted with the MSEs to validate their replies.

Results

All 30 countries answered the questionnaire, but comparison was possible only for 28 countries that participated both in 2010 and 2014. Between 2010 and 2014, the % countries that had recommendations for IC/HH management and had a definition for an IC/HH team increased from 86% to 96% and from 79% to 93%, respectively. The % countries having mandatory basic IC/HH training in medical and nursing schools increased from 29% to 57% and from 54% to 61%, respectively. Presence of a national curriculum or programme for IC/HH training was available for medical doctors in 50% of countries in 2010 and 46% in 2014, and for nurses in 61% of countries in 2010 and in 54 % in 2014.

Conclusion

Although some progress was observed regarding national recommendations for IC/HH management, IC/HH teams and basic IC/HH training, there was no improvement in countries' commitment to post-graduate training of IC/HH professionals. Sustained investment in training at national and EU level is crucial.

Keywords: TRICE-IS, Infection control professionals, Hospital hygiene, Training needs, European Countries.

PRESENTED BY: Elisa Fabbro (elisa.fabbro@uniud.it)

REFERENCE NUMBER: 2986

A 3-year outbreak of Multidrug resistant Salmonella Montevideo infections in a mother and baby unit, France: basic hygiene control measures still needed

Nathalie Jourdan-Da Silva (1), Laure Fonteneau (1,2), Anne Bernadou (3), Philippe Germonneau (4), Marianne Chemaly (5), Olivier Barraud (6), Simon Le Hello (7)

1. National Institute for Public Health Surveillance, Department of Infectious Disease, France
2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden
3. French Institute for public health surveillance, Limoges regional office, France
4. French Institute for public health surveillance, Poitiers regional office, France
5. French agency for food, environmental and occupational health safety (Anses), France
6. Department of Bacteriology, Medical Faculty, University of Limoges, France
7. Institut Pasteur, Unité des Bactéries Pathogènes Entériques, Centre National de Référence des Escherichia coli, Shigella et Salmonella, WHO Collaborating Centre for Reference and Research on Salmonella, Paris, France

Background

In May 2012, hospital X reported 4 cases of Salmonella Montevideo infections in infants hospitalized in a mother and baby unit (MBU). Three strains were multidrug resistant (MDR). Despite implementation of hygiene measures, cases continued to be identified. In November 2013, we visited the unit to describe the outbreak, formulate hypothesis about a persisting source and propose additional control measures.

Methods

A case was defined as a person hospitalized in hospital X with isolation of S. Montevideo between October 2010 and November 2013.We obtained data on the clinical presentation of the cases and their infant foods through staff interviews and medical records. We subtyped Salmonella strains by Antibiotic Susceptibility Testing (AST), Pulse Field Gel Electrophoresis (PFGE) and Whole genome Sequencing (WGS).We took 105 environmental swabs throughout the unit.Auditing of hygiene practices was carried out.

Results

Sixteen cases were identified: 14 infants (median age of 2.5 months), and 2 adults. No milk formula, food nor drink was common to the cases. S. Montevideo was identified on the floor of a cleaned case's bedroom. Plasmids with genetic features of MDR to third cephalosporin and quinolone were variably found among the S.Montevideo strains. A unique PFGE and WGS cluster was identified for all S. Montevideo strains whatever their resistance.Significant gaps in good cleaning and disinfection practice were identified.No new cases have been identified since the replacement of the cleaning staff and the implementation of a new cleaning protocol in January 2014.

Conclusion

The prolonged duration of this outbreak was most probably due to the persistence of S. Montevideo in the environment. Disinfection of the patient's environment is essential to avoid nosocomial transmission of Salmonella.

Keywords: Salmonella, Disease outbreak, Cross contamination, Hygiene, Infants

PRESENTED BY: Nathalie Jourdan-da Silva (n.jourdan@invs.sante.fr)

REFERENCE NUMBER: 3140

Knowledge, Attitude and Practice (KAP) Survey on Peripheral Intravenous Catheter Related Phlebitis among Nurses in Tbilisi, Georgia, 2014

Irma Burjanadze (1,2), Marika Geleishvili (3), Eka Khabazi (1,2), Thomas H. Rush (3), Edd Maes (4), Jon E. Tongren (3)

1. National Center for Disease Control and Public Health
2. South Caucasus Field Epidemiology and Laboratory Training Program
3. US CDC-Georgia Country Office
4. CDC Atlanta

Background

Nine-point prevalence studies in 1996-2003 of all hospitalized patients with a peripheral venous catheter (IVC) revealed IVC-associated phlebitis in 2.6%-12.7% of patients in Israel. Occurrence of IVC-associated phlebitis was significantly associated with insertion and management practices. Burden of IVC-associated phlebitis is not studied in Georgia. The aim of the study was to evaluate IVC-phlebitis related knowledge, attitude and practices among hospital nurses.

Methods

A Survey was conducted in the Intensive Care Unit (ICU) and Emergency Department (ED) of two tertiary hospitals during April-May, 2014 in Tbilisi, Georgia. Anonymized structured questionnaires were developed with 4 key questions and 152 (92%) out of 166 nurses were interviewed; 14 refused due to busy work schedules. Data were analyzed with Epi InfoTM and StatCalc for sample size and 95% confidence intervals. Respondents had never been trained on Phlebitis management and prevention.

Results

No one responded correctly to all key questions. Twenty eight percent of nurses in ED were significantly (RR=3.1; 95% CI:1.5-6.5) more likely than nurses (9%) of ICUs to know the link between length of PIC with the development of phlebitis. Eighty nine percent of nurses in ED were more likely (RR= 1.4; 95% CI:1.1-1.6) to use 70% alcohol instead of 0,5% chlorhexidine to process the skin before catheterization. Twenty percent of males were more likely (RR=2.9: 95% CI:1.4-7.5) to know the phlebitis time course and 80% nurses working less than 3 years were less likely (RR= 1.3; 95% CI:1.07-1.67) to have knowledge of phlebitis.

Conclusion

Given the findings, we recommend implementing a mandatory learning module about peripheral intravenous catheterization for hospitals and routine supervision targeting inexperienced nurses by more experienced nurses at the workplace.

Keywords: Phlebitis, Nurses, knowledge, Attitude, Catheterization.

PRESENTED BY: Irma Burjanadze (irmaepi@gmail.com)

REFERENCE NUMBER: 3203

Cluster of patients with multidrug resistant Klebsiella pneumoniae in a neurological early rehabilitation unit, South West Germany 2014

Christiane Wagner-Wiening (1,2), Friederike Ley (3), Elisabeth Czekalla (4), Edeltraud Herb (4), Elisabeth Aichinger (1), Guenter Pfaff (1)

1. Baden Wuerttemberg State Health Office, Stuttgart, Germany
2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Dis-ease Prevention and Control, (ECDC), Stockholm, Sweden
3. Local Health Office Karlsruhe County, Baden-Wuerttemberg, Germany
4. Hospital Karlsbad, Baden-Wuerttemberg, Germany

Background

Multidrug-resistant Klebsiella pneumoniae (MRKP) is a frequent opportunistic pathogen in hospital settings. In January 2014, a neurological rehabilitation hospital in South-West Germany reported four cases of positivity for MRKP, sharing closely related pulsed-field gel electrophoresis (PFGE) profiles (defined as outbreak strain) on one hospital ward. An outbreak investigation was initiated to identify the source of infection and colonisation and to provide recommendations for prevention.

Methods

We defined probable cases as patients hospitalised in the affected hospital unit between 1 and 28 January 2014 with a negative KP rectal screening test on admission, as routinely performed in this department, and culture-confirmed MRKP-colonization or infection acquired during hospital stay. A retrospective cohort study was performed to identify risk factors for acquiring MRKP.We defined confirmed cases as probable cases in whom the outbreak strain was detected. We actively searched for cases of colonization by singular rectal swabbing of patients of the affected ward. We collected information on demographics, period of stay and contact to a case, defined by sharing the same room and/or bathroom. We also collected environmental swab samples.

Results

Nine probable cases were identified; 8 male (median age 67, range 47-81 years), of which 7 were confirmed and five colonized. Patients who shared a room with an outbreak case were more likely to acquire MRKP than patients who did not (RR= 6.0 (95%CI 2.4-15); p<0.001). The outbreak strain was found on a shower chair used by several patients on the ward.

Conclusion

Patients with unrecognized MRKP-positivity probably served as a source of transmission. Based on our finding we recommend regular screening for MRKP during hospital stay and molecular typing of all detected MRKP-isolates.

Keywords: multidrug-resistant, Klebsiella pneumoniae, cohort study, molecular typing, outbreak strain

PRESENTED BY: Christiane Wagner-Wiening (christiane.wagner-wiening@rps.bwl.de)

REFERENCE NUMBER: 2887

Track 24: Late Breakers

MODERATOR: Josep Jansa (ECDC, Head of section, Epi intelligence & response)

Swimming in urban canals may be more risky for health than previously thought: a gastrointestinal outbreak among triathletes, Utrecht, the Netherlands, July 2015

Ewout Fanoy (1,2,3), Saara Parkkali (2,3), Rosa Joosten (1), Roan Pijnacker (2,3), Janko van Beek (2), Diederik Brandwagt (1), Erik Ruland (1), Wilfrid van Pelt (2)

1. Public Health Service region of Utrecht, the Netherlands
2. National Institute for Public Health and the Environment, the Netherlands
3. The European Programme for Intervention Epidemiology Training, Sweden

Background
On July 14th, two days after a triathlon event in urban canals of the city of Utrecht, 56 participants were reported with gastrointestinal symptoms to the Public Health Service. We investigated the outbreak to identify risk factors for infection.

Methods
We sent an online questionnaire to 900 event participants. A case with gastroenteritis was defined as a participant with diarrhea, vomiting or abdominal pain. We calculated risk ratios (RR) and 95% confidence intervals (95%CI) using univariable and multivariable Poisson regression. Fecal specimens from 6 patients were collected and tested for bacterial and viral gastroenteritis agents.

Results
239 (27%) participants responded within 1-2 weeks of the event. Of those, 24 did not swim but only cycled and ran. 67 (28%) met the case definition; 66/67 had swum in the canal. Swimming (RR 7.9; 95%CI 1.1-55) and consumption of energy drink (RR 1.6; 95%CI 1.0-2.6) increased the risk for gastroenteritis. The risk increased by 13% (95%CI 1.0-1.3) with increasing amounts of swallowed water (categorized as 1, 2, 3, 4-5, 6-9, ›9 mouthfuls). In 4 of 6 patient specimens, an identical norovirus genogroup II genotype 4 (GII.4) was detected.

Conclusion
Epidemiological and microbiological evidence suggested that ingesting water while swimming was associated with this norovirus outbreak, highlighting the existence of health risks related to swimming events in urban canals. As these events are becoming increasingly popular, we recommend developing preventive guidelines and advice for swimmers and event organizers, testing water for microbiological quality and standard follow-up on the health status of the participants.

Keywords: infectious disease outbreaks, outbreaks, norovirus, swimming

PRESENTED BY: Ewout Fanoy (ewout.fanoy@rivm.nl)
REFERENCE NUMBER: 3497

Post earthquake outbreak of Cholera in Kathmandu-2015

Bhim Prasad Sapkota (1), Isabelle Devaux (2), Gunanidhi Sharma (1), Baburam Marasini (1)

1. Epidemiology and Disease Control Division,Department of Health Services
2. Medicines Sans Frontiers (MSF)

Background
In Nepal, Sporadic cases of cholera occur almost every monsoon. A particular public health concern is highlighted this year due to the impact of the earthquake that took place on 25 April 2015.

Methods
Following an alert reported to EDCD on 2 August, an ad-hoc surveillance system was setup to monitor Acute Gastro-enteritis (AGE) and Cholera cases amongst patients seeking for care at Shukraraj Tropical and Infectious Disease Hospital (STIDH).A confirmed cholera case was defined as a patient aged five years of more with acute diarrhea and Vibrio Cholerae O1 or O139 isolated from stool. A detail line listing of all AGE cases was compiled daily using STIDH patient's treatment register. Home visits of the confirmed cholera cases were operated and drinking water samples were taken for the purpose of outbreak investigation.

Results
As of 17 September 2015, 666 AGE cases were reported, including 76 laboratory confirmed cholera cases from STIDH. Among 76 cholera cases only one case is O1 Inaba remaining 75 cases are O1 Ogawa serotype. Mean age was 35 (S.D of 1.5) years and 60% of the cases were male. Among 325 water sample analyzed, 72% were found to be unfit for drinking purpose due to presence coliforms organisms. Vibrio Cholerae was isolated from one deep well. GIS mapping showed the clustering cholera cases at the peripheral settlements of Bishnumati River.

Conclusion
Post-earthquake outbreak of cholera in Kathmandu might be due to the contamination of drinking water as a result of damages in the water supply system. Preventive measures for water treatment and awareness campaign were operated, inter-sectorial investigation including health, environment, water supply and sanitation is essential for disease control.

Keywords: Acute gastro enteritis, Cholera, Outbreak investigation

PRESENTED BY: Bhim Prasad Sapkota (bhimprasadsapkota@gmail.com)
REFERENCE NUMBER: 3500

High and rapid effectiveness of polysaccharide vaccines against clinical meningitis in Niger, 2015.

Marc Rondy (1), Issifou Djibo (2), Zaneidou Maman (3), Ibrahim Alkassoum (3), Kadade Goumbi (3), Hamidou Oumoulkair (4), Sidikou Fati (5), Esther Kissling (1), Sarah Meyer (6), Olivier Ronveaux (4)

1. EpiConcept, Paris, France
2. District sanitaire de Niamey 2, Niger
3. Direction de la surveillance et de la riposte aux épidémies, ministry of health, Niamey, Niger
4. World Health Organization, Geneva, Switzerland
5. Centre de Recherche Médicale et Sanitaire, Réseau International des Instituts Pasteur, Niamey, Niger
6. Meningitis and Vaccine Preventable Diseases Branch, Centers for Disease Control and Prevention, Atlanta, USA

Background

In 2015, a large outbreak of meningococcal C meningitis hit Niger. In late April, a vaccination campaign was held in Niamey. Using a case-control study we measured the vaccine effectiveness (VE) of tri - (ACW) and quadrivalent (ACYW) polysaccharide vaccines against clinical meningitis among 2-15 year olds in Niamey II district between 28 April and 30 June.

Methods

We selected all clinical cases registered in health centres and conducted a household- vaccination coverage (VC) cluster survey (control group). We ascertained vaccination from children/parent reports. Using odds of vaccination among controls and cases with onset after 10 May, we computed VE as 1-OR. In a sensitivity analysis we simulated a density case control design randomly attributing recruitment dates to controls based on case dates of onset. We considered children vaccinated less than 10 days before symptoms onset or recruitment dates as either vaccinated (VVE) or unvaccinated (UVE). We modelled VE by days since vaccination.

Results

Among 523 cases and 1800 controls, 57% and 92% were vaccinated respectively. In the principal analysis, VE was 84% (95%CI: 75-89) and 97% (94-99) for the tri- and quadrivalent vaccines respectively. In the sensitivity analysis, VVE and UVE were 86% (80- 90) and 80% (70 -88) for trivalent vaccine and 94% (91-96) and 98% (96-99) for quadrivalent vaccine. VE at day 5 and 10 after any vaccination was 83% (73-89) and 91% (86-94) respectively.

Conclusion

Results suggest a high VE of the polysaccharide vaccines against clinical meningitis, an outcome of low specificity, and a rapid protection after vaccination. We identified no potential biases leading to VE overestimation. Measuring VE and rapidity of protection against laboratory confirmed meningococcal meningitis is needed.

Keywords: Meningococcal meningitis, vaccine effectiveness, vaccine effectiveness, case control, meningitis belt

PRESENTED BY: Marc Rondy (m.rondy@epiconcept.fr)

Could sand be the missing link? An outbreak of sorbitol-fermenting enterohaemorrhagic Escherichia coli O157:H- in Northern Germany, 2015

Salla Eliisa Toikkanen (1,2), Martina Scharlach (1), Angelika Fruth (3), Rita Prager (3), Ute Messelhaeusser (4), Regina Konrad (4), Johannes Dreesman (1), Anne Mazick (5)

1. Governmental Institute of Public Health of Lower Saxony (NLGA)
2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden
3. National Reference Centre for Salmonella and other Bacterial Enteric Robert Koch-Institute, Branch Wernigerode, Germany
4. Bavarian Health and Food Safety Authority (LGL), Department Oberschleissheim, Germany
5. Local Public Health Authority of Cuxhaven, Germany

Background

On 13th July 2015, district of Cuxhaven in Northern Germany reported two cases of Hemolytic Uremic Syndrome (HUS) caused by sorbitol-fermenting enterohaemorrhagic Escherichia coli O157:H- (SF EHEC O157:H-). The cases were children. We initiated an investigation to identify the extent of the outbreak and its source to prevent further infections.

Methods

We performed a retrospective cohort study and defined a case as a participant on the common events 3-5th July with SF EHEC O157:H- confirmation from the first stool specimen. We collected information on symptoms, water- and food exposures and outdoor activities and calculated risk ratios (RR) with 95% confidence intervals (95%CI). Food, water and environmental specimens were microbiologically tested and human isolates were subtyped with pulse-field gel electrophoresis (PFGE).

Results

Eighteen persons were included in the study. Six children met the case definition: three HUS patients and three asymptomatic. Playing in sandbox (RR=13, 95%CI 2.0-85) and eating bananas (RR=8.0, 95%CI 1.3-50) were associated with being a case. SF EHEC O157:H- with indistinguishable PFGE pattern was identified from all six human specimens. Water and food samples tested negative for E.coli. One specimen from the sandbox was positive for SF EHEC O157:H-.

Conclusion

Our findings suggest sand being the source of this outbreak. Environmental source for SF EHEC O157:H- infections was proposed previously, but this is the first time it was detected in both human and environmental specimens. The PFGE-pattern was novel to the German National Reference Centre. To confirm sand as a plausible vehicle of infections, it should be considered as an exposure and tested when cases of SF EHEC O157:H- are observed.

Keywords: Outbreak, Hemolytic-Uremic Syndrome, Escherichia coli O157, Germany

PRESENTED BY: Anne Mazick (a.mazick@landkreis-cuxhaven.de)

REFERENCE NUMBER: 3527

A province-crossing Nalidixic acid and Ciprofloxacin resistant Salmonella Stanley outbreak, Austria, 2015

Sabine Maritschnik (1), Elisabeth Eva Kanitz (1), Christian Kornschober (2), Franz Allerberger (1), Daniela Schmid (1)

1. Austrian Agency for Health and Food Safety (AGES), Wahringerstrasse 25a, 1096 Vienna, Austria
2. Austrian Agency for Health and Food Safety (AGES), National Reference Laboratory for Salmonella, Beethovenstrasse 6, 8010 Graz

Background

On July 30, 2015, the National Reference Laboratory for Salmonella reported an increase in cases of infection with Salmonella (S.) Stanley resistant to nalidixic acid (Nx) and ciprofloxacin (Cip). On August 3, 2015, the Ministry of Health mandated an investigation to identify the source and propose preventive measures.

Methods

A probable outbreak case was a person (1) living in Austria or with a stay in Austria for at least 3 days prior to onset of illness with (2) diarrhoea or vomiting with disease onset after January 1, 2015, and who (3) had a laboratory confirmed infection with Nx/Cip resistant S. Stanley. A confirmed outbreak case was a probable case with a specific PFGE pattern "Perg". We conducted a retrospective case series investigation among cases.

Results

Of 141 registered cases, 123 (87%) fulfilled the probable case definition and 18 were confirmed cases. The median age was 19 years (4 months - 81 years) and 95 (67%) of 115 cases are male. The cases fell ill between January and September with a peak in week 30 (July). Cases were geographically spread throughout eight of the nine Austrian provinces with the highest number of cases reported in Upper Austria. Three clusters were identified by time and place. Cluster cases were linked by turkey kebap consumption and a trace-back analysis showed that turkey meat was supplied from a single transportation company located in Slovakia. It is suspected that the source of the turkey meat is from a turkey fattening and slaughtering facility in Hungary.

Conclusion

Epidemiological and microbiological information gathered, strongly suggests that consumption of contaminated turkey and turkey products are one of the sources of the outbreak.

Keywords: Salmonella infection, meat products, disease outbreak, food safety

PRESENTED BY: Sabine Maritschnik (sabine.maritschnik@ages.at)

REFERENCE NUMBER: 3534

Second Confirmed MERS-CoV Case in the Philippines, July 2, 2015

Lilia Ligon - Imperio (1), Imelda Deveraturda (1), Imelda Deveraturda (1), Vikki Carr Delos Reyes (2), Ma. Nemia Sucaldito (2), Rio Magpantay (2)

1. FETP Fellow
2. Department of Health

Background

On July 4, 2015, the Epidemiology Bureau (EB) received a confirmed MERS-CoV from the National Reference Laboratory. We conducted epidemiologic investigation: to profile the case, to conduct contact tracing and to recommend preventive and control measures.

Methods

We conducted a case report study. We interviewed the index case using the form by Public Health England and reviewed medical records. Closed contacts were identified and tested for MERS-CoV by real time polymerase chain reaction (RT-PCR). All traced contacts were monitored daily for appearance of illness for 14 days starting from the date of the last exposure to the confirmed case. A standard log sheet was used for symptoms monitoring. The close contacts were categorized as to close contact passengers, household close contacts, health workers close contacts and ancillary close contacts.

Results

The case was a 36 year old male, single. On June 30, he had cough. On July 2, respiratory samples were tested for MERS-CoV and yielded a positive result. There were 131 closed contact passengers listed on board. Eighty two (65%) were traced. One household contact was identified. There were 30 health workers close contacts from two hospitals. Ancillary close contacts were other passengers of air flight, friends, taxi driver and spa massage parlor staff. A total of 167 close contacts were identified, and 118 (71%) were traced. Of those traced, six developed respiratory symptoms but tested negative for MERS-CoV.

Conclusion

This is the second confirmed MERS-CoV case in the country. There were no secondary cases seen. A review of interim guidelines for MERS contact tracing was done.

Keywords MERS, Philippines, review, contact tracing

PRESENTED BY: Lilia Ligon - Imperio (doclily_229@yahoo.com.ph)

REFERENCE NUMBER: 3547

National outbreak of verocytotoxigenic Escherichia coli (VTEC) amongst adults exposed to prepacked salad detected by whole genome sequencing in England and Wales, August 2015

Amy Mikhail (1), Isidro Carrion (1,2), John Harris (1), Ian Fisher (1), Kirsten Glen (1), Claire Jenkins (1), Timothy Dallman (1), Gillian Beasley (3), Thomas Inns (4), Nicola Elviss (5), Drazenka Tubin-Delic (6), Paul Cleary (4), Jeremy Hawker (1,7)

1. National Infection Service, Public Health England, London, UK
2. European Program for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, Stockholm, Sweden
3. East of England Health Protection Team, Public Health England, Cambridge, UK
4. Field Epidemiology Services North West, Public Health England, Liverpool, UK
5. Food, Water and Environmental Microbiology Laboratory, Public Health England, London, UK
6. Food Standards Agency, London, UK
7. Field Epidemiology Services West Midlands, Public Health England, Birmingham, UK

Background

In August 2015, Public Health England detected a phylogenetic cluster of VTEC cases widely dispersed across England with one case in Wales. We investigated to identify the vehicle of infection and determine suitable control measures.

Methods

We defined cases as those with VTEC serotype O157 phage type 8 verotoxin 2a clustering within five single-nucleotide-polymorphisms of the outbreak sequence by whole genome sequencing (WGS). Standardised VTEC Enhanced Surveillance Questionnaires were completed for all cases. Exposures common to at least 70% of cases were assessed further with a focused questionnaire. A case – case study was conducted to test the resultant hypothesis on primary cases from 2015, aged over 18, resident in England or Wales, without history of foreign travel in the week before onset. Sporadic (non-outbreak) controls meeting these criteria were selected from the National VTEC database. We used multivariable logistic regression to calculate odds ratios (OR) and 95% confidence intervals (95%CI) for exposures.

Results

Forty-four cases were identified; 73% were female (median age 36, range 2-73 years). Thirty-six cases and 78 controls were included in the case-case study. Consumption of prepacked salad from one supermarket-chain was identified as the primary exposure associated with the outbreak (OR: 54, 95%CI: 11-247). Further investigations implicated two prepacked salad products, with one common ingredient, processed by one distributor who was supplied by six salad leaf producers during the outbreak period.

Conclusion

A national VTEC outbreak was successfully detected using WGS. The routine application of a standardised questionnaire to all VTEC cases facilitated a rapid investigation which identified prepacked salads as the likely vehicle of infection. Protection of salad leaves from possible sources of contamination from harvest to distribution is strongly recommended.

Keywords: VTEC, Escherichia coli, Whole genome sequencing, Standardised questionnaires, Surveillance, Salad leaves

PRESENTED BY: Amy Mikhail (amy.mikhail@gmail.com)

REFERENCE NUMBER: 3553

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European Centre for Disease Prevention and Control (ECDC)

Postal address:
ECDC, SE171 83 Stockholm, SWEDEN

Visiting address:
Tomtebodavägen 11A, Solna, SWEDEN

Tel. +46858601000
Fax +46858601001
http://www.ecdc.europa.eu

An agency of the European Union
http://www.europa.eu