ESCAIDE 10 YEARS

ABSTRACT BOOK

European Scientific Conference on Applied Infectious Disease Epidemiology 2016

Stockholm Waterfront Congress Centre
28-30 November 2016
Stockholm, Sweden

ecdc
EUROPEAN CENTRE FOR
DISEASE PREVENTION
AND CONTROL

www.escaide.eu

ESCAIDE is organised by the European Centre of Disease Prevention and Control, ECDC, in collaboration with the ECDC Fellowship Programme, i.e. EPIET and EUPHEM, as well as EAN (EPIET Alumni Network) and TEPHINET Europe (Training Programmes in Epidemiology and Public Health Interventions NETwork)

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European Scientific Conference on Applied Infectious Disease Epidemiology

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Warm welcome to ESCAIDE 2016!

This year marks the 10th anniversary of ESCAIDE. Over the past years, ESCAIDE has evolved from a scientific seminar for training fellows in the EPIET programme to a leading international conference in the field of infectious diseases.

This and the future success of ESCAIDE we owe to:

- You, who submitted and continue to submit abstracts to ESCAIDE. This is because the core of ESCAIDE is your work in applying epidemiology, microbiology and other scientific disciplines to dealing with real-world issues, showcased in the parallel and poster sessions;
- You, who contributed and continue to contribute your time and expertise as reviewers and moderators;
- You, who attended and continue to attend ESCAIDE, because you create the amazing atmosphere and spirit of the Conference.

One of the key aims of ESCAIDE is sharing of scientific knowledge and experience in all areas applied to infectious disease epidemiology, public health microbiology and related scientific fields. To highlight the importance of sharing data, we will open this year's ESCAIDE with a keynote address on open data (Plenary A). We will then continue with looking into how using data across disciplines and applying an integrated approach could advance models on disease transmission and improve communicable disease prevention and control (Plenary B).

On the second day of ESCAIDE, the topic of migrant health will return to the plenary forum. This is a subject that has gained even greater prominence as a public health issue than when it was last discussed as a plenary topic at ESCAIDE 2008. We will note what we have learned and achieved, and discuss what still needs to be done (Plenary C).

The third day of ESCAIDE will open with a discussion on the needs and roles of the public and private sector in delivering effective immunisation programmes (Plenary D).

This year's public health event is unquestionably the Zika epidemic (Plenary E). Its complexities have posed new challenges for the public health community, which we will discuss in the context of the need for multidisciplinary approaches to address such challenges.

Let me finish by reminding you what the other aims of ESCAIDE are. Namely:

- Discussing and debating scientific advances and current public health challenges;
- Strengthening and expanding the human network of all involved in this field in Europe and globally;
- Providing opportunities for further professional development for fellows and students in this field, e.g. EPIET, EUPHEM, FETP and other national/international training programmes.

Therefore I encourage you to take every opportunity to meet new peers, share your knowledge, ask questions, learn as much new information as you can and importantly, have fun!

Wishing you a productive and memorable ESCAIDE 2016!

Prof. Mike Catchpole
Chair, ESCAIDE Scientific Committee

Other Conference organisers

Networking and the use of a common language in field epidemiology, together with capacity building in surveillance and response, have been fundamental objectives of EPIET since its start in 1995. Inspired by the EPIET Scientific Seminar, ESCAIDE represents for fellows a unique forum to present their field investigations, and exchange experience with peers, supervisors, and different professionals in the area of communicable disease surveillance and response.

The ECDC Fellowship Programme, with the EPIET and EUPHEM paths, is a new step towards interdisciplinary work. Thanks to partnerships with the public health institutes who host the fellows and supervise their projects, the field epidemiology and public health microbiology networks can only be strengthened by the greater coordination and interaction among disciplines, as core values of the Fellowship Programme. This indeed will be crucial when considering the fast pace of advances in methods and technology in communicable disease surveillance and response.

Public health institutes, the national Field Epidemiology Training Programmes, TEPHINET, the EPIET Alumni Network and ECDC, as key partners in this expanding scientific community, work together to strengthen collaboration in training and building capacity for a competent workforce who can make Europe and the world better prepared to deal with public health emergencies.

On the 10th Anniversary of ESCAIDE, we wish a Happy Birthday and long life to both the conference and this network of networks!

Carmen Varela Santos, Acting Head of Public Health Training Section, ECDC

When EPIET was created in 1995, its purpose was to create a network of highly trained field epidemiologists in the EU, strengthening the public health epidemiology workforce at Member State and EU/EEA level. During the course of the 2-year fellowship, fellows build strong links both within, and between the cohorts. The challenge of developing and maintaining this network after the fellowship ends led to the establishment of the EPIET Alumni Network (EAN) as an independent association in 2000.

The EAN continues to grow each year (currently 490+ members), and now also includes alumni from EUPHEM and the EU/EEA FETPs, as well as external members. Having a network of professionals that know each other, speak the same ‘language’ (professionally), and can easily access each other’s expertise represents an important resource for European and global public health. As well as helping to develop and maintain the network, the EAN also aims to share and exchange professional experiences, constitute and enable access to a pool of expertise, promote and deliver ongoing training for members, and provide support to current fellows.

ESCAIDE has its roots in the EPIET Scientific Seminar, and since the first ESCAIDE the EAN has contributed to both the logistical and scientific organisation of the conference. The EAN President sits on the ESCAIDE Scientific Committee, and the EAN Board provides travel grants to 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. EAN members act as moderators for oral and poster sessions, as judges for prizes, and innovate with ideas such as BarCamp. They volunteer their time, ideas and boundless enthusiasm to ensure that, year on year, all these activities are a success.

We all know how easy it is to lose touch and the annual ESCAIDE also provides members with the opportunity to catch up face to face with each other. 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 EAN Board.

But, ESCAIDE is also a social event. As alumni, we look forward to ESCAIDE each year, knowing that it provides a welcome chance to meet the new fellows and to reconnect with old friends and colleagues, developing and maintaining those strong links between the growing family of field epidemiologists and public health microbiologists to which we belong!

We wish ESCAIDE a happy 10th birthday, and wish you all a personally and professionally enriching conference!

Dr Aileen Kitching, EAN President

TEPHINET
Training Programs in Epidemiology and Public Health Interventions Network

The Training Programs in Epidemiology & Public Health Interventions Network (TEPHINET) is a member-led global network of field epidemiology training programs (FETPs) or field epidemiology and laboratory training programmes (FELTPs) founded in June 1997. With a secretariat based in Atlanta, Georgia, USA, TEPHINET has existed for nearly two decades as a global network of field epidemiology training programs, spanning multiple regional networks, sub-regional programs, and national programs around the world. Overall, TEPHINET comprises 65 member programs in more than 90 countries. Currently, there are more than 10,000 FETP trainees, 6,500 graduates, and 1,000 students.

The principal mission of TEPHINET is to strengthen international public health capacity through initiating, supporting, and networking field-based training programs that enhance competencies in applied epidemiology and public health practice. Its training programs are mostly hosted within local departments of health, independent research institutes, or academic institutions and consist of one to two years of training. In general, graduates complete a two-year training program and receive their certificate of completion from the institutions in which their programs function.

TEPHINET's vision is to improve health through a global network dedicated to quality training in applied epidemiology and public health practices. Toward this end, it strives to support and strengthen existing programs, assist in the development of new ones, enhance applied research activities of programs, improve response to public health emergencies, and link competent professionals in field epidemiology to responding agencies.

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

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

ESCAIDE offers opportunities for networking and information sharing where FE(L)TP fellows, alumni and other PH professionals can show their achievements and learn from each other's experience in order to acquire new ideas and skills that can be put into action.

As every year TEPHINET has participated in the organization of ESCAIDE and wishes all the participants an inspiring conference with interesting presentations and discussions relevant for your work.

Dr. Fehminaz Temel, TEPHINET Representative, European Region

Scientific Committee

Mike Catchpole – ECDC, Chair of ESCAIDE Scientific Committee

Mike is the Chief Scientist at ECDC. As Head of the Office of the Chief Scientist, he is responsible for driving the scientific agenda 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 working in infectious disease epidemiology at national and international levels. 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 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, written a textbook on infectious disease epidemiology and co-edited another.

Aileen Kitching – President of the EPIET Alumni Network (EAN)

Aileen is a specialist in Public Health Medicine in the Department of Public Health (Cork/Kerry) of the Health Service Executive in Ireland, where her portfolio includes HIV/STIs, hepatitis B and C, and health inequalities. After a background in clinical medicine (hospital & general practice in Ireland, Scotland and Australia; MSF in Liberia), she completed EPIET from 2007-2009 at the Health Protection Agency in London, and from 2009-2015 completed her specialisation in public health medicine, with a main interest in and experience of communicable disease control (surveillance and outbreak response), at local, regional and national level in the UK (at the Health Protection Agency/ Public Health England), as well as internationally. This included three months in the Outbreak Response Unit at NICD in South Africa in 2012; three months as Health Cluster Coordinator with WHO in the Philippines supporting the response to Typhoon Haiyan (Yolanda) in 2014; and three months as part of the Ebola Response Team with WHO in Sierra Leone in 2015 (in a national role as WHO lead for contact tracing). As president of the EAN board, she represents the vast alumni of EPIET, EU-FETP and EUPHEM on the scientific committee and remains committed to training in field epidemiology.

Panayotis T. Tassios – University of Athens, Greece

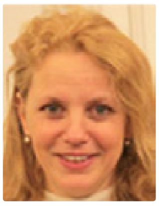
Panayotis is Associate Professor in Molecular Microbiology at the National & Kapodistrian University of Athens, Greece. His research focuses on the molecular typing of bacterial strains –from both healthcare-associated and community-onset infections– and their antimicrobial drug resistance mechanisms, 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 Eurosurveillance and Clinical Microbiology and Infection.

Andrea Ammon – ECDC

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.

Aftab Jasir – ECDC/EUPHEM

Aftab is an associate professor, working as head of the 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). Her specialisations include healthcare-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.



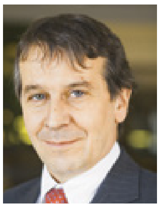
Ines Steffens - ECDC

Ines is the Editor-in-Chief of Eurosurveillance journal. She joined ECDC in 2006 as Managing Editor for Eurosurveillance, and between 2007-2011 set up ECDC's Scientific Communication Section. Before Joining ECDC, Ines was Editor-in-Chief for Germany's national epidemiological and public health bulletin, the Epidemiologisches Bulletin at Robert Koch Institute, Berlin, Germany. Ines is a trained internist, with broad clinical experience and expertise in infectious diseases. She holds a masters degree in public health, and has a special interest in communication-related issues.

Thea Kølsen Fischer – SSI

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 specialised in epidemiology and laboratory outbreak management as an EIS Officer at CDC (2003-2005). Thea is a member of the ECDC National Microbiology Focal Points forum.

Scientific Committee

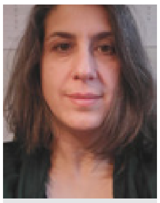


Denis Coulombier – ECDC

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.

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.

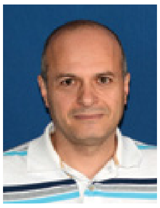


Helena de Carvalho Gomes - ECDC

A medical doctor by training, Helena first worked in obstetrics and gynaecology before moving to public health where she holds a masters degree. Helena joined ECDC in 2008 to work with the vaccine-preventable diseases programme, and is currently Head of the Scientific Advice Coordination Section. After leaving clinical practice and before joining ECDC, Helena was member of the subcommittee on prevention and represented the National Association of Statutory Health Insurance Physicians in the German Federal Joint Committee. In this function she developed systematic reviews, health technology assessments and directives for the Committee, mainly in the area of screening and early detection of disease, as well as maternal and child health. Helena has a special interest in methods and tools for evidence-based practice and decision-making in healthcare and public health, and their application in infectious diseases epidemiology, prevention and control.

Fehminaz Temel - MoH, PHI, Turkey

Fehminaz is a medical doctor, epidemiologist and public health specialist, working as head of Field Epidemiology Unit and Director of Turkey Field Epidemiology Training Programme in the Public Health Institution of Turkey. She is a member of TEPHINET (Training Programs in Epidemiology and Public Health Interventions Network) Europe.

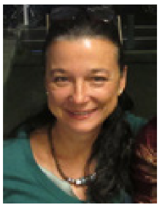


Fortunato (Paolo) D'Ancona – ISS, Italy

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).

Osamah Hamouda - Robert Koch Institute , Germany

Osamah Hamouda MD, MPH is head of the Department of Infectious Disease Epidemiology at the Robert Koch Institute, the national public health institute in Germany. Prior to his appointment, Dr. Hamouda was deputy head of the department since 2003 and head of the HIV/AIDS, STI and Bloodborne Infections Unit since 1995, responsible for HIV/AIDS, STI and blood donor surveillance in Germany. He studied medicine at the Free University Berlin and completed his post-graduate training in public health also in Berlin. He has worked in prevention, surveillance and epidemiology since 1987 and has lead numerous surveillance and research projects in the field.



Marion Muehlen – ECDC

Marion currently heads the EPIET programme in the Public Health Training section. After training and working as a medical doctor in Brazil, Marion moved to Germany to specialize in occupational health. She then moved on to clinical pharmacology, where she worked for 15 years in clinical trials. Drug trials for neglected diseases sparked her interest in epidemiology and public health, leading her to complete a masters degree in tropical medicine and international health, and later the EPIET programme as an FETP fellow at the Robert Koch Institute. After completing EPIET, Marion received a two-year Marie Curie fellowship to help develop mathematical models of infectious disease transmission in the Theoretical Epidemiology group at the Gulbenkian Institute of Science in Portugal. Following these two years, Marion joined the EPIET Scientific Coordinator team in 2008, first as coordinator based at the Robert Koch Institute, Germany, and later as coordinator at PHE (former HPA) in Colindale, UK. She joined ECDC in 2010 as an EPIET coordinator based in Stockholm, and has been appointed acting Head of EPIET since April 2015.

Abstract Reviewers

The Scientific Committee warmly thanks everyone who participated in the reviewing of the abstracts submitted for ESCAIDE 2016

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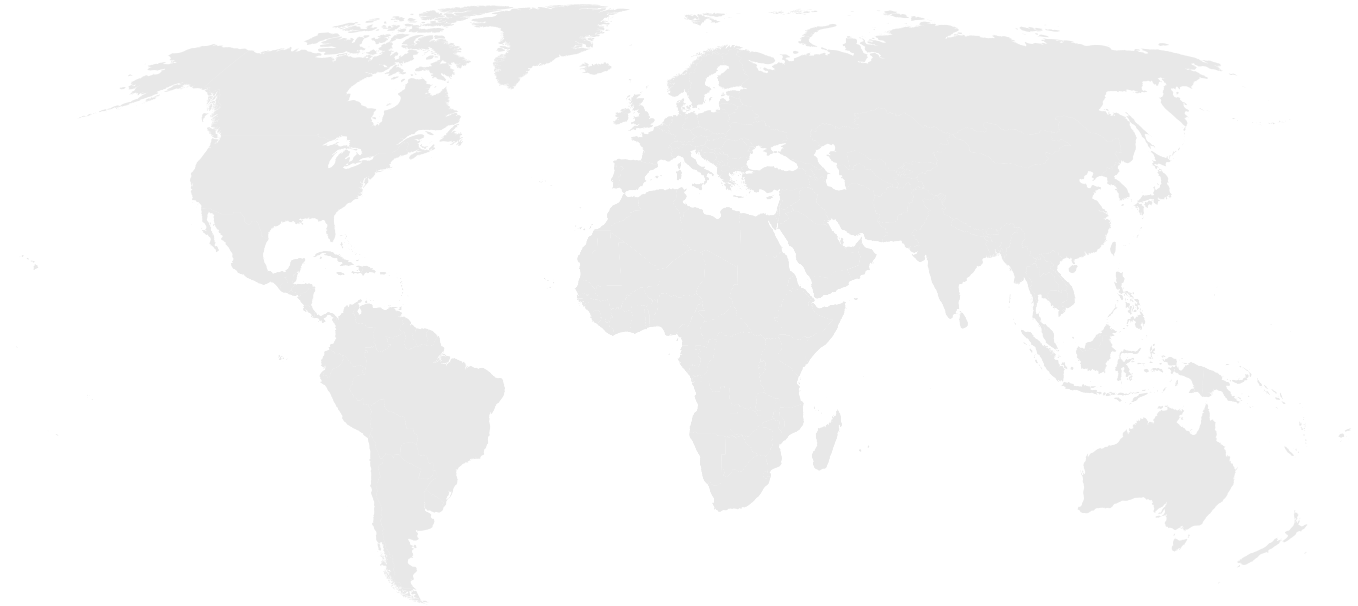

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Information Stands

Eurosurveillance - ECDC

Eurosurveillance is a European peer-reviewed scientific journal devoted to the epidemiology, surveillance, prevention and control of communicable diseases, with a focus on such topics that are of relevance to Europe. It is a weekly online journal, with 50 issues per year published on Thursdays, and features short rapid communications, longer in-depth research articles, surveillance and outbreak reports, reviews and perspective papers, as well as short news items. Timely publication of short authoritative papers on ongoing outbreaks or other relevant public health events is one of the major assets of the journal. Under special circumstances when current events need to be urgently communicated to readers for rapid public health action, e-alerts can be released outside of the regular publishing schedule. Topical compilations of selected articles and special issues are also published in print.

The entire content is open access, free of charge for both readers and authors. All articles are indexed in the PubMed/MEDLINE, Scopus, EMBASE and EBSCO databases. In 2015, Eurosurveillance reapplied successfully to be listed in the Directory of Open Access Journals (DOAJ) and is listed in the Sherpa/Romeo database as a journal that complies with the open access standards required by funders such as the Wellcome Trust.

The journal has been selected for coverage by Thomson Reuters and is indexed and abstracted in the Science Citation Index Expanded (also known as SciSearch) and in the Journal Citation Reports/Science Edition beginning with volume 14(1) 2009. The current impact factor, for the year 2015, is 5.98 (Journal Citation Reports, Thomson Reuters, 2016). This places Eurosurveillance at rank 7 among the 83 journals in the category Infectious Diseases. The Scopus-based SCImago Journal Rank (SJR) for 2014 ranks Eurosurveillance 92 of 1,775 journals in the category Medicine. The journal is also in the first quarter (Q1) in the categories Epidemiology, Public Health, Environmental and Occupational Health and Virology. Google Scholar metrics in mid-2014 listed Eurosurveillance at ranks 4 and 10 among journals in the categories Epidemiology and Communicable Diseases.

www.eurosurveillance.org

Reimbursements – ECDC

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

Training Network Strengthening (TNS) Group Public Health Training Section, Public Health Capacity and Communication Unit, ECDC

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The Training Network Strengthening Group (TNS) works in close collaboration with ECDC Disease Programmes and public health core functions as a reference team for adult learning methodology and quality assurance of ECDC training activities.

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.

The ECDC Virtual Academy (EVA) and FEM-wiki are platforms where EPIET and EUPHEM fellows, supervisors and scientific coordinators and in general participants in our ECDC training activities can access online courses, interact in communities of practice, among other opportunities for sharing training materials and networking.

ecdc.europa.eu

ECDC Fellowship Programme (EPIET and EUPHEM)

The European Programme for Intervention Epidemiology Training (EPIET) and the European Programme for Public Health Microbiology Training (EUPHEM) are two-year fellowships 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/

EPIET Alumni Network (EAN)

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

epietalumni.net

European Society for Clinical Virology (ESCV)

The European Society for Clinical Virology (ESCV) was formed from the European Group for Rapid Viral Diagnosis and the European Society against Virus Diseases which merged on 1 January 1997. aims are to promote knowledge in the field of basic and clinical virology, including aspects of Public Health virology. This is achieved through the organisation of educational meetings and workshops, as well as providing travel grants to attend meetings and the ECDC Observership programme. It also provides awards for work in the fields of basic and clinical virology.

The ESCV is registered as a "Company Limited by Guarantee" and listed in the Central Register of Charities in England and Wales (No 1099537).

www.escv.org

European Society of Clinical Microbiology and Infectious Diseases (ESCMID)

Since its founding in 1983, ESCMID has evolved to become Europe's leading society in clinical microbiology and infectious diseases with members from all European countries and all continents. For more than 30 years, ESCMID has been an influential component in the professional lives of microbiologists and infectious disease specialists and now reaches more than 33,000 individual and affiliated members around the world. ESCMID is registered in Switzerland with offices in Basel.

www.escmid.org

Invited Speaker Biographies

Plenary Session A: Key Note Address – Open data

Prof. Henrik Wegener

Prof. Henrik Wegener is the Executive Vice President at Technical University of Denmark (DTU) and an expert on food safety, zoonosis, antimicrobial resistance as well as emerging infectious diseases.

He has served as advisor to national and international authorities & governments, international organizations and private companies, and universities and research foundations, and is presently serving, on several national and international committees and boards on food safety, veterinary public health, and research policy.

Most recently he was appointed Chair of the High Level Group of the EC Scientific Advice Mechanism (SAM).

Plenary B: Modelling

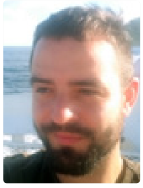
Prof. Anne-Mieke Vandamme

Prof. Anne-Mieke Vandamme joined the Rega Institute at the University of Leuven in 1990, where she started a unit on virus genetic testing for clinical practice. Together with Professor Van Ranst, she founded a new division, Clinical and Epidemiological Virology.

Anne-Mieke Vandamme and her team perform research on the molecular epidemiology of HIV, HTLV and HCV, on HIV and HCV drug resistance testing (genotyping, phenotyping) in clinical context, and on bioinformatics (data mining, phylogenetic analysis) technology. In the fields of HIV molecular epidemiology and drug resistance, she has an extensive and widely recognized expertise. She has been participating in several European projects (ENVA, SPREAD, EHR, Virolab, CHAIN, VIROGENESIS). She supported the development of a few widely used (bioinformatics) tools, the Rega HIV Drug Resistance algorithm, the Rega HIV typing and subtyping tool, and recently also RegaDB, a free and open source software for collecting and sharing HIV epidemiological, clinical and virological data.

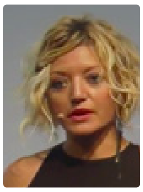
In her address Professor Vandamme will talk about reconstruction and visualising HIV global dissemination networks and its relevance to public health policy.

Dr. Thibaut Jombart



Dr. Thibaut Jombart is a lecturer in biostatistics and genetic analysis in the MRC Center for Outbreak Analysis and Modelling, Imperial College London. His work is dedicated to developing new methods and tools for understanding how infectious disease spread, and help informing public health response in outbreak situations. He has made a number of theoretical contributions for integrating pathogen genomic data into infectious disease epidemiology. This includes the reconstruction of the historical spread of specific pathogens, the inference of transmission trees ('who infects whom') from genetic and epidemiological data, and more recently the identification of the likely origins of contamination in food-borne disease outbreaks, and new algorithms for detecting outbreaks from genomic surveillance data. Besides his theoretical work, he has also been involved first-hand in several outbreak responses, including the 2009 influenza pandemic, the Middle-East Respiratory Syndrome (MERS), and more recently as a member of the WHO Ebola response team since August 2014. Part of his work over the last years has focused on developing free, open-source tools for outbreak response. He has organised a series of international hackathons dedicated to building a platform for handling and analysing outbreak data. The most recent one, Hackout 3, took place in Berkeley (CA) in June 2016. In his allocution Dr. Thibaut Jombart will introduce the use of biogenomic data in mathematical models of infectious disease transmission.

Dr. Vittoria Colizza



Dr. Vittoria Colizza is senior researcher at Inserm (French National Institute of Health and Medical Research) & Universite Pierre et Marie Curie, Faculte de Medecine, Paris, France. She also has a joint appointment at ISI Foundation, Turin, Italy.

After receiving her PhD in Statistical and Biological Physics at the International School for Advanced Studies in Trieste, Italy, in 2004, she spent 3 years in the US at the Indiana University School of Informatics (Bloomington, IN). In 2007 she moved back to Europe after being awarded a Starting Independent Career Grant in Life Sciences by the European Research Council, starting her first lab at ISI Foundation. In 2011 Vittoria joined the Inserm in Paris where she now leads the EPIcx lab (Epidemics in complex environments, www.epicx-lab.com) within the Pierre Louis Institute of Epidemiology and Public Health.

Through her work she has made important contributions to the development of the field of computational epidemiology (50+ publications in international peer-reviewed journals), based on sophisticated models and massive empirical datasets aimed at producing advances in the surveillance, modeling and prediction of epidemic spread. These research activities are further supported by theoretical approaches integrating methods of complex systems, network science and statistical physics aimed at underpinning the mechanisms behind observed spreading phenomena. In addition to the ERC Starting Grant in 2007, Colizza received the Young Talent Award by the Italian Ministry of Youth in 2010, the Prix Louis-Daniel Beauperthuy 2012 for Human biology and Medical sciences by the French Academy of Sciences, the Young Scientist Award for Socio-Econophysics in 2013. She also served as Young Advisor to the Vice President of the European Commission Mrs. Neelie Kroes for the Digital Agenda for Europe.

In her talk, Dr. Vittoria Colizza will discuss the usage of data on travel, social networks, human movement, and disease occurrence, in order to explain how pathogens spread.

Plenary Session C: Migrant Health

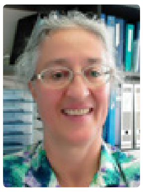
Dr. Bayard Roberts

Dr. Bayard Roberts is Senior Lecturer in Health Policy and Systems at London School of Hygiene and Tropical Medicine (LSHTM). Bayard has a public health background, much of it related to forced migration and health.

His PhD (2009) examined the health impacts of forced migration in northern Uganda, and he has subsequently led quantitative and qualitative research on forced migration and health in Ukraine, Georgia, South Sudan, Tanzania, and elsewhere. He has also led a number of systematic reviews related to health needs among populations affected by armed conflict. In addition, Bayard has examined the health impact of major social, political and economic change in studies in the countries of the former Soviet Union. The main health outcomes of interest to him are mental health disorders, diabetes and other non-communicable diseases, and related harmful health behaviours.

Bayard has over 100 publications – the majority on health in Europe and/or health of migrant populations. He is Editor-in-Chief of the journal Conflict and Health, and has taught on the subject of conflict and health and forced migration at LSHTM, WHO, King's College London and Imperial College London. He is also the Director of ECOHOST – The Centre for Health and Social Change at LSHTM.

Dr. Silvia Declich



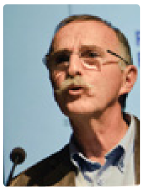
Dr. Silvia Declich, MSc in Epidemiology from the University of Ottawa (Canada), started working in Africa in cooperation Projects in the field of Primary Health Care and Nutrition. In 1993 she joined the Istituto Superiore di Sanità (ISS) in Rome and is currently Director of the Communicable Disease Epidemiology Unit of the Centre of Epidemiology, Surveillance and Health Promotion.

Dr Declich, a senior researcher, has extensive experience in the direction and management of scientific research projects, national and international, on various areas related to communicable diseases, including those pertinent to migrant health and preparedness.

She has a long standing working experience with the European Commission (in particular with DG SANCO and DG DEVCO) and WHO, as well as with academic and research institutions in Europe and in European Neighbourhood Countries. Additionally Dr Declich, as member of the ECDC Advisory Forum.

Plenary Session D: Vaccines

Dr. Alain Moren



Dr Moren was trained as an EIS officer at the US CDC (1985-7). He holds a master degree from Johns Hopkins University, USA, and a PhD in epidemiology from Bordeaux University in France and is certified as a research director in France.

He has been Director of the medical department of MSF (1983-4); Director of Epicentre, the scientific department of MSF (1987-95); Coordinator of the EPIET programme (1995-2006); since 2006, Dr Moren has been heading the epidemiology department of EpiConcept. He is mainly involved in supervising vaccine preventable disease research studies aiming at measuring the effectiveness and the impact of vaccines (influenza, pneumococcal, rotavirus, pertussis vaccines).

Andrea Rappagliosi

Andrea Rappagliosi joined the Sanofi Pasteur MSD Executive Committee in July 2012 as Vice President Market Access, Health Policy and Medical Affairs.

Born in Rome, Andrea received a law degree from the University of Rome "La Sapienza". He began his professional career in the Italian Senate. Before joining SPMSD, he worked at Baxter Healthcare, Serono International and GSK in different European and International positions in the market access and policy area.

Andrea is currently President of Vaccines Europe and Chair of the EFPIA HTA Priority WG. He represents the healthcare Industry in several European EU Commission and Member States initiatives such as the HTANetwork, EUnetHTA, the EU Active & Healthy Aging Innovation Partnership. He was member of the High Level Pharmaceutical Forum (2005-2008).

Dr. Marco Cavaleri

Dr. Marco Cavaleri, Head of Anti-infectives and Vaccines, Scientific and Regulatory management Department at EMA, is responsible for the management of pre- and post-authorisation activities of centralised applications/marketing authorisations, and particularly the Safety and Efficacy part, related to medicinal products in the above-mentioned therapeutic areas.

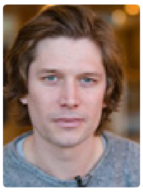
Dr. Marco Cavaleri is a Pharmacologist who spent several years in industry in R&D mainly in the area of antibacterials and antifungals covering different positions in preclinical and clinical development. In 2005 he joined the EMEA as Scientific Administrator in the Scientific Advice and Orphan Drugs Sector, specifically being in charge of anti-infectives and vaccines scientific advice procedures.

He returned to the Agency in 2008 as Group Leader Anti-infectives in the Safety&Efficacy Sector, Pre-Authorisation Human Unit following a short period in industry leading clinical and preclinical development in the area of Gastroenterology and Infectious Diseases. In 2009 he was appointed as Head of Section for Anti-infectives and vaccines in the Safety&Efficacy Sector, Human Medicines Development and Evaluation Unit.

Invited Speaker Biographies

Plenary Session E: Zika/ Public Health Event 2016

Dr. Joacim Rocklöv



Dr. Rocklöv an Associate Professor in epidemiology with application to infectious disease. His main focus is with vector-borne disease, such as dengue and Zika. He has a specific interest in disease dynamics, understanding drivers of spread, and establishing predictions and forecasting models to inform policy and facilitate timely preparedness.

Dr. Lyle Petersen

Lyle R. Petersen, M.D., M.P.H., has served as the director of the Division of Vector-borne Diseases since 2004.

Dr. Petersen began his training at the University of California, San Diego where he received an undergraduate degree in biology. He then studied medicine at the University of California, San Francisco, where he was awarded a Regent's Scholarship. After medical school, Dr. Petersen completed his internship and residency in internal medicine at Stanford University. He then joined Tulane University's tropical medicine research efforts in Cali, Colombia before starting CDC's Epidemic Intelligence Service (EIS) applied epidemiology training program in 1985. After his EIS training at the Connecticut State Health Department, he joined the CDC's Division of HIV/AIDS where he worked until 1995.

During that time, he completed CDC's Preventive Medicine Residency Program, received an MPH degree from Emory University, and served in several posts, including the Chief of the HIV Seroepidemiology Branch. From 1996 to February 2000, Dr. Petersen guided Germany's efforts in creating a new national infectious disease epidemiology program at the Robert Koch Institute in Berlin. From 2000 to 2003, he served as the Deputy Director for Science of the Division of Vector-borne Diseases. He is the author of more than 175 scientific publications.

Dr. Petersen has been the recipient of several scientific awards including the Charles B. Shepard Science Award, the Alexander D. Langmuir Award, James H. Nakano Citation, and twice the HHS Secretary's Award for Distinguished Service. He served on the National Security Staff at the White House, currently serves on the editorial boards of two medical journals, is a member of the Faculty of 1000, and is the Incident Manager of the Zika Response at the CDC. Dr. Petersen's current research focuses on the epidemiology of arboviral and bacterial vector-borne zoonoses.

Dr Anna Thorson

Dr Anna Thorson joined the Department of Reproductive Health and Research at WHO as Research Manager in 2016. She also works with Dr Nathalie Broutet, RHR, WHO in the Ebola Viral Persistence Study in Sierra Leone, which investigates Ebola viral persistence in a cohort of male and female survivors, and in the research investigating viral persistence and sexual transmission of the Zika virus.

Anna is affiliated to the Department of Public Health, Global Health, Karolinska Institutet, where she holds a Professorship in Global Infectious Disease Epidemiology. Anna has extensive experiences of leading research focused on HIV and TB epidemiology, health systems and implementation research, specifically in low-income settings and vulnerable groups. Anna´s research also includes infectious disease epidemiology related to influenza, as well as innovative m- and e- health methods for sampling and modelling related to sexual risk behaviour, HIV and PMTCT. Anna was awareded an honorary professorship at Hanoi Medical University, Vietnam in 2011. She is a member of the Global Fund Technical Evaluation Reference Group (TERG).

Anna's talk will focus on the latest evidence-base on sexual transmission of the Zika virus, and the methodology and rationale adopted by WHO for making recommendations on the prevention of sexual transmission of Zika virus.

Dr Colleen Acosta

Dr Colleen Acosta is an epidemiologist at the World Health Organization Regional Office for Europe, Copenhagen, Denmark. She currently works with the Alert and Response Operations Team, WHO Health Emergencies Programme. She is also the focal point for Zika surveillance, information and planning for the European Region under the WHO Incident Management System.

Colleen was awarded her PhD in perinatal epidemiology from the University of Oxford in 2014. Prior to that, Colleen received her bachelor degree from Stanford University and master degree from the Johns Hopkins Bloomberg School of Public Health. Colleen has extensive experience in research, having been a research associate at the Stanford University School of Medicine. She was also the research focal point for the WHO TB and Multidrug resistant TB Programme, WHO Regional Office for Europe, where she coordinated research capacity building in Eastern Europe and Central Asia. Colleen additionally served as a field epidemiologist for the WHO Ebola Response Team in Sierra Leone, and has a long experience of working in outbreak investigation and early warning surveillance.

Plenary Session Abstracts

16	PLENARY SESSION A	MONDAY 28 NOVEMBER	9:00-10:30
16	PLENARY SESSION B	MONDAY 28 NOVEMBER	17:00-18:30
18	PLENARY SESSION C	TUESDAY 29 NOVEMBER	9:00-10:30
19	PLENARY SESSION D	WEDNESDAY 30 NOVEMBER	9:00-10:30
20	PLENARY SESSION E	WEDNESDAY 30 NOVEMBER	17:00-18:30

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Plenary Session Abstracts

PLENARY SESSION A
MONDAY 28 NOVEMBER
9:00-10:30

Plenary Session A: Keynote

Chair: Andrea Ammon, ECDC

Open data – maximizing the societal value of research

Presented by

Prof. Henrik C. Wegener

Affiliation

Technical University of Denmark, Lyngby, Denmark; High Level Group of the Science Advice Mechanism, European Commission, Bruxelles, Belgium

Abstract

All research builds on former work and depends on the possibilities for scientists to access and share scientific information. The Internet has fundamentally changed the world and we have also witnessed its impact on the scientific system, which is currently undergoing significant changes ("Science 2.0"/"Digital Science"). In particular, fuller and wider access to scientific publications and data can help to:

- Accelerate innovation;
- Foster collaboration and avoid duplication of efforts;
- Build on previous research results;
- Involve citizens and society.

What is at stake is the speed of scientific progress and the return on R&D investment, and in particular publicly-funded investment, which has enormous potential for boosting productivity, competitiveness and growth. Affordable and easy access to scientific information is very important for the scientific community itself, but also increasingly important for innovative small businesses. Improving access to scientific information is also about increasing openness and transparency, which are essential features of Responsible Research and Innovation and contributes to better policy-making.

The presentation will describe the background and the first stages of implementation of the EU policy on open science and open data, and put it into perspective in the context of research, as well as surveillance and control of infectious diseases in Europe and beyond.

Finally, the recently established Scientific Advice Mechanism of the European Commission will be presented, and the importance of open access to scientific information for better policy-making will be discussed.

Keywords: Open Science, Open Data, Science 2.0, Digital Science

PLENARY SESSION B
MONDAY 28 NOVEMBER
17:00-18:30

Plenary Session B: Modelling

Chairs: Marc Struelens and Marion Muehlen, ECDC

How to bridge phylogenetics and epidemiology: visualization of metadata on trees

Presented by

Prof. Anne-Mieke Vandamme

Affiliation

KU Leuven - University of Leuven, Department of Microbiology and Immunology, Rega Institute for Medical Research, Clinical and Epidemiological Virology, Leuven, Belgium; Center for Global Health and Tropical Medicine, Unidade de Microbiologia, Instituto de Higiene e Medicina Tropical, Universidade Nova de Lisboa, Lisbon, Portugal

Abstract

Phylodynamic and phylogeographic techniques are increasingly used to understand the origin and spread of epidemics. However, in addition to time and place, many other epidemiological data are available, and the visualization of all these metadata on trees can help classical epidemiologists to appreciate the kind of hypotheses that can be tested using phylogenetics. One of the aims of the EC project VIROGENESIS is to bridge the gap between bioinformatics developers and public health workers, by providing easy to use visualization tools for viral disease epidemics and outbreaks.

HIV-1 subtype B has been shown to have originated in Haiti during the 1960's as a heterosexually transmitted virus, but has then spread to the US among men-who-have-sex-with-men (MSM). Starting in the 1980's, the virus caused a worldwide pandemic in mainly three risk groups, MSM, heterosexuals and injecting drug users. The timing and magnitude of the jumps between these three risk groups, and where geographically they occurred, can be visualized in an interactive tool.

Keywords: Virus diseases, phylogeny, HIV-1, epidemics, Heterosexuality, Male Homosexuality, Drug Users

The R Epidemics Consortium: building the next generation of statistical tools for outbreak response using R

Presented by

Dr. Thibaut Jombart

Affiliation

MRC Centre for Outbreak Analysis and Modelling, Department of Infectious Disease Epidemiology, Imperial College London

Abstract

The recent West African Ebola outbreak has been a terrible reminder for the need to gain timely situation awareness, in order to inform and guide public health intervention and maximise the chances of mitigating disease outbreaks. Unfortunately, many tools are still lacking for addressing the challenges, both statistical and technical, posed by the analysis of outbreak data. This presentation will introduce the R Epidemics Consortium (RECON), an initiative bringing together public health officers, statisticians, modellers and software developers to develop a new generation of tools for outbreak response using the R software. We will argue that R is a platform of choice for the development of cutting-edge methodology which can further our understanding of disease dynamics. This point will be illustrated using outbreaker2, a new R package for reconstructing disease outbreaks using various kinds of epidemiological and genetic data. We will also show how R can be used for addressing some of the more technical challenges inherent to the outbreak response context, taking the packages incidence and epicontacts as examples. We will conclude by reflecting on how the typical life-cycle of methodological development is altered during emergency outbreak response, and on what novel practices may be considered to address some of these issues.

Keywords: methods, R, statistics, software, RECON, tools

Facing the complexity of infectious disease spread

Presented by

Dr. Vittoria Colizza

Affiliation

IPLESP, Pierre Louis Institute of Epidemiology and Public Health, Inserm, Paris, France; Université Pierre et Marie Curie, Faculté de Médecine, Paris, France

Abstract

New advances in science and medicine help us gain ground against certain infectious diseases, yet new infections continue to emerge that spread rapidly into the population and may reach pandemic proportions. We face a perpetual challenge against the capacity of new pathogens to lead to emerging epidemics. And our global, mobile and interconnected world contributes with dangerous mechanisms that may potentially greatly magnify the global burden of diseases. Understanding how epidemics spread in a host population represents a crucial step for prevention and control, with broad implications on the system's functioning, population's health, and associated costs.

Mathematical and computational models that integrate epidemiological information with data on the disease-transmission paths (from transmission contacts to movement-mediated transmission) can be built to provide crucial insights into the complexities of the spreading dynamics as well as predictions for its future evolution. Focusing on a range of different infections I will discuss how models can help us facing epidemics in the phases of preparedness, outbreak emergence, and epidemic invasion, and how they can be used to advise public health policies.

PLENARY SESSION C
TUESDAY 29 NOVEMBER
9:00-10:30

Plenary Session C: Migrant Health

Chairs: Aileen Kitching, HSE, Ireland, President of EAN & Paolo D'Ancona, ISS, Italy, Chair of the EPIET Training Site Forum (ETSF)

Forced migration and meeting health needs: the needs for better data

Presented by

Dr Bayard Roberts

Affiliation

Director of ECOHOST – The Centre for Health and Social Change, London School of Hygiene and Tropical Medicine, United Kingdom

Abstract

There are unprecedented numbers of refugees and other forcibly displaced persons globally, and migration has become one of the most pressing public health and political issues of our time – nowhere more so than in Europe. Refugee migration in Europe has raised important concerns about the risk of communicable diseases, but non-communicable diseases and poor mental health arguably present greater health needs among refugees in Europe. However, our ability to detect and monitor such needs and evaluate responses to them appears limited. This presentation will explore key data needs in developing appropriate and effective health services, systems and policies in addressing mental health and non-communicable diseases among refugees in Europe. It will then provide some suggestions for methods to improve our understanding of refugee health needs and responses to them. It will draw on work and evidence in Europe but also with forcibly displaced populations more globally.

Key words: Refugees, migration, chronic disease, non-communicable disease, mental health, Europe

Experiences and challenges in monitoring migrant health in migration centres and at community level

Presented by

Dr. Silvia Declich

Affiliation

National Institute of Health (Istituto Superiore di Sanità), Centre for Epidemiology, Surveillance and Health Promotion, Rome, Italy

Abstract

The increasing number of people entering the EU as asylum seekers and irregular migrants has challenged public health authorities to provide relevant, proportionate and appropriately targeted action.

While media and scientific attention has been focussed on the recurring humanitarian crises triggered in several EU countries by large unexpected migration inflows, it is also true that migration is a long-term phenomenon, recognised as one of the key components of population change in Europe. Therefore Member States need to monitor the health not only of newly arrived migrants but also of longer term resident migrant populations in their countries. To do this, appropriate and diverse approaches and tools need to be adopted.

There are several issues that hamper the feasibility of monitoring migrant health in an affective way. These occur when targeting both newly arrived and longer term resident migrants and include data incompleteness for migrant related variables and lack/diversity of data availability between countries, under/over/misreporting of cases of disease and misalignment with appropriate denominators, excessive aggregations that do not account for the diversity of migrant populations.

The talk will discuss several options developed towards monitoring Migrant health in migration centres and at community level both internationally and at Member State level.

PLENARY SESSION D
WEDNESDAY 30 NOVEMBER
9:00-10:30

Plenary Session D: Vaccines

Chairs: Mike Catchpole & Lucia Pastore Celentano, ECDC

Public private partnerships for evaluation research: pure pragmatism and impure science?

Presented by

Dr. Alain Moren

Affiliation

Director of the Epidemiology Department, EpiConcept, France

Abstract

The ECDC has been coordinating vaccine preventable disease (VPD) programmes aiming at measuring the coverage, the effectiveness, and the impact of vaccination strategies in EU for more than 10 years. Large EU/EEA networks have developed (I MOVE & +, SpIDnet, Pertinent, VENICE, etc.). They are funded with public resources provided by member states (MS), EC, and EU agencies. This mechanism allows vaccine researchers to address public health research questions that go beyond regulatory requirements.

This development is now facing two important challenges. 1) The European Medicine Agency (EMA) requires vaccine producers to provide post-authorisation vaccine effectiveness, impact, and safety estimates. This now includes providing annual brand specific effectiveness measurement for influenza vaccines, an objective not currently achievable due to sample size and associated cost. 2) The European financial and economical context has led the EC, its agencies, and national public health institutes (NPHI) to dramatically reduce funding devoted to post-authorisation vaccine research. EC and some NPHIs are now turning to vaccine producers to seek funding for surveillance and evaluation research. The EC, through the Innovative Medicine Initiative (IMI) programme, promotes public private partnerships (PPP) to help vaccine producers fulfil their obligations in collaboration with NPHIs.

The current context and funding mechanisms proposed raise questions that will be discussed. Is public funding still available and if so what would be the best EC agency to channel it? How can we preserve scientific independence and public confidence in vaccines in the context of joint public and private funding? What are the consequences of PPP on public health surveillance and research, and on the future of public services in Europe?

The Needs and Roles of the Public and Private Sector in Delivering Effective Immunisation Programmes: the Yin and Yang of Vaccination

Presented by

Dr. Marco Cavaleri

Affiliation

European Medicines Agency (EMA)

Abstract

Vaccination is one of the most effective and widely used public health interventions, whose benefits for individuals and the community have been abundantly demonstrated. As with any other pharmaceutical product, however, no vaccine is without risks. Robust systems and procedures must be in place to continuously monitor quality, safety and efficacy. Risk Management Plans (RMPs) are developed by manufacturers and agreed with EMA in order to allow a proper monitoring of the benefit/risk balance for each vaccine once authorised.

As emphasised in the recently released EMA guideline on influenza vaccines, effectiveness and safety data are expected to be collected for each approved influenza vaccine in order to allow a continuous monitoring of the benefit-risk over time. The need of collaboration between the private and public health sector in order to achieve such goal is acknowledged and warrants further reflection on how best to build an efficient and effective infrastructure for the benefit of public health in the EU.

Keywords: vaccines, Benefit risk, effectiveness, RMP

PLENARY SESSION E
WEDNESDAY 30 NOVEMBER
17:00-18:30

Plenary Session E: Zika

Chairs: Denis Coulombier, ECDC and Dr Larry Madoff, Director of ProMED

Challenges to achieve optimal immunisation programmes

Presented by

Andrea Rappagliosi

Affiliation

President, Vaccines Europe, Brussels, Belgium; Vice President, Market Access, Health Policy and Medical Affairs at Sanofi Pasteur MSD, Lyon, France

Abstract

Over the past years, Europe has been experiencing a worrying surge in cases of vaccine-preventable diseases. Such a situation puts avertable strains on healthcare systems, as the necessary vaccines and infrastructures to deliver the programmes are often in place but remain suboptimal in their use. Vaccination also continues to still be primarily regarded as a childhood intervention. The value of immunisation beyond childhood is currently not being sufficiently considered, leaving the healthcare system with a missed opportunity to comprehensively promote active and healthy aging policies in response to the demographic changes in Europe.

The recently adopted Council Conclusions on vaccinations as an effective tool in public health well highlight the common challenges that are being faced by all of the EU Member States at present. Such challenges are affecting the successful implementation of existing immunisation programmes in Europe today. More so in a climate of increasing uncertainties posed by risks of supply shortages that could be further exacerbated with the recent wave of migration towards EU countries and the growth of "vaccine hesitancy" in Europe.

Vaccines Europe considers that a continuous dialogue between manufacturers and public health authorities will allow both sides to better anticipate the evolution of vaccine recommendations and more accurately forecast vaccine demand. Vaccine effectiveness measurement will no longer only be a tool for programme evaluation by public health institutions, but also an important tool for regulators to assess the balance of benefit and risk of vaccines available on the market. In view of responding to this regulatory request, capacity to monitor the effectiveness of vaccines will require the expertise and experience from both the manufacturers and the public sector.

Keywords: Vaccination, immunisation, healthy aging, immunisation programs

What we know about Zika epidemiology, dynamics and future risks

Presented by

Dr Joacim Rocklöv

Affiliations:

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Abstract:

The Zika epidemic and public health emergency situation (PHEIC) has been followed by a large number of epidemiological studies based on experimental and observational data. Part of these studies has tried to characterize the ZIKV transmission dynamic, risk areas, risk period, determinants and drivers, and make use of this information for risk assessments and policy and response strategies. As a part of the PHEIC publishers changed their routines regarding peer-review latencies and pre-publishing. In the first phase of the emergency, early risk assessments, local epidemiological observations, and studies focusing on estimating specific parameters of importance for disease dynamics were dominating. Later on, closing in to the peak of published studies in June 2016, studies provided estimations of the basic reproduction number, and further assessments of the spread of Zika outside Latin America became available. More recently, in a later phase between a first and a second wave of Zika in Latin America, studies have assessed the contribution of sexual transmission to the dynamics and spread of the virus. There is currently a lack of studies assessing the future of Zika, although surveillance registers point to a second wave despite herd protection, and active transmission cluster outside Latin America in regions where Aedes vectors are known to be abundant.

Keywords: Epidemiology, Zika, Review, Mathematics, Statistics

Zika risk assessment for the WHO European Region – What have we learned for Europe at the end of the transmission season?

Presented by

Dr. Colleen Acosta

Affiliation

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Abstract

In March-April 2016, the risk for a Zika virus outbreak in the WHO European Region was assessed. Outbreak risk was considered to be a function of the likelihood of local Zika virus transmission and the capacity of countries to contain transmission at an early stage based on a number of factors. Many countries extending from the Mediterranean Basin were found to be at moderate risk for local Zika virus transmission. In addition, three geographical areas (Madeira Island and the Black Sea coastal areas of Georgia and the Russian Federation) with established populations of Ae. aegypti, were classified as having high likelihood for local transmission. Anecdotal evidence, however, suggests that the distribution of Ae. aegypti and Ae. albopictus may be wider than originally known. Overall, there was good capacity in the Region to contain Zika virus transmission at an early stage. At the end of the 2016 transmission season, there has been no mosquito-borne Zika virus transmission in the region, although imported cases continue to be reported. Detection and notification of imported cases to Europe, particularly from areas with previously unknown transmission, highlight the importance of reporting under the International Health Regulations (2005) to inform the global epidemiological picture, and to implement necessary response measures. In addition, since the initial assessment, many countries at high or moderate likelihood of local Zika virus transmission have strengthened their vector control activities, clinical surveillance and laboratory capacities to test for Zika virus and offered advice to populations at risk. Follow-up analyses given changes in country capacities and geographical distribution of the virus and competent vectors will further inform the future risk for a Zika virus outbreak in the region.

Keywords: Zika, risk assessment, European Region

Sexual transmission of Zika virus

Presented by

Dr Anna Thorson

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Department of Reproductive Health and Research, The Human Reproduction Programme (HRP), World Health Organization, Geneva, Switzerland

Abstract:

Zika virus (ZIKV) is a mosquito-borne arbovirus from the genus Flavivirus (family Flaviviridae) whose first isolation occurred in 1947 from a rhesus monkey in the Zika forest of Uganda. The virus is almost exclusively transmitted by the Aedes aegypti mosquito but has been isolated from several other species of the genus Aedes.

Up to 10/11/2016 ZIKV infection in humans had been documented in 75 countries and territories. During the ongoing epidemic, mounting evidence has shown that sexual transmission of Zika virus is more common than previously assumed. Sexual transmission was first suggested in 2008 and has since then been identified as a source of infection in 12 countries without an ongoing vector borne epidemic. Studies investigating post-acute infection persistence of ZIKV in body fluids of relevance to sexual transmission, show that up to date the longest persistence of ZIKV has been shown in semen, as detected by RT-PCR 188 days after onset of acute infection.

In response to the emerging epidemic context the WHO reviewed the evidence-base and published recommendations and updates on how to avoid sexual transmission of ZIKV. This talk will describe the latest evidence-base on persistence and sexual transmission of Zika, and the methodology and rationale adopted by WHO in order to make recommendations on the prevention of sexual transmission of Zika virus.

Keywords: Zika, infection, sexual, transmission

Parallel Session Abstracts

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60 Parallel Session 19: Food- and waterborne diseases and zoonoses (4)
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PARALLEL SESSION PROGRAMME
MONDAY, 28 NOVEMBER
11:00-12:40

Parallel Session 1: Antimicrobial resistance and healthcare-associated infections (1)

Moderator: Aftab Jasir, ESCAIDE Scientific Committee & ECDC, Head Scientific Coordinator EUPHEM

O1.1 Spread of mupirocin-resistant methicillin-resistant Staphylococcus aureus (MR-MRSA) and high patient dependency: lessons to be learned

Patricia Garvey (1,5), M Skally (2), H Humphreys (2,4), K Burns (1,2), K O'Connell (1,2), F Fitzpatrick (2,4), M Fitzpatrick (2), S Donlon (3), F Duffy (3), T P Devassy (3), C Finn (3), H Good (3), B O'Connell (6), G Brennan (6) and E Smyth (2,4)

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Background
In June 2014, an outbreak of mupirocin-resistant (MR)-MRSA spa type t127 (and closely-related t922) was identified in a large tertiary hospital in Ireland. We described the extent of the outbreak and undertook a matched case-control study to investigate risk factors for infection/colonisation.

Methods
Cases were diagnosed by the hospital laboratory following routine and active screening. Controls were randomly-selected from in-patients on affected wards with negative MRSA screening swab results within 10 days of the matched case. We collected information from hospital databases and patient charts. We calculated adjusted matched odds ratios (amOR) using conditional logistic regression.

Results
Between November 2013 and June 2015, there were 41 cases; the median age was 73 (range 47-96) years; 78% were male. Case numbers peaked in July 2014. Overall, 27 (67%) of cases were linked to Ward W either at detection or historically, with cases on other wards more common later in the outbreak. The weekly number of patient bed days on Ward W exceeded maximum capacity (n=245) for four consecutive weeks (weeks 17-21 2014), peaking at 252 bed days in week 20 2014. Male sex (amOR=21; 95%CI 0.99-454), urinary catheterisation (amOR=12; 95%CI 0.98-154), occupational therapy (amOR=9.9; 95%CI 1.6-61), vascular consultation (amOR=5.1; 95%CI 0.89-29), and length of stay (amOR=1.1; 95%CI 1.0-1.1 per in-patient day) were associated with MR-MRSA.

Conclusion
Underlying high-dependency, including prolonged hospitalisation, urinary catheterisation, vascular surgery and occupational therapy consultation, were associated with MR-MRSA. High bed-occupancy rates may also have contributed to transmission on Ward W. Prospectively recording the dependency of patients to optimise infection prevention and control measures, and the avoidance of overcrowding, are recommended to prevent/control future outbreaks.

Keywords: Methicillin-Resistant Staphylococcus aureus, Case-Control Studies, Outbreaks, Hospitals

ABSTRACT ID: 55

PRESENTED BY: Patricia Garvey (patricia.garvey@hse.ie)

O1.2 Using Whole Genome Sequencing as a tool for MRSA national surveillance

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Background
The national surveillance system of methicillin-resistant Staphylococcus aureus (MRSA) in England is restricted to cases of bacteraemia. The referral of isolates for typing and characterisation is not mandatory but hospitals send samples to Public Health England (PHE) for surveillance and to assist with outbreak investigations. Traditional techniques like spa-typing and pulsed-field gel-electrophoresis (PFGE) have limited discriminatory power to distinguish between strains of the same lineage. We tested the utility and feasibility of whole genome sequencing (WGS) as tool for routine surveillance of EMRSA-15 (CC22-SCCmecIV), the dominant healthcare-associated clone in the UK.

Methods
We sequenced whole genomes of 505 EMRSA-15 isolates received from 61 hospitals across England between 2010 and 2014. An alignment based on 15,958 Single Nucleotide Polymorphisms (SNPs) was used for maximum likelihood (ML) phylogenetic analysis to confirm or refute suspected clusters.

Results
Of all isolates, 353 were submitted as epidemiologically linked, i.e. containing more than one case. Thirteen clusters were identified comprising ≥5 cases with at least one isolate that was phylogenetically distinct in the ML tree. Conversely, we identified instances of probable transmission events that had been missed. We confirmed the known regional clustering for EMRSA-15, and were able to identify intra-regional transmission events. Furthermore, preliminary analyses show closely related isolates re-occurring in the same hospitals in different years, suggesting persistence of particular clades.

Conclusion
Results generated in this study add to the available genomic framework and thereby serve as long term resource for contextualizing novel sequences. SNP based analysis will prospectively allow for rapid distinction between linked and sporadic cases that are difficult to discern through traditional methods and facilitate rapid public health action where appropriate.

Keywords: MRSA, EMRSA-15, Whole genome sequencing, phylogeography, Single nucleotide polymorphism

ABSTRACT ID: 213

PRESENTED BY: Sabrina Weiss (sabrinanweiss@gmail.com)

O1.3 The emergence and spread of moxifloxacin-resistant Clostridium difficile ribotype 231 in Sweden between 2006 and 2015

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Background

A newly emerging moxifloxacin-resistant C. difficile ribotype 231 (RT231) was identified in the Stockholm area in 2008 as a result of national surveillance. By the end of 2015, C. difficile RT231 had spread to 13 out of 21 Swedish counties. We have investigated the epidemiology of C. difficile RT231 in Sweden between 2006 and 2015 in order to determine transmission of this type within and between counties.

Methods

From a total of 189 C. difficile RT231 isolates identified in Sweden between 2006 and 2015, 51 geographically and temporally representative isolates were selected for whole genome sequencing. The genomic relatedness of isolates was assessed by whole-genome SNP analysis: up to three SNPs per genome was expected to be seen between related isolates collected up to one year apart.

Results

We demonstrated the circulation of three phylogenetically distinct lineages of moxifloxacin-resistant C. difficile RT231 in Sweden during the 10-year study period; one lineage circulating in the counties of Stockholm and Uppsala 2007-2012, one in the Stockholm-Gotland Health Care region 2008-2009, and one in the Uppsala-Örebro Health Care region 2009-2015. An identical strain was identified in four different hospitals in Stockholm during 2008, whereas another identical strain was demonstrated in the Uppsala, Södermanland, Västmanland and Örebro counties between 2009 and 2015.

Conclusion

The continued transmission of moxifloxacin-resistant C. difficile RT231 within and between different close-proximity counties was likely due to patient transfers between hospitals. The spread in the Stockholm Health Care region stopped in 2012, and since then only the Uppsala-Örebro Health Care region has been perpetuating the spread. Our results support the need for careful monitoring and isolation routines of hospitalised individuals infected with moxifloxacin-resistant C. difficile.

Keywords: Clostridium difficile, Whole genome sequencing, outbreak, moxifloxacin-resistant

ABSTRACT ID: 253

PRESENTED BY: Heli Harvala (heli.simmonds@hotmail.com)

O1.4 Reconstructing transmission of extended-spectrum β-lactamase-producing Klebsiella pneumoniae in a German neurorehabilitation centre using epidemiology and next generation sequencing, 2015/2016

Gerit Korr (1,2), T. Eckmanns (2), D. Sissolak (3), M. Friedrichs (4), E. Zill (5), M. Tung (4), L. Becker (6), Y. Pfeifer (6), S. Fuchs (6), M. Kaase (7), C. Dohle (4), G. Werner (6), S. Haller (2)

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7. National Reference Laboratory for multidrug-resistant gram-negative bacteria, Department for Medical Microbiology, Ruhr-University Bochum, Germany

Background

Neurorehabilitation inpatients with multiple antibiotic pretreatments are particularly susceptible to acquire multidrug-resistant gram-negative bacilli (MDRGN). Yet, evidence on epidemiology and prevention of MDRGN in neurorehabilitation settings is scarce. We investigated an extended-spectrum β-lactamase -K. pneumoniae (ESBL-KP) outbreak in a neurorehabilitation centre where ESBL-KP had been detected in 36 patients from April to September 2015 and transmission continued despite intensified hygiene measures and intermittently halted admissions.

Methods

We defined patients with evidence of ESBL-KP and a stay since 01/04/15 as confirmed cases when typing confirmed an outbreak strain and as probable cases when no typing results were available. Information on gender, age and ward allocation of cases was extracted from patient-charts. We performed case finding using repeated microbiological screenings. Additionally, approximately 200 environmental samples were taken. Phenotypic resistance testing, pulsed-field gel electrophoresis (PFGE) and next generation sequencing (NGS) were performed on all available isolates.

Results

We identified three outbreaks of ESBL-KP (ST-15, ST-414, ST-405) with a total of 45 cases (39 confirmed, 6 probable) until 29/02/16. Median age of cases was 69 (31-90) years, 34/45 (75%) were males and 21/45 (46%) developed an invasive infection. Since April 2015, at least one case of each outbreak strain was present on overall five affected wards. No ESBL-KP were detected in the environment. NGS confirmed PFGE results and identified gene loci responsible for carbapenem-resistance of an outbreak strain in one and colistin-resistance in another case.

Conclusion

Epidemiology and microbiological typing suggest person-to-person transmission. When linked to epidemiological findings NGS is helpful to understand transmission chains. The extent of the transmission and the development of additional antibiotic resistances illustrate the importance to look for MDRGN in neurorehabilitation settings and implement suitable prevention measures.

Keywords: Nosocomial infections, Klebsiella pneumoniae, Neurological Rehabilitation, Multiple Antibacterial Drug Resistance, High-Throughput Nucleotide Sequencing

ABSTRACT ID: 74

PRESENTED BY: Gerit Solveig Korr (KorrG@rki.de)

Parallel Session 2: Travel and migrant health (1)

Moderator: Chris Williams, EPIET Coordinator/ EPIET Alumni Network/ Public Health Wales

O2.1 Assessing the status of the International Health Regulations (2005) core capacities: Lessons learned from using mixed methodologies in the occupied Palestinian territory and Malawi in 2015

Emily MacDonald (1, 2, 3, #), Bernardo Guzman Herrador (1, #), Eirik Vikum (2), Karin Nygård (1), Didrik Frimann Vestrheim (4), Line Vold (1), Ambonishe Mwalwimba (3), Thokozani Kalua (3), Austin Mnthambala (3), Yousef Muhaisen (5), Abdelnaser Soboh (6), Wesam Sbehat (7), Frode Forland (2), Bjørn Iversen (2)

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6. World Health Organization, occupied Palestinian territory, Gaza City
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Background

The Norwegian Institute of Public Health (NIPH) supports the implementation and strengthening of the International Health Regulations (IHR) 2005 core capacities in countries with long-term partnerships. In 2015, NIPH supported cross-sectional joint assessments in Malawi and the occupied Palestinian territory (oPt) to determine the status of IHR implementation in order to develop prioritized action plans. To inform best practices, we present the strengths and weaknesses of the assessment methodologies.

Methods

In both countries, interviews and site visits were conducted using adapted questionnaires from the WHO IHR assessment protocol with a purposive sample of central, district, health facility and laboratory informants. Quantitative and qualitative data were collected from 19 districts in Malawi. In oPt qualitative data from six districts were collected. To assess alert and response to a fictional emerging zoonotic event, one national tabletop exercise with district representation was held in Malawi, while two national and six district exercises were held in oPt. Descriptive and SWOT analyses were completed in both countries.

Results

Interviews were vital for documenting experiences at different levels and identifying discrepancies, but were time-consuming and may not reflect functionality of systems. The exercises provided a better reflection of operational status of the IHR core capacities and the level of cooperation between multi-sectoral actors across central, district and facility levels.

Conclusion

A mixed-method approach using questionnaires to document the strengths and weaknesses in combination with exercises to test functionality was successful in both countries. Linking qualitative assessment results to quantitative indicators would allow for developing clear action plans and monitoring progress in implementing the core capacities. Long-term partnering between countries may have positive impact on strengthening IHR core capacities through sharing experiences and best practices.

Keywords: Research design, Global health, Public health, Africa

ABSTRACT ID: 183

PRESENTED BY: Emily MacDonald (emacdonald.mw@gmail.com)

O2.2 Syndromic surveillance for early detection of infectious disease outbreaks in emergency shelters for refugees in Berlin: pilot phase

Navina Sarma, H. Wilking, A. Jansen, K. Stark, S. Vygen-Bonnet Department for Infectious Disease Epidemiology, Robert Koch-Institute, Berlin, Germany

Background

In 2015, 79,034 refugees arrived in Berlin. Large emergency shelters were opened due to a lack of regular housing capacities, increasing the risk of infectious disease outbreaks. We describe the pilot phase of a syndromic surveillance system aiming to timely detect and control potential outbreaks and generate data on refugees' health situation.

Methods

In January 2016, we identified important stakeholders and piloted a preliminary paper data sheet including infectious and non-infectious syndromes in a large camp (population size ~2500). We tested transmission modes (mobile phone, e-mail, postal mail) and descriptively analysed data.

In May 2016, we will expand the pilot to two other camps (population size ~1000 each) with daily transmission of data. We will analyse data and test applicability of signal algorithm and outbreak verification.

Results

The pilot camp sent completed data sheets for each day in irregular frequency by postal mail. Updated figures on population size were not available. From week 3 to 15 2016, 2,026 syndromes were reported; of these 1,228 (61%) were infectious syndromes: 758 (37%) acute respiratory infections, 167 (8%) dermatological diseases and 111 (5%) gastrointestinal infections. Based on these experiences, the final data sheet was developed. It includes 15 infectious disease categories with standardised case definitions. We identified the need of regular meetings with the health staff. Health authorities supported the project.

Conclusion

Acceptance of syndromic surveillance is high and implementation in camps with health facilities based on a paper tool is feasible. However, adaptation of the system to varying conditions is essential. Timeliness of data transmission needs improvement. Infectious diseases accounted for the largest part of syndromes. Interpretability of disease pattern is limited by absence of denominators.

Keywords: Infectious Disease Outbreaks, Refugee Camps, Surveillance, Crowding

ABSTRACT ID: 196

PRESENTED BY: Navina Sarma (sarman@rki.de)

O2.3 A review on the effects of Mass Meningococcal Meningitis vaccinationin Indonesian Hajj Pilgrims, 1987 to 2015

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2. Hajj Health Center, Ministry of Health, Republic of Indonesia
3. The University of Hong Kong, Hong Kong SAR.

Background

The Hajj in Mecca, Kingdom of Saudi Arabia (KSA), is a religious mass gathering which takes place annually. As a mass gathering of more than 2 million pilgrims a year, it provides an opportunity for the efficient spread of N. meningitidis. After the 1987 outbreak, the KSA health authorities made it mandatory forHajjpilgrims to be vaccinated against N. meningitides. From an initial compulsory vaccination with bivalent A and C vaccine for all pilgrims, the quadrivalent meningococcal vaccine is now usedwhich covers four serogroups with the exception of serogroup B. The review shows the impact of meningococcal vaccination on the Indonesian Hajj pilgrims to date.

Methods

Data was extracted from the Hajj mortality surveillance, medical and laboratory reports from Hajj pilgrimages in 1987 to 2015. An attack rate and case fatality rates were generated from the merged data. The attack rate and case fatality rate was calculated per year.

Results

In five years (1989-5, and 2004-05), there were no reported cases of meningococcal meningitis. Without the inclusion of 1987, the highest attack rates were 8.02 and 9.33 in 2001 respectively during the W135 serotype outbreak in the Hajj but the highest case fatality rate was 76.92 in 1998. In 1998 there was a cluster of serotype B reported during the hajj. At that time, there was no known vaccine for serotype B. After 2006 until 2015, there were no reported cases of meningococcal meningitis from the Hajj.

Conclusion

The effectiveness of the vaccine can be seen in the reduction of cases when compared to 1987.The results strongly suggest that the mass vaccination requirement had protected Indonesian Hajj pilgrims.

Keywords: Meningococcal Meningitis, Vaccination, Review, Effects

ABSTRACT ID: 345

PRESENTED BY: Masdalina Pane (masdalina.pane@gmail.com)

O2.4 High proportion of asylum seekers consent to vaccinations after counselling, April-August 2014, Rhineland-Palatinate, Germany

Maja George (1), A. Mund (2), M. Vogt (3), F. Burckhardt (1), P. Zanger (1,4)

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2. Asylum seeker reception centre Trier, MEDEUS, Trier, Germany
3. Federal State Agency for Consumer & Health Protection Rhineland-Palatinate, Germany
4. Institute for Public Health, University Heidelberg, Heidelberg, Germany

Background

In Germany informed consent prior vaccination is mandatory. Since April 2014 the asylum seeker (AS) reception centre in Trier is offering vaccinations (e.g. MMR, Tdap-IPV). AS are invited for vaccine counselling (VC) and to sign consent on a different day prior to vaccination. We analysed vaccination uptake and risk factors for non-vaccination among AS invited for vaccinations from April – August 2014.

Methods

Following variables were transcribed from vaccination lists: id number, country of origin, age, gender, vaccinated, missed VC, missed vaccination, and actively refused vaccination. The last three variables were merged as „not vaccinated“ (NV). We analysed AS aged 14+ years (y) only, since 0-13y old were vaccinated elsewhere. Country of origin and age category (14-19, 20-29 30-39 and 40+y) were used as exposure variables. Univariable poisson regression was performed in Stata 13.1.

Results

1784 14+y AS from 33 countries were invited. 494 (28%) were from Syria, 304 (17%) from Eritrea and 122 (7%) from Serbia. The median age was 27y. Of the 1112 AS, who followed the invitation, 95% (1061) gave consent, 84% (931) were vaccinated, 5% (51) refused vaccinations and 12% (130) did not attend VC. AS from Russia (IRR for NV=2.3; p=0.004) and Georgia (IRR for NV=1.8; p=0.01) were less likely to be vaccinated. Age was not associated with NV-status.

Conclusion

Vaccination acceptance is very high among counselled AS. Country of origin is a risk factor for NV. A mixed-methods approach is needed to further elucidate potential obstacles and their association with NV-status.

Keywords: asylum seekers, vaccination, reception centre, Germany, vaccination uptake

ABSTRACT ID: 371

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

Parallel Session 3: HIV, sexually transmitted infections and viral hepatitis (1)

Moderator: Osamah Hamouda, ESCAIDE Scientific Committee, Germany

O3.1 Changing molecular epidemiology of Neisseria gonorrhoeae in Europe: the first international survey combining Neisseria gonorrhoeae Multi Antigen Sequence Typing and Whole Genome Sequencing

Simon R. Harris (1), MJ. Cole (2), G. Spiteri (3), S. Jacobsson (4), D. Golparian (4), F. Tripodo (2), Beatrice Bercout (5), Maria José Borrego (6), Brendan Crowley (7), Paola Stefanelli (8), Julio Vazquez (9), A. Amato (3), C. Glasner (10), DM. Aanensen(10), M. Unemo (4), the Euro-GASP network

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6. National Institute of Health, Lisbon, Portugal
7. St James's Hospital, Dublin, Ireland
8. Istituto Superiore di Sanitá, Rome, Italy
9. Institute of Health Carlos III, Madrid, Spain
10. Centre for Genomic Pathogen Surveillance, Wellcome Genome Campus, Cambridgeshire, United Kingdom

Background

Molecular typing of Neisseria gonorrhoeae isolates collected in 2009/2010 through the European Gonococcal Antimicrobial Surveillance Programme (Euro-GASP) identified genogroup 1407, associated with cefixime resistance, as the most prevalent in Europe. The objectives of this typing survey were to describe the molecular epidemiology of isolates collected in 2013, compare with 2009/2010 and assess the public health value of whole genome sequencing (WGS).

Methods

Susceptibility of isolates collected through Euro-GASP in 2013 to ceftriaxone, cefixime, azithromycin and ciprofloxacin was determined through Etest/agar dilution and interpreted using European Committee on Antimicrobial Susceptibility Testing breakpoints. Isolates were typed using Neisseria gonorrhoeae Multi-Antigen Sequence Typing (NG-MAST) and sequenced using Illumina HiSeq. Genogroup distribution, associations with sexual orientation and resistance patterns were analysed using logistic regression. Results were compared to the 2009-2010 study. Additional value of WGS was assessed by comparing resolution and additional information provided to NG-MAST.

Results

Among the 1189 isolates from 21 EU/EEA countries typed by NG-MAST, G1407 was most prevalent but prevalence decreased from 23.3% in 2009/2010 to 14.8% in 2013 (p<0.01). G1407 was associated with resistance to cefixime (p<0.01), ciprofloxacin (p<0.01; Fisher's exact test) and azithromycin (p<0.01) as in 2009/2010. G1407 isolates were associated with heterosexuals (OR 5.97 p<0.01) in contrast to men who have sex with men in 2009/2010. WGS provided additional resolution, identified isolates not sharing the genetic backbone of other members of genogroups, identified samples with multiple sequences and allowed evaluation of multiple markers (e.g. resistance).

Conclusion

The 2013 survey provided an updated picture of the genetic heterogeneity of Neisseria gonorrhoeae in the

EU/EEA. Decreasing prevalence of G1407 correspondeds with increasing susceptibility to cefixime reported by Euro-GASP. WGS provides additional public health benefit compared to NG-MAST.

Keywords: Neisseria gonorrhoeae, Drug Resistance, Microbial, DNA Sequencing, Anti-Infective Agents, Sexually Transmitted Diseases

ABSTRACT ID: 342

PRESENTED BY: Simon R Harris (sh16@sanger.ac.uk)

O3.2 People who inject drugs are often susceptible to hepatitis B despite recommended vaccination - results from the first large integrated sero-behavioural study in eight German cities, 2011-2015

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Background

The German Standing Committee on Vaccination recommends vaccinating people who inject drugs (PWID) against hepatitis B (HBV) among other groups. To determine HBV prevalence and investigate factors associated with HBV-vaccination status (HBV-VS) among PWID we analysed data from a multicentre sero-behavioural survey.

Methods

Current injectors aged ≥16 years consuming in one of eight German study cities were recruited by respondent-driven sampling in low-threshold drug services from 2011-2014. Capillary blood samples (dried blood spots) were tested for HBV-DNA, HBsAg, anti-HBc and anti-HBs. Participants exclusively positive for anti-HBs were defined as HBV-vaccinated, those positive for anti-HBc and HBsAg/HBV-DNA/anti-HBs as (chronically or previously) HBV-infected. Face-to-face-interviews included questions on HBV infection, vaccinations and socio-demographic factors. We used univariable and multivariable logistic regression to identify factors associated with not being HBV-vaccinated. HBV-infected participants were excluded from this analysis.

Results

Among 2,077 participants, 32% were HBV-vaccinated (city range: 15-52%) and 25% (5-33%) were chronically/previously HBV infected. In 43% (16-69%) no HBV markers were detected. Knowledge of HBV-VS was incorrect in 47% (41-57%) and 10% (5-15%) were unaware of their HBV infection. Non-vaccinated PWID were more likely to belong to age-group 25-39 years (adjusted Odds Ratio (aOR): 1.6, 95%-confidence interval: 1.0-2.6) (reference: a higher education level (aOR: 2.8, 95%-CI: 1.0-2.6) and consume drugs in Berlin (aOR: 16.1, 95%-CI: 10.0-26.0) or Leipzig (aOR: 13.3, 95%-CI: 7.1-24.8) (reference: Hanover).

Conclusion

Many PWID are not vaccinated against HBV and are at risk of HBV infection. Poor knowledge of own HBV infection and vaccination status pose the risk of further HBV transmission. The local setting seems to have the greatest influence on the HBV-VS. Our results emphasize the need for targeted information and vaccination campaigns.

Keywords: Hepatitis B; Hepatitis B Vaccines; Substance Abuse, Intravenous; Seroepidemiological Study

ABSTRACT ID: 148

PRESENTED BY: Joana Haussig (haussigj@rki.de)

O3.3 HIV testing in Europe: Evaluating impact, added value, relevance and usability of ECDC's 2010 HIV testing guidance

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Background

To increase coverage of HIV testing in the EU/EEA, the European Centre for Disease Prevention and Control (ECDC) published a guidance on HIV testing in 2010 targeting primarily EU/EEA Member States (MS) policy advisors and programme managers. The impact, added value, relevance and usability of the guidance were evaluated, and needs for an update assessed.

Methods

The evaluation conducted from October 2015 to January 2016 gathered data from: two surveys - one for a primary target group (PTG) (ECDC official contact points in the 31 EU/EEA MS) and one for a broader target group (BTG) (e.g. clinicians, civil society, international agencies); two moderated focus group discussions (N=17); webpage access data and literature citation review; and finally an expert consultation (N=16) on the evaluation.

Results

28 PTG (from 23/31 EU/EEA countries) and 51 BTG (from 18 EU/EEA countries and one international organisation) responded to the surveys. Overall, the guidance reached a broader audience than intended. 10/23 (48%) MS reported having used the guidance in the development, monitoring and/or evaluation of their national HIV testing policy/guidelines/programme/strategy. 29/51 (56%) BTG respondents reported having used the guidance for their work. The majority of respondents considered it of added value having an EU/EEA-level guidance. 15/25 (60%) PTG and 26/50 (52%) BTG respondents considered that the guidance fostered change in individual countries by providing an EU/EEA standard.

Conclusion

Stakeholders used the guidance and valued having an EU/EEA-level guidance. Limitations may be related to sub-optimal representativeness of the sample, overrepresentation of respondents familiar with ECDC guidance and validity of data collection sources. For the future, a new guidance should be updated regularly; include more guidance on monitoring and evaluation; and be supplemented with practical tools.

Keywords: HIV, diagnosis, evaluation, Europe

ABSTRACT ID: 198

PRESENTED BY: Ida Sperle (ida.sperle@regionh.dk)

O3.4 Investigating the association between long-acting reversible contraceptives (LARCs) and chlamydia diagnosis: addressing the gap in the literature

Hannah Evans (1,2,3,8), L.Emmett (3), T. Inns (4), G.Crowe (5), M.Ramogi (6), T.Balachandran (7), A.G. Shankar (1,2,8)

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Background

LARCs are not protective against sexually transmitted infections (STIs) but there is limited research on the association with STI risk. We investigated whether LARC users have a higher rate of chlamydia infection (the most commonly diagnosed STI in England) than non-LARC users in three integrated sexual-health clinics providing contraception and STI testing, in the East of England, to help inform safe sex education.

Methods

Our study required a sample size of 365 women aged ›15 years who attended a clinic twice between 01/01/2010-31/12/2013; were taking contraception (for the first time/changed method), and who had a negative chlamydia test at first attendance. Outcome measure was a first positive chlamydia trachomatis NAAT during the study. We collected exposure information on demographics, LARC use, any condom use and number of sexual partners in the 3-months preceding last attendance, and compared outcome by exposures, calculating crude and stratified ORs with exact p-values and 95% CIs.

Results

We recruited 192 women in the study: 86 (48%) were LARC users and were significantly older (median: 23.5 years) than non-LARC users (median: 22 years, p-value=0.02). LARC users had a lower crude chlamydia incidence rate (OR 0.85, p-value=0.77, 95% CI 0.31–2.36), but were significantly less likely to use condoms than non-LARC users (p-value=0.006), and less likely to report multiple sexual partners (p-value=0.431).

Conclusion

Our study shows that LARC users change partners less frequently and may have a lower risk of acquiring chlamydia despite lower condom usage. A larger, better-powered study, comparing sexual health outcomes with risk factors will strengthen the evidence base on LARC use and STI acquisition. We recommend replicating this study in a larger number of integrated sexual-health clinics.

Keywords: Chlamydia, Contraceptive Agents, Female, Sexually Transmitted Diseases, Contraceptive Methods, Contraceptive Devices, Female. Reproductive Health

ABSTRACT ID: 138

PRESENTED BY: Hannah Evans (hannah.evans@phe.gov.uk)

PARALLEL SESSION PROGRAMME
MONDAY, 28 NOVEMBER
14:30-15:30

Parallel Session 4: Emerging and vector-borne diseases (1)

Moderator: Henriette de Valk, EPIET Alumni Network/ Santé Publique France: Head of Foodborne/ Vector-borne/ Zoonotic Infections at DMI

O4.1 The Impact of Hotspot-Targeted Interventions on Malaria Transmission in Rachuonyo South District in the Western Kenyan Highlands: Paving the road towards malaria elimination

Amrish Y. Baidjoe(1), Gillian Stresman(2)*, John Bradley(3), Philip Knight(4), William Stone(1), Victor Osoti(5), Euniah Makori(5), Chrispin Owaga(5), Wycliffe Odongo(5), Pauline China(5), Shehu Shagari(5), Ogobara K. Doumbo(6), Robert W. Sauerwein(1), Simon Kariuki(5), Chris Drakeley(2), Jennifer Stevenson(2,7), Jonathan Cox(2)¥, Teun Bousema(1,2)¥*

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*AYB and GS contributed equally to this article; ¥JC and TB contributed equally to this abstract. **This work was done outside the ECDC/EUPHEM fellowship of Amrish Baidjoe ***Work was very recently (end of April) published in PLoS Medicine but is very relevant towards the field of malaria elimination and novel intervention programmes.

Background

Malaria risk is not uniformly distributed between districts, villages and even between neighbouring households. This is mostly observed in areas transitioning to a state of (pre-)elimination. Whilst mean levels of malaria transmission may decline, geographical hotspots of intense transmission may persist inter-seasonally leading to a local increase of the R_0 up to five-fold. This study, conducted in the western Kenyan highlands utilizes serological and molecular markers aiming to identify hotspots, and assess the efficaciousness and cost-effectiveness of targeted interventions.

Methods

Samples from 17.503 individuals residing in 100km2 area were collected on filterpaper. Parasite prevalence (PCR) and serological markers of malaria exposure (AMA-1/MSP-119) were used in spatial scans for the detection of hotspots with localized levels of increased transmission. Within a cluster-randomized trial, 5 hotspots were randomly allocated for targeted interventions with larviciding, long-lasting insecticide-treated nets, indoor-residual spraying and focal mass drug administration; 5 control hotspots received routine malaria control. Efficacy of interventions was determined within and surrounding hotspots at baseline, 8 and 16 weeks post-intervention.

Results

Twenty-seven hotspots were discovered, parasite positivity and malaria-specific antibodies were strongly related at individual level, (OR1.94, 95%CI 1.77-2.13,$p<0.001$) exhibiting similar spatial patterns. Hotspots covered 34.7% of the total field area and included 44.4% of all sampled individuals. Intervention coverage ≥87% for all interventions. Combined hotspot-targeted interventions resulted in an average reduction of parasite prevalence of 10.2% (95%CI 1.3–21.7%) post-intervention after adjustment for covariates. In areas surrounding hotspots no significant reduction was observed.

Conclusion

This study shows that malaria prevalence varies within smaller foci of transmission resulting in the formation of hotspots which can potentially be utilized for more widely deployed targeted interventions leading to an increase of cost-efficacy.

Keywords: Malaria, Plasmodium falciparum, hotspots, PCR, serology

ABSTRACT ID: 65

PRESENTED BY: Amrish Baidjoe (amrish.baidjoe@gmail.com)

O4.2 Importance of active case detection for malaria cases in Evrotas, Lakonia, Greece, 2015

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Background

Greece has been malaria-free since 1974. In October 2011, following an outbreak of 36 locally-acquired malaria cases in Evrotas, an Active Case Detection (ACD) programme for malaria was implemented among migrants from malaria-endemic countries to support early diagnosis and treatment of cases. We evaluated the sensitivity of this surveillance programme and timeliness of diagnosis for 2015.

Methods

From 30 July to 7 December 2015, we visited each migrant home every 10-15 days to screen for fever and other malaria symptoms. We performed Rapid Diagnostic Tests (RDTs) and blood sampling on symptomatic patients. We estimated i)the sensitivity (Se) of ACD using the total number of reported malaria cases as denominator and ii)the timeliness as the time between onset of symptoms and diagnosis.

Results

During the study period, we undertook 2762 fever screenings, 169 RDTs and 133 blood samples among migrants (median monthly population size: 384, range: 348-453). In 2015, eight Plasmodium vivax cases were reported in Evrotas, seven of whom during the ACD period. Through ACD, we identified six imported cases in males from Pakistan and one locally-acquired case in a migrant from a non-endemic country was detected through the passive surveillance system (Se: 86%). The median age of cases identified through ACD was 24 years (range: 19-30). Four of the six imported cases had fever as the main symptom, with a median temperature of 37.60C (range: 37.20C-400C). The median time between onset and diagnosis was 2.5 days (range 0-10).

Conclusion

ACD in Evrotas promptly identified most of the reported malaria cases, suggesting that it contributed to reduced disease transmission. ACD must be continued to prevent re-establishment of malaria in the area.

Keywords: malaria, plasmodium vivax, active case detection, Greece

ABSTRACT ID: 60

PRESENTED BY: Maria Tseroni (mariatseroni@googlemail.com)

O4.3 A secondary case of Lassa fever in Germany identified the need to revise existing tools for VHF contact tracing and exposure risk classification

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Background

Lassa fever is a viral haemorrhagic fever (VHF) endemic to West Africa. Disease onset is characterized by flu-like symptoms. Person-to-person transmission occurs particularly in nosocomial settings of low-income countries. In March 2016, a nurse with malaria was evacuated from Togo to Germany and died shortly after hospital admission. Six days after the corpse was transferred to a mortuary in Rhineland-Palatinate, autopsy samples tested PCR-positive for Lassa virus (LV). We describe contact tracing and risk classification within Rhineland-Palatinate.

Methods

We traced potential contacts, classified them into risk categories according to national VHF-guidelines, and initiated symptom monitoring for 21 days post-exposure. Based on category, and presence of fever and other symptoms, we imposed additional measures (e.g. PCR-testing, quarantine/isolation, occupational ban). Regarding flu-like symptoms without fever, we defined a three-day disease progression as the threshold for enforcing these measures. We later conducted in-depth interviews to fill information gaps, and re-assessed initial risk classifications.

Results

We identified eight contacts exposed to the corpse, including a mortician recovering from a flu-like illness while handling the corpse. His condition deteriorated five days post-exposure and he tested PCR-positive for LV. He was isolated, treated with ribavirin, and recovered. We identified eleven contacts of the mortician. Via in-depth interviews we identified two additional contacts and re-classified two contacts into a higher category. Five contacts were quarantined and one received an occupational ban. Nine contacts reported flu-like symptoms without fever during follow-up, none of them triggering additional measures.

Conclusion

Contact tracing and respective measures interrupted the transmission chain. Rapid assessment directed by VHF-guidelines may underestimate LV-exposure risk. We suggest additional in-depth interviews for improved risk classification, and using algorithms to assess flu-like symptoms without fever during follow-up.

Keywords: Disease Outbreaks; Lassa Fever; Hemorrhagic Fevers, Viral; Risk Assessment; Contact Tracing;

ABSTRACT ID: 126

PRESENTED BY: Lutz Ehlkes (lutz.ehlkes@gmail.com)

Parallel Session 5: Vaccine preventable diseases (1)

Moderator: Helena de Carvalho Gomes, ESCAIDE Scientific Committee & ECDC, Head of Section Scientific Advice Coordination

O5.1 Estimating the burden of pertussis in 23 EU/EEA countries, 2010-2014

Vincenza Gianfredi (1,2), Sabrina Bacci1, Lucia Pastore Celentano (1), Robert Whittaker (1), Alessandro Cassini (1)

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Background

Despite sustained high vaccination coverage worldwide, pertussis remains not fully controlled in several EU countries. Its burden isn`t well known due to underestimation of cases, particularly in older age groups. Our aim was to estimate the burden of pertussis, expressed in disability-adjusted life years (DALYs) in 23 European Union and European Economic Area (EU/EEA) countries by age groups; in these countries the mean annual reported incidence for 2010-14 was 7.4 per 100,000.

Methods

We analyzed cases of pertussis reported to ECDC between 2010-14. The data were corrected with a multiplication factor to adjust for underestimation and DALYs were estimated using The Burden of Communicable Diseases in Europe software application. The annual data were averaged.

Results

The estimated annual number of cases was 942,774 (309 per 100,000 population), resulting in 3.6 (95% uncertainty intervals, UI 3.29-3.90) DALYs/ 100,000 total population. Age groups with highest DALYs per 100,000 total population were infants (< 1 year), 10-19 year and 40-49 year olds, respectively with 2.79 (95% UI 2.78-2.80); 5.33 (95%UI 4.25-6.44); and 3.42 (95% UI 2.71-4.14) DALYs. Infants also had the highest DALYs per 100,000 stratum specific population. No significant differences were observed by year and sex.

Conclusion

This preliminary analysis confirmed that infants were the group with the highest risk for disability and premature mortality compared to other groups, as estimated by DALY per 100,000 stratum specific population. In addition, the estimated DALYs/total population indicated that adolescents and adults were the groups where pertussis had the highest impact as compared to the whole population, therefore suggesting that they also carry a significant burden. Vaccination strategies should take this into account to reduce the number of complications among adolescents and adults.

Keywords: pertussis, Bordetella pertussis infection, adults, whooping cough, burden of illness

ABSTRACT ID: 217

PRESENTED BY: Sabrina Bacci (sabrina.bacci@ecdc.europa.eu)

O5.2 Investigation of an outbreak of pertussis in children with high vaccination coverage in Kiel, Germany, 2015-2016

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Background

From 16/11/2015-26/1/2016, 82 pertussis cases, mainly mild and in vaccinated children, were notified in Kiel, Germany. We investigated to assess symptoms in relation to vaccination status and laboratory confirmation and estimate pertussis-vaccine effectiveness (VE).

Methods

Three educational establishments participated in a retrospective cohort study from 27/1/2016-4/2/2016, providing information on risk factors and symptoms from parent-completed questionnaires. We reviewed vaccination cards and analysed laboratory results, including cycle thresholds (CT) for real-time PCR (assuming high bacterial load when CT<34). Cases were children with physician-diagnosed pertussis and cough since 1/11/2015 either lasting ≥14 days or of any duration if lab-confirmed. We estimated relative VE using binomial regression (VE=(1-RR)x100%).

Results

271/595 (46%) children provided questionnaires (aged 2-15, median 11 years; 56% females) and 193/595 (32%) vaccination cards (190 without prior pertussis of whom 187 had ≥1 pertussis vaccination). We identified 16 cases (attack rate (AR) 6%, 3 unvaccinated, 13 lab-confirmed (all PCR)). Being a case was associated with age ≤6 years (RR=4.8; 95%CI:1.8-12.7) and no/incomplete primary vaccination (RR=10.9; 95%CI:4.4-27.1). Age-adjusted VE for complete primary vaccination was 88% (95%CI:68-95%). We found no association with booster vaccinations. Cough lasted longer in cases with no/incomplete primary vaccination (42.7 vs 15.1 days (p=0.15)) and higher bacterial load (42 vs 9.4 days (p=0.08)).

Conclusion

Complete primary vaccination prevented pertussis disease effectively and may have mitigated symptoms in breakthrough infections. However, some milder cases may have been only colonised by Bordetella pertussis with symptoms caused by other pathogens, possibly explaining why booster vaccinations had no effect on the AR. Comprehensive analysis of outbreaks affecting populations with high vaccination coverage may be challenging if case ascertainment is solely based on PCR without considering bacterial load or further serologic/cultural confirmation.

Keywords: pertussis, outbreak, vaccine effectiveness, laboratory confirmation

ABSTRACT ID: 82

PRESENTED BY: Viktoria Schönfeld (SchoenfeldV@rki.de)

O5.3 Are pertussis cases reported too late for public health interventions? Cross sectional study in London and the South East of England, 2010 to 2015.

Helen Crabbe (1), M. Saavedra-Campos (2), J. Morris (1), A. Leonard (2), S. Balasegaram (2)

1. Public Health England South East Centre, Chilton, UK
2. Field Epidemiology Service, National Infections Service, Public Health England, London, UK

Background

In the UK, pertussis guidance recommends prophylaxis of all household contacts within 21 days of case symptom onset when an under-immunised infant (<1 year) or individuals likely to transmit them (health care workers (HCW) and >32 weeks pregnant) are identified as contacts, to reduce severe disease in infants. We undertook a cross sectional study to assess timeliness of reporting pertussis cases to public health teams in London and the South East of England, 2010-15.

Methods

We extracted information on laboratory confirmed and clinically suspected pertussis cases from case management systems. We defined cases as late if the interval from symptom onset to report date was >21 days. We identified risk factors for late reporting compared to non-late on univariate analysis. We calculated adjusted odds ratios and 95% confidence intervals (aOR; CI) using a stepwise logistic regression model.

Results

Of 8761 cases (6688 confirmed, 2073 suspected), 61% were reported from laboratories and 63% were reported late. After adjusting for seasonality and source, older age groups (aged 1-12 months; aOR=1.9 [95%CI 1.1-3.4]; 1-9 years; aOR=3.8 [95%CI 2.2-6.8]; 10+ years; aOR=5.9 [95%CI 3.3-10] compared to neonates age <1 month), confirmed cases (aOR=1.9; 95% CI 1.6-2.2) compared to suspected and area team (highest aOR=2.4; 95%CI 1.9-3.0) were associated with late reporting. HCW (aOR=0.53; 95%CI 0.35-0.78 or being hospitalised (aOR=0.56, 95%CI 0.32-0.92) was associated with timeley reporting. Report year, socioeconomic status and pregnancy had no effect.

Conclusion

Timely reporting is associated with younger age, severity and HCWs. However most cases were reported late, potentially missing opportunities for secondary prevention. We recommend further exploration of the geographical variation and feedback to local general practitioners groups to improve reporting on clinical suspicion.

Keywords: Pertussis, Whooping Cough, epidemiology, late reporting, risk factors, disease notification

ABSTRACT ID: 186

PRESENTED BY: Helen Crabbe (helen.crabbe@phe.gov.uk)

Parallel Session 6: Late Breakers

Moderator: Ines Steffens, ESCAIDE Scientific Committee & ECDC, Editor-in-Chief Eurosurveillance

O6.1 National outbreak of Pseudomonas aeruginosa associated with body piercings, July-September 2016, England

Ellen Heinsbroek (1), Peter English (2), Samia Latif (3), Sue Ibbotson (4), David Spence (3), Hikaru Bolt (5), Liz Loosemore (2), Max Courteney-Pillinger (2), Bryony Lloyd (3), Neil Anstey (3), Rob Johnston (6), Russell Sinclair (3), Jonathan Lloyd (5) , Gail Beckett (3), Jane Turton (7), Dervla Kenna (7), Peter Hoffman (7), Nicola Elviss (8), Caroline Willis (9), Sarah Collins (10), Julian Wilks (11), Amanda Wright (1), Maria Saavedra-Campos (1), Sophie Newitt (3), John Paul (12), Theresa Lamagni (13), Colin Brown (12), Derrick Crook (12), Shaun Whelan (14), Paul Cosford (15), Helen Maguire (1), Paul Crook (1), Richard Puleston (5)

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13. Public Health England, Department of Healthcare-Associated Infection and Antimicrobial Resistance , London, UK
14. Public Health England, Communications, London, UK
15. Public Health England, Health Protection, London, UK

Background

On 31st August 2016 two clusters of Pseudomonas aeruginosa ear infections were reported following cartilaginous ear piercings performed at two geographically distinct studios in England. Sporadic infections following cartilaginous ear piercing are well documented, common source outbreaks are rare. We report the incident investigation findings.

Methods

We defined confirmed cases as persons in England with Pseudomonas aeruginosa infection following any body piercing since 1st July 2016, and probable cases as persons with infection (consistent with Pseudomonas) following any cartilaginous piercing at a studio with confirmed case(s). We carried out active case finding, explored common exposures, took various environmental samples from studios, and typed human and environmental samples using variable number tandem repeats (VNTR).

Results

As of 29th September 2016, there were 49 confirmed and 10 probable cases. Median age was 17 years (range 13-48 years); 92% were female (54/59). Piercing dates ranged from July to September 2016. Fifty-four cases had cartilaginous ear piercings (5 unknown). Cases resided in eight English regions and attended 17 different piercing studios. At least 32 cases required surgery. Pseudomonas aeruginosa was cultured from eight bottles of an aftercare solution prepared at a single location in the Midlands, and used by at least 33 cases, and from four environmental samples from its production. Isolate typing by VNTR identified that all environmental samples matched 24/33 cases typed. The 24 cases matched on VNTR attended seven different piercing studios supplied with the suspected aftercare solution. No common VNTR type was identified for the remaining nine cases.

Conclusion

There is strong microbiological and epidemiological evidence implicating contaminated aftercare solution. It was recalled on 9th September. A review of piercing industry regulation and infection control practice is required.

Keywords: Pseudomonas aeruginosa, body piercing, outbreaks, infection

ABSTRACT ID: 715

PRESENTED BY: Hikaru Bolt (Hikaru.bolt@phe.gov.uk)

O6.2 Zika virus in pregnant women in French Guiana

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Background

An epidemic of Zika virus (ZIKV) is ongoing in the Americas and has been associated with complications such as microcephaly during pregnancy. Although the presence of symptoms might be a risk factor for complication, the proportion of ZIKV-infected pregnant women with symptoms remains unknown.

Methods

Following the emergence of ZIKV in French Guiana, all pregnancies were monitored in the territory. Pregnant women were regularly tested for ZIKV infection by RT-PCR and/or detection of antibodies against ZIKV. Follow-up data were collected during pregnancy monitoring interviews and analyzed from 1 February to 1 June 2016.

Results

A total of 3,050 pregnant women aged 14-48 years old were enrolled and 573 (18.8%) had laboratory-confirmed ZIKV infection. Rash, arthralgia, myalgia and hyperemic conjunctivitis were more frequently observed in ZIKV positive women. Twenty three percent (95% CI 19.7%-26.7%) of ZIKV positive women had at least one symptom compatible with a ZIKV infection. ZIKV positive women aged ≥ 30 years were significantly more symptomatic than those aged <30 years (28.0% vs 19.9%). The proportion of symptomatic infections varied from 16.5% in the remote interior to 34.8% in the more mixed and urbanized population in the coastal area (Risk Ratio: 1.64; 95% CI: 1.39-1.92.)

Conclusion

This is the first study documenting the proportion of symptomatic infections among ZIKV-positive pregnant women. These estimates are important to put findings based on cohorts of symptomatic ZIKV-positive pregnant women into the wider context of an epidemic where most infections are asymptomatic. The proportion of symptomatic ZIKV infections appears to vary substantially between populations.

Keywords: Zika virus infection, Pregnant women, Outbreak, Epidemiology, French Guiana

ABSTRACT ID: 722

PRESENTED BY: Claude Flamand (cflamand@pasteur-cayenne.fr)

O6.3 Implementation of infectious disease syndromic surveillance in points of care for refugees/ migrants, Greece, April – July 2016

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Background

In March 2016, the sealing of the Western Balkan migration route resulted in about 50,000 refugees/migrants being stranded in camps across Greece. Since mid-April Greek public health authorities with the support of two EPIET fellows implemented a syndromic surveillance system at points of care (POC) in centres hosting refugees/migrants to rapidly detect and respond to potential public health emergencies.

Methods

Health care providers in POC daily reported data on 14 syndromes/ conditions to the Hellenic Center for Disease Control and Prevention. During the initial phase of the establishment of the system, we identified constraints through site visits and delivered training to health care providers. We analyzed data daily, determining whether observed morbidity exceeded significantly the expected proportional morbidity for each syndrome.

Results

During 11/4/2016-31/7/2016, 50 of the 55 centres (covering 99% of the refugee/migrant population hosted in centres) were gradually included. Respiratory tract infections with fever were most frequently reported (n=5831; 55%), followed by gastroenteritis (n=3071; 29%), scabies (n=868; 8.3%) and rash with fever (n=668; 6.4%). Of the reported rash with fever cases, 88% (n=586) were chickenpox, from which 84% were among children <15 years old. Eighteen clusters of gastroenteritis without blood from 12 different centres were reported, all of small size (median:14 cases, range: 7-34), and low severity. All nine reported cases of jaundice with acute onset were hepatitis A, for which appropriate measures, including vaccination of close contacts, were implemented. No cases of serious communicable conditions were reported.

Conclusion

Syndromic surveillance in POC for refugees/migrants allowed monitoring the morbidity of the refugees/migrants, enabling health authorities to detect and respond to events of public health importance. We recommend maintenance of the system for the duration of POC operation.

Keywords: syndromic surveillance, Greece, refugee, migrant, early warning, morbidity

ABSTRACT ID: 734

PRESENTED BY: Lamprini Veneti (lambrinive@gmail.com)

PARALLEL SESSION PROGRAMME
TUESDAY, 29 NOVEMBER
11:00-12:40

Parallel Session 7: HIV, sexually transmitted infections and viral hepatitis (2)

Moderator: Andrew Amato, ECDC, Head of Disease Programme HIV, Sexually Transmitted Infections and Viral Hepatitis

O7.1 Inequalities in sexual health and risk behaviour among men who have sex with men living in Ireland

Kate O'Donnell (1), M. Fitzgerald (1), P. Barrett (1,2), M. Quinlan (3,4), D. Igoe (1)

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3. Gay Health Network, Dublin, Ireland
4. Gay Men's Health Service, Dublin, Ireland

Background

MISI 2015 is the largest community-based internet survey among men who have sex with men (MSM) living in Ireland. The purpose of the study was to monitor behaviour, and prevention interventions, and to identify needs and gaps among this group.

Methods

It was an anonymous, self-completed and cross-sectional survey over a three-month period in 2015. It recruited 3,090 MSM who provided information about HIV/STI testing, sexual behaviour, knowledge and prevention strategies.

Results

Fifty-three percent of men were single, 13% identified as bisexual and 51% were out to all or almost all. Overall, 37% had never tested for HIV and this proportion was significantly higher in 18-19 year olds (84%), men who were not out (77%) and men with low education levels (53%). Five percent of men were HIV positive (8% among those ever tested) and this proportion was highest among men in their 40s (14%). Thirty eight percent never had an STI test and this proportion was highest among 18-19 year olds (83%) followed by men aged 60 years and over (68%). Fifty-five percent reported having at least one episode of unprotected anal intercourse (UAI) in the last year. Twenty-four percent reported lack of access to a condom when needed within the last year (44% of 18-19 year olds) and 30% reported awareness of and confidence in getting post exposure prophylaxis (PEP) if needed (13% of 18-19 year olds).

Conclusion

Inequalities in sexual health and risk behaviour in Irish MSM are evident. The challenge for policy makers and service providers is to implement tailored interventions to target the groups at most risk of HIV and STI infection thereby improving the health and wellbeing of MSM in Ireland.

Keywords: Surveys and Questionnaires, Homosexuality Male, Ireland, HIV Infections, Sexual Behaviour, Sexually Transmitted Diseases

ABSTRACT ID: 287

PRESENTED BY: Kate O'Donnell (kateodonnella@gmail.com)

O7.2 Point-of-care management of gonococcal infections among men who have sex with men

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4. Center for Infection and Immunology Amsterdam (CINIMA), Academic Medical Center (AMC), University of Amsterdam, Amsterdam, The Netherlands

Background

Point-of-care (POC) management for gonorrhoea infections involves rapid testing with a result on the same day as the sample was obtained. This allows immediate treatment, thus averting new infections that could occur in the time between testing and treatment or due to loss to follow-up. We investigate the impact of POC management on the transmission of gonorrhoea among men who have sex with men (MSM).

Methods

We develop a mathematical model and distinguish infected MSM according to whether they are tested with rapid tests (and treated immediately) or with NAAT (and wait for test results to get treated). We compare the current POC management in Amsterdam offered only to symptomatic MSM to (a) POC for all MSM or (b) no POC for MSM.

Results

With the current 7% loss to follow-up in Amsterdam and an average of 12 days between testing and treatment for those not tested with rapid tests, expanding POC management (from symptomatic MSM to all MSM) could result in a decline of 4.21% in prevalence after 10 years. Greater reductions in prevalence could be attained with higher loss to follow-up or longer time between testing and treatment. Terminating the current POC management for symptomatic MSM could result in an increase of 14.70% in prevalence after 10 years; the increase could be greater if the loss to follow-up is higher and/or the time between testing and treatment is longer.

Conclusion

POC management for gonorrhea infections among MSM can considerably contribute to reducing gonorrhea transmission and prevalence, even if offered only to symptomatic MSM.

Keywords: Gonorrhea, point-of-care management, rapid test, mathematical model, men who have sex with men

ABSTRACT ID: 134

PRESENTED BY: Maria Xiridou (maria.xiridou@rivm.nl)

07.3 Drugs, alcohol and sexual behaviour among Irish men who have sex with men: results from a national cross-sectional survey

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2. Department of Public Health, HSE-South, Cork, Ireland
3. Gay Men's Health Service, HSE, Dublin, Ireland
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Background

Men-who-have-sex-with-men (MSM) account for 58% of new HIV diagnoses in Ireland. Drug use has increased in the general population, and chemsex is a growing cause for concern. Little is known about drug/alcohol use in Irish MSM, and whether they are associated with sexual risk behaviour or HIV/STIs.

Methods

Community-based opportunistic sampling recruited 3,090 men to Ireland's largest MSM internet survey. Respondents reported on substance use, demographic characteristics, sexual behaviours and HIV/STIs. Multivariable logistic regression was used to examine associations between substance use and other factors.

Results

Thirty-six percent of MSM used drugs last year. One third used poppers, 7% used chemsex drugs (methamphetamine, GBL/GHB, mephedrone, ketamine), and 36% used other illicit drugs. Two percent had ever injected drugs. Overall, drug use was most prevalent among those <25 years (48%) and was more likely among men with HIV (AOR1.6, 95%CI 1.0-2.6) and men who had unprotected anal intercourse (UAI) with ≥10 partners last year (AOR2.4, 95%CI 1.3-4.3). Use of chemsex drugs was most prevalent among those aged 25-29 (9%), and users were more likely to have ≥10 recent UAI partners (AOR5.1, 95%CI 2.3-11.1) and have a recent STI(AOR2.1, 95%CI 1.3-3.4). Drug users had higher odds of smoking (AOR3.9, 95%CI3.2-4.8) and bringe drinking (AOR1.4, 95%CI 1.2-1.8). Overall fifty-eight precent of men reported binge drinking, and this was most prevalent among those <25 years (69%) and those with low education (66%). Thirty-five per cent smoked and smoking was more likely among HIV-positive men (AOR2.0, 95%CI 1.3-3.2).

Conclusion

We found high prevalence of drug use and binge drinking among Irish MSM. Drug use was associated with sexual risk-taking and HIV/STIs. Risk reduction interventions are being planned nationally in response to our findings.

Keywords: Alcohol drinking, drug use, chemsex, male homosexuality, HIV, sexually transmitted diseases

ABSTRACT ID: 384

PRESENTED BY: Peter Barrett (peterm.barrett@hse.ie)

07.4 Tuberculosis and HIV co-infection: looking at one reality from two angles

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Background

Information on the burden of tuberculosis (TB) and human immunodeficiency virus (HIV) co-infection is critical for planning and evaluating TB/HIV prevention and control activities. Mitigation measures include increase testing coverage of TB patients for HIV co-infection and HIV-positive individuals for TB.

The aim of this study is to estimate the burden and identify risk-factors for TB/HIV co-infection in the EU/EEA for planning of prevention and control measures.

Methods

We performed an analysis of the 2014 TB and AIDS cases with TB disease reported to the European Centre for Disease Prevention and Control to estimate the burden of TB/HIV co-infection and employed multivariable logistic regression to identify risk factors for co-infection.

Results

Twenty-one of 31 EU/EEA countries included HIV testing results for 64.6% (N=21,243) of the 32,892 reported TB cases. Among tested, 1,051(4.9%) were reported as HIV-positive. Males (adjusted odds ratio [aOR] 1.25; 95% Confidence Interval [95% CI] 1.07-1.45), and persons aged 25-44 were more frequently co-infected. TB cases originating from the WHO African Region had the highest proportion of co-infection (aOR 2.82; 95% CI 2.07-3.86). TB treatment was completed successfully by 57.9% of HIV-positive TB cases and 83.5% of HIV-negative cases reported in 2013.

The same 21 countries reported 1,934 AIDS cases in 2014 with TB reported as an AIDS-defining illness at diagnosis in 436 (22.5%) of them. Persons with acquired HIV through injecting drug use had higher odds of TB as an AIDS-defining illness (aOR 1.96; 95% CI 1.50-2.55).

Conclusion

TB/HIV co-infection is substantial in the EU/EEA. The international guidelines for prevention and treatment of TB in HIV-infected adults need to be better implemented by increasing of testing coverage for TB and HIV within vulnerable population.

Keywords: Tuberculosis, HIV, AIDS, European Union, Europe, co-infection

ABSTRACT ID: 200

PRESENTED BY: Csaba Ködmön (csaba.kodmon@ecdc.europa.eu)

O7.5 Late breaker: Drug use in sexual settings ('chemsex') by men who have sex with men: a survey of sexual health clinic users in Dublin, Ireland

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Background

The use of drugs for/during sex –'chemsex'– among MSM is causing concern, because of the direct effects of the drugs, and because of the increased risk of STIs amongst those who engage in these practices. In the context of increasing STIs/HIV in MSM in Ireland, this study aimed to assess the prevalence of chemsex among attendees at Ireland's only MSM-specific sexual health clinic in Dublin in 2016.

Methods

All attendees were invited to participate over a six-week period in June and July 2016. The self-completed survey collected demographic data, and information on sexuality and sexual practice, STIs, and chemsex. Multi-variable modelling was used to identify variables independently associated with a prior diagnosis of a range of STIs.

Results

The response rate was 89.7%(510/568). One in four respondents(27%) had engaged in chemsex within the previous 12 months, the majority(57%) of whom had used GHB/GBL. Half had taken ≥ 2 drugs on his last chemsex occasion. One in five(23%) respondents/their partners had lost consciousness as a result of chemsex. Those engaging in chemsex were more likely to have had more sexual partners($p<0.001$), more partners for anal intercourse($p<0.001$) and to have had unprotected sex at last anal intercourse($p=0.041$). They were also more likely to have ever been diagnosed with chlamydia(OR1.95, 95% CI 1.22-3.13) and gonorrhoea(OR1.95, 95% CI 1.23-3.08). One third(31%) reported that they would like help or advice.

Conclusion

There is a substantial culture of chemsex among MSM in Ireland, with significant implications for sexual health and addiction services. Ireland's next National Drug's Strategy is currently being developed; these results will inform this process and support the implementation of an effective, targeted response which simultaneously addresses addiction and sexual ill-health among MSM.

Keywords: Sexually transmitted infections; Risk behaviour; Chemsex; Gonorrhoea; Chlamydia; Recreational Drugs

ABSTRACT ID: 737

PRESENTED BY: Ronan Glynn (ronan.glynn@hse.ie)

Parallel Session 8: Food- and waterborne diseases and zoonoses (1)

Moderator: Birgitta de Jong, ECDC, Senior Expert Respiratory Diseases / Group Leader EU Preparedness

O8.1 An outbreak of invasive Listeria monocytogenes serotype 1/2a with a rare pulsotype associated to processed pork meat-stuff in central Italy, 2015-2016.

Michela Sabbatucci (1,2), G. Tagliavento (3), A. Duranti (4), F. Pomilio (5); inter-institutional outbreak investigation group (*). (*) G. Scavia (1), C. Rizzo (1), A. Bella (1), C. Graziani (1), P. Pezzotti (1), M.V. Gianfranceschi (1), A. Gattuso (1), D. De Medici (1), L. Busani (1), D. Fiacchini, (3), A. Tibaldi (3), G. Migliorati (5), P. Colangeli (6), G. Blasi (7), G. Filippini (8).

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8. Istituto Zooprofilattico Sperimentale dell'Umbria e delle Marche, Perugia, Italy

Background

In 2015 the local surveillance system in region Marche (central Italy) reported a four-fold increase in listeriosis compared to 2013-2014. As part of the official operational group, we investigated the outbreak to identify the source(s) of infection and prevent further cases.

Methods

We defined a case as a patient resident in Marche region, symptoms onset after January 1st 2015 and culture-confirmed Listeria monocytogenes (L.m.) isolated from a normally sterile site. We performed serotyping, Pulsed-Field Gel Electrophoresis (PFGE) typing and uploaded BioNumerics PFGE profiles in The European Surveillance System (TESSy), identifying a rare cluster-pulsotype. We interviewed cases with a food-consumption questionnaire. We conducted retrospective case-case study (i.e. cluster-cases infected with L.m. rare pulsotype vs not cluster-cases (other pulsotypes) using unconditional logistic regression (STATA 12.0).

Results

We identified L.m. serotype 1/2a with a rare pulsotype (ECDC_PFGE_ApaI.0246_AscI.0356) never reported before in Europe. As of April 30 2016, 23 cluster-cases and 11 not cluster-cases were reported (median age 75±17 years, 56% female). Cases increased until a peak at the 23th week in 2015 and at the 3rd week in 2016. Five patients died. Cluster-cases were more likely to consume coppa di testa (OR 3.5, 95%CI 0.3-35), a typical pork-meat product, than not cluster-cases. Local health authority isolated the outbreak strain from coppa di testa sampled in a local retail.

Conclusion

Epidemiological and microbiological investigations suggested coppa di testa as the likely source of the infection. Coppa di testa was withdrawn from the market and the manufacturer activity suspended. A sharp decline in the occurrence of cases was observed. We recommend to maintain surveillance and typing of listeria cases, inform risk categories (elderly and pregnants) and increase control of L.m. in food plants.

Keywords: Listeriosis, Disease Outbreaks, Case-Control Studies, Pulsed-Field Gel Electrophoresis, Disease Notification

ABSTRACT ID: 207

PRESENTED BY: Michela Sabbatucci (michela.sabbatucci@iss.it)

O8.2 A combined case control and source attribution study in Germany, 2011-2014, suggests reduction of Campylobacter on chicken meat as the most effective strategy to reduce human campylobacteriosis

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5. Department for Biological Safety, Federal Institute for Risk Assessment, Berlin, Germany

Background

Campylobacteriosis is the most commonly reported bacterial gastroenteritis in Germany. We performed a large case control study combined with source attribution analysis to identify specific risk factors and routes of transmission in Germany and to quantify the proportion of human cases attributable to certain sources. The aim of this study was to build a basis for evidence-based prioritisation of possible prevention strategies.

Methods

Case patients and randomly selected controls completed a questionnaire (study period Nov 2011-Feb 2014). Campylobacter isolates of case patients as well as from food, animals and the environment collected in temporal and geographical relation were further analysed by multilocus sequence typing. We conducted univariable and multivariable logistic regression analyses. Source attribution analysis was performed using Bayesian inference on an asymmetric island model.

Results

We analysed questionnaires from 1,812 case patients and 3,983 control persons. Most important risk factors based on the population attributable fractions (PAF) were: consumption of chicken meat (adjusted odds ratio [aOD] 1.6; 95% confidence interval [CI] 1.2-2.0; PAF 32%) and eating out (aOD 1.6; 95% CI 1.3-2.0; PAF 30%). We also identified factors reflecting insufficient kitchen hygiene as important routes of transmission: preparation of packaged poultry meat in the household (aOD 1.4; 95% CI 1.1-1.6; PAF 13%) and of non-heated food together with raw meat (aOD 1.3; 95% CI 1.1-1.5; PAF 12). Of 230 attributable human Campylobacter isolates, 63% (n=146) were assigned to the source chicken.

Conclusion

Our study confirms chicken as the major source of human campylobacteriosis in Germany. Thus, efforts should be stepped up to reduce bacterial load on chicken meat and to educate consumers on handling chicken meat safely.

Keywords: Campylobacter, Case-Control Studies, Risk Factors, Foodborne Diseases, Gastroenteritis

ABSTRACT ID: 197

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

O8.3 Cholera Outbreak in Gajala, Birnin Kudu, Jigawa State, Nigeria, September 2015.

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Background

Cholera outbreaks are seasonal in Nigeria with high case fatality rates (CFRs) 5.1%, 3.87%, 2010 and 2015 respectively. An outbreak of cholera was reported in Gajala community, Birinin Kudu Local Government Area, Jigawa State, Nigeria September 16th, 2015. We investigated the outbreak to characterize the outbreak and institute control measures.

Methods

We reviewed surviellance records, conducted active case search, and described the outbreak. We collected five stool and water samples each for Rapid Diagnostic Test (RDT) using smart kit and culture respectively. We carried out an un-matched (1:2) Case Control Studies (CCS). Case definition was any person ≥ 2 years from Gajala presenting with Acute Watery Diarrhea (AWD) with or without vomiting from 11th-25th September 2015. Similarly a control was defined as stated but without AWD. We examined the environment for possible food or water contamination. Data analysis was done using Epi info version 3.5.3.

Results

Overall 50 cases were identified, median age 21years (range:2-80), more female affected, 27(54%), overall attack rate 10.5%, 1 died CFR 2%.Mean duration of illness before presentation 17.2 ± 15.2 hrs. All 5 water samples tested positive to RDT while vibrio cholerae was not issolated from the water cultures. The 138 respondents (46 cases and 92 controls) in the CCS have median age 20 (range: 2-70). Poor knowledge of cholera [aOR=2.52 95%CI (1.23-5.28)]. Not washing hand before eating [adjusted Odds Ratio (aOR)= 2.78, 95%CI (1.16-6.63)], Not washing hand after using toilet [aOR=2.63, 95%CI (1.18-5.85)]. The environment showed poor sanitation.

Conclusion

A confirmed Cholera outbreak occurred in Gajala due to Poor knowledge of cholera and hand hygiene. We conducted health education on cholera and hand hygiene practices which stopped the outbreak.

Keywords: Cholera, outbreak, Gajala, Jigawa State, Nigeria.

ABSTRACT ID: 28

PRESENTED BY: Robinson Nnaji (robinsonnnaji@yahoo.com)

O8.4 Serogroup-specific seasonality of verotoxigenic Escherichia coli, Ireland, 2004-2014

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5. Public Health England London, United Kingdom
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Background

Typically, human verotoxigenic Escherichia coli (VTEC) infections are reported as being more common in late summer, but this may vary by serogroup. The aim of this study was to describe the seasonality of VTEC infections in Ireland and the potential serogroup differences in seasonality.

Methods

Using national notification data for VTEC serogroups O157 and O26 for the period 2004-2014 (n=2,569), we calculated the phase for seasonality for each serogroup, and the difference between the two phases. We used times series quasi-Poisson regression, fitting a term for temporal trend, a sine wave with a period of 12 months for seasonality, and terms for interaction by serogroup. We compared the phase shifts of the two serogroups using the Wald test.

Results

The two VTEC serogroups appeared to differ in their seasonality with the peak in VTEC O26 notifications generally occurring around eight weeks earlier than VTEC O157. This earlier peak in incidence for VTEC O26 has become progressively more consistent as the number of reported VTEC O26 notifications has risen. Using times series quasi-Poisson regression, the predicted peak in cases occurred in July for VTEC O26 and in September for VTEC O157, with the two month difference in phase (seasonality) by serogroup being statistically significant (p-value <0.001). The difference in seasonality remained significant (p-value <0.001) for sporadic cases alone, with the same predicted two month difference.

Conclusion

The consistent differences in seasonality identified here between the two most common VTEC serogroups suggest that there are noteworthy underlying differences in disease aetiology between the strains. Possibilities include differences in primary animal reservoirs, in seasonal distribution in the environment or in human behaviours. We recommend further exploration.

Garvey P, et al.EID. http://dx.doi.org/10.3201/eid2204.151160

Keywords: Shiga-Toxigenic Escherichia coli, seasons, etiology, time-series

ABSTRACT ID: 54

PRESENTED BY: Patricia Garvey (patricia.garvey@hse.ie)

O8.5 Virulence factors of Shiga toxin-producing Escherichia coli and the risk of developing Haemolytic uremic syndrome in Norway 1992-2013

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Background

Shiga toxin-producing Escherichia coli (STEC) may cause haemolytic uremic syndrome (HUS). Young age, presence of stx2a and eae are reported risk factors for the development of HUS. In this study we explore the presence of adhesins, toxins and molecular risk assessment (MRA) factors among STEC isolates in Norway from 1992 to 2013, to identify novel risk factors for HUS development in order to improve the STEC surveillance system in Norway.

Methods

We included non-duplicate isolates of all STEC cases (n=340) reported from 1992-2013 (one isolate per outbreak, 32 HUS cases). Median age of cases were 14 years (range: <1-97), female 56%. Most common STEC were O157:H7 (19%), O103:H2 (14%) and O26:H11 (10%). We screened the isolates by PCRs for 35 virulence factors (adhesins (n=13), toxins (n=8), and MRA (n=14)) and calculated odds ratios (OR) and adjusted odds ratios (aOR) for associations to HUS development.

Results

All STEC isolates from HUS cases were positive for intimin (eae) and the long polar fimbriae lpfAO26. Age ≤ 5 years (aOR 13.4, $p<0.005$) and stx2a (aOR 29.3, $p<0.005$) were identified as independent risk factors for HUS development. Furthermore, O145 (aOR 14.9, $p<0.05$) and the non-LEE-encoded effector that inhibits apoptosis and phagocytosis, nleH1-2 (aOR 31.4, $p<0.005$) were identified as independent risk factors for HUS development. None of the cases between 20-60 years (n=117), O103:H2 isolates (n=47) and isolates producing stx2b (n=32) developed HUS.

Conclusion

This study demonstrates that the presence of O145 or nleH1-2 may be predictors for elevated risk for HUS development, and conversely stx2b or O103:H2 isolates, predictors of low-virulent STEC infections. We recommend the Norwegian National Reference Laboratory for Enteropathogenic Bacteria to consider including nleH1-2 screen into routine STEC surveillance.

Keywords: Shiga-Toxigenic Escherichia coli, Virulence factors, Haemolytic-Uremic Syndrome, Shiga toxin

ABSTRACT ID: 131

PRESENTED BY: Umaer Naseer (mohammed.umaer.naseer@fhi.no)

Parallel Session 9: Vaccine preventable diseases and healthcare- associated infections (2)

Moderator: Natasha Crowcroft, EPIET Alumni Network, Canada

O9.1 PCV13 effectiveness and overall effect of higher valency pneumococcal conjugate vaccination programmes in children under five years from nine European countries: results of SpIDnet multicentre studies

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Background

The Streptococcus pneumoniae invasive disease network (SpIDnet) conducts population-based surveillance for invasive pneumococcal disease (IPD) in 13 sites from nine European countries. Using surveillance data, we measured the effectiveness of 13-valent pneumococcal conjugate vaccine (PCV) and the overall effect of higher valency PCV (PCV10/13) vaccination programmes on IPD incidence in children under five years of age.

Methods

To measure vaccine effectiveness, we compared the vaccination status of cases of IPD due to PCV13 serotypes (cases) to that of nonPCV13 IPD (controls) reported from January 2012 to December 2014. We calculated pooled vaccine effectiveness as (1-odds ratio)*100, adjusted for age, gender, underlying conditions, notification year and site. To measure PCV10/13 overall effect, we calculated incidence rate ratios (IRR) comparing specific PCV13 serotypes (PCV13non7) and nonPCV13 IPD serotype incidences in each of the five PCV10/13 years to PCV7 reference period, by site. We calculated pooled IRR and 95% confidence intervals (CI) using random effects meta-analysis.

Results

Effectiveness of at least one dose PCV13 was 87.0% (95%CI: 79.9-91.6) against PCV13 IPD (n=877), 85.5% (95%CI: 76.9-90.9) against PCV13non7 IPD (n=806) and 86.3% (95%CI: 73.9-92.8) against serotype 19A IPD (n=667). The pooled PCV13non7 IPD IRR decreased from 0.89 (95%CI: 0.74-1.07) for the first year to 0.18 (95%CI: 0.10-0.31) for the fifth year postPCV10/13. The pooled nonPCV13 IPD IRR was 1.10 (95%CI: 0.84-1.45), 1.53 (95%CI: 1.15-2.03), 1.53 (95%CI: 1.18-1.99), 1.70 (95%CI: 1.31-2.22) and 1.60 (95%CI: 1.26-2.04) for each year postPCV10/13, respectively.

Conclusion

Our results indicate a high PCV13 effectiveness and overall effect of PCV10/13 vaccination programmes against vaccine serotypes. The increase of nonPCV13 incidence indicates serotype replacement. Active IPD surveillance in children is needed to guide research on new generations of pneumococcal vaccines.

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

ABSTRACT ID: 145

PRESENTED BY: Camelia Savulescu (c.savulescu@epiconcept.fr)

O9.2 Indirect effect of five years of infant PCV10/13 vaccination on invasive pneumococcal disease among the elderly: pooled analysis from 10 European countries

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Background

SpIDnet and I-MOVE+ networks conduct population-based surveillance for invasive pneumococcal disease (IPD) in elderly from 10 European countries (11 sites). Universal infant vaccination programme is implemented with PCV13 in 5 countries, PCV10 in 2 and both PCV10/13 in 3. We estimated the indirect effect of infant PCV10/13 vaccination on IPD in elderly.

Methods

Using PCV7 period as reference, we calculated IPD incidence rate ratios (IRR) for each of the five PCV10/13 years in persons ≥65 years by serotype-group (All, PCV7, PCV13non7 and non-PCV13). We calculated pooled IRR and confidence intervals, using random effect meta-analysis, and the indirect effect as 1-IRR (in percent).

Results

During the PCV10/13 period, the annual decrease in all IPD in ›65 years ranged from 7% (IRR 0.93, 95%CI:0.89-0.98) in year 1 to 22% (IRR 0.78, 95%CI:0.67-0.90) in year 5. PCV7 serotype IPD declined by 55% (IRR 0.45, 95%CI:0.35-0.58) and 76% (IRR 0.24, 95%CI:0.14-0.39) in year 1 and 5, respectively. Rates of IPD due to PCV13non7 serotypes increased in year 1 and then declined by 43% (IRR 0.57, 95%CI:0.44-0.74) in year 5. Incidence of non-PCV13 IPD gradually increased in each country, up to +44% in year 5 in the pooled analysis (IRR 1.44, 95%CI:1.29-1.61).

Conclusion

Declines in PCV serotype IPD indicate an annual progressive indirect effect of infant PCV10/13 vaccination on IPD burden in the elderly. However, the gradual increase in non-PCV13 IPD, suggesting serotype replacement, partly countered the herd protection effect on overall IPD. Progressive decreases in PCV13 serotype IPD limit the potential benefit of direct PCV13 vaccination of the elderly. Further monitoring of trends in IPD in older adults is needed to better estimate the balance of herd protection and serotype replacement.

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

ABSTRACT ID: 286

PRESENTED BY: Germaine Hanquet (ghanquet@skynet.be)

09.3 Comparison of the epidemiology of vaccine preventable and non-vaccine preventable invasive Haemophilus influenzae disease in Canada, 2011-2015

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Background

The pan-Canadian implementation of routine childhood vaccination programs against Haemophilus influenzae type b (Hib) in 1988 has resulted in a 95% decrease in the incidence of invasive disease due to Hib. A review of national Hi epidemiology has not been done since invasive disease due to non-b H. influenzae serotypes (Hi non-b) became nationally notifiable.

Methods

This study compares the epidemiology of invasive Hib and Hi non-b in Canada. Data sources included the Canadian Notifiable Disease Surveillance System, the International Circumpolar Surveillance (ICS) and provinces and territories. Death data were obtained from the Statistics Canada Death Database. Descriptive analyses were conducted for the time period 2011-2015, except most recent death data were 2008-2012. Incidence rates (IRs) were calculated per 100,000 population.

Results

The average IR for Hi non-b was 16.5 times higher compared to the IR for Hib (1.47 and 0.08, respectively). Hib IRs were stable during this time, while Hi non-b IRs showed an increasing trend. The highest IRs for both Hib and Hi non-b were in infants < 1 year (1.32 and 10.27) followed by those ≥ 60 years (0.11 and 3.60). On average, 10 deaths occurred annually; 44% in adults ≥60 years and 12.5% in infants <1 year. In Northern Canada, the most common serotypes identified were a (69.5%), b(7.1%) and f(5.7%); non-typeable represented 11.5%.

Conclusion

While Hib incidence remains low, Hi non-b, appears to be an important cause of morbidity in Canada, particularly Hi type a, as a significance cause of invasive disease in Northern Canada. Expansion of surveillance activities is warranted to support further understanding of changing Hi epidemiology and vaccine development.

Keywords: Invasive Haemophilus influenzae, Canada, Epidemiology Surveillance

ABSTRACT ID: 298

PRESENTED BY: Susan Squires (Susan.Squires@phac-aspc.gc.ca)

09.4 Increase in invasive serogroup W meningococcal disease in 2015 and 2016 in the Netherlands

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Background

In the Netherlands, the incidence of invasive serogroup W meningococcal disease (MenW) has been very low in the last decade. However, increased numbers of MenW cases were observed in 2015 and 2016. MenW vaccination is not included in our national program. We assessed changes in the MenW incidence in the last 2 years in the Netherlands and described the recent cases.

Methods

All microbiological laboratories in the Netherlands submit Neisseria meningitidis isolated from blood or cerebrospinal fluid (i.e. invasive meningococcal infections) to the Netherlands Reference Laboratory for Bacterial Meningitis for serogrouping and finetyping. We compared the incidence rate (IR) of MenW in 2015 and 2016 (up to May 6) with the IR in 2005-2014. We describe age, mortality and finetype of the MenW cases diagnosed since October 2015.

Results

During 2005-2014, there were on average four MenW cases per year (range: 1-6; IR=0.022/100,000/year). The IR increased significantly in 2015 to 0.053/100,000/year (n=9; IRR=2.4 [95%CI:1.1-4.9]) and 2016 to 0.273/100,000/year (n=16; IRR2016vs2005-2014=12.2 [6.8-22.0]; IRR2016vs2015=5.1 [2.3-11.6]). In 2016, 28% of Men cases were MenW (16/58); this was 10% (9/90) in 2015 and 3% (37/1453) in 2005-2014. Of 21 MenW cases since October 2015, two were <5 years (10%), five were 20-29 years (24%), five were 30-64 years (24%) and nine were ≥65 years (43%). Mortality was 11% (2/18). The majority of cases had finetype P1.5,2:F1-1 (17/20; 85%).

Conclusion

The MenW incidence increased in 2015 and 2016 in the Netherlands due to a specific finetype, which is associated with the hypervirulent clonal complex 11. Meningococcal disease is unpredictable, but patterns of increase suggest we may expect increasing rates in the coming years. Continuous surveillance is performed to support timely vaccine policy decisions.

Keywords: meningococcal serogroup W, incidence, surveillance, vaccination

ABSTRACT ID: 296

PRESENTED BY: Mirjam Knol (mirjam.knol@rivm.nl)

O9.5 Meningococcal carriage in university students and military recruits during the pre MenB vaccination era in Greece (2014-2015)

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Background

Meningococcal carriage studies are valuable tools in order to monitor the circulating clones and obtain information for decision making on vaccine policy. The aim of the study was to estimate the meningococcal carriage rate, and characterize the strains isolated from healthy young adults in Greece.

Methods

1,420 oropharyngeal swab samples were collected from military recruits and university students (680 and 740 respectively) in 2014 and 2015. Identification and molecular characterisation were carried by mPCR, MLST and WGS analysis. The odds ratios for known factors associated with N.meningitidis carriage and the respective 95% confidence intervals were calculated by the use of Open Epi, v3. The Z- test for two population proportions was used and a two-tailed $p<0.05$ was considered as significant.

Results

The carriage rates were 15% in recruits and 10.4% in university students; significant lower compared to our previous studies (25% and 18% for recruits and students, $p<0.05$ and $p=0.002$ respectively). Median age for military recruits and university students was 20 and 21 years respectively. 35% were smokers; higher among military recruits (77% and 23%). Prevalent genogroups were MenB (39.4%) MenY (12.8%), MenE (8.3%), MenW (4.4%) and MenX (3.3%), while 29.4% were non-groupable. Among the MenB, 6 clonal complexes were identified; 41/44 cc was the most predominant.

Conclusion

Carriage studies remain crucial for the epidemiology of meningococcal disease. According to the data provided, a decrease on carriage rates was observed in comparison to previous studies, while, an increasing trend was observed among the MenB isolates. These data could potentially serve as basis for comparisons and estimations of the possible effect of immunization with the new MenB vaccine and on the dynamics of meningococcal carriage and disease in Greece.

Keywords: N. meningitidis, meningococcal carriage, genogroups, clonal complexes, university students, military recruits

ABSTRACT ID: 105

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

PARALLEL SESSION PROGRAMME
TUESDAY, 29 NOVEMBER
14:30-15:30

Parallel Session 10: Emerging and vector-borne diseases (2)

Moderator: Herve Zeller, ECDC, Head of Disease Programme Emerging and Vector-borne Diseases

O10.1 High impact of flooding on mental health outcomes: a cohort study in response to the 2013/14 floods in England

Daiga Jermacane[1,2], Thomas David Waite[1,2,3] Katerina Chaintarli[1,9], Charles R Beck[3,4,9], Angie Bone[5], Richard Amlôt[6], Sari Kovats[7], Ben Armstrong[7], Giovanni Leonardi[5], G James Rubin[8], Isabel Oliver[3,4,9]

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Background

The longer term impact of flooding on health is poorly understood. In 2015, following widespread flooding in the UK, Public Health England launched the National Study of Flooding and Health, a ten-year cohort study to examine the effect of flooding and related disruption on mental health and wellbeing.

Methods

In 2015 and 2016, participants affected by the winter 2013/14 floods, completed i) a standardised questionnaire on a comprehensive assessment of flooding-related exposures and ii) validated instruments to screen for anxiety, depression and post-traumatic stress disorder (PTSD). We classified exposures into three categories: flooded, disrupted and unaffected, based on flood-related damage to accommodation, access to services and secondary stressors (such as economic and social disruption). We calculated adjusted odds ratios (aOR) with 95% confidence intervals (95%CI), using logistic regression.

Results

In year 1 (2015), of the 8,761 invited households, 2,126 (23%) responded and of those 1,406 (16%) participated in the year 2 follow-up (2016). At 12 months post-flooding, the odds of PTSD were higher for flooded (aOR 7.2; 95% CI 4.3–12) and disrupted participants (aOR 2.1;95% CI 1.3–3.4), compared with unaffected individuals. Amongst participants who reported flooding of the liveable rooms, the odds of anxiety or depression were higher (aOR 6.5; 95%CI 3.8–11 and aOR 5.9; 95%CI 3.2–11, respectively), compared with unaffected participants. Data analysis for year 2 is underway.

Conclusion

Both flooding of liveable rooms in the home and disruption from flooding were associated with poor mental health outcomes. Providers of primary care and mental health services should take into account the potential impact of flooding on mental health, when planning services, especially in areas at high risk of flooding.

Keywords: floods, mental health outcomes, exposure assessment, disruption, environmental exposure

ABSTRACT ID: 38

PRESENTED BY: Daiga Jermacane (jermacane@gmail.com)

O10.2 Prepare, detect and respond - Portugal's preparedness for Zika virus in 2016

Guilherme Duarte (1,2), R. Sá Machado (1), N. Pereira (1), P. Silva (1), S. Ferreira (1), I. Falcão (1), C. Santos (1), P. Nogueira (1)

1. Direção-Geral da Saúde
2. European Programme for Intervention Epidemiology Training

Background

Portugal faces special challenges from the current Zika virus (ZIKV) outbreak, having a historical relationship with Brazil and Venezuela (aprox. 44000 passengers/week from Central and South America). Early detection of cases is particularly important in Madeira, due to the risk of autochthonous transmission; Madeira has both the vector (Aedes aegypti) and 0.5% of residents from affected countries.

Methods

Portugal's ZIKV surveillance uses data from the National Laboratory (INSA), clinicians and National Notifiable Disease system. Cases are classified as probable or confirmed, using the ECDC criteria. Pregnant cases are offered monthly follow-up. Congenital anomalies are notified through an existing surveillance system; neurological disease is not currently part but is being considered for ZIKV surveillance. Entomological surveillance is established since 2005 (Madeira) and 2008 (continent) consisting of grid placement of ovitraps (larvae) and BG-traps (adult mosquitoes).

Results

To 21st April 2016, 295 samples were tested in INSA, of which 16 (5,4%) were confirmed. Most (15/16) were travel-associated with a single case of sexual transmission. 9/16 were non-nationals. No pregnant, or locally acquired cases were reported. Two were reported in Madeira including the sexual transmission. At this point none of the ZIKV cases have been associated with neurological disorders. The mean/median delay between symptoms leading to diagnosis and reporting has been 19,8 days. Entomological survey in Madeira showed no signs of ZIKV infected mosquitoes.

Conclusion

More ZIKV cases are expected in upcoming months prompting the need to improve already existing surveillance systems. Notification delays must be minimized in order to prevent infection of invading mosquitos in Madeira, while promoting consistent sexual precautions and maintaining mosquito control. Neurologic surveillance should be established.

Keywords: Zika Virus Infection, Portugal, Madeira Island, Communicable Disease Control

ABSTRACT ID: 222

PRESENTED BY: Guilherme Duarte (guilhermegduarte@gmail.com)

O10.3 Surveillance of Zika Virus infection in mainland France, 2015-2016: an essential tool to limit local transmission

Alexandra Septfons (1-2), I.Lepart-Goffart (3), F.Franke (4), C.Six (4), A.Guinard (5), A-H.Liebert (6), I.Poujol (7), S.Raguet (8), C.Rousseau (9), A. Saidouni-Oulebsir (10), M.Subiros (1), V.Servas (11), E.Terrien (12), D.Viriot (1), , H.Noel (1), H.De Valk (1), MC.Paty (1)

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Background

Zika virus (ZIKV) is an emerging mosquito-borne flavivirus which typically causes mild disease. Since 2015, ZIKV has spread rapidly throughout the Americas including the French territories (FTA) and revealed new modes of transmission and clinical manifestations, including sexual transmission, congenital malformations and neurological syndromes. There is a risk of introduction and transmission of ZIKV in mainland France, because of the number of travellers from FTA and the presence of the vector Aedes albopictus. Surveillance of Zika infection and its complications in mainland France was established, based on existing surveillance for chikungunya and dengue, to rapidly detect cases, prevent local transmission including vector control measures, and ensure clinical follow up of infected pregnant women.

Methods

The surveillance included (i) notification of laboratory-confirmed cases (detection of specific IgM or IgG by plaque-reduction neutralization test or seroconversion or viral nucleic acids by RT-PCR), (ii) notification by Prenatal Diagnostic Centers of microcephaly (foetal head circumference < 3rd percentile, or < 2 standard deviations in newborns) and other malformations in foetuses or newborns of women with Zika infection or exposed to sexual or mosquito-borne transmission.

Results

From 1st January to 3rd May 2016, 242 ZIKV cases were reported including 8 in pregnant women, 5 sexually-transmitted case, and one meningoencephalitis case. Eighty-seven (36%) cases lived in an area where Ae.albopictus is established. No Zika-related congenital malformation has been detected.

Conclusion

The high proportion of ZIKV cases in areas where Ae.albopictus is established and the severe Zika-related adverse outcomes trigger the need to monitor closely the autochthonous and vertical transmission. Vector control measures are essential during the active period of the vector (May to November), around each arbovirus case in Ae.albopictus infested areas

Keywords: Zika, surveillance, Aedes, France

ABSTRACT ID: 78

PRESENTED BY: Alexandra Septfons (alexandra.septfons@santepubliquefrance.fr)

Parallel Session 11: Antimicrobial resistance and healthcare-associated infections (2)

Moderator: Panayotis Tassios, ESCAIDE Scientific Committee, Greece

O11.1 Incidents and Outbreak Logging system (IoLog): a rapid communication tool for reporting care home outbreaks in the East of England

Hannah Evans (1,2,3,4), I. Roddick (3), M. Reacher (3), B. Nazareth (2), A.G. Shankar (1,2,4)

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Background

In 2012, the Incidents and Outbreak Logging (IoLog) system (a web-based tool for communicating descriptive epidemiological information on care home outbreaks to hospitals in the East of England) was implemented. Previously, care homes reported to Health Protection Teams (HPTs), who reported to Infection Prevention and Control (IPC) teams via telephone, requiring significant time resource. Of three HPTs, two use the system, one since inception. We evaluated the simplicity, completeness and timeliness of IoLog to record outbreaks focusing on care home norovirus, known to cause considerable burden.

Methods

We emailed an online questionnaire to HPTs and IPCs users. Simplicity was self-reported, and defined as <5 minutes to create a record. We extracted data on care home outbreaks from loLog and HPZone (a case management system) from 01/01/2013-31/12/2015. We calculated completeness as the proportion of norovirus outbreaks logged on loLog compared with HPZone, matched by postcode and report date as no common identifier was available. We calculated timelines as percentages of outbreaks reported on the same day as HPZone.

Results

44 questionnaires were received from IPC (70%) and HPT (30%) staff. Among users that create records, 38% (8/21) reported that it took <5 minutes. Norovirus accounted for 72% (633/885) of IoLog outbreak records. Completeness of IoLog reporting was 86% (572/665), and timeliness was 76% (435/572).

Conclusion

IoLog is a rapid outbreak information communication tool, and its use should be considered by all HPTs. IoLog record completeness is likely underestimated due to the lack of a common identifier with HPZone, but the time to create a record should be explored. IoLog could be further utilised to record other infection outbreaks (e.g. influenza) and expanded to other settings (e.g. schools).

Keywords: Evaluation Studies as Topic, Disease Outbreaks, Risk Management, Infectious Disease Reporting

ABSTRACT ID: 143

PRESENTED BY: Hannah Evans (hannah.evans@phe.gov.uk)

O11.2 Hospital admission-prevalence and determinants of C. difficile colonisation: a cross-sectional survey with nested case-control and case-case studies among patients of Vienna General Hospital 2013-2015

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Background

Estimated hospital-admission C. difficile (CD) colonization (CDC) prevalence is 3-5% in industrialised countries. CDC risk factors knowledge is sparse. We aimed to estimate CDC admission-prevalence at Vienna General Hospital and identify colonisation determinants.

Methods

Non-diarrhoeal patients, admitted to five non-oncological departments (selected based on availability) between July 2013-July 2015, submitting admission stool samples were included in the CDC-admission-prevalence study. Consenting CDC-patients were included as cases in the nested case-control (CD negatives) study. CD infection (CDI) patients from departments were included in the CDC/CDI case-case study. Investigated colonisation determinants were age, sex, comorbidities, comorbidity-severity, proton pump inhibitor (PPI) use 7 days, antibiotic use 2 months and previous hospital stay 6 months prior to admission and pathogen characteristics (toxin encoding genes, risk-associated ribotypes and antimicrobial resistance). A study-coordinator collected information using hospital discharge data, personal interviews and laboratory data. CDC-cases were compared with controls and CDI-cases using univariate and stratified logistic-regression.

Results

CDC admission-prevalence was 5.5% (n= 63/1136; 95%CI: 4.4-7.0). Comparing 29 CDC-cases to 116 controls, CDC-cases were more likely exposed to PPI (OR 3.4; 95%CI 1.4-9.1), antibiotics (OR 2.6; 95%CI 1.1-6.3) and previous hospitalisation (OR 3.3; 95%CI 1.3-9.6). Comparing 29 CDC-cases to 35 CDI-cases, CDC-cases were less likely to be ≥60 years (OR 0.2; 95%CI 0.1-0.5) and to have diabetes (OR 0.3; 95%CI 0.1-1.0). Stratified outcomes were similar. Isolates did not differ in pathogen characteristics.

Conclusion

Admission-prevalence results confirm previous international findings. Results suggest an association of CDC with PPI, antibiotics use or hospital stay. Despite low study power, we found that following CD-acquisition, older patients and those with diabetes are more likely to develop CDI than CDC, while CD-strain characteristics seemed to not be associated with clinical presentation.

Keywords: Clostridium difficile, Carrier state, Epidemiological determinants, Antimicrobial drug resistance, Ribotyping, Bacterial toxins

ABSTRACT ID: 121

PRESENTED BY: Alexander Spina (alexander.spina@ages.at)

O11.3 Is it valid to compare surgical site infections rates between countries? Results from a study of the English and Norwegian surveillance systems

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2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden
3. National Infection Service, Public Health England, London, United Kingdom

Background

ECDC coordinates a European surveillance network for surgical site infections (SSI), collating and publishing data from national surveillance programmes to shape public health policy. We assessed whether differences in surveillance methods could significantly influence national SSI rates through comparison of two countries' surveillance.

Methods

We assessed surveillance methodology and compared SSI rates in England and Norway (September 2012-January 2015) for common surgical categories: coronary artery bypass graft (CABG), colon surgery, cholecystectomy and hip prosthesis (HPRO). Category-specific SSI rates were compared between countries using univariable and multivariable logistic regression adjusting for sex, age, American Society of Anaesthesiologists' (ASA) score, wound contamination, operation duration and length of postoperative stay. We performed these analyses on all reported procedures in each surgical category and on a subset reported by both countries.

Results

In-patient and readmission surveillance methods were comparable with exception of the case definition for superficial infection, restricting analyses to deep-organ-space SSI. For CABG, the crude odds ratio (OR) for England compared to Norway was 2.4 (95%CI: 1.4-4.4) whereas adjusted OR (aOR) lost significance (1.1, 95%CI: 0.57-2.0). For colon surgery the decreased odds (0.68, 95%CI: 0.56-0.81) remained significant after adjustment (0.42, 95%CI: 0.34-0.51). We found no associations in cholecystectomy. For HPRO the crude OR suggested no significant difference (1.2, 95%CI: 0.72-2.1), whereas the aOR was significantly lower in England (0.45, 95%CI: 0.25-0.81). Including only the subset of procedures reported by both countries yielded comparable results.

Conclusion

Differences in case definitions and population under surveillance in the English and Norwegian SSI surveillance systems affected SSI estimates making comparison of crude rates unreliable. Standardised definitions and adjustment for established risk factors are essential for European comparisons in order to guide public health action.

Keywords: Surgical Wound Infection, Surveillance, Infection control, Public health policy, Epidemiology,

ABSTRACT ID: 113

PRESENTED BY: Hinta Meijerink (hinta.meijerink@fhi.no)

Parallel Session 12: Vaccine preventable diseases (3)

Moderator: Tarik Derrough, ECDC, Expert Vaccine-preventable Diseases

O12.1 The impact of herd immunity on cost-effectiveness when modelling rotavirus vaccination

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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. Herd immunity, i.e. the indirect protection of unvaccinated individuals as a result of others being vaccinated, could affect the cost-effectiveness (CE) of rotavirus vaccine, since rotavirus is highly contagious. The aim with this study was to estimate how much impact the inclusion of herd immunity in the epidemiological model has on the CE.

Methods

We performed two CE-analyses of rotavirus vaccination based on different epidemiological models; a dynamic simulation model that included herd immunity, and a static model in which herd-immunity was not included. Both epidemiological models simulated the course of rotavirus in the Swedish population over a period of six years, with and without vaccination. Vaccination coverage was set to 95% among children 0-2 years old, and the vaccine-effect to 68% and 98% for mild and severe infection respectively. The number of infected, and thus the risk of infection, were calibrated to correspond to Swedish incidence. Both CE-analyses included costs for health care consumption and health effects, measured as quality-adjusted life years (QALY). Output from the epidemiological models, and input to the CE-analysis, were annual number of mild and severe cases of rotavirus gastroenteritis among children under five.

Results

Results show that the effect of vaccination is underestimated when herd immunity is excluded and increased the cost per QALY gained by 27%, from about 58 000 euro to 74 000 euro.

Conclusion

Herd immunity has a great impact when modelling cost-effectiveness of rotavirus vaccination, predominantly since it is a highly contagious infection.

Keywords: Modelling, rotavirus, herd immunity, health economics, sensitivity analysis

ABSTRACT ID: 331

PRESENTED BY: Ellen Wolff (ellen.wolff@folkhalsomyndigheten.se)

O12.2 Sex-differences in IgG-responses to childhood vaccinations

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2. Department of Pediatric Immunology and Infectious Diseases, Wilhelmina Children's Hospital, University Medical Center Utrecht, Utrecht, The Netherlands

Background

If immune responses to vaccination differ between males and females, sex-specific vaccination schedules may be indicated. A recent meta-analysis found higher responses in girls for diphtheria, pneumococcal and some meningococcal vaccines and similar responses for tetanus and Hib vaccines. To investigate this in a different population and for an additional pathogen (pertussis), we systematically reanalysed clinical childhood vaccination studies conducted in The Netherlands for sex-differences in IgG-responses.

Methods

Five studies with IgG-measurements following infant pneumococcal (PCV7/PCV10/PCV13) and/or DTaP-IPV-Hib(-HepB) vaccinations for 1118 children were included. We performed one-stage individual participant data meta-analyses of the effect of sex on log-transformed IgG-levels per time-point using linear mixed models. Separate analyses were performed for IgG against pneumococcal serotypes (plus pooled across serotypes), diphtheria toxoid, tetanus toxoid, pertussis Ptx/FHA/Prn and Hib-PRP. A fixed effect for study-group was included to account for differences in measurement technique and vaccination type and schedule. Where applicable, clustering of measurements by individual was accounted for through a random intercept.

Results

For pneumococcal vaccination, the geometric mean ratio (GMR) of IgG-levels in girls versus boys pooled across serotypes was 1.16 (95%CI 0.99-1.37) following the primary series, 1.16 (1.02-1.31) at age 8 months, 1.12 (1.02-1.23) prebooster (age 11 months) and 0.99 (0.90-1.09) postbooster (age 12 months). This pattern was relatively consistent for the different serotypes. Diphtheria toxoid, tetanus toxoid, pertussis Ptx/FHA/Prn and Hib-PRP IgG-levels did not differ between girls and boys, except for Hib postbooster (GMR 1.24; 95%CI 1.01-1.52).

Conclusion

Responses to infant pneumococcal conjugate vaccination were generally higher in girls between primary series and booster. However, we found no differences following booster vaccination. We found no consistent evidence of sex-differential IgG-responses to infant diphtheria, tetanus, pertussis or Hib vaccination.

Keywords: pneumococcal vaccines, DTaP-IPV-Hib-HBV vaccine, IgG, female, male

ABSTRACT ID: 265

PRESENTED BY: Anna Boef (anna.boef@rivm.nl)

O12.3 Non-specific effects of vaccines with live attenuated pathogens

H. Nieminen, A.A. Palmu, H. Rinta-Kokko, R. Syrjänen, H. Nohynek, E. Ruokokoski, M. Lahdenkari and J. Jokinen

Department of Health Protection, National Institute for Health and Welfare, Finland

Background

Recent studies have suggested live vaccines to have non-specific effects that protect against other than the specific infections the vaccines are targeted against. In Finland we have excellent opportunities to study the non-specific effects as we have nation-wide health registers and altogether three changes in the national vaccination programme (NVP) that serve as "natural experiments".

1. September 2006: The target group for live tuberculosis vaccine (BCG) was changed from all newborn babies to babies of parents in defined risk groups (mainly immigrants).Thus, the vaccination coverage in children of Finland-borne parents diminished from almost 100% to 0% overnight.
2. September 2009: Rotavirus vaccine was included into NVP. The vaccination coverage was about 30% before inclusion and afterwards about 90%.
3. May 2011: Recommended administration time of the measles-mumps-rubella –vaccine (MMR) was changed from 14-18 months to 12 months. The vaccination data of each individual will be obtained from Vaccination Register.

Methods

Before-after design will be used to study the potential non-specific impact. The outcome data will be obtained from National Care Register (hospitalisations with ICD10 codes compatible with outcomes) and National Infectious Diseases Register (notifications of infections). We will compare incidences of pneumonia, urinary tract infections, confirmed viral and bacterial infections and asthma among BCG and rotavirus vaccine-eligible children and MMR vaccinated children in comparison to unvaccinated children.

Results

In our first analysis pneumonia incidence was lower among BCG-eligible infants (n=125 626) under three months of age than among unvaccinated (n=127 004), 5.1 vs. 6.9 per 1000 person-years, respectively. Incidence rate ratio was 0.74 (0.60-0.91).

Conclusion

We will continue analyses for BCG, rota and MMR vaccinations for other outcomes to evaluate the non-specific effects further.

Keywords: Non-spesific effects, vaccines, BCG, MMR, pneumonia

ABSTRACT ID: 258

PRESENTED BY: Heta Nieminen (heta.nieminen@thl.fi)

PARALLEL SESSION PROGRAMME
TUESDAY, 29 NOVEMBER
17:00-18:30

Parallel Session 13: Vaccine preventable diseases (4)

Moderator: Thea Fischer, ESCAIDE Scientific Committee, Denmark

O13.1 General practitioners and pediatricians' perceptions, beliefs, attitudes and acceptance towards vaccinations in Baden-Wuerttemberg, 2016

Nobila Ouédraogo (1,2,4), G. Pfaff (1), D. Lohr (1), O. Wichmann (3), B. Bödeker (3), E. Aichinger (1)

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2. Postgraduate Training for Applied Epidemiology (PAE, German FETP), Robert Koch-Institute, Berlin, Germany
3. Robert Koch-Institute, Berlin, Germany
4. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden

Background
Vaccine-preventable diseases and vaccination gaps remain a public health concern in Baden-Wuerttemberg (BW). We adopted a "Guide to Tailoring Immunization Programmes" by WHO to investigate perceptions, beliefs and attitudes of general practitioners (GP) and pediatricians toward vaccinations and their acceptance of providing vaccination services.

Methods
We selected six of 44 counties by second-dose measles vaccine coverage below (5) and above (1) the statewide coverage (88.4%) and mailed anonymous questionnaires with 50 main items to all 1149 GPs and pediatricians in the study area. We categorized response scores for physicians´ beliefs toward vaccination, attitudes and acceptance. We compared counties above (A-county) vs. below (B-county) statewide coverage and GPs vs. pediatricians regarding variables of interest.

Results
Overall 459 GPs and pediatricians replied (40%). Respondents considered fear of side effects (86%) and missed vaccination appointments (76%) as most frequent causes of incomplete vaccination coverage. Roughly 18% of respondents use electronic reminder systems for their patients. We ascertained 67% physicians with positive and 33% with neutral beliefs. Attitude towards vaccination was stated as supportive by 82%, neutral by 17% and non-supportive by 1% of respondents. We observed medium acceptance of providing the vaccinations in 51% (high: 38%; low: 11%). Except positive beliefs (A-county: 85%; B-county: 65%) (p=0.048), there was no significant difference between these two county categories. Supportive attitudes towards vaccination were significantly higher among pediatricians (89%) compared to GPs (79%)(p=0.038).

Conclusion
Two-third of respondents held positive beliefs and support vaccinations. Physicians accentuated uncertainty of parents about vaccination safety and missed appointments as explanations for vaccination gaps. We propose continuing training of vaccination providers on communication strategies especially for GPs and increased use of appointment reminder systems in order to improve vaccination coverage.

Keywords: tailoring immunization programmes, general practitioners and pediatricians, perceptions, beliefs, attitudes, acceptance

ABSTRACT ID: 249

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

O13.2 Determinants of early MMR vaccine uptake during a measles outbreak in the Netherlands in 2013-2014: a multi-level study

Laura M. Nic Lochlainn(1,2), T. Woudenberg(1), H.E. de Melker(1), S.J.M. Hahné(1)

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2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, Stockholm, Sweden

Background
During a large measles outbreak in the Netherlands among orthodox-Protestants in 2013-2014, a novel intervention was implemented by personally inviting all 6–14 month-olds for an early measles-mumps-rubella (MMR) vaccination in 29 municipalities with ~83% MMR vaccination coverage. We estimated uptake and assessed determinants for early MMR vaccination.

Methods
Using vaccination records from the National Immunisation Register (Præventis) we defined early MMR by receipt before 415 days of age. A multi-level multivariable logistic regression model, restricted to infants with three diphtheria-tetanus-pertussis (DTaP) vaccinations, was used to examine the association between sex, parents' country of birth, socioeconomic status (SES; at postcode level) and voting proportions for the Reformed political party (SGP; at municipal level) on early MMR uptake.

Results
In total, 5,800 (57%) infants received an early MMR vaccination, of whom 86% was vaccinated within one month of invitation. Only 1% of infants without prior DTaP vaccinations (n=1773, 18% of all infants) received an early MMR. Early MMR uptake did not differ by sex (OR 1.02 95%CI 0.93–1.13). Infants whose parents were born abroad were less likely to have received the early MMR (OR 0.80 95%CI 0.70-0.93). Compared with very high SES areas, early MMR vaccination was lowest in areas of high SES (OR 0.66 95%CI 0.49-0.87). A higher proportion of SGP voters (OR 0.89 per 5% increase, 95%CI 0.83-0.96) was also associated with lower uptake.

Conclusion
The uptake of early MMR vaccination was satisfactory, considering low vaccination coverage in these municipalities. However, among DTaP unvaccinated infants, uptake of early MMR was extremely low. In future outbreaks, information on determinants of the uptake of the early MMR found in our study could be used to tailor communication strategies.

Keywords: Measles-Mumps-Rubella Vaccine; Measles; Prevention & control; infant; Immunization; Disease Outbreaks

ABSTRACT ID: 376

PRESENTED BY: Tom Woudenberg (tom.woudenberg@rivm.nl)

O13.3 Low measles vaccination coverage in a mobile population and reasons for non-vaccination: results from a household survey in Kinkondja, DRC, 2015.

Georgios Theocharopoulos (1, 2, 3), J. N. Mwenge (3), C. I. Yumba (4), A. Lenglet(5)

1. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Sweden
2. Institute de Veille Sanitaire, Paris, France
3. Médecins Sans Frontières (OCA), Lubumbashi, Democratic Republic of Congo
4. Bureau Centrale de Zone (BCZ) , Democratic Republic of Congo
5. Médecins Sans Frontières (OCA), Amsterdam, The Netherlands

Background

In response to a measles outbreak in Haute Lomami region, Democratic Republic of Congo (DRC) (3,022 clinical cases and 154 deaths from March to August 2015), Médecins Sans Frontières (MSF) conducted a measles vaccination campaign (MVC) in a highly mobile population in Kinkondja prefecture and a household survey to estimate the measles vaccination coverage and understand reasons for non-vaccination.

Methods

We used two-stage cluster sampling to randomly select households. We collected data on measles vaccination status for children 6 months to 15 years and reasons for non-vaccination during the MVC in July-August 2015. We estimated the coverage in the MVC by age and gender. To identify factors associated with low coverage, we calculated adjusted prevalence ratios (aPR) using Poisson regression.

Results

We included 2,980 children from 709 households in 40 clusters. Of them, 50% were female. Measles coverage was 64% (95%CI: 63-66) and 85% (95%CI: 84-86) documented by vaccination card and by card and oral vaccination history, respectively. Coverage was higher when children's guardians were over 25 years (aPR: 1.2; 95%CI: 1.0 –1.4), communities were accessible by car or boat (aPR: 1.2; 95%CI: 1.0–1.4) and social mobilisers promoted the MVC (aPR: 1.3; 95%Cl; 1.1–1.5). For the 441 unvaccinated children, displacement (49%; 95%CI: 36-61) and inadequate information about the MVC (12%; 95%CI: 3.0-20), were the most frequent reasons for non-vaccination.

Conclusion

The MVC did not achieve the global standard of 95% coverage in Kinkondja in 2015. Better access to vaccination sites and knowledge about the MVC were predictive factors, suggesting that extensive social mobilization is required to achieve adequate measles coverage in these communities.

Keywords: Measles, Measles Vaccine, Mass Immunization

ABSTRACT ID: 129

PRESENTED BY: Georgios Theocharopoulos (theocharopoulos1@yahoo.com)

O13.4 Comparative Evaluation of District Health Information System 2 and District vaccine Data Management tools, Enugu State, Nigeria - 2015

Robinson Nnaemeka Nnaji (1), O. Ajumobi (1), J. Adegoke (2), A. Anagor (2),P Ossai (3), P. Nguku(1)

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2. African Field Epidemiology Network. Asokoro, Abuja
3. Ministry of health Enugu state

Background

Surviellance is an integral part of every health system. All along Nigeria uses district vaccine data management tool (DVDMT) for collection of surviellance data at all level including routine immunization. In 2012 Nigeria introduced the district health informaton system (DHIS2) as surviellance data collection tool. Enugu state commenced the use of DHIS2 alongside the usual DVDMT. We conducted a comparative evalluation of the operations of the old and new system and user preference for decision making.

Methods

We quantitatively and qualitatively assessed the surviellance attributes of DHIS2 and DVDMT in Enugu state 2015 using CDC guidlines 2001. We administered semi-structured questionnaire to all the local immunisation officers (LIOs) in the 17 local gorvernment area (LGAs) of enugu state to assess surviellance attributes. We assesed quality of the data captured by the two tools, interviewed six key informants(KI)(Enugu state director of public health, data manager, cold chain officer, state epidermiologist state immunisation officer and DHIS2 state implimentation officer)and conducted focus group discussion (FGD) with six randomly selected heads of department of health in the LGAs.

Results

All the LIOs accepted the intr,.loduction of the new tool. 16(94%) said that DHIS2 is more user friendly compared to DVDMT. 13(76%) agreed that DHIS2 is simpler than DVDMT. Completness of data is 100% in both systems. Timeliness of reporting is 100% and 90% in DHIS2 and DVDMT respectively. All KIs opined that dhis2 is better than DVDMT because it has features of data visualisation and real time reaporting. The FGD agreed that DHIS2 is better but it requries computer proficency of users.

Conclusion

DHIS2 is prefeared over DVDMT in Enugu state as it provides high quality data in real-time for prompt decision making. We recomended the use of DHIS2 over DVDMT in Enugu state, although training of users should be done.

Keywords: Surveillance evaluation, routine immunization, Enugu state, Health information system, Nigeria.

ABSTRACT ID: 89

PRESENTED BY: Robinson Nnaji (robinsonnnaji@yahoo.com)

Parallel Session 14: Food- and waterborne diseases and zoonoses (2)

Moderator: Ettore Severi, ECDC, Expert Outbreak Response: Food- and Waterborne Diseases

O14.1 Norovirus outbreak following a high school gala dinner in Denmark, April 2016

Celine Barnadas (1,2), C. Kjelsø (3), L. D. Rasmussen (2), C. W. Jensen (4), K. V. Sigsgaard (4), T. Jensen (4), S. Ethelberg (3), L. Muller (3).

1. European Public Health Microbiology (EUPHEM) training programme, European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
2. Microbiological Diagnostics and Virology, Statens Serum Institut, Copenhagen, Denmark
3. Department of Infectious Diseases Epidemiology, Statens Serum Institut, Copenhagen, Denmark
4. Danish Veterinary and Food Administration, Copenhagen, Denmark

Background

On April 6th 2016 an outbreak of gastroenteritis was reported in a high school in Zealand (Denmark) concurrently with a series of norovirus genogroup I outbreaks related to contaminated Lollo Bionda lettuce from France. The school kitchen initially indicated not having served this lettuce and that lettuce purchased in that period originated from Spain. An investigation was conducted to identify the outbreak source and propose adequate control measures.

Methods

School employees and students were requested to fill an electronic questionnaire to gather demographic, clinical and exposure information. Cases were defined as individuals who presented with diarrhea and/or vomiting from April 2nd to April 7th. Relative risks (RR) with 95% confidence intervals (CI) were calculated using multivariate analysis. One stool specimen was received for microbiological analyses.

Results

250/327 respondents attended a school gala dinner on April 1st. Analysis was restricted to 234 individuals. From those, 83 (35.5%) were cases. Individuals who consumed the dinner starter (salmon mousse) were 7 times more likely to become ill (RR 7.7, CI 2.2-26.7). Two individuals reported that the mousse was served on lettuce. Further inquiries with the kitchen staff revealed that about 150 starters individually served at the dinner contained Lollo Bionda lettuce and that it was of French origin and not from Spain (mistake on the invoice from supplier). The stool specimen was positive for norovirus genogroup I.

Conclusion

This investigation suggested that this outbreak was part of a series of norovirus outbreaks caused by Lollo Bionda lettuce. It shows how thorough epidemiological and microbiological investigations can bring to light associations hidden in misinformation and mistakes. The importance of record keeping and traceability was communicated to the wholesaler and the kitchen staff.

Keywords: Disease Outbreaks, Norovirus, Gastroenteritis, Denmark, Lettuce, Genotype

ABSTRACT ID: 156

PRESENTED BY: Celine Barnadas (cebs@ssi.dk)

O14.2 An outbreak of Norovirus infections from recreational lake water, Tampere, Finland 2014

Aleksandra Polkowska (1), S. Räsänen (2), M. Bojang (2), O. Lyytikainen (3), P. Nuorti (1, 3), K. Jalava (2, 4)

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2. City of Tampere, Tampere, Finland
3. National Institute for Health and Welfare, Helsinki, Finland
4. University of Helsinki, Helsinki, Finland

Background

In July 2014, an outbreak of gastroenteritis was detected among visitors to public beaches at several lakes around Tampere, Finland. We conducted an investigation to identify agent and source of infection and implemented control measures.

Methods

Cases were persons who had visited one or more of six public beaches during 21.07.-06.08.2014 and developed diarrhea, vomiting or two other symptoms (nausea, stomachache or fever). Case ascertainment and data collection was done using an internet-based survey, solicited by public announcement. We conducted retrospective cohort study to determine risk factors for illness. Stool and water samples were obtained for microbiological analysis.

Results

Of 1453 persons enrolled in the study, 244 met the case definition (attack rate: 17%, 68% were females, median age, 33 years). Cases peaked during 27-29.07. Cases were significantly younger than non-cases (p value 0.000). In univariate analysis, significant risk factors for gastroenteritis included ingestion of lake water (Risk Ratio (RR) 2.85; 95%CI: 2.17-3.71) and playing on wet sand at the beach (RR 1.90; 95%CI: 1.50-2.40). Increasing time spent in the water was associated with gastroenteritis in a dose-dependent manner. As many cases visited several beaches, initial outbreak reports were received from multiple locations. In a multivariate model, however, the source of the infection was likely at four beaches of two lakes adjacent to each other. Norovirus was found in 19 stool samples (genotype I in 17 samples, genotype II in 5 samples), all beach water samples were negative.

Conclusion

The likely source of this widespread outbreak was lake-water contaminated with norovirus at two popular lakes. Regular cleaning of the beach sites is recommended and informing the public about personal hygiene is key in preventing this type of outbreaks.

Keywords: Norovirus, outbreak, waterborne, gastroenteritis

ABSTRACT ID: 351

PRESENTED BY: Aleksandra Polkowska (apolkowska84@gmail.com)

O14.3 A large outbreak of giardiasis linked to a private swimming pool, North Yorkshire, UK, July–December 2015.

James Elston (1,2), S Padfield (3), L Coole (1,2), D Harmer (3), I Karagiannis (1), G.J Hughes (2)

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2. Field Epidemiology Service (Leeds), National Infection Service, Public Health England, UK
3. Public Health England, Yorkshire and the Humber, UK

Background

In October 2015, the local Health Protection Team was notified of four cases of giardiasis who had participated in a swim school for children. On inspection, inadequate pool filtration and flocculation practices were noted. Following preliminary investigations, an outbreak was declared and the pool closed.

Our objectives were to describe the outbreak and to identify exposures associated with increased risk of illness to inform recommendations.

Methods

Individuals reporting diarrhoea or illness with gastrointestinal symptoms after attending the swim school (open July–October 2015) were defined as cases and considered laboratory-confirmed if Giardia was identified by stool microscopy. We described outbreak-associated cases and undertook a retrospective cohort study among individuals who attended the swim school. We distributed an online questionnaire on exposures and illness via social media. We estimated adjusted risk ratios (aRR) and 95% CIs for relevant exposures.

Results

Of 316 swim school attendees, 186 (58.9%) were cases, of which 159 (85.5%) were laboratory-confirmed. 105 (56.5%) cases were ≤5 years old. Amongst 93 cases where symptom details were available, median symptom duration was 21 days; 43 (46.2%) experienced (median of three) recurrence(s) of symptoms after initial recovery. The outbreak was responsible for a >50-fold increase in local incidence of confirmed giardiasis. Risk of illness was higher in those who entered the water than those observing lessons (aRR 1.39; 95% CI: 0.99-1.94). Swimming during certain weeks was associated with significantly higher risk.

Conclusion

To our knowledge, this is the largest reported outbreak of giardiasis linked to a swimming pool. There was substantial associated morbidity, particularly among young children. This outbreak highlights the need for regulation and monitoring of hygiene and maintenance of privately owned swimming pools, to protect population health.

Keywords: Giardia, Giardiasis, Disease Outbreaks,Swimming Pools.

ABSTRACT ID: 58

PRESENTED BY: James Elston (james.elston@phe.gov.uk)

O14.4 Risk of gastroenteritis among participants of city canal swimming events in Amsterdam and Utrecht, the Netherlands, summer 2015

Rosa Joosten (1), G. Sonder (2,3), S. Parkkali (4,5), D. Brandwagt (1), E. Fanoy (1,4), L. Mughini Gras (4), J. van Beek (4), E. Ruland (1) , E. Siedenburg (2), S. Kliffen (2), W. van Pelt (4)

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3. Division of Infectious Diseases, Department of Internal Medicine, Academic Medical Center (AMC), University of Amsterdam, Amsterdam, The Netherlands
4. National Institute for Public Health and the Environment (RIVM), Centre for Infectious Disease Control, the Netherlands
5. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden

Background

In summer 2015 two city canal swimming events took place, the Utrecht Singel Swim (USS) and the Amsterdam City Swim (ACS). We investigated the occurrence of and risk factors for infections caused by swimming in urban canals to develop targeted preventive measures for future similar events.

Methods

An online questionnaire was sent to 160 USS and 2692 ACS participants and to three of their relatives who were not participating in the swimming events. A gastroenteritis case was defined as a participant with diarrhea, vomiting, nausea or abdominal pain. We calculated adjusted risk ratios (RR) and 95% confidence intervals (95%CI) using multivariable binominal regression. For the ACS, water and stool specimens were collected.

Results

106 USS and 1,964 ACS questionnaires were returned. 75% of USS-respondents and 70% of ACS-respondents were swimmers. The attack rate (AR) among USS swimmers was 9%, among non-swimmers 4% (RR 2.0; 95%CI 0.3-16.0). In ACS among swimmers AR was 31%, among non-swimmers 5% (RR 6.3; 95%CI: 4.1-9.5). Among ACS participants the risk for gastroenteritis increased by 44% (95%CI: 1.3-1.6) per interval of mouthfuls water swallowed (i.e. none, ≤3, >3 mouthfuls). Swimming in open water in the past 3 months and being male was protective among ACS participants (both RR 0.8; 95%CI 0.7-0.9). In 5 stool- and 3 water specimens, norovirus was detected, albeit with different typing.

Conclusion

Swimming and swallowing water was associated with gastrointestinal complaints. In the ACS event, norovirus was the most likely cause. As these events are becoming increasingly popular, we recommend organizers to inform participants about the health risks of swimming in canals. Training in open water and avoiding swallowing water could prevent gastrointestinal complaints.

Keywords: Gastrointestinal diseases/ epidemiology, prospective studies, swimming, risk factors, water pollution.

ABSTRACT ID: 77

PRESENTED BY: Rosa Joosten (RJoosten@ggdru.nl)

O14.5 Investigation of a Shiga toxin-producing Escherichia coli infection outbreak associated with haemolytic uraemic syndrome, Romania, Italy, January – April 2016.

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Background

Reports of shiga-toxin producing Escherichia coli (STEC) infections increased in the European Union (EU). STEC O26 is the second most frequently reported serogroup. We investigated a STEC outbreak in Romania and Italy to identify the source and prevent further cases.

Methods

In our investigation we included EU residents with an epidemiological link to Romania. Confirmed cases were individuals with laboratory-confirmed STEC O26 infection. Probable cases were individuals either diagnosed with haemolytic uraemic syndrome (HUS) or tested positive for stx1 and/or stx2 and eae or other STEC serogroups after 15/01/2016. We queried cases' food consumption during 10 days before disease onset. We tested suspected food items for STEC using the ISO/TS 13136:2012. We characterised isolates by Pulsed-Field Gel Electrophoresis (PFGE).

Results

From 25/01/2016 to 08/04/2016, we identified 13 confirmed cases (11 in Romania, two in Italy) and 14 probable cases (all in Romania): 21 were less than 2 years old, 19 had HUS, three fatalities. Italian cases consumed cow soft-cheese from one Romanian dairy mentioned twice in interviews in Romania that exported to other EU countries. Human and cheese isolates were obtained in both countries, PFGE was performed on seven human and three cheese isolates: both Italian STEC O26 isolates from humans and cheese showed >98% similarity. Alert was given through Epidemic Intelligence Information System for food- and waterborne diseases (EPIS-FWD) and Rapid Alert System for Food and Feed (RASFF). The Romanian dairy suspended operation on 28/02/2016; products were withdrawn from the EU market.

Conclusion

Results implicated contaminated cheese as a persistent common source of infection and emphasized that dairy production can be source for STEC O26 infection. Communication at the European level was crucial to prevent further cases.

Keywords: STEC O26, HUS, EU, dairy products

ABSTRACT ID: 146

PRESENTED BY: Emilie Peron (perone@rki.de)

Parallel Session 15: Influenza and other respiratory viruses (1)

Moderator: Pasi Penttinen, ECDC, Head of Disease Programme Influenza and other Respiratory Viruses

O15.1 In-season time trends of seasonal influenza vaccine effectiveness (SIVE) estimates – a pilot study, week 40 (w40) 2015 to week 18 (w18) 2016, Finland

Ulrike Baum, H. Nohynek, N. Ikonen, R. Syrjänen, J. Sundman, J. Jokinen National

Institute for Health and Welfare, Finland

Background

Finnish National Immunization Program (NIP) recommends seasonal influenza vaccination i.a. to elderly and young children. National register data allows on-line monitoring of epidemic course, coverage, and effectiveness, i.e. indicators important for evaluating NIP. Differences in mid-season and end-season SIVE were observed before, but time trends were not investigated. Objectives: monitoring potential in-season SIVE time trends in 2015-16, concluding how to improve analysis in 2016-17.

Methods

Since w4, we have weekly extracted vaccination and laboratory-confirmed influenza (LCI) records of w40 and later from Vaccination and Infectious Disease Register. We calculated SIVE (1 minus hazard ratio) against LCI in elderly (≥65years) and children (6-35months) on-line and retrospectively, i.e. in w8, w12, and w16, we recalculated w4, w8, and w12 SIVE based on up-to-date data.

Results

Through w18, 11381 LCI-A and 4157 LCI-B cases were detected. Epidemic curves peaked in w4 (2103 new LCI-A cases, 5892 cumulated) and w13 (449 new LCI-B cases, 3004 cumulated). 42% of elderly and 24% of children were vaccinated; 40% and 23% before w4. In elderly, SIVE reached 57%(95%CI:47%-65%) in w4 and slowly decreased to 51%(46%-56%); no differences between on-line and retrospective estimates. In children, on-line SIVE reached 50%(25%-67%) in w4, peaked at 60%(49%-68%) in w10 and decreased to 51%(40%-59%); retrospective estimates indicate SIVE plateau at ~60% (w4-w10) followed by substantial decline in w12 (53%;42%-61%).

Conclusion

Study revealed decreasing SIVE within season. Waning immunity could explain in-season time trend in both age groups and needs further investigation. SIVE decline in children appears timely associated with LCI-B epidemic, which could reflect poor match between vaccine and circulating B-virus. Discrepancies between on-line and retrospective estimates indicate register data delay. Consequently, register-based mid-season SIVE figures must be interpreted carefully.

Keywords: Coverage, Effectiveness, Immunization, Influenza, Vaccination

ABSTRACT ID: 191

PRESENTED BY: Ulrike Baum (ulrike.baum@thl.fi)

O15.2 Moderate vaccine effectiveness against hospitalization with severe influenza but low protective effect against mild influenza in elderly, season 2015-16, Spain

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4. Miguel Servet Universitary Hospital, Zaragoza, Aragon, Spain
5. CIBERESP, Institute Of Health Carlos III, Madrid, Spain

Background

The 2015-16 influenza season in Spain was dominated by Influenza A(H1N1)pdm09 with an increase of Influenza B circulation towards the end. We present the 2015-16 influenza vaccine effectiveness (IVE) estimates against mild confirmed influenza attended in primary care and against Influenza confirmed hospitalised severe acute respiratory sindrome (SARI), in elderly (above 64 years-old).

Methods

We used the Spanish Influenza Sentinel Surveillance Sistem (SISSS) data and the results from the two influenza reference regional hospitals (Donostia – Basque Country and Miguel Servet – Aragon) participating in the European I-MOVE+ study for measuring VE. For both studies we used a test-negative case control design, cases having a positive swab for influenza while controles were negative for all influenza viruses. We estimated the IVE as 1-Odds Ratio of vaccination, using logistic regression models and adjusting by age, onset of symptoms, sex, sentinel network/hospital, chronic condition and Barthel Index (for hospitalized patients).

Results

We included 113 cases and 112 controls within the SISSS study and 135 cases and 233 controls from the hospital study, between weeks 50/2015-16/2016. Adjusted IVE within the SISSS was 12% (95%CI: -75; 56), -15% (95%CI: -153; 47) and 9% (95%CI: -474; 86), while in the hospital study was 57% (95%CI: 22; 76), 45% (95%CI: -6; 72) and 69% (95%Ci: 1; 90) against any Influenza, A(H1N1)pdm09 and B Influenza, respectively.

Conclusion

Our results suggest no protective effect against mild influenza A(H1N1) pdm09 and a low IVE against mild B influenza, but a moderate-high protective effect against hospitalisation of patients with A(H1N1)pdm09 and B influenza. We highlight the importance of influenza vaccination in elderly as a potential preventive measure against severe forms of Influenza.

Keywords: Test negative design, Influenza vaccination, Influenza A(H1N1)pdm, vaccine effectiveness

ABSTRACT ID: 327

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

O15.3 Enteroviruses and their role in respiratory illness in Denmark, 2009-2015.

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4. Center for Global Health and Department of Infectious Diseases, Clinical Institute, University of Southern Denmark, Odense

Background

Enteroviruses (EV) are a common cause of hand-foot-and-mouth disease and meningitis and are globally monitored using EV screening of cerebrospinal fluids and stools. However, the recent extensive EV-D68 outbreak in USA/Canada, increased the awareness on respiratory EVs. Our objectives were to investigate the extend of respiratory disease caused by EVs and describe which EV genotypes are associated with these illnesses.

Methods

All respiratory samples (5607) submitted for viral diagnostic testing at SSI, from all regions of Denmark, were included in the study. Samples were tested using reverse transcriptase-PCR and subsequently sequenced followed by BLAST analysis against the NCBI/SSI-EV databases.

Results

During 2009-2015, 905 (16%) respiratory samples tested positive for EV, representing 745 disease episodes. Of these 399 episodes (54%) occurred in males and 390 episodes (52%) occurred in children aged ‹5 years. Of EV species indentified, rhinovirus (RV) was detected in 390 episodes (52%), followed by EV-A (11%) and EV-B (8%). For EV species A-D, 28 different EV genotypes were detected. The most frequent were Coxsackievirus A6 (12%), EV-D68 (4%), and Coxsackievirus A16 (4%). Of note, new emerging EV genotypes C104, C109 and C117 were indentified in three individual cases.

Conclusion

Our findings are the first to demonstrate that EVs constitute a major burden of viral respiratory disease among Danish patients. Further, we have documented a large variety of EV genotypes in respiratory specimens, of which some (EV-D68, EV-C104, EV-C109 and EV-C117) are not detectable in stools. In order to detect novel and emerging EVs, and allow for timely intervention in the event of outbreaks such as EV-D68, the existing EV surveillance-system needs to be enhanced to include typing of EV positive respiratory samples.

Keywords: Enterovirus,Genotype,Respiratory Tract Infections,Surveillance

ABSTRACT ID: 372

PRESENTED BY: Susanne Schjørring (SSC@ssi.dk)

O15.4 Seasonal influenza vaccination recommendations and vaccination coverage in EU/EEA countries, 2008/09 – 2014/15 influenza season. Results from surveys conducted by the VENICE network

Jolita Mereckiene (1,9), S. Cotter (1,9), K. Johansen (2), S. Tsolova (2), P. Penttinen (2), F. D'Ancona (3,9), D. Levy-Bruhl (4,9), O. Wichmann (7,9), L. Demattè (5,9), P. Valentiner-Branth (6,9), I. Stankiewicz (7,9), D. O'Flanagan (1,9) on behalf of the VENICE project gatekeepers group (10)

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9. Vaccine European New Integrated Collaboration Effort (VENICE) Project
10. The list of gatekeepers is available in the final report on VENICE website: http://venice.cineca.org

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Background

Since 2008 VENICE has conducted annual surveys to follow-up on changes in seasonal influenza vaccination policy and to identify compliance with the European Commission recommendation to achieve the European Union (EU) goal of 75% coverage in older age and risk-groups by 2014-15. Methods

In 2015 a survey was undertaken for influenza season 2014-15 across EU/EEA Member States (MS). Vaccination policy and coverage was compared between countries using data obtained from previous surveys. The questionnaire was completed on-line by MS gatekeepers. The questionnaire for United Kingdom was completed separately for England, Northern Ireland, Scotland and Wales.

Results

Of 30 responding MSs, all recommend seasonal influenza vaccines to older age-groups: 19 for individuals aged ≥ 65 years and 11 with lower age cut-offs (ranging from ≥ 50 to ≥ 60 years of age).Nine MSs recommend vaccination of healthy children. All MSs recommend influenza vaccine for clinical risk groups(n=30) and most for pregnant women(n=27) and health care workers (HCWs)(n=29).

Reported vaccination coverage varied by country and targeted group in 2014-15, ranging from 1.0%-76.3% (median 45.5%) for older age-groups(n=25) and 0.1%-79.7% for healthy children(n=7). Coverage in clinical risk-groups (n=7), HCWs (n=13) and pregnant women(n=5) ranged between 21%-71.8% (median 50%), 5%-54.9%(median 24%) and 0.3%- 56.1%(median 23.6%), respectively. Netherlands and United Kingdom have achieved or almost achieved the EU goal in older age-groups.

Conclusion

Most countries recommend influenza vaccination for the known risk-groups. However, few countries have achieved the recommended vaccination coverage among older age groups, and coverage information is not available in most countries for clinical risk-groups, HCWs and pregnant women. Additional work is needed to improve coverage and respective data across the EU region, and lessons learnt in countries with high coverage should be utilized.

Keywords: influenza, immunisation, vaccination, vaccination coverage, risk groups

ABSTRACT ID: 98

PRESENTED BY: Jolita Mereckiene (jolita.mereckiene@hse.ie)

O15.5 Possible impact of H1N1 flu pandemic in 2009 on the uptake of seasonal influenza vaccine in persons aged 65 years and older in Ireland, 2004-2015

Katerina Chaintarli (1,2), L. Domegan (2), J. O'Donnell (2), A. Barrasaa (1)

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2. Health Protection Surveillance Centre, Dublin, Ireland

Background

In Ireland, seasonal influenza vaccination is recommended for persons aged 65 years and older and is free for medical/GP cardholders. There is a year-on-year variation in the uptake and anecdotally the 2009 pandemic is thought to have influenced this. We conducted this study to determine whether the uptake has been influenced by the 2009 pandemic, age or deprivation status.

Methods

Aggregated seasonal influenza vaccine uptake data (2004-2015) by health authority area and age group were obtained from the national database. The Haase-Pratschke relative deprivation score (2011) was applied to these same areas. Using Poisson regression model, we estimated the associations between uptake before and after the pandemic, age and deprivation status.

Results

The median uptake was 62% before the pandemic (2004-2009) and 59% after (2010-2015). After adjusting for age, season and deprivation status, overall people aged ≥ 65 years were less likely to receive the seasonal influenza vaccine after the pandemic compared to before (Risk Ratio (RR)=0.89, 95% Confidence Interval (CI): 0.82-0.96).

Vaccine uptake increased with age; both those in the "70-74" and "above 75" years age groups were more likely to receive the vaccine compared to those aged 65-69 years (RR=1.18, 95%CI:1.14-1.24; RR=1.34, 95%CI:1.28-1.39 respectively).

There was no significant association between uptake and deprivation score. Areas with the highest/lowest uptake remained consistent across all seasons.

Conclusion

This study demonstrated that seasonal influenza vaccine uptake increased with age but decreased after the influenza pandemic. Qualitative studies should be undertaken to explore whether changes in public funding and/or people's perceptions on the risks of disease and the vaccine influenced the uptake. No association was found between uptake and deprivation status but disaggregated data are required to further explore this.

Keywords: Influenza Vaccine, Pandemics, Trends, Poisson Distribution

ABSTRACT ID: 94

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

PARALLEL SESSION PROGRAMME
WEDNESDAY, 30 NOVEMBER
11:00-12:40

Parallel Session 16: Food- and waterborne diseases and zoonoses (3)

Moderator: Johanna Takkinen, ECDC, Head of Disease Programme Food- and Waterborne Diseases and Zoonoses

O16.1 Risk of chronic Q fever in patients with cardiac valvulopathy, after a large outbreak of Q fever in the Netherlands

Marit M.A. de Lange (1,2,3), A. Scheepmaker (2), W. van der Hoek (1), P.M. Schneeberger (2,3).

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2. Bernhoven Hospital, Uden, the Netherlands
3. Jeroen Bosch Hospital, Den Bosch, the Netherlands

Background

From 2007 through 2010, the largest outbreak in the world of acute Q fever occurred in the Netherlands. Patients with cardiac valvulopathy have a high risk to develop chronic Q fever presenting as endocarditis, after experiencing an acute infection. However, patients with valvulopathy were not routinely screened for Q fever during and after the outbreak. Therefore, it is not known if all patients with chronic Q fever of the heart valves were diagnosed in time. The objective of this study is to investigate how many chronic Q fever patients can be identified, by routinely screening patients with valvulopathy, to establish whether the policy of not routinely screening should be adapted.

Methods

This study is a cross sectional study and is performed in one hospital in the epicentre of the outbreak. One blood sample was taken from patients above 17 years with a valvulopathy, who attended the hospital (admitted or routine check-up). The blood sample was tested for IgG antibodies against phase I and II of the Coxiella burnetii bacterium, with an immunofluorescence assay (IFA). Patients with an IgG phase I titre of ≥ 1:512 were suspected for a chronic Q fever infection. This study will run for one year or until 2,000 patients are screened.

Results

On 10 May 2016, after a three months study period, 222 patients were included, of whom 26 (12%) experienced an acute Q fever infection and no one had an indication for a chronic infection.

Conclusion

No definite conclusions can be drawn yet from these preliminary results. However, if the number of chronic infections will remain this low, no adjustment of the policy will be needed.

Keywords: Chronic Q fever, Coxiella burnetii, Netherlands, Heart valve diseases

ABSTRACT ID: 208

PRESENTED BY: Marit de Lange (marit.de.lange@rivm.nl)

O16.2 Do not feed the pigeons! First recorded outbreak of psittacosis in office workers with little or no exposure to birds in England, August 2015

John Mair-Jenkins (1), T. Lamming (2), A.Dziadosz (3), D. Flecknoe (2), T. Stubington (2), P. Monk (2)

1. Field Epidemiology Training Programme Fellow, Public Health England, UK
2. Public Health England East Midlands, Nottingham, UK
3. Environmental Health, Ashfield District Council, UK

Background

On 14th August 2015 an office manager informed Public Health England of five workers diagnosed with pneumonia within two weeks. We investigated to determine whether an outbreak had occurred and to identify and control the source.

Methods

We undertook case finding for self-reported pneumonia (confirmed by medical records) at local businesses (July-August 2015) and tested samples from a hospitalised case for common respiratory pathogens and Chlamydophila psittaci (serology/PCR). We subsequently undertook serology on all cases, redefining cases as confirmed (C.psittaci PCR/serological positive) or probable (inconclusive C.psittaci serology). Twenty-eight day exposure histories informed descriptive analysis. We conducted an environmental investigation at the office to identify sources of exposure.

Results

We identified six office workers with pneumonia; four met case definitions (three confirmed, one probable) with symptom onset between 29th July and 4th August. Three cases reported no contact with birds or guano, but the index case reported handling a dead pigeon. Workplace was the only epidemiological link between cases, two cases reported close contact at work. Environmental investigations identified pigeons being fed by workers (non-cases) and a flock roosting nearby. Actions included stopping the feeding of pigeons, a deep clean of office ventilation systems, and advising workers to avoid bird contact. Cases recovered after receiving appropriate antibiotics and no further cases were identified.

Conclusion

Our investigation revealed this unusual diagnosis in a novel setting. Little or no contact between cases suggested person-to-person transmission was unlikely. We hypothesised that transient environmental exposure to infected pigeons or guano was the source of this outbreak, but it was unclear how zoonotic transmission occurred. Health professionals should consider psittacosis in the differential diagnosis of cases of severe respiratory illness reporting no overt bird contact.

Keywords: psittacosis, outbreaks, zoonotic infections

ABSTRACT ID: 30

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

O16.3 Risk factors associated with seropositivity against Toxoplasma gondii: Results from the first representative serosurvey of adults in Germany

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3. Department for Mycotic and Parasitic Agents and Mycobacteria, Robert Koch Institute, Berlin, Germany

Background

Toxoplasmosis, caused by Toxoplasma (T.) gondii, is a zoonotic infection contracted by contaminated food or contact to infested cat faeces. Primary infection during pregnancy may lead to malformations in neonates. Immunocompromised persons may experience severe disease. Data on the extent of endemicity and characteristics associated with seropositivity are scarce. Our objectives were to conduct a representative serosurvey among adults in Germany to assess the seroprevalence of T. gondii and to identify associated factors.

Methods

Sera from a nationwide representative survey of adults were tested by an enzyme-linked fluorescence assay for anti-toxoplasma IgG-antibodies Data collected by interview were used to evaluate possible associated factors. Multivariable logistic regression used sampling weights and accounted for survey design cluster effects.

Results

Out of 6,663 individuals, 3,602 were seropositive. Seroprevalence increased from 20.0% (95%-CI:17.1%-23.1%) in the 18-29 age-group to 76.8% (95%-CI:72.7%-80.5%) in the 70-79 age-group. Male gender (OR:1.8; 95%-CI:1.1-2.9), keeping cats (OR:1.27; 95%-CI:1.06-1.51) and BMI≥40 (OR:2.6; 95%-CI:1.6-4.2) were independent risk factors for seropositivity; vegetarian status was negatively associated with seropositivity (OR:0.6; 95%-CI:0.4-1.0) as was a high socio economic status (OR:0.7; 95%-CI:0.6-0.9). Based on these data, we estimate 1.1% of adults and 1.3% of women aged 18–49 to seroconvert each year. This implies annually 6,393 seroconversions during pregnancies.

Conclusion

Our study demonstrates significant seroprevalence of T. gondii IgG. Variations in eating habits and cat ownership apparently influence seroprevalence. Seropositivity is not equivalent with a history of clinical manifestation, but disease burden and seroprevalence are likely to be correlated. Toxoplasmosis is often neglected in public health programs targeting foodborne disease. Medical doctors and public health authorities should be aware. Food hygiene standards regarding T. gondii should be kept high.

Keywords: toxoplasma gondii, toxoplasmosis, foodborne diseases, congenital infection, prevalence

ABSTRACT ID: 204

PRESENTED BY: Hendrik Wilking (WilkingH@rki.de)

O16.4 Avian Newcastle disease: a farm case-control study in Mananjary, Madagascar, 2015 – 2016

Nivohanitra Perle Razafindraibe (1,2,6), M.A. Andriamananjara (2), M. Biarmann(2), P.S. Fenozara (2), A. Halm (3), M. Tajding (4), F. Ravaomanana(5), O.F. Maminiaina (6), H. Razafimandimby (3), E. Cardinale (3), A.H. Rasamoelina(3)

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Background

Newcastle disease (ND) is a poultry-affecting viral disease with high mortality. In Madagascar, it causes significant (4.2 million Euros) losses each year. In December 2015, Mananjary district reported suspected ND cases. On 9 March 2016 we initiated an investigation to describe the outbreak and to identify associated factors to inform control measures.

Methods

We visited all farms of affected neighbourhoods. We interviewed farmers on number of sick and dead poultry, symptoms and lesions, disease onset date, poultry supply origin, vaccination. A farm-case was a farm in Mananjary district with poultry mortality and animals presenting at least two of these: diarrhoea, respiratory, nervous symptoms, swollen head, prostration, between July 2015 and March 2016. Farm-controls were “healthy” farms in the same villages. We took samples for PCR analysis. We calculated adjusted odds ratios (OR) and 95% confidence intervals (95%CI).

Results

Fifteen of twenty neighbourhoods were affected with 171 farm-cases and 74 farm-controls. The first farm-case appeared in July 2015. Predominant clinical signs were prostration (132/171, 77%) and torticollis (88/171, 51%). PCR results are pending. Of 4550 animals, 3149 (69%) were sick; 2896 (92%) died. Farm-cases were more likely to report passage of poultry resellers (OR=2.83; 95%CI=1.43-5.62), and poultry purchase on markets (OR=2.76; 95%CI=1.42-5.34). Twenty-three percent of farm-cases and 70% of farm-controls were vaccinated (OR=0.13; 95%CI=-2.02-0.25).

Conclusion

The symptoms, high attack rate and case fatality are compatible with an outbreak of ND. Our results suggest that poultry resellers and markets contributed to introduction and spread of the outbreak while vaccination protected.

The veterinary services should educate breeders regarding the risk of buying poultry on the market and resellers visits during outbreak periods. The central veterinary services should reinforce vaccination campaigns.

Keywords: Newcastle disease, outbreak, poultry, risk factors, Madagascar

ABSTRACT ID: 163

PRESENTED BY: Nivohanitra Perle Razafindraibe (nhperle@gmail.com)

Parallel Session 17: Travel and migrant health (2)

Moderator: Josep Jansa, ECDC, Head of Section Epidemic Intelligence and Response

O17.1 Communicable disease transmission pathways in migrant holding centres in Europe: a literature review

Flavia Riccardo (1,2), J. E. Suk (3), A. Bella (2), C. Giambi (2), M. Del Manso (2), C. Napoli (2), MG Dente (2), G. Nacca (2), S. Declich (2)

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3. European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden

Background

Migrant holding centres (MHC) host closed/semi-open communities. In order to identify the most frequent communicable disease transmission routes (CDTR) and issues for outbreak prevention/management, we conducted a systematic scientific and grey literature review.

Methods

We included studies and reports from 2000-2015 in English/French/Italian that focussed on CDTR in closed settings (educational, correctional, and military facilities). We retrieved articles through PubMED and reports from official websites. Only articles and reports considered to be relevant were reviewed in full text. We assessed if human resources (HR), physical infrastructure (PI), sanitation&disinfection (S), and medicines&vaccines (M) were critical for prevention and management of outbreaks.

Results

We identified 551 articles and 62 reports: 35 articles (24 outbreak investigations, 8 reviews, a modelling study, a survey and an exercise) and 21 reports focussed on CDTR in closed settings. 24 articles described human-to-human transmission (HH) in different settings, 4 articles gastro-intestinal infections (GI) in schools and jails/prisons. Blood-borne and/or sexually transmitted diseases (BBV/STD) and skin infections (5 and 1 respectively) were described only in jails/prisons. S (20 studies, 57%) was most frequently a critical dimension, followed by M (18; 51%), PI (12; 34%) and HR (5; 14%).

All reports focussed on migrant health, 20 covered MHC in Europe. All mentioned diseases with different CDTR (HH, GI, Skin infections). HR was most frequently critical (15 reports; 75%) followed by PI (13; 65%), S (12; 60%) and M (7; 35%). Overcrowding and health financing were also recurrent issues.

Conclusion

MHC face outbreaks from a wide range of pathogens. As in jails/prisons, specific challenges, such as BBV/STD, might apply to migrant detention centres. In contrast to other closed settings, HR and PI are most frequently critical in MHC.

Keywords: Transients and Migrants; Disease Outbreaks

ABSTRACT ID: 153

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

O17.2 Refugee crisis in Europe: health status, life experiences, and mental health problems of transiting refugees and migrants on the Balkan route in 2015

Iro Evlampidou (1), C. Baruzzi (2), C. Peruzzo (3), A. Meimaridou (2), E. Loyens (2), E. Faga (1), A. Ponthieu (1), M.E. Ingres (2), S. Moissaing (3), F. Zamatto (4), N. Severy (1), S. Argenziano (1), M. Van Herp (1), JP. Jemmy (1), C. Montaldo (1)

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Background

In 2015, over 1 million refugees/migrants reached Europe mainly through the Balkans. MSF provided medical and mental health (MH) care at entry/exit points in Greece and Serbia. We aimed to assess the medical and MH burden and document the experiences of transiting refugees/migrants.

Methods

We analysed routine outpatient (Jan-Dec 2015) and individual MH data (May-Dec 2015) from MSF clinics (Greece/Serbia). Information included socio-demographics, health status, traumatic life-events and MH symptoms.

Results

We performed 81,868 consultations (Greece: 43,619[53%]; Serbia: 38,249[47%]) in:<18 years:22,165(27%); women:15852 (19%). Most were Syrians (36,729;45%), Afghanis (26,332;32%) and Iraqis (8,848;11%); 12,796(16%) were vulnerable (pregnant, young/unaccompanied children, disabled) Presenting symptoms: resporatory tract (33,331;41%), physical trauma (12,792;16%), gastrointestinal (8965;11%), dermatological (8484;10%) complaints; 93% (74,232/79,784) reported onset during migration. 6% (n=4560) reported chronic diseases. We proposed referral to 680 (0.8%) of whom 129 (19%) were trauma cases; 77(11%) refused referral.

We performed 1064 individual MH sessions (Greece:733 [69%]; Serbia:331[31%]); 116(11%) were <18 years, 330(31%) women, 329(31%) vulnerable. Pateints experienced a median (IQR) of 3(2-4) traumatic life events:866(81%) forced to flee;281(26%) bombing;210(20%) life-threatening event;170(16%) family member(s) killed;203(19%) physical violence;156(15%) ill-treatment. State authorities perpertrated violence for 123(12%) and ill-treatment for 74(7%). MH symptoms (831/1052;79%): anxiety (246;30%), adjustment/acute reasons (198;24%), depression (165;20%), post-traumatic symptoms (60;7%). We followed-up only 120(11%), due to patients' need to move onwards: single orientation sessions/patient moved:937/1064(88%). We referred 356(33%) for social, medical/psychiatric care.

Conclusion

Many refugees/migrants were vulnerable, fled conflict and experienced physical and mental trauma and life-threatening events. The population's high mobility renders follow-up care challenging. Safety and early vulnerability screening should be ensured. Free and accessible health services, including MH and follow-up care, should be provided along a continuum in transit/destination countries through innovative ways.

Keywords: Refugees, Transients and Migrants, Health Status, Mental Health, Vulnerable populations, Europe

ABSTRACT ID: 268

PRESENTED BY: Iro Evlampidou (iro.evlampidou@gmail.com)

O17.3 Cross-sectional participatory study assessing the impact of HIV knowledge on testing uptake among migrants from sub-Saharan Africa in Berlin, Germany, 2015

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Background

Of the 3,674 new HIV diagnoses notified in Germany in 2015 15% were among migrants from Subsaharan Africa (MISSA). We conducted a participatory quantitative cross-sectional study with MISSA in Berlin in 2015 to improve the knowledge of sexual health and HIV, to identify determinants associated with HIV knowledge and testing uptake and to develop prevention strategies with stakeholders.

Methods

After community mapping, African peer researchers recruited MISSA in Berlin to fill in a paper-based standardized questionnaire about sexual health and HIV in German, English or French (October-December 2015). We conducted multivariable analysis to assess the impact of HIV knowledge on the odds of getting tested for HIV, adjusted for age and gender.

Results

Peer researchers recruited 536 participants. Eighty-one percent (403/498) knew eight out of 10 statements about HIV (transmission, symptoms and treatment). Additionally 59% (308/521) knew where to go for HIV testing in Berlin, and 66% (347/526) knew that no one can be deported for being HIV-positive. Sixty-nine percent (360/525) were ever tested for HIV. With every fact known about HIV, the odds of getting tested increased by 41% (OR 95%CI: 1.21-1.66); knowing HIV diagnosis does not lead to deportation increased odds of getting tested by 67% (OR 95%CI: 1.03-2.70).

Conclusion

While general knowledge of HIV was high among participants, the finding that more than one third of MISSA had misconceptions about the consequences of HIV diagnosis or did not know where to get tested for HIV, needs to be addressed in order to increase testing uptake. We recommend the training and funding of trusted community representatives to convey context specific HIV information in close collaboration with MISSA communities and local public health authorities.

Keywords: HIV, migration, migrants, sub-Saharan Africa, participatory research, Germany

ABSTRACT ID: 114

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

O17.4 Novel use of community-based surveillance with integrated cross-sectional surveys to identify health priorities in Mtendeli Refugee camp, Tanzania, February-March 2016.

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5. Médecins Sans Frontières - OCA, Mtendeli, Tanzania

Background

In February 2016, approximately 5000 Burundian refugees were accommodated in newly-built Mtendeli camp, Tanzania. No public health data were available. To provide more timely and comprehensive health data with limited additional resources, Médecins Sans Frontières implemented community-based surveillance (CBS) with additional integrated cross-sectional surveys carried out by the same outreach team. With this new surveillance design we aimed to identify health priorities and inform public health action.

Methods

We trained 17 outreach workers who conducted weekly visits to all households in Mtendeli and collected structured CBS data on demographic breakdown of households; births, deaths, self-reported diarrhoea and fever in the preceding week. In different weeks, they additionally included surveys for mosquito net coverage, measles and cholera vaccination coverage, and malnutrition. We calculated morbidity prevalence, mortality rates, vaccination/mosquito net coverage and severe acute malnutrition (SAM). Data from epidemiological weeks 9-12 are presented.

Results

We collected information for an average 5,051 refugees (1,072 households) weekly; 21% were (under)5 years and 51% female. Fever and diarrhoea prevalence was 9.2% and 2.1% in (under)5 years respectively and 4.6% and 0.4% in (over)5 years. Two (neonatal) deaths were reported during this period. Households owned a mean of 0.3 intact mosquito nets. Vaccination coverage in children (under)15 years was 83% for measles, 30% for cholera. SAM was estimated at 0.5% in children (under)5 years.

Conclusion

Standard emergency thresholds for mortality, morbidity and malnutrition were not reached during the reporting period. Our novel approach integrating targeted surveys into CBS allowed us to efficiently identify public health priorities such as measles vaccination and mosquito net distribution utilising the available infrastructure. We recommend consideration and evaluation of further use of CBS with integrated surveys in similar settings.

Keywords: surveillance, refugee health, mortality, vaccination coverage, mosquito net coverage, malnutrition

ABSTRACT ID: 71

PRESENTED BY: Suzan Trienekens (scmtrienekens@gmail.com)

Parallel Session 18: Vaccine preventable diseases (5)

Moderator: Johan Giesecke, ESCAIDE Scientific Committee, Sweden

O18.1 Large outbreak of mumps virus genotype G among vaccinated students in Norway, 2015-2016

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7. Department of Microbiology, Haukeland University Hospital, Bergen, Norway

Background
Since 1983, when mumps vaccination (genotype A) was introduced in the Norwegian childhood vaccination schedule, vaccination coverage exceeded 90% and mumps incidence has declined to an annual mean of 0.4 cases per 100,000 population during 2000-2014. We here describe the first large mumps outbreak in Norway occurring from September 2015.

Methods
We defined a case as a person with clinical mumps notified infection from 01/09/2015 and laboratory confirmation (IgG seroconversion, IgM or PCR) (confirmed) or an epidemiological link (probable). PCR positive specimens were genotyped. We described the cases using notification data and obtained vaccination status from the Norwegian vaccination registry.

Results
Between September 2015 and April 2016, 227 cases were notified (225 confirmed). The median age of all cases was 22 years (range 4-66); 89% were 19-28 years old; 140 (62%) were male; >75% occurred among students. Of all cases, 13 (5.7%) were diagnosed with orchitis; 6 (2.6%) were hospitalized. Out of 190 PCR positive specimens, 65 (34%) were genotyped, and they were all genotype G. Genotyping suggested that the index case was a student in Trondheim infected in Italy. 154 (68%) cases were infected in Trondheim, 56 (25%) in Bergen and 16 (7%) in other locations in Norway. Of 199 cases with known vaccination status, 192 (96.5%) were vaccinated (12 once and 180 twice). The health authorities in Trondheim and Bergen vaccinated unvaccinated students and close contacts.

Conclusion
This large outbreak occurring among vaccinated students suggests suboptimal protection of the current genotype A vaccine in preventing genotype G mumps outbreaks. However, the outbreak may have been larger if the population was unvaccinated. We therefore recommend maintaining high vaccination coverage and offering the vaccine to all unimmunized individuals.

Keywords: mumps, vaccine, outbreak, genotype G, students, Norway

ABSTRACT ID: 275

PRESENTED BY: Lamprini Veneti (lambrinive@gmail.com)

O18.2 Environmental surveillance for poliovirus in the United Kingdom (UK)... getting ready.

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Background
WHO recommends Poliomyelitis Environmental Surveillance (PES) in populations where acute flaccid paralysis surveillance is not in place and where conditions exist that render the population at potential risk for poliovirus circulation. The UK has close links with geographical areas where endemic wild (WPV) and circulating Vaccine Derived Poliovirus (cVDPV) are still present. We describe a protocol for implementing PES in the UK as part of the National Polio Plan.

Methods
We reviewed the WHO guidelines and literature on PES, obtained information from colleagues in countries using PES and sewage network companies in the UK. We developed a protocol for sewage sampling procedures, proposed scenarios of poliovirus detection, based on mathematical modelling, and described the required public health actions following detection.

Results
We propose using grab method sampling to collect raw sewage at least once a month from converging sewers networks serving populations of optimal size: 100,000–300,000. WPV or cVDPV detected through this environmental surveillance would represent a public health emergency warranting immediate further investigation and notification to the Public Health Authorities and WHO. To determine if there is local poliovirus transmission, actions would include: enhanced environmental sampling (more frequently, smaller target populations, more sites), active search for poliovirus-infected persons, estimating local polio immunisation coverage in target groups and genome characterization to determine length of transmission chains and possible source. We present four levels of possible detection scenarios and associated public health actions, including mop-up vaccination when genetic and epidemiological evidence indicate widespread transmission of WPV or cVDPV.

Conclusion
This new surveillance system will allow the early identification of poliovirus transmission in the UK and inform optimal implementation of a rapid public health response.

Keywords: Polio, environmental surveillance, erradication

ABSTRACT ID: 56

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

O18.3 Sequential administration of inactivated followed by oral poliovirus vaccine in Poland between 2000 and 2014 did not completely prevent vaccine associated paralytic poliomyelitis

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Background

Existing serologic and limited epidemiologic evidence suggests that inactivated polio vaccine (IPV) completely prevents vaccine-associated paralytic poliomyelitis (VAPP) upon subsequent administration of oral polio vaccine (OPV). Children born in Poland between 2000-2007 were vaccinated under three different schedules: 1 IPV + 4 OPV (S1), 2 IPV + 3 OPV (S2), and 3 IPV + 1 OPV (S3). We described VAPP notified in Poland between 2000 and 2014 by schedule.

Methods

We included probable VAPP cases (confirmed paralytic poliomyelitis, onset 4-30 days following receipt of OPV or 4-75 days after contact with OPV recipient, residual paralysis 60 days after onset) and confirmed cases (additionally, identification of vaccine virus). Using birth date and vaccination history obtained from case reports, we assigned cases to schedule. We pooled 2000-2007 birth cohorts by schedule, estimated total OPV doses to be administered per schedule (2000-2014 “intention-to-treat”), and calculated attack rates (VAPP per pooled birth cohort/million (bcm)) and incidence per million OPV doses.

Results

We identified seven cases of VAPP: one probable and one confirmed under S1, one probable and one confirmed under S2, and three confirmed under S3. This corresponds to 1.85 cases/bcm (S1); 5.83 cases/bcm (S2); and 2.07 cases/bcm (S3) and to 0.46, 1.94 and 2.07 cases/million OPV doses for S1, S2, and S3 respectively.

Conclusion

Our results indicate that sequential administration of IPV followed by OPV in Poland between 2000 and 2014 did not completely prevent VAPP. After introduction of single/multiple doses of IPV prior to OPV administration in immunization schedules, vigilant surveillance of VAPP should continue, in order to identify cases in a timely manner, and gain more knowledge on the association of VAPP with polio vaccine schedules.

Keywords: poliomyelitis, oral poliovirus vaccine, inactivated poliovirus vaccine, immunization schedule

ABSTRACT ID: 236

PRESENTED BY: Savina Stoitsova (savinaos@yahoo.com)

O18.4 Evaluation of the Acute Flaccid Paralysis Surveillance (AFP) system in Oyo State, southern Nigeria, (2008-2014)

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Background

In September, 2015, Nigeria was removed from the list of Polio-endemic countries globally. To be certified polio free, the country must demonstrate the absence of wild poliovirus (WPV) transmission for additional two consecutive years. In Oyo State, the last case of WPV was reported in February, 2009. We evaluated the AFP surveillance system in Oyo State to assess its attributes and determine if it was meeting its set objectives.

Methods

We used the Centre for Disease Control and Prevention guidelines for evaluating public health surveillance system. We conducted a retrospective review of AFP surveillance data between 1st January, 2008 and 31st December, 2014. We conducted in-depth interviews with identified stakeholders. Semi-structured questionnaires were administered to Disease Surveillance and Notification Officers (DSNOs) and AFP focal persons. Univariate analysis was performed using Microsoft Excel 2010.

Results

The case definition and channel of reporting are simple. Of the 897 AFP cases detected between 2008 and 2014, 20 (2.2%) were laboratory confirmed WPV. The sensitivity of the system, measured by the Annualized Non-Polio AFP (NPAFP) rate was consistently above the target of ≥ 2/100,000 population. The mean NPAFP rate for underperforming LGAs was 1.6, SD: 0.31.The mean Stool adequacy and Timeliness were 91.43% (SD: 18.3) and 91.3% above the target of ≥ 80% respectively. Positive Predictive Value (PVP) was 2% (2008 -2009), and 0% in 2010-2014.

Conclusion

The Oyo State AFP surveillance system is simple, sensitive and meeting its set objectives. However, PVP was low and all the LGAs, at one point, between 2008 and 2014, did not meet the NPAFP target. We recommended that more logistic support should be provided for underperforming LGAs to improve case reporting, investigation, and response.

Keywords: Acute Flaccid Paralysis, Surveillance evaluation, Wild poliovirus, Nigeria

ABSTRACT ID: 42

PRESENTED BY: Maureen Anyanwu (maureenanyanwu23@yahoo.com)

PARALLEL SESSION PROGRAMME WEDNESDAY, 30 NOVEMBER 14:30-15:30

Parallel Session 19: Food- and waterborne diseases and zoonoses (4)

Moderator: Fehminaz Temel, ESCAIDE Scientific Committee, Turkey

O19.1 Whole Genome Sequencing (WGS) offers high resolution discriminative data for rare serovars of Salmonella; examples from epidemiologically well characterized outbreaks in France in the period 2014-2016

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Background

Routine microbiological detection of Salmonella relies on classical laboratory techniques for surveillance (serotyping) and additional molecular subtyping methods for outbreaks investigation (e.g. PFGE, MLVA). For emerging and rare serotypes, these subtyping methods are more likely to lack sufficient resolution to detect distinctive causative clusters. To address this challenge we utilize WGS in two retrospective and one ongoing outbreak. Additionally, we showcase methods to present complex phylogenetic trees linked with epidemiological parameters.

Methods

Three epidemiologically and microbiologically well-characterized nationwide Salmonella outbreaks by serotypes Dublin(2015-2016,N=200),Havana(2014,N=29) and Kedougou(2014,N=44) were studied. Samples from different sources were subtyped by PFGE or MLVA according to serotype, WGS was performed on all samples. Maximum-likelihood phylogenetic trees based on SNP divergence were co-joined with temporal and spatial data in Microreact and iTOL to generate interactive trees.

Results

The total intrinsic strain SNP divergence was 210 for Dublin, 565 for Kedougou and 88.500 for Havana indicating different levels of diversity between serotypes. For S. Dublin and S. Kedougou outbreaks, PFGE revealed one unique profile. WGS and epidemiological spatio-temporal analyses indicated three simultaneously occurring outbreaks for S. Dublin linked to three different unpasteurized cheeses, something MLVA did not reveal. S.Kedougou occurred in two batches of cheese and for S.Havana, cross-contamination between flocks was confirmed by WGS.

Conclusion

This study shows that co-joined WGS and epidemiological data has proven specifically useful in more accurately estimating the context and multitude of the outbreak and pinpointing specific batches or contamination between production chains. This was the case for outbreaks involving rare serotypes with both homogeneous and heterogeneous levels of intrinsic SNP diversity. Where possible we would recommend the use of WGS especially in outbreaks involving serotypes which are homogeneous by nature.

Keywords: Salmonella, WGS, outbreaks, phylogeny

ABSTRACT ID: 291

PRESENTED BY: Amrish Baidjoe (amrish.baidjoe@gmail.com)

O19.2 Disentangling a complex nationwide Salmonella Dublin outbreak associated with rawmilk cheese consumption, France, 2015-2016: findings from a case-case, a case-control study and Whole Genome Sequencing

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Background

On 18 January 2016, the National Reference Centre (NRC) for Salmonella in France reported an excess of Salmonella enterica serotype Dublin (S. Dublin) infections. We conducted an investigation to identify the source of infection and inform control measures.

Methods

Cases were S. Dublin infections among French residents diagnosed at the NRC between 17 November 2015 and 11 March 2016. We used Whole Genome Sequencing (WGS) to identify clusters of outbreak-related cases. We compared food histories of each cluster with those i) of the other cases, and ii) of controls recruited online from a web-based cohort. Cases were interviewed using a trawling questionnaire and controls completed a shorter online questionnaire on food consumption. We calculated crude odds ratios (OR) and adjusted-OR (aOR) using logistic regression.

Results

We interviewed 63 (73%) of the 86 cases. WGS analysis on 58 (92%) isolates identified two major clusters, A and B (28% and 19% of the cases, respectively). Compared with other cases, cluster A cases were more likely to have consumed Morbier cheese (OR 2.6, 95%CI 0.6-12) and cluster B cases were more likely to have eaten Vacherin cheese (OR 6.3, 95%CI 1.1-43). Compared with controls, cluster A cases were more likely to consume Morbier (aOR 6.5, 95%CI 2.2-19) and cluster B cases were more likely to eat Vacherin (aOR 20, 95%CI 5.4-73).

Conclusion

WGS contributed to the identification of at least two outbreaks of S. Dublin, and two different raw-milk cheeses from different processing plants as potential vehicles. Findings from both studies were consistent. Based on those, the Ministry of Agriculture launched a reinforced control plan for processing plants of raw-milk cheeses in the region of production, to prevent future outbreaks.

Keywords: Disease Outbreaks, Salmonella, Cheese, Case-Case Studies, Case-Control Studies, Whole Genome Sequencing

ABSTRACT ID: 224

PRESENTED BY: Aymeric Bun Ung (aymeric.ung@santepubliquefrance.fr)

O19.3 Whole genome sequencing of the major Listeria MLVA-cluster in Norway 2005-2015

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Background

All Listeria monocytogenes isolates in Norway are submitted to the National Reference Laboratory for Enteropathogenic Bacteria (NRL). Since 2005 three outbreaks of listeriosis have been detected using multi-locus variable number of tandem repeat analyses (MLVA). Whole-genome sequencing (WGS) provides ultimate resolution and has shown great promise for typing L. monocytogenes. In this study we investigate WGS typing of the major MLVA-profile using two different bioinformatical approaches, in order assess their usefulness in future surveillance.

Methods

We selected 29/82 L. monocytogenes MLVA-type 7-7-9/10-10-6 isolates from the NRL collection (2005-2015) including; 8 outbreak associated isolates (from 2 outbreaks), 4 isolates from cases with suspected epidemiological links, and 17 sporadic isolates distant in time and geography. We sequenced the genomes (MiSeq) and analysed the sequences using reference genome mapping (RGM) with L. monocytogenes 10403S and compared to gene-by-gene (GbG) in SeqSphere.

Results

RGM identified 658 single nucleotide polymorphisms (SNPs), distributed into 20 partitions (of ≤10 SNPs) including five clusters (of >1 isolates). All previously identified outbreak isolates were clustered. Only 2/4 suspected linked isolates were seen clustered, and two new clusters of two isolates each were identified that were distant in time (2-3 years) and place. Using GbG, 2570/2866 genes were identified in all isolates varying at 286 loci. Isolates were distributed into 20 partitions (of ≤1 SNPs) including five clusters (of >1 isolates). Clustered and non-clustered isolates were in complete agreement with RGM.

Conclusion

This study demonstrates that WGS has superior discriminatory power to MLVA regardless of analytical approach. Both RGM and GbG uncovered new clusters of epidemiological relevant isolates. We recommend introducing WGS into routine typing of L. monocytogenes for accurate and timely detection of future outbreaks.

Keywords: Listeria monocytogenes, Sequence Analysis, DNA, Multilocus Sequence Typing, VNTR Sequences

ABSTRACT ID: 130

PRESENTED BY: Umaer Naseer (mohammed.umaer.naseer@fhi.no)

Parallel Session 20: Influenza and other respiratory viruses (2)

Moderator: Eeva Broberg, ECDC, Expert Virology / Influenza

O20.1 A large school outbreak of H1N1 pdm09 amongst vaccine-eligible primary school children with low vaccine uptake, UK, 2016

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5. Screening and Immunisation, Public Health England, South West, United Kingdom

Background

In January 2016, a large outbreak of influenza A(H1N1)pdm09 (predominant for 2015/16 season) was notified in a primary school (4-11 year-olds). We aimed to describe the outbreak and estimate the vaccine effectiveness (VE) of the 2015/16 nasal spray influenza vaccine (LAIV).

Methods

A possible case was a child with at least one influenza-like-illness (ILI) symptom recorded on school absence records. We used the EU case definitions for probable and confirmed cases. We obtained confirmatory diagnosis from HPZone and vaccination status from linked GP records. To estimate VE, we conducted a cohort study amongst vaccine-eligible school children (4-7 year olds) and calculated VE as 1-risk ratio for confirmed/probable cases.

Results

The overall ILI attack rate (AR) at the school was 48% (191/395), with 165 possible, 23 probable and 3 confirmed influenza A cases, of whom 2 were H1N1 pdm09. The AR of confirmed and probable influenza was highest (4.7%) in 4-5 year olds who were LAIV vaccine-eligible. Higher AR (3.1%) was also observed among 9-10 year old children. Of the 180 vaccine-eligible children, only 57 (32%) had been vaccinated in the 2015/16 season. The 2015/16 VE was 33% (95% CI,-100% to 78%); VE of a single dose (received at any point between 2013 and 2015) was 43% (95% CI,-62% to 80%).

Conclusion

The vaccine uptake was lower than the England average of 55% in 2014/15 and was likely to have facilited the spread of infection. Our VE results are compatible with the UK mid-season VE estimate for confirmed infection. Further work is needed to encourage uptake of the vaccine amongst eligible children.

Keywords: influenza like illnesses, ILI, vaccine effectiveness, vaccine coverage, school absence, Influenza A, influenza vaccines

ABSTRACT ID: 35

PRESENTED BY: Daiga Jermacane (jermacane@gmail.com)

O20.2 Vaccinating young, healthy children against seasonal influenza – effects of introducing the live attenuated vaccine (LAIV) to the National Immunization Program (NIP), Finland, 2015-16

Ulrike Baum, H. Nohynek, N. Ikonen, R. Syrjänen, J. Sundman, J. Jokinen

National Institute for Health and Welfare, Finland

Background

In Finland, vaccinating healthy children aged (0.5-)2 years with trivalent inactivated influenza vaccine (TIV) against seasonal influenza is covered by NIP since 2007. Post-pandemic TIV coverage (2010-15) was constantly low (~13.5%). In 2015-16, for first time, vaccination with tetravalent LAIV was available for 2-year-olds and covered by NIP; LAIV and TIV were used in parallel. We investigate effect of introducing LAIV on vaccination coverage (VC) and differences in vaccines' effectiveness (VE).

Methods

We linked National Population Register, Vaccination Register (NVR), Infectious Disease Register (NIDR), Primary Health Care Register (AvoHILMO) data via a unique personal identifier. Study population comprised children of birth cohort 2013 living in Finland. We extracted records of first influenza vaccination in 2015-16 from NVR, laboratory-confirmed influenza, influenza-like illness (ILI; ICD-10:J09-J11, ICPC-2:R80) from NIDR, AvoHILMO. We used Cox models with time-dependent vaccination status and calculated VE as 1 minus hazard ratio.

Results

From 58804 children, 8358(14.2%) were vaccinated with LAIV, 4425(7.5%) with TIV; altogether 21.7%. Counting 300 influenzaA (25 vaccinated with LAIV; 5 with TIV), 69 influenzaB (6;6), 227 ILI cases (17;9) by April, LAIVE against influenzaA, influenzaB, ILI was estimated at 47.0%(20.3%-64.8%), 40.0%(-42.7%-74.8%), 51.8%(20.8%-70.6%); TIVE at 77.8%(46.3%-90.9%), -11.1%(-157.5%-52%), 48.0%(-1.2%-73.3%).

Conclusion

Introducing intranasal LAIV to NIP raised VC by half, probably due to less invasive route of administration. Direct effect on vaccinated, indirect effects of elevated VC contribute to impact on disease burden. Crude figures indicate moderate LAIVE against influenza and ILI. LAIVE against influenzaA seems lower, against influenzaB higher than TIVE. Till November, we adjust results for medical history, time since vaccination and review them considering vaccine antigen (mis)matches with circulating strains. We recommend children's immunization with TIV and/or LAIV, continue VC and VE monitoring.

Keywords: Coverage, Effectiveness, Immunization, Influenza, Vaccination

ABSTRACT ID: 81

PRESENTED BY: Ulrike Baum (ulrike.baum@thl.fi)

O20.3 Late breaker: New screening strategy in a nosocomial outbreak of human parainfluenza 3 virus in a haematology-oncology ward, in a tertiary hospital in the Netherlands

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Background

Outbreaks of human parainfluenza 3 (HPIV -3) are common on haematology-oncology wards and prolonged shedding in this population can lead to prolonged outbreaks. Previous studies have shown that symptomatic surveillance and isolation are not always effective in terminating an outbreak. Therefore, during a HPIV-3 outbreak in this ward, we initiated screening of all patients, to implemented preventive measures for all HPIV-3 positive patients.

Methods

Typically, pharyngeal swabs are used for the diagnosis of HPIV-3. To screen frequently with minimum patient burden, the HPIV-3 PCR was validated on oropharyngeal rinse material, used in screening after selective oropharyngeal decontamination. Screening was implemented thrice weekly for all inpatients. Additionally, new patients were screened before admittance to the ward. Screening allowed cohort isolation of HPIV-3 positive patients before onset of symptoms, thereby possibly limiting HPIV-3 spread. Patients remained in isolation until three consecutive negative PCR results in a period of at least 7 days, or until discharge from the hospital.

Results

The total outbreak consisted of 53 patients between 14 July and 28 September 2016. Validation of oropharyngeal rinse fluids demonstrated up to tenfold higher sensitivity compared to pharyngeal swabs. After implementation of screening, an initial increase in cases was observed, including asymptomatic cases. At first positive HPIV-3 PCR, 22/53 (42%) cases were asymptomatic. Fourteen HPIV-3 positive cases remained asymptomatic. A reduction in nosocomial transmission occurred within 2 weeks of implementation, as all new cases since implementation lacked an epidemiological link. Confirmation of decline of nosocomial transmission will follow using molecular epidemiology.

Conclusion

Screening of both symptomatic and non-symptomatic patients, using a sensitive screening method with low patient burden, helped control the outbreak of HPIV-3 in a haematology-oncology ward.

Keywords: Nosocomial Infections, Human Parainfluenza, Screening, Outbreak

ABSTRACT ID: 723

PRESENTED BY: Lieke van Alphen (lieke.van.alphen@mumc.nl)

Parallel Session 21: Tuberculosis and other respiratory diseases (excluding viruses)

Moderator: Marieke van der Werf, ECDC, Head of Disease Programme Tuberculosis

O21.1 Evaluation of Toronto's Tuberculosis Contact Screening Parameters Tool

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Background

In 2007, Toronto Public Health (TPH) developed and implemented the Contact Screening Parameters Tool (CSPT) to provide a more systematic risk-based approach for prioritizing follow-up of contacts of pulmonary tuberculosis (TB) cases, according to case infectivity, circumstances of exposure, and susceptibility of contacts. After using this tool for several years, we decided to evaluate it for effectiveness of its operational use in an applied public health setting.

Methods

Data were extracted from an electronic reporting database and line lists for pulmonary TB cases, with one or more household contacts, reported from June 1, 2007 to May 31, 2012 and the respective household contacts. Poisson regression was used to evaluate the predictive value of the CSPT risk categories (low, medium, high) and case infectivity parameters (chest x-ray, smear, cough) in identifying transmission.

Results

There were a total of 746 pulmonary cases, 43.3% low, 28.6% medium and 28.2% high risk. There were 2,508 household contacts; of these, 211 (8.4%) became a converter and/or secondary case. High risk cases were 2.4 times more likely to generate a transmission event than medium risk cases (95% confidence interval 1.7-3.5). There was no significant difference between medium and low risk cases. Chest x-ray and smear were both significant predictors of transmission (p=0.004 and p=0.001, respectively); cough was not significant (p=0.682).

Conclusion

The CSPT appropriately differentiated contacts with the highest potential for TB infection and development of active disease. TPH will continue to use the tool, and will simplify it by combining the medium and low risk categories, and removing cough from the case infectivity rating assessment.

Keywords: tuberculosis, public health, program evaluation, risk, transmission

ABSTRACT ID: 100

PRESENTED BY: Rebecca Stuart (rstuart2@toronto.ca)

O21.2 Determinants of site of tuberculosis disease in the EU/EEA: an updated analysis of EU surveillance data from 2003–2014

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Background

In most countries of the European Union (EU) and European Economic Area (EU/EEA), tuberculosis (TB) incidence is declining; however, its clinical profile is changing. Extrapulmonary TB (EPTB) has increased from 16.4% in 2003 to 21.8% in 2014 of all TB cases reported.

The site of TB disease influences transmissibility, diagnosis, and patient outcome. We explored host-related factors associated with the site of disease using variables routinely collected by countries in the EU/EEA for the national TB surveillance.

Methods

Logistic regression models were fitted to case-based TB surveillance data reported to the European Surveillance System for 2003-2014 to identify determinants of site of disease including the following covariates: age, gender, previous TB treatment, country of report, and geographic area of origin.

Results

564,916 TB cases reported by 27 EU/EEA countries had exclusive pulmonary (83%) or extrapulmonary (17%) disease, and complete data on all five explanatory variables. Exclusive EPTB was associated with age with age ‹15 years (adjusted OR [aOR]:5.50; 95%CI 5.32-5.68; reference age-group 15-44y), female gender (aOR:1.60;1.58-1.63), previously not treated status (aOR:3.1; 3.05-3.25), and patients origin from Indian subcontinent (aOR3.74; 3.56-3.94; reference: Western Europe). Age ‹15y and origin from the Indian subcontinent or Africa were strongly associated with lymphatic, peritoneal/digestive and osteo-articular localization (aOR›3.8), as well as central nervious system with age ‹15y and peritoneal/digestive with persons originating from the Indian subcontinent or Africa.

Conclusion

Awareness by clinicians of host-related determinants of site of TB is relevant to diagnosis, particularly in children and patients showing atypical clinical pictures. Association of EPTB with patients originating from certain countries outside EU/EEA may reflect mycobacterial strain preferences for disease localization, ethnic differences in disease manifestation and higher HIV prevalence.

Keywords: European Union, epidemiology; tuberculosis, pulmonary; extra-pulmonary tuberculosis,

ABSTRACT ID: 341

PRESENTED BY: Vahur Hollo (gsotgiu@uniss.it)

O21.3 Childhood Tuberculosis in Germany 2002-2014: a comparison of contact tracing and passive case finding

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Background
Tuberculosis (TB) poses a challenge in children, as rapid progression of infection to active TB (ATB) and severe disease are more likely. Contact tracing is important as it aims to identify infection or disease earlier. We investigated sociodemographic and clinical factors among children with ATB to determine whether they were associated with contact tracing.

Methods
We analysed national surveillance data for children aged ‹15y notified with ATB in Germany, 2002 through 2014. We performed univariable and multivariable logistic regression to examine the association between mode of case finding (contact tracing vs. passive case finding) and the following covariates: notification year, age, gender, birth place, disease site and bacteriological confirmation.

Results
Of 2,276 children, 51.5% were found through contact tracing; 49.5% were female, 68.0% were German born and median age was 4y (IQR:2-9y).

In the multivariable analysis, cases found through contact tracing were likelier to have pulmonary TB (adjusted odds ratio (aOR)=8.01, 95% confidence interval (CI):5.31-12.08) or intrathoracic lymphnode disease (aOR=11.39, 95%CI:6.74-19.25). Contact tracing was associated with later notification year (aOR=1.03, 95%CI:1.01-1.06, per year). Foreign born children (aOR=0.48, 95%CI:0.38-0.60), age group 10-14y (aOR=0.58, 95%CI:0.45-0.76) and bacteriologically confirmed TB (aOR 0.47,95%CI:0.38-0.57) were less likely to be found through contact tracing. Gender wasn't associated with contact tracing (aOR=0.99, 95%CI:0.81-1.21).

Conclusion
We found increasing proportions of children identified through contact tracing over time and ATB detected at an earlier stage of disease. Younger children, who have greater risk of severe disease, were likelier to be identified by contact tracing. The reasons for foreign born children being less likely to be found through contact tracing will be investigated in a wider clinical cohort study to guide the development of targeted public health recommendations.

Keywords: Tuberculosis, Children, Contact tracing

ABSTRACT ID: 170

PRESENTED BY: Janine Thoulass (ThoulassJ@rki.de)

Poster Abstracts

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MODERATED POSTER SESSION A
MONDAY, 28 NOVEMBER
15:30-16:30

Track 1: Antimicrobial resistance and healthcare-associated infections (1)

Moderator: Diamantis Plachouras, ECDC, Expert Antimicrobial Resistance and Healthcare-associated Infections

A 1.1 Prevalence of and determinants for carriage of extended-spectrum β-lactamase – and pAmpC-producing Enterobacteriaceae in the general population in a livestock-dense area

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2. Institute for Risk Assessment Sciences (IRAS), Utrecht University, Utrecht, the Netherlands

Background

In the Netherlands there is a debate regarding environmental health risks of livestock farming for neighbouring residents. This explorative study aims to determine the prevalence of carriage of ESBL/pAmpC-producing Enterobacteriaceae (ESBL/pAmpC-E) in the general population living in a livestock-dense area, and to study associations between determinants, including exposure through contact with animals and the environment, and human carriage of ESBL/pAmpC-E.

Methods

A cross-sectional study was performed among 2,432 adults (aged 20–72 years) in twelve temporary research centres in the south of the Netherlands. Subjects completed a questionnaire, and carriage of ESBL/pAmpC-E was assessed in a faecal sample. Residential proximity to cattle, goat, horse, mink, pig, poultry, and sheep farms was available. Risk factors were determined using multiple logistic regression analysis.

Results

ESBL/pAmpC resistance genes were found in 109 participants, resulting in a prevalence of 4.5% (95%CI: 3.7–5.4) ranging from 1.4–10.9% among the research centres. People travelling to Asia, Latin-America, Caribbean or Africa (last 12 months) (OR: 2.82 (95%CI: 1.71–4.63)), having kept cows for a hobby (last 5 years) (OR: 3.77 (95%CI: 1.22–11.64)), using proton-pump inhibitors (OR: 1.84 (95%CI: 1.05–3.23)), and living within 1,000 meters of a mink farm (OR: 2.26 (95%CI: 1.28–3.98)) were at increased risk for carriage of ESBL/pAmpC-E . Residential proximity to any other livestock was not associated with an increased risk.

Conclusion

This large population-based study showed that living in close proximity to livestock farms was not associated with carriage of ESBL/pAmpC-E. Based on the findings public health measures regarding livestock-related environmental exposure are not warranted, but the unexpected association with mink farms needs more research. Reducing PPI usage is a potential measure to decrease carriage of ESBL/pAmpC-E.

Keywords: antimicrobial drug resistance, beta-lactam resistance, AmpC beta-lactamases, livestock, environment, risk factors

ABSTRACT ID: 174

PRESENTED BY: Cornelia C H (Lieke) Wielders (lieke.wielders@rivm.nl)

A 1.2 Adverse outcomes of colonisation with vancomycin-resistant enterococci: a retrospective cohort study, Norway, 2010–2015

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Background

Before 2010, vancomycin-resistant enterococci (VRE) were rare in Norway. Since then several hospital outbreaks have been reported. To prevent the spread of VRE in healthcare institutions, resource intensive infection-control measures are implemented for both VRE colonization and invasive VRE-infections. However, in Norway the risk of developing an invasive VRE-infection and associated mortality among previously colonised patients is unknown.

Methods

We collected data on VRE-positive isolates from patients aged ≥18 years from Norwegian laboratories (January 2010 – July 2015), excluding patients where the first positive test result indicated an invasive VRE-infection (isolation from normally sterile site). We estimated the incidence of invasive VRE-infection and used binomial regression to identify risk factors (age, sex, species, and resistance genotype). Using Cox regression we calculated adjusted hazard ratios (aHR) with 95% confidence intervals (CI) for all-cause-mortality taking the development of invasive VRE-infection into account as a time-dependent variable, adjusting for age and sex.

Results

We included 717 isolates (99% Enterococcus faecium, 80% vanB) from 560 VRE-colonised patients (318 males, median 72 years), 18% (n=100) had multiple positive tests. After a median of 29 days (interquartile range: 13-62 days), 4.8% (n=27, 95% CI: 3.3%-6.9%) developed an invasive VRE-infection. We found no association between risk of developing an invasive VRE-infection and age, sex, species, or resistance genotype. The all-cause 30-day and 1-year mortality were respectively 15.3 (95% CI: 7.55-31.2) and 3.35 (95% CI: 1.93-5.81) times higher among patients who developed an invasive VRE-infection compared to those that did not develop an invasive VRE-infection.

Conclusion

Five percent of VRE-colonised patients developed an invasive VRE-infection. Patients that developing an invasive VRE-infection showed increased all-cause mortality. These results have implications for control routines and burden estimations.

Keywords: Vancomycin-Resistant Enterococci, Infection Control, Norway, Incidence, Mortality

ABSTRACT ID: 119

PRESENTED BY: Hinta Meijerink (hinta.meijerink@fhi.no)

A 1.3 Implementation of an enhanced surveillance system for carbapenemase producing organisms in Scotland through innovative and efficient data integration

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Background

The global spread of carbapenemase producing organisms (CPO) is alarming and represents an increasing threat to healthcare delivery, patient safety and public health. The establishment of a national surveillance system is vital for effective CPO prevention and control. Our aim was to develop a surveillance system that would allow us to monitor and describe changes in the epidemiology of CPO cases in relation to known risk factors, and would inform policy and guidelines to prevent and better manage patients infected or colonised by CPO.

Methods

We undertook a novel approach to data integration through the NHS Scotland Infection Intelligence Platform (IIP). This platform provides a secure data linkage between laboratory results from confirmed CPO isolates and existing national datasets on hospital admissions, medicines use and patient outcomes.

Results

Upon suspicion of resistance caused by the expression of an acquired carbapenemase, Scottish diagnostic laboratories submit isolates to the PHE reference laboratory for further characterisation. Results are shared with both Scottish diagnostic laboratories and HPS. These data are then linked to hospital, prescribing and mortality data available in IIP to identify main risk factors for CPO infection. Such data linkage is complemented by an enhanced surveillance questionnaire on information not available in the IIP datasets, e.g. travel history.

Conclusion

This surveillance system was developed as a proof-of-concept that the IIP can be used to respond to public health threats through innovative and efficient data integration. Our approach is more resource efficient than the administration of long detailed questionnaires and can be easily modified to adapt to the constant evolution of this challenging area. Further evaluations are required to assess the system's acceptability, sensitivity, representativeness and timeliness.

Keywords: carbapenemase, antimicrobial drug resistance, microbiology, surveillance

ABSTRACT ID: 237

PRESENTED BY: Diogo Marques (diogo.marques@nhs.net)

A 1.4 Identification of the potential source of an international healthcare-associated Mycobacterium chimaera outbreak: Contamination during production of heater-cooler units, Germany, Apr. 2015 – Feb. 2016

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Background

Invasive infections with Mycobacterium chimaera were reported in patients with previous open chest surgery and exposure to contaminated heater-cooler units (HCUs) from different countries. We present results of the surveillance of clinical cases and of contaminated HCUs as well as environmental investigations in Germany.

Methods

A case was defined as a patient who had undergone surgery with extracorporeal circulation in the five years before onset of symptoms of non-tuberculous-mycobacteria infection and M. chimaera detection in an invasive sample. For prospective case-finding and identification of contaminated HCUs, we used the established German mandatory surveillance systems. We informed public health authorities and healthcare professionals about the outbreak, case definitions and notifications. Environmental investigations were conducted at the HCU manufacturing site and at a HCU-service centre.

Results

We identified five cases (all male and aged 53–80 years) with severe invasive M. chimaera infection. Cases had been exposed to HCUs from one single manufacturer during open chest surgery up to five years prior to symptom onset. We received reports about contaminated HCUs from 16 of a total 78 German cardiac surgery centres. Environmental investigations at the manufacturing site in Germany detected M. chimaera in: 1. eight samples from used HCUs from three countries; 2. two samples from new HCUs; 3. a sample from the manufacturing line.

Conclusion

Our investigation suggests that at least some of the M. chimaera infections may have been caused by contamination of HCUs at the manufacturing site. We recommend that until sustainable measures for a safe use of HCUs are implemented, users continue to adhere to Field-Safety-Notices issued by the manufacturer and continuously check the websites of national and European authorities for current recommendations for safe HCU operation.

Keywords: health care associated infection; thoracic surgery; nontuberculous mycobacteria; disease outbreak

ABSTRACT ID: 263

PRESENTED BY: Sebastian Haller (HallerS@rki.de)

A 1.5 The added value of participation in the newly launched European surveillance of Clostridium difficile infections: the case of Hungary

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3. National Center for Epidemiology, Dept. of Phage-Typing and Molecular Epidemiology, Budapest, Hungary

Background

Since 2012, mandatory notification of healthcare-associated Clostridium difficile infections (HA-CDI) has been in place in Hungary, following a national protocol used both in acute and chronic care hospitals. To further improve the national surveillance, a start-up data collection following the newly launched European CDI surveillance protocol was organised.

Methods

We invited all hospitals in Hungary to complement the mandatory HA-CDI surveillance in February 2016 with additional variables of the European protocol: hospital data on testing frequency, positivity rate, diagnostic algorithm used; case-based data on community-acquired CDI (CA-CDI), CDI of unknown origin (UO-CDI), and recurrent cases. Twenty hospitals were asked to participate in the enhanced surveillance by sending five C. difficile isolates per hospital for PCR-ribotyping to the National Center for Epidemiology, Budapest.

Results

Forty-five hospitals participated in the European CDI start-up data collection, 42 reporting at least one case (59% of the hospitals reporting into the mandatory surveillance in February 2016). The overall testing frequency was 2.9/1000 patient days with 22% positivity rate. Combined diagnostic assays (GDH+toxin A/B) were used predominantly (73%). In total, 441 CDIs were reported. The proportion of HA-CDI, CA-CDI and UO-CDI was 89%, 5% and 6%, respectively. The proportion of primary episodes and recurrent cases was 59% and 5%, respectively (36% unknown). Eighty-seven isolates were ribotyped: 57 (65%) were RT027, 14 (16%) belonged to other types (e.g. RT012, RT014, RT035, RT036, RT081), and 16 (18%) still require ribotype designation.

Conclusion

The European CDI start-up data collection gave additional information on CDIs in Hungary. Further participation in the European surveillance can offer a better understanding of the diagnostic practices, total CDI burden and circulating C. difficile ribotypes in Hungarian hospitals, also through future inter-country comparisons.

Keywords: Clostridium difficile infections, Healthcare-associated infections, Hospital-based surveillance, PCR-ribotyping

ABSTRACT ID: 346

PRESENTED BY: Ágnes Hajdu (hajdu.agnes@oek.antsz.hu)

A 1.6 Inter-hospital comparison of surgical site infection rates in orthopaedic surgery

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Background

Giving feedback to hospitals on their surgical site infection (SSI) rates can provide information to support reducing SSIs. Overall crude rates, including both superficial and deep SSIs, are widely used when ranking hospitals. We investigated whether comparison by overall, deep or adjusted deep SSI rates are a better basis for a feedback to Finnish hospitals.

Methods

We analyzed surveillance data on 73,227 hip and 56,860 knee arthroplasties from 18 hospitals participating in Finnish Hospital Infection Program, from 1999 to 2014. For each hospital, by dividing number of SSIs and procedures, the rates of overall, deep and adjusted deep SSIs with 95% confidence intervals (CIs) were calculated, and the hospital ranking positions simulated in the Bayesian framework. We adjusted deep SSI rates by relevant patient and hospital characteristics. The correlation between the median theoretical hospital ranks in overall vs. deep and in deep vs. adjusted deep rate was assessed by Spearman's correlation coefficient (ρ).

Results

The overall, deep and adjusted deep hospital-specific SSI rates varied between 0.96-7.10, 0.57-1.82 and 0.37-1.85 for hip surgeries, and from 0.65-4.80, 0.45-1.59 and 0.56-1.55 for knee surgeries. In both procedures, the 95%CIs of the rates between hospitals largely overlapped; only single outliers were detected. Ranking order of hospitals did not correlate between overall and deep SSI rates (hip: $\rho=0.03$; knee: $\rho=0.46$), but a correlation was observed for hospital rank of deep and adjusted deep SSI rates (hip: $\rho=0.89$, knee: $\rho=0.95$).

Conclusion

Deep SSI rates may be a better tool for inter-hospital comparison instead of the overall rates. The current analysis also suggests that although the adjustment could lead to fairer hospital ranking, it is not necessary for useful feedback.

Keywords: Surgical Wound Infection, Orthopedics, Hospital Comparison, Feedback

ABSTRACT ID: 39

PRESENTED BY: Jozica Skufca (josie.skufca@gmail.com)

Track 2: Emerging and vector-borne diseases (1)

Moderator: Kostas Danis, EPIET coordinator/ EPIET Alumni Network, France

A 2.1 Designs and Concepts of 42 Different Mobile Phone Applications for the Management of the West African Ebola Outbreak 2014/15 – Results of a Systematic Literature Review

Daniel Tom-Aba(1), P. Nguku (2), C. Arinze (2,3), G. Krause (1,4)

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2. Nigeria Field Epidemiology and Laboratory Training Programme, Abuja, Nigeria
3. Crestoville Technologies & Data Consults ltd
4. Hannover medical School

Background

Multiple mobile health (mHealth) tools intend to improve surveillance and outbreak management. We therefore conducted a systematic review on mHealth-tools in the context of the recent Ebola-Virus-Disease (EVD) outbreak in order to provide an overview on functionalities these tools offer and identify the most promising approaches.

Methods

We searched in Google Scholar for publications in any language from 01.01.2014 until 31.12.2015 using the following search strategy: (“outbreak” OR “epidemic”) AND (“mobile phone” OR “smartphone” OR “smart phone” OR “mobilephone”) AND (“Ebola” OR “EVD” OR “hemorrhagic”). Two reviewers independently screened titles and abstracts, selecting original publications on tools running on smartphones and dealing with management of hemorrhagic fever outbreaks. We used a standardized form to extract information on the tools’ technical design and functionality.

Results

The automated search generated 690 publications, of which we identified 118 (17%) as relevant for the topic, among which 50 (42%) described a total of 42 different tools. Thirteen tools contained outbreak management functionalities (33% of 39 for which that information was retrievable); 9 (47% of 19) were programmed in open source technology; 31 (84% of 37) contained the feature of bi-directional communication. Surveillance notification was supported by 14 (36% of 39), case management by 6 (18% of 34), and contact tracing by 4 (25% of 16). Three tools support all three of these key functionalities (CommCare, Sense-Follow Up, SORMAS). Two tools (6% of 32) adhere to the data standards of the Integrated Disease Surveillance and Response System (Sense-Follow Up, SORMAS).

Conclusion

Among the large number of mHealth-tools for EVD outbreak management, only 3 appear to contain all three key functionalities for outbreak management and may be the most promising for comprehensive implementation.

Keywords: Mobile health, Ebola Virus Disease, Nigeria, Information and Communication Technology(ICT), Surveillance, Infectious diseases, Outbreak management, Mobile phone, Outbreaks

ABSTRACT ID: 262

PRESENTED BY: Daniel Tom-Aba (Daniel.tom-aba@helmholtz-hzi.de)

A 2.2 Investigation of suspected Ebola cases in Spain through the National Early Warning and Response System

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Background

During the Ebola Outbreak in West Africa, the action protocol against suspected cases of Ebola Virus Disease (EVD) was activated in Spain. The aim of the study is to describe investigated suspected cases through the National Early Warning and Response System.

Methods

All cases investigated between 3rd April 2014 and 14th January 2016 were included. The information sources were notifications from the regional Public Health Departments received at the Coordinating Centre for Health Alerts and Emergencies and microbiological reports from the National Center of Microbiology. We described socio-demographic, diseases-related and laboratory data, as well as epidemiological and clinical compliance with the case definition. Data were analyzed using SPSS.21.

Results

Between April 2014 and January 2016, 56 suspected cases were reported from 14 out of the 17 regions: 75.0% were travelers to the affected countries, 12.5% were field workers and 12.5% were contacts of the three EVD cases treated in Spain. The most frequently visited country was Nigeria (36.7%) followed by Guinea (22.4%). The most commonly reported symptoms were headache (57.1%) and arthralgia (48.2%). From the 51 cases with accurately recorded body temperature, 84.3% had 37.7°C or higher. Case definition was met by 33.9% of the investigated cases. Compliance with the epidemiological criteria was superior to compliance with the clinical criteria (82.1% versus 41.1%). EVD was confirmed in one of the suspected cases. Among travelers and field workers the most frequent diagnosis was malaria (55.1%).

Conclusion

The low specificity of initial symptoms of EVD may have contributed to the low compliance with the case definition. However, the opportunity for detection, reporting and implement control measures highlights the adequate functioning of the National Early Warning and Response System in Spain.

Keywords: Ebola Virus Disease; surveillance; outbreaks; epidemiology; Spain

ABSTRACT ID: 311

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A 2.3 Utilizing a novel focal screening and treatment approach to identify clusters of subpatent 'invisible' infections of malaria in the Kenyan Highlands

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** part of this work was very recently published in the Journal of Infectious Diseases, however asymptomatic/subpatent infections pose a very big problem in intervention and surveillance programmes aiming for elimination. This work addresses this problem

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Background

Mass screening and treatment campaigns have had limited success in curbing malaria transmission, most likely due to the prevalence of subpatent infections missed using the field based diagnostic tools. It has been shown that subpatent malaria infections are more likely to occur in households where patent infections are identified and are often more prevalent in low-endemic areas. Therefore, it is possible that a more focal approach to treatment campaigns using patent infections as a proxy for the presence of a subpatent reservoir may be more effective at reducing the malaria burden.

Methods

To test this strategy, a focal Mass Drug Administration and treatment (fMDA) intervention in foci of malaria transmission was conducted in the Western-Kenyan highlands as part of a larger cluster randomized trial. All consenting individuals under 15 years old or febrile adults residing within the foci were tested for malaria with a rapid diagnostic test and if found positive all individuals residing in the compound received a curative dose of artemisinin combination therapy. Blood spots on filter paper were collected from all household members (N=2083). nested polymerase chain reaction and merozoite surface protein-2 genotyping was performed on all samples to characterize the parasite reservoir.

Results

Of the compounds within the intervention foci, 168 of 406 (41.4%) households sampled received treatment. Initial results indicate that, at baseline, PCR prevalence in compounds with a patent infection and therefore targeted for treatment was 34.0% compared to 11.1% in those that had no patent infections ($p<0.0001$) with the fMDA approach successfully identifying 78.3% of all parasite carriers.

Conclusion

This strategy could provide a useful and operationally attractive alternative to detecting subpatent, 'invisible' infections in foci of declining malaria transmission.

Keywords: Malaria, P. Falciparum, elimination, malaria transmission, screening subpatent infection.

ABSTRACT ID: 66

PRESENTED BY: Amrish Baidjoe (amrish.baidjoe@gmail.com)

A 2.4 Introduction of whole-genome sequencing (WGS) to the nationwide surveillance of invasive group A streptococcal infections in Denmark in 2015

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Background

The number of submitted isolates of invasive group A streptococci (iGAS) in Denmark was 30% higher in the period 2010-2015 than during 2005-2009. The current routine laboratory surveillance methods include T-typing and antimicrobial resistance (AMR) testing (penicillin, erythromycin, and clindamycin). The aim of the study was to evaluate implementation of whole genome sequencing (WGS) and compare with results from traditional laboratory methods for surveillance.

Methods

We performed WGS on all 163 iGAS isolates received in 2015. Emm-typing by Sanger sequencing was performed on the first 56 isolates. Emm types and resistance genes were extracted from WGS and compared to routine laboratory results. Single nucleotide polymorphism (SNP) based phylogeny and pairwise comparisons were constructed.

Results

Twenty-nine different emm types were identified by WGS. Emm types 28.0 (N=27), 3.1 (N=26), and 1.0 (N=23) were the most prevalent types. Fifty-five (98%) among 56 isolates typed by traditional Sanger sequencing had emm types identical to that found by WGS. Isolates with the same emm types could be further distinguished WGS (0-191 SNPs within each emm type). Traditional T-typing identified only 16 different types while 40 isolates (23%) were non-typeable. Only few AMR genes were demonstrated: erm(A) was found in one of each of emm types 77.0, 87.0 and 108.1, in agreement with the results of phenotypic AMR tests.

Conclusion

Based on our study WGS forms a reliable system that can be implemented for typing of iGAS since it replaces many different methodologies for characterisation of iGAS, are simple to perform, have comparable cost, and can improve the data available for surveillance. Hence we recommend WGS to be used for surveillance of iGAS.

Keywords: Streptococcus pyogenes, group A streptococci, whole genome sequencing, surveillance

ABSTRACT ID: 195

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A 2.5 Differences in data collection parameters distorts of comparative analyses of morbidity data between countries, Azerbaijan and Georgia, 2012-2014

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Background

Anthrax is endemic disease for Azerbaijan and Georgia. New cases of cutaneous form of anthrax were registered in the both countries during last five years. We aimed to conduct comparative evaluation of anthrax trends between the countries.

Methods

The descriptive analysis of anthrax morbidity was conducted using the Electronic Integrated Disease Surveillance System (EIDSS) of the Ministries of Health of Azerbaijan and Georgia for 2012-2014. For evaluation of case definition and diagnostic algorithms, official health and CDC guidelines were used.

Results

In 2014, incidence rate of anthrax was 1.3 and 0.7 per 100,000 in Georgia and Azerbaijan respectively. Since 2012, anthrax incidence has declined by 2.8 and 3.2 times, respectively. However, district incidence rates were high (10.0-13.3 per 100,000) in the bordering districts of Georgia (Sagarejo, Gardabany). Males accounted for 54-83% (average 74.6 and 60.4 respectively). However, in 2014, number of cases among women increased by 7% in Azerbaijan compared to 2012. The highest proportion was in 30-59 age group (64-81%). Similar distribution by occupation was observed in both countries. Intercountry differences in parameters for data collection such as case definitions, laboratory algorithms, and algorithms of reporting were identified. Variations in case confirmation due distinctive confirmatory tests and assigning cases in the report using different dates were found.

Conclusion

Over the past three years, we identified similar trends for anthrax in Azerbaijan and Georgia. However, country comparisons are complicated by differences in parameters of data collection which could entail a possible misrepresentation of trends. To promote information exchange between the countries, the standardization of parameters for data collection is essential.

Keywords: Anthrax,data exchange,comparative analyse

ABSTRACT ID: 90

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A 2.6 Outbreak detection: determinants of statistical algorithms' performances, a simulation based study

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Background

Early detection of outbreaks is crucial in infectious disease surveillance, in order to enable rapid control measures. However, statistical methods used for it can be influenced by time series (TS) characteristics. Aim was to explore relationships between time series characteristics and outbreak detection algorithms.

Methods

We tested 23 outbreak detection algorithms on a previously published simulated database: 231,000 624-week TS were generated using a negative binomial model, under 42 scenarios depending on different secular trends, baseline frequencies of reports, seasonalities (annual or biannual) and dispersion. We simulated outbreaks with varying duration and amplitude (tuning coefficients: k1 = 0, 2, 5 or 10 for past outbreaks, and k2 = 1 to 10 for current outbreaks). We computed for each method False positive rate without current outbreak (FPR) and probability of detection (POD: at least one alarm during the current outbreak period). We performed Poisson regression of FPR or POD on simulation parameters.

Results

Adjusted FPR ratios decreased when k1 increased and were greater for TS with secular trends or seasonality (annual or biannual). Worst FPR were observed for increasing dispersion parameter. We observed a nonlinear relation between FPR and baseline frequency. For the POD model, outbreak detection probability decreased when k1 increased and when k2 decreased. POD increased for TS with secular trends but was lower in case of annual seasonality than without any seasonality.

Conclusion

Baseline TS may impact performances of detection methods, depending on trend, seasonality, baseline frequency, overdispersion and outbreaks amplitude and duration. An original approach was here to compare performance indicators adjusted on these parameters in a regression model. This could help epidemiologists to select the method the most adapted to a given situation.

Keywords: Health surveillance, Outbreak detection algorithm, Statistical method, Performance assessment, Simulation study

ABSTRACT ID: 343

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Track 3: Food- and waterborne diseases and zoonoses (1)

Moderator: Louise Coole, EPIET Coordinator/ Public Health England

A 3.1 Surveillance for outbreaks of gastroenteritis in elderly care facilities in France contributes to the rapid implementation of control measures

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Background

Outbreaks of acute gastroenteritis (AGE) are frequent in long-term care facilities for elderly (LTCFE), causing a considerable health and economic burden; outbreak surveillance was implemented in 2010 to improve detection and control. We aimed to document the burden of AGE in LTCFE in France, evaluate the system and identify factors associated with a high attack rate in order to recommend future developments.

Methods

An outbreak was defined as at least five cases of AGE within a four day period among LTCFE residents. Surveillance operated from November to May, and included data collection on control measures, dates of report and onset, and population at risk. We calculated delay from onset to report, attack rate (AR), frequency of implementation of control measures. We measured associations between attack rate and outbreak parameters using negative binomial regression.

Results

From 2010 to 2015, a total of 3549 outbreaks were reported in 3404 LTCFE causing 88930 cases of AGE. The annual AR among residents ranged from 28% to 32% depending on the year of surveillance; The median delay in notifying an outbreak decreased from 5 days in 2010-2011 to 4 days in 2014-2015. For each of the recommended control measures, the frequency of implementation increased significantly over the years. The AR among residents was lower when control measures were implemented within three days from the date of symptom onset of the first case (IRR=0,90;p<0,001).

Conclusion

Surveillance for AGE outbreaks in LTCFE helped improving response time for outbreak control measures associated with quicker reporting and implementation of control measures. Recommendations should be to focus on speedy implementation of control measures in order to reduce the AR of outbreaks.

Keywords: gastroenteritis, outbreaks, elderly care, France

ABSTRACT ID: 165

PRESENTED BY: Alexandra Septfons (alexandra.septfons@santepubliquefrance.fr)

A 3.2 Gastroenteritis school outbreak linked to reheated prepared food, Ireland, 2016

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Background

On 25th January 2016, the environmental health service received a report of 70 cases of gastroenteritis at a school event in the south of Ireland. Students from several schools participated. We undertook a cohort study to identify the source of infection.

Methods

We defined a case as an attendee with diarrhoea or abdominal pain, with symptom onset within 96 hours of the event start. We employed an anonymous online questionnaire to collect data on clinical symptoms and food exposures. Poisson regression was used to estimate adjusted risk ratios (aRR).

Results

Of the 177 attendees, 108 (61%) responded. Among those, 76 (70%) cases occurred. The epidemic curve was indicative of a common point source. Diarrhoea (93%) and abdominal cramps (99%) were the predominant symptoms. One person was hospitalised. No organism was identified. Chicken curry was associated with illness [aRR=3.8 (95% CI 1.4-11)]. It was consumed by 95% of cases, with a nine hour median interval between consumption and onset. Environmental health investigations suggested that reheating of the ready-made chicken curry was likely to have been inadequate. Anecdotal participant reports of 'cool' chicken supported this. No leftovers were available for testing.

Conclusion

Epidemiological and environmental investigations pointed towards the chicken curry as the most likely outbreak vehicle. The clinical presentation, interval between consumption and onset, and deficiencies identified by environmental health were consistent with Clostridium perfringens or Bacillus cereus contamination. Foodborne outbreak investigations without microbiological findings pose a particular challenge. The foodhandlers were advised of the importance of thorough reheating of pre-prepared foods and were retrained. Extensive prompt environmental investigations, together with timely commencement of the epidemiological study, were key to outbreak management and institution of early control measures.

Keywords: Disease outbreak, cohort study, foodborne disease

ABSTRACT ID: 44

PRESENTED BY: Patricia Garvey (patricia.garvey@hse.ie)

A 3.3 Remaining open minded: A potential mixed-pathogen outbreak of Campylobacter and secondary pathogen from Christmas meals served at an entertainment venue, England, December 2015

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Background

Public Health England was alerted to gastrointestinal illness amongst persons who ate from the Christmas menu served at an entertainment venue throughout December 2015. Prior to the alert, Campylobacter spp was isolated from stool specimens and environmental investigations identified inappropriate cooking techniques for chicken liver parfait. Descriptive analysis identified persons with short incubation periods inconsistent with Campylobacter infection. Here we present a post-hoc analysis to identify factors associated with illness in these cases.

Methods

A retrospective cohort study was conducted using a bespoke questionnaire among respondents who ate from the Christmas menu. Cases were defined as (1) Campylobacter case: gastrointestinal symptoms or fever which developed 24 hours to 12 days after exposure (± laboratory confirmation), or (2) possible secondary pathogen case: gastrointestinal symptoms or fever which developed 6 to 24 hours after exposure. We performed multinomial regression analyses informed by descriptive and logistic regression analyses for each case definition.

Results

Of 230 valid responses, we identified 44 Campylobacter (nine microbiologically confirmed) and nine possible secondary pathogen cases. Vomiting was more prevalent amongst possible secondary pathogen cases (56% vs 27%) whilst diarrhoea was more prevalent amongst Campylobacter cases (91% vs 67%). A multinomial regression model showed chicken liver parfait (OR=15.4, 95% CI=6.0-39.2) and gravy (OR=2.9, 95% CI=1.3-6.6) were associated with Campylobacter cases; vegetable pesto salad (OR=9.7, 95% CI=2.1-45.5) and gravy (OR=4.8, 95% CI=0.9-25.1) were associated with possible secondary pathogen cases although the latter exposure was not statistically significant.

Conclusion

Our post-hoc analysis suggests a mixed pathogen outbreak with aetiological causes of illness different to those associated with Campylobacter. Failing to identify a cause of infection may result in missed opportunities to implement control measures and provide public health advice.

Keywords: mixed-pathogen, Campylobacter, cohort, food poisoning, multinomial regression

ABSTRACT ID: 189

PRESENTED BY: Daniel Gardiner (daniel.gardiner@phe.gov.uk)

A 3.4 Risk factors for sporadic cryptosporidiosis cases in the Netherlands, analysis of a three-year population-based case-control study, 2013-2016

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Background

In 2012, cryptosporidiosis cases increased in the Netherlands, but no single source was identified. The predominant species was C. hominis (88%). In 2013, we began a three-year population-based case-control study to identify risk factors for sporadic cryptosporidiosis in collaboration with 17 Dutch microbiology laboratories.

Methods

We defined cryptosporidiosis cases as laboratory confirmation via microscopy or PCR. Cryptosporidium samples were further analysed by RT-PCR for C. hominis or C. parvum speciation. Cases received the study questionnaire from their GP. Controls were selected from the population register and frequency matched on age. We calculated adjusted odds ratios (aOR) using logistic regression.

Results

Overall, 650 Cryptosporidium samples were speciated. In study-year-one, 240 samples were C. parvum (81%) and 55 C. hominis (19%); study-year-two, 182 samples were C. parvum (90%) and 21 C. hominis (10%), and study-year-three, 65 samples were C. parvum (43%) and 87 C. hominis (57%). In risk factor analysis, cases in study-year-one were more likely than controls to swim in a river or lake (aOR 4.9; 95%CI:2.0-12), have contact with cattle (aOR 3.8; 95%CI:2.0-7), eat barbequed foods (aOR 3.8; 95%CI:2.4-6.1) and have a household diarrhoeal case (aOR 1.8; 95%CI:1.1-3.7). In study-year-two, cases were more likely than controls to have contact with a non-household diarrhoeal case (aOR 3.0; 95%CI:1.2-7) or household diarrhoeal case (aOR 2.8; 95%CI:1.3-5.8). In study-year-three, cases were more likely than controls to have a household diarrhoeal case (aOR 2.5; 95%CI:1.7-3.9), changed infants' diaper(s) (aOR 1.8; 95%CI:1.1-2.8) and bathed in an inflatable pool (aOR 1.6; 95%CI:1.1-2.5).

Conclusion

During the three-year study, we identified a species shift from C. parvum to C. hominis. Information about Cryptosporidium exposure during outdoor recreational activities and household hand-hygiene improvements could prevent future infections.

Keywords: Cryptosporidiosis, Case-control, Sporadic, Risk factors, the Netherlands

ABSTRACT ID: 264

PRESENTED BY: Titia Kortbeek (titia.kortbeek@rivm.nl)

A 3.5 Staphylococcus aureus enterotoxin outbreak in Lisbon, 2015: need for active enforcement of public health recommendations

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3. Unidade de Saúde Pública Dr. António Luz

Background

On 15th December 2015, 30 schoolchildren presented to the emergency room of Amadora hospital with gastrointestinal symptoms. A common exposure to a community kitchen from a social program was identified; this facility had been previously inspected twice due to unsanitary conditions. The local Public Health Unit undertook an investigation into the source of disease.

Methods

We defined cases as anyone with vomiting, prostration or abdominal pain who ate lunch prepared by the kitchen on 15th December. We interviewed 350 people to explore potential exposures. Leftover food samples, vomitus from cases, and swabs from food handlers were sent to the reference laboratory and tested for foodborne pathogens. Environmental investigations were carried out for flaws in food preparation chains.

Results

S. aureus enterotoxin was detected in samples from 4 patients, 1 food handler and 1 food item. The epidemic curve suggested a point source outbreak with contamination on 15th December; food was distributed from the common kitchen leading to approximately 600 people being exposed to the same meal. 226 children and 49 adults sought hospital care; 9% were admitted.

Flaws identified on previous kitchen visits persisted, including deficient food temperature control, hand hygiene, and improper handling of food utensils risking cross-contamination.

Conclusion

Epidemiological investigation, symptom and microbiological profile suggest an S. aureus toxin outbreak with a food handler source. Deficient kitchen processes and conditions were previously identified but not remediated, leading to contamination of food, bacterial growth and dissemination.

The local Public Health Unit could have averted hospitalization, human and economic costs in this case by using existing powers to enforce changes by temporary kitchen closure.

Keywords: Disease Outbreaks, Staphylococcal Food Poisoning, Health Policy, Portugal

ABSTRACT ID: 219

PRESENTED BY: Guilherme Duarte (guilhermegduarte@gmail.com)

A 3.6 Restaurant-associated typhoid fever outbreak, Taiwan, 2015

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Background

Indigenous typhoid fever is rare in Taiwan. In March and November 2015, three indigenous typhoid fever cases emerged in Longtan District and the Salmonella enterica serovar Typhi isolates shared a common pulsed-field gel electrophoresis (PFGE) pattern, SIX.001.

Methods

All cases were interviewed using a standard investigation form to trace common sources of infection. Active case finding were conducted among the contacts. Stool specimens were collected from households of cases and food handlers of implicated restaurants for isolation of pathogens. Bacterial isolates were characterized using PFGE and multilocus variable number tandem repeat analysis (MLVA). The genotypic patterns were compared with those in the Salmonella DNA Fingerprint database constructed by Taiwan Centers for Disease Control.

Results

Three cases were all female aged 21 to 39. Epidemiological investigation revealed two restaurants as the suspected sources of infection. Stool cultures from two asymptomatic food handlers of restaurant A yielded S.Typhi, who had stool specimens tested negative in the first investigation in March, 2015. The PFGE profiles of isolates from the two employees were indistinguishable from the isolates from the three cases and matched the isolates from two cases emerged in November 2012, who also resided in Longtan District and admitted that they patronized the restaurant A before onset. No further cases occurred after the closure of the implicated restaurant. By MLVA, isolates associated with the outbreak can be discerned from other SIX.001 isolates which were frequently recovered from Indonesian migrant workers in Taiwan.

Conclusion

The source of infection for this outbreak was successfully traced and molecular subtyping of bacterial isolates was helpful for outbreak investigation. Repeated epidemiological and laboratory investigation should be considered because chronic typhoid carriers could excrete the organism intermittently.

Keywords: outbreaks, molecular epidemiology, typhoid fever, pulsed-field gel electrophoresis

ABSTRACT ID: 50

PRESENTED BY: Hao-Hsin Wu (wuhaushing@cdc.gov.tw)

Track 4: HIV, sexually transmitted infections and viral hepatitis (1)

Moderator: Lelia Thornton, EPIET supervisor, Ireland / Hepatitis expert

A 4.1 Former Soviet Union migrants in Germany: HIV and hepatitis C infections among people who inject drugs.

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Background

High proportions of drug use and injection-related risk behaviours have been reported among Former Soviet Union (FSU)-migrants. To investigate this group in Germany regarding hepatitis C (HCV) and HIV prevalence and related risk behaviours and to focus prevention/control strategies, we compared drug-injecting first generation FSU-migrants and native Germans by using data from a sero-behavioural survey among people who inject drugs (PWID).

Methods

Current injectors were recruited using respondent-driven sampling in eight German cities between 2011-2014. Questionnaire-guided interviews were conducted and dried blood spots collected and anonymously tested for anti-HCV, HCV-RNA, and anti-HIV1/2. We performed Chi2 or Fisher's exact tests to describe differences between FSU-migrants and native Germans, and developed a multivariable logistic regression (MVR) model to investigate the risk for HCV-infection.

Results

A total of 208 FSU-born migrants and 1,318 native Germans were included in the analysis. FSU-migrants were younger than Germans (median age: 33 vs. 38), and more often male (83.1% vs. 75.9%, p=0.022). HCV prevalence was 74.5% in FSU-migrants vs. 64.6% in Germans (p=0.006), HIV prevalence 5.8% and 4.6%, respectively (p=0.474). The proportion of FSU-migrants reporting injecting-related risk behaviours was higher than among Germans: injecting daily (p=0.015), with friends (p=0.038), cocaine (p=0.044), more than one drug (p=0.006), and sharing drug paraphernalia (filters/cookers) (p=0.045). In the MVR, risk for HCV-infection was increased in FSU-migrant compared to German males (OR 2.7, p=0.005), but no difference was identified between FSU-migrant and German females (OR: 0.79, p=0.528).

Conclusion

Identification of subgroups among PWID is important to focus prevention strategies. Among the subgroups analysed male FSU-migrants were at highest risk for HCV, therefore access to and acceptance of harm reduction measures, HCV-testing and – treatment should be investigated further for this population.

Keywords: Intravenous substance abuse, HIV infections, Hepatitis C, Migrants, USSR, Germany

ABSTRACT ID: 361

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A 4.2 Advancing HIV+ migrants access to health care services in Spain

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Background

In Spain, migrants are disproportionately affected by HIV and experience higher rates of late diagnosis. We investigated the barriers to health care access among HIV+ migrants in Spain.

Methods

Between July 2013 and July 2015, we surveyed 765 HIV+ migrants living in Spain, over 18 years old and diagnosed within 5 years before the survey. We collected epidemiological, demographic and behavioural data. We estimated the prevalence of self-reported barriers to health care, and determined their association with socio-demographic factors and immigration status using chi-squared analysis and logistic regression.

Results

Of those surveyed, 672 (88%) individuals had information on health care access: 23% were women. Men were more likely to report barriers than women (24% vs. 14%, p=0.009). The main barriers were: lengthy waiting times for an appointment (9%) or in the clinic (7%) and lack of a health card (7%). Having an irregular immigration status was a risk factor for experiencing barriers for both men (OR: 4.5 [95%CI: 2.5-8.0]) and women (OR: 9.0 [95%CI: 2.9-28.3]). Financially dependent men (OR: 2.3 [95%CI: 1.3-4.0]) were more likely to report barriers compared to men who earned an income. Women with a university degree were more likely to report barriers (4.6 [95%CI: 1.8-18.0]), mostly related to waiting times.

Conclusion

Health services barriers are more frequently reported among migrant men in Spain, and are primarily structural. These barriers are determined by socio-economic and legal status. Facilitating health card acquisition for all migrants, and reducing the waiting time for appointments would ensure prompt and ongoing access to HIV treatment and care services.

Keywords: HIV, migrants, immigration, Health care

ABSTRACT ID: 99

PRESENTED BY: Patricia Ndumbi (patricia.ndumbi@gmail.com)

A 4.3

Is shigellosis among MSM a widespread problem? An analysis of the European surveillance data.

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Background

Shigellosis outbreaks associated with sexual transmission among men who have sex with men (MSM) were recently reported from the United Kingdom, Germany and Spain, with severe infections among HIV-positive MSM. We explored surveillance data to assess whether men are over-represented among domestic shigellosis cases in Europe, suggesting sexual transmission among MSM.

Methods

We analysed EU/EEA shigellosis surveillance data submitted to The European Surveillance System between 2009 and 2014. We assessed trends by gender and origin of infection among cases aged 16-65 years to determine the contribution of males among domestically-acquired infections. Male-to-female ratios were calculated for domestically-acquired cases by country (aggregated for 2012-2014) and by Shigella species (and serotype for S. flexneri) over time.

Results

During 2009 to 2014, travel-related shigellosis cases decreased overall (1378 to 1013) and among both genders. Domestically-acquired cases increased from 691 to 1071; among men, cases doubled from 364 to 735. Male-to-female ratios increased among both travel-related (0.7 to 0.8) and domestic cases (1.1 to 2.3). Among domestic cases (2012-2014), the male-to-female ratio was 2.0 or above in the EU/EEA and in the Netherlands, France, Austria, Germany, United Kingdom, Poland, Spain and Ireland. Male-to-female ratios were 2.0 or above among domestic cases for: S. flexneri serotype 3a (all years), 2a (2010-2014), 1b (2010, 2012), 6 (2013) and other serotypes (all years); S. sonnei (2011); and unknown Shigella species (2014).

Conclusion

The excess of male cases among domestically-acquired cases in several countries suggest ongoing sexual transmission among MSM in Europe. Reporting of transmission mode will facilitate interpretation of national and European trends and allow public health interventions, including raising awareness among clinicians and MSM, particularly HIV-positive individuals at risk of severe outcomes.

Keywords: Shigella, Sexually Transmitted Diseases, Gastroenteritis, Surveillance

ABSTRACT ID: 185

PRESENTED BY: Gianfranco Spiteri (gianfranco.spiteri@ecdc.europa.eu)

A 4.4

Chlamydia trachomatis Infection in Women in Germany, 2008-2015

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Background

Chlamydia trachomatis (CT) infections are not reportable in Germany. Gynaecologists offer CT-Screening to pregnant women (SP) since 1995 and women and women ‹ 25 years since 2008 (S25). Diagnostic testing (DT) is offered for symptomatic women. In 2010 a nationwide, laboratory-based, voluntary sentinel, conducting retro – (since 2008) and prospective information on routin CT-diagnostics, was initiated. We analysed Ct-diagnostic practices to develop recommendations for prevention.

Methods

We analysed CT-tests from 15-59 years old women with information on test result, age-group in years (15-19, 20-24, 25-29, ›=30), and test reason (TR). We extrapolated ratio of S25 – and SP-tests to the ratio of the respective populations in Germany and estimated S25 coverage.

We calculated proportion of positive tests (PPT) by age-group and TR and compared those with Chi-squared test. We estimated trends of the PPT by age-group and TR with multivariable Poisson regression.

Results

We analysed 4,632,770 CT-tests from 24 laboratories. Most frequent TR was SP (40%), followed by S25 (24%), DT (26%), and unknown (10%). The S25 coverage was 8% in 2008, 11% in 2009, and 12% in 2015.

In age-groups 15-19 and 20-24 the S25 PPT was 5.0% and 5.1%, respectively. SP and DT PPT was higher in age-groups 15-19 (10.1% and 9.2%) and 20-24 (5.7% and 8.0%) compared to 25-29 (2.1% and 5.2%), and ›=30 (0.9% and 2.3%), p-value‹0.001. Over time the PPT slightly decreased in age-groups 15-19 and 20-24 (0.9%/year and 2.0%/year, p-value‹0.001).

Conclusion

Despite a gradual slight decrease, PPT is high among young women. S25 coverage is low and did not increase substantially. S25 should be promoted among young women and gynaecologists. CT awareness campaigns should be implemented. Gynaecologists should be remunerated for S25 counselling.

Keywords: Chlamydia trachomatis, Chlamydia, sexually transmitted infections, Germany, women, screening

ABSTRACT ID: 63

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

A 4.5 Current prevalence of chronic hepatitis B and C virus infection in the general population and other low-risk populations of the EU/EEA: a systematic review.

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Background

Hepatitis B (HBV) and C (HCV) prevalence estimates are necessary to inform policymaking and to design appropriate secondary prevention interventions.

Methods

We conducted a systematic review of literature published between 2005 and 2015 on hepatitis B and C prevalence in the EU/EEA Member States in the general population, pregnant women and first-time blood donors. We defined HBV and HCV prevalence based on HBsAg and anti-HCV antibody markers, respectively. A risk of bias assessment was performed for each study and was used to classify included studies by quality. To assess the prevalence of HBV and HCV among first-time blood donors, data from the Council of Europe was used. An algorithm based on study quality was used to calculate an EU/EEA general population HBV and HCV prevalence estimate.

Results

In total 211 prevalence data points were identified, ranging from zero to 33 estimates per country. For HBV, general population estimates were available for 13 countries, with prevalence ranging from 0.1% to 4.4%. For HCV, prevalence estimates for the general population were available for 13 countries, with reported prevalence ranging from 0.1% to 5.9%. Based on general population and first-time blood donor estimates, the HBV prevalence in the EU/EEA as a whole is estimated to be 0.9%, corresponding to around 4.7 million HBsAg positive cases. For HCV, the estimated EU/EEA prevalence is 1.1% corresponding to around 5.6 million anti-HCV positive cases.

Conclusion

Our findings indicate a high HCV and HBV chronic infection burden in the EU/EEA with significant variability between countries. The lack of high quality, recent, nationwide prevalence estimates makes it challenging to gain an EU/EEA overview of the current situation regarding chronic viral hepatitis.

Keywords: Hepatitis B, Hepatitis C, Prevalence, Systematic Review [Publication Type]

ABSTRACT ID: 223

PRESENTED BY: Irene Veldhuijzen (Irene.veldhuijzen@rivm.nl)

A 4.6 Knowledge, Attitude and Practices on Hepatitis B and C among health care workers, Armenia, 2016

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Background

Hepatitis B and C (HBV, HCV) are chronic viral infections causing liver cirrhosis and carcinoma. They are serious global public health problems and health care workers (HCWs) are at high risk. This study aims to evaluate knowledge, attitude and practices (KAP) about HBV and HCV among HCWs in Armenia.

Methods

We conducted a cross sectional study using randomized sampling among 389 HCWs, working in Yerevan and two districts. KAP information on hepatitis was collected using a standardized questionnaire.

Results

Out of 400 respondents, 389 (97%) responded (median 46 years); 328 were female (84%); 210 (54%) completed college; 179 (46%) graduated university. Only 216 (56%) passed continuing medical training during last 5 years. 101 (29%) believed that HBV and HCV are the same and 100 (26%) thought HCV can be prevented by vaccine. 360 (93%) knew HBV and HCV transmission is blood-borne. 291 (75%) HWCs reported not receiving HBV vaccine and 83 (21%) didn't recommend it for children due to severe adverse reactions. Only 80 (21%) of HCWs had been trained on hospital infection control; 381 (98%) HCWs were exposed to blood, 272 (71%) never used eye protection during patient contact.

Conclusion

HCWs showed varied knowledge, attitudes, and practices on HBV and HCV. The majority were not HBV vaccinated and a fourth would not vaccinate their children. Although the majority knew that HBV and HCV were bloodborne infections, only a fourth received infection control training.

In order to mitigate the burden of HBV and HCV, HCWs need to receive HBV vaccinations. HCWs require more training in bloodborne infections and hospital infection control. Armenia also needs to develop and implement a hospital acquired infection (HAI) surveillance system.

Keywords: knowledge, attitude, practices (KAP), hepatitis, medical workers

ABSTRACT ID: 187

PRESENTED BY: Mher Davidyants (davidyants@gmail.com)

Track 5: Influenza and other respiratory viruses (1)

Moderator: Cornelia Adlhoch, ECDC, Expert Respiratory Diseases / Influenza

A 5.1 Estimating the community burden of influenza-like illness (ILI) in Sweden, 2013-2014.

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Background

Traditional healthcare-based surveillance systems underestimate the burden of influenza in the community, since most cases do not require medical attention. We used a population-based cohort to estimate the burden of influenza in the community in Sweden during the 2013-2014 season.

Methods

We randomly selected individuals aged 3 months-85 years from the National Population Registry. Between November 2013 and November 2014, cohort participants completed weekly online questionnaires reporting new occurrence of ILI symptoms, and related medical consultations and hospitalisations. We estimated the ILI weekly incidence as the proportion of cases fulfilling the EU case definition over the number of responders per week, standardised for the age of the Swedish population. We also estimated the proportion of all episodes receiving medical care and those requiring hospitalization.

Results

Of the 34,970 selected individuals, 3,245 (9.3%) completed at least one questionnaire and reported 1,863 ILI episodes. The weekly ILI incidence ranged from 1.4 cases/1,000 population in week 13, 2014 to 18/1,000 in week 30, 2014 (median 9.7/1,000). Overall, the highest proportions of episodes requiring medical consultation were observed among <2 (26%) and ≥65 (26%) year olds. The highest hospitalization proportions were also observed among those groups (1.6% and 5.9%, respectively).

Conclusion

The study estimated the ILI burden in the community in Sweden during an entire year with a mild influenza season. These findings can serve as baseline figures for severity assessments of future epidemics or pandemics. We also recommend the use of these estimates for i) estimating the community ILI-associated costs, ii) evidence-based resource allocation, and iii) assessing additional needs during pandemics, in order to improve preparedness strategies and health communication to the general population.

Keywords: Influenza, Incidence studies, severity

ABSTRACT ID: 180

PRESENTED BY: Hanna Merk (hanna.merk@falkhalsomy)

A 5.2 European enterovirus surveillance and laboratory detection – are we prepared to detect an enterovirus outbreak?

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Background

Enteroviruses (EVs) are known to cause large and severe outbreaks as previously demonstrated with EV-D68. The risk for poliovirus importation exists until the eradication has been completed, as seen earlier in Israel. This is particularly true in the EU/EEA region where inactivated polio vaccine only vaccination strategy could lead to silent transmission of vaccine derived polioviruses. We evaluated the European preparedness for detection of EVs in order to improve our response for (re)-emergencing EVs linked to severe disease.

Methods

Two on-line surveys were submitted to all EU/EEA Member States (MS) national coordinating competent bodies. The first questionnaire was on non-polio enterovirus surveillance and laboratory detection, and the other on poliovirus environmental surveillance.

Results

23 MS responded to the surveys by 2 May 2016; 21 conduct non-polio enterovirus surveillance by typing clinical specimens. Twelve MS have established surveillance for EV-D68, either via sentinel influenza surveillance (n=7) and/or by typing EV-positive respiratory samples (n=11). EV-PCR is provided by 21 MS, and virus isolation by 18. Nine MS type/characterise only culture-positive EV isolates, whereas twelve MS also subject PCR-positive samples for typing/characterisation. Neutralisation assay, sequencing or both are utilised by seven MS each. Ten MS perform environmental surveillance for poliovirus; five plan its introduction.

Conclusion

Our surveys demonstrated partial EV-D68 and poliovirus environmental surveillance in the EU/EEA region. They revealed issues related to EV typing/characterisation in those countries which rely on virus isolation, as most emerging EV types are refractory to isolation and antibodies used in neutralisation assays are unlikely available. A situation report will be shared with MS, and European algorithms for polio and other EV identification will be developed to strengthen the European enterovirus laboratory preparedness.

Keywords: Enterovirus, Poliovirus, Surveillance, Detection, Typing, Outbreak

ABSTRACT ID: 250

PRESENTED BY: Heli Harvala (heli.simmonds@hotmail.com)

A 5.3 Emerging Enterovirus C104, C105 and C109 in Denmark in 2015 and 2016

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Background

New genotypes of enterovirus (EV) species C associated with respiratory infections and severe disease including paralysis have recently emerged worldwide. These new EVs are typically not detected in stools and therefore missed by the standard EV surveillance systems. In Denmark, the EV surveillance system was extended in 2014 to include respiratory samples in response to the North American outbreak of EV-D68. We investigated the emerging EVs in order to improve future surveillance and control measures.

Methods

Between January 2015 and March 2016, 192 EV positive respiratory samples were received and genotyped by RT-PCR and sequencing of partial coding sequences of the VP1 and VP2 capsid proteins. Phylogenetic analyses were performed using partial sequences of these genes together with all available published sequences downloaded from GenBank.

Results

Two, one and three cases of EV C104, C105 and C109 respectively, were detected during this 15 month period in three of Denmark's five regions. Age ranged from 1 to 24 years. Four cases had known underlying co-morbidities, and all presented with influenza-like symptoms. Phylogenetic analysis demonstrated 95% and 98% sequence homology among the Danish C104 and C109 sequences, respectively. Danish EV sequences showed 85% to 99% sequence homology with available EV sequences.

Conclusion

Three new emerging EV strains were detected in Denmark. Unique EV C104 and C109 sequences argue against common sources of introduction. Future detection and characterization of these emerging non-poliovirus EVs in a timely manner will not only improve our understanding of their nature and estimate their potential health burden but also enable a prompt response in case of outbreaks. Hence, we recommend the expansion of the current EV surveillance system to include respiratory specimens in Denmark.

Keywords: Enterovirus C, Human – Denmark – Phylogeny – Genotype – Respiratory infections

ABSTRACT ID: 157

PRESENTED BY: Celine Barnadas (cebs@ssi.dk)

A 5.4 Facebook versus telephone: comparison of samples from two different recruitment approaches in a survey on parental acceptance of seasonal influenza vaccination for children, Germany 2015

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Background

Since recruitment of participants into health research is challenging, recruitment via social networking sites has become increasingly popular. However, it is unknown if samples of online-recruited participants are comparable to those recruited via conventional methods. We conducted a survey on parental acceptance of seasonal influenza vaccination for children with recruitment of participants via Facebook and telephone and compared characteristics of both samples.

Methods

We targeted parents with children aged <18 years living in Germany. Between May and July 2015 we invited Facebook users to participate in an online-survey by showing various advertisements. Simultaneously, we conducted a telephone survey with identical questions using random-digit dialing. We compared participants regarding sociodemographic characteristics, acceptance of influenza vaccination, general vaccination attitude and costs per completed questionnaire.

Results

On Facebook 4,821 clicks at the advertisements resulted in 1,419 completed questionnaires. During telephone interviews 518 questionnaires were completed (response 22%). Compared to the telephone sample, Facebook-recruited participants were younger (mean age 36.4 vs. 42.1 years, $p<0.001$), more often female (85% vs. 73%, $p<0.001$), more likely to work in the medical field (29% vs. 17%, $p<0.001$) and less likely to have a migration Background (14% vs. 32%, $p<0.001$). Facebook-recruited participants were less likely to have their children vaccinated against influenza (50% vs. 66%, $p<0.001$) and were more often against vaccinations in general (24% vs. 1.9%, $p<0.001$). Total costs per completed questionnaire were lower for recruitment on Facebook (10.60 vs. 28.50 Euro).

Conclusion

Characteristics of participants differed considerably between both samples. In particular, an unexpected high proportion of persons with negative attitudes towards vaccination were attracted by Facebook. Even if recruitment of participants via Facebook is feasible and cost-effective, results should be interpreted with caution.

Keywords: influenza, vaccination, acceptance, children, online recruitment, comparison

ABSTRACT ID: 142

PRESENTED BY: Lena Boes (BoesL@rki.de)

A 5.5 The ECDC Surveillance Systems Reengineering (SSR) project: improved surveillance for tomorrow

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Background

Feedback from internal and external stakeholders pointed out inefficiencies in ECDC surveillance processes, data flows and IT systems. We started the Surveillance Systems Reengineering (SSR) project to address these inefficiencies, to reduce the reporting burden and to maximise the EU/EEA surveillance benefits for the Member States. We report here the results of the project and the remaining challenges before new EU surveillance system is developed.

Methods

We described the surveillance vision using relevant parts of the ECDC Long Term Surveillance Strategy 2014-20. We defined optimal processes and data models through structured interviews with key ECDC experts. We consolidated their views during externally moderated workshops. We held two experts consultations with national representatives to collect data reporting and validation requirements. We applied an Enterprise Architecture methodology based on The Open Group Architecture Framework (TOGAF) to document processes, data and IT applications models.

Results

The project delivered 'to be' surveillance-related processes and a global data model integrating indicator-, event-, and laboratory-based surveillance. The new system allows for machine-to-machine data transmission and online-guided data validation. Data providers did not yet agree on a common approach for automatic data transmission. A number of algorithms, electronic workflows and interactive decision trees allows for automation of processes and data flows. Dashboards allows for timely dissemination of communicable diseases data, their determinants and emerging threats. ECDC is currently estimating the resources and timeframe needed to develop the new system.

Conclusion

The development of an integrated EU surveillance system is technically feasible and can address most of the current inefficiencies. In the absence of agreed data transmission standards ECDC should be ready to support data providers in developing suitable data transmission tools.

Keywords: Public Health Surveillance, Health Information Systems, Surveillance, Electronic Health Records, Database

ABSTRACT ID: 364

PRESENTED BY: Gaetan Guyodo (gaetan.guyodo@ecdc.europa.eu)

A 5.6 Comparison of nine serological assays for the specific detection of avian influenza A(H7) antibodies

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Background

In 2013, a novel avian Influenza A(H7N9) virus causing severe respiratory infections in humans was discovered in China. Zoonotic influenza viruses exhibit a high pandemic potential and accurate diagnostic and surveillance activities are crucial for proper disease management. Serological assays play a fundamental role in this regard. Virus neutralization tests (VNT) are complex and require advanced biosafety conditions. Hemagglutination inhibition tests (HIT) are more feasible but are described as less sensitive for the diagnosis of new viruses. The use of tween-diethyl-ether split antigen in HIT assays (TW/E-HIT) demonstrated increased sensitivity but lower specificity compared to standard HIT.

This study compares the performance and specificity of nine serological assays for the detection of avian influenza A(H7) antibodies.

Methods

VNT, HIT and TW/E-HIT assays were performed with two viral strains (A/Anhui1/2013/H7N9 and A/Oregon/1971/H7N3) using turkey or horse red blood cells (RBC). Assay performance was assessed with positive animal control sera. Geometric mean titres (GMT) were calculated and differences between groups of sera or assays were determined using logistic regression models. Specificity was evaluated using 1028 paired human serum samples, collected from patients with respiratory symptoms (thereof 100 with confirmed Influenza A infection) between 1998 and 2013 in a non-endemic area.

Results

Assay performance based on GMT levels was best in TW/E-HIT assays performed with horse RBCs and A/Oregon antigen. The viral strain in combination with the method of antigen preparation influenced considerably the GMT level. Specificity was ›99% in all assays.

Conclusion

TW/E-HIT assays represent a specific alternative for the diagnosis of avian Influenza A(H7N9)infections. In order to evaluate this method for endemic regions, sensitivity and specificity tests should be repeated with an Asian serum panel.

Keywords: Avian Influenza, A(H7N9), Serology, Virus neutralization, Hemagglutination inhibition, Tween-diethyl-ether split viral antigen

ABSTRACT ID: 388

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Track 6: Novel methods in epidemiology (1)

Moderator: Bruno Ciancio, ECDC, Head of Section Epidemiological Methods

A 6.1 Introducing dot map cartograms for detection of infectious disease outbreaks

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Background

Geographical mapping of infectious disease cases is an important tool for detecting and studying outbreaks. Two main mapping methods, dot maps and incidence maps, are problematic, as the first does not present the population density and often violates the privacy of cases, and the second is depended on pre-defined regional boundaries. We developed a new method for mapping infectious disease data, which overcomes these limitations: dot map cartograms.

Methods

Dot map cartograms are created by taking a point pattern of cases and reshaping spatial units such that each area becomes proportional to its population size. We compared dot map cartograms with dot maps and incidence maps considering their ability to show both absolute numbers and incidence of the disease, sensitivity to choices regarding spatial scale and classification system, ability to secure the privacy of cases and ability to recognize locations. As an example we created dot map cartograms for a point source outbreak (Q-fever, the Netherlands, 2009) and for human-to-human transmission (pertussis, Germany, 2015).

Results

Dot map cartograms were able to show both absolute numbers of cases and incidence. In the Q-fever outbreak it revealed potential sources (goat farms) and for pertussis it identified clusters with high incidence. Unlike incidence maps, dot map cartograms were insensitive to choices regarding spatial scale. Furthermore, dot map cartograms secured the privacy of cases by spatial distortion, at the expense of recognition of locations.

Conclusion

We demonstrated that dot map cartograms can be a valuable method for detection and presentation of infectious disease outbreaks. Showing both absolute numbers and incidence on the same map informs public health professionals, upon which they can take more informed and appropriate actions to prevent further spread.

Keywords: Geographic Mapping, Cluster analysis, Disease Outbreaks, Communicable Disease Control, Spatial Visualization

ABSTRACT ID: 120

PRESENTED BY: Loes Soetens (loes.soetens@rivm.nl)

A 6.2 A tool for speedy foodborne outbreak investigations based on population food surveys.

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Background

Low participation rates among controls in case-control studies has created the need for alternatives methods to investigate foodborne outbreaks. To avoid sampling controls and based on ideas from Keene (2011), we compared the exposure of cases to specific food items with the population rate of consumption in existing food survey databases (FSD). The results can be used as a quick hypothesis generating tool in the early stages of an outbreak.

Methods

The FSD from the National Food Agency consists food items collected in a web-based 4-day food record completed by a national sample of 1797 adults during 2010-2011. Trawling questionnaires were used to reduce FSD to relevant items. We calculated binomial probabilities that x cases out of n had been exposed to a food item, given the population rate of consumption in the FSD. To test, we analyzed confirmed foodborne outbreaks and extracted food items with p-value < 0.05: EHEC with 67 cases and Salmonella entiriditis with 11 cases.

Results

Standardized trawling questionnaires included 204 items of which 158 were possible to map to FSD. In the EHEC outbreak we found 41 out of 47 items in the questionnaire statistically significant; and in the S entiriditis outbreak, 5 out of 8 items. In both the confirmed source was included in the short list.

Conclusion

We identified food items with higher risk of exposure among cases in foodborne outbreaks than was expected in the population. During an outbreak investigation, these results can be used to generate hypotheses on which items in the trawling questionnaire require further investigation. In the near future we will include stratified analysis by age and sex to increase the statistical power.

Keywords: Disease Outbreaks Foodborne Diseases Surveys and Questionnaires Binomial Distribution Risk Probability

ABSTRACT ID: 385

PRESENTED BY: Sharon Kühlmann-Berenzon (sharon.kuhlmann-b@folkhalsomyndigheten.se)

A 6.3 Use of multi locus sequence typing (MLST) to obtain discriminatory information and Leptospira species directly from clinical specimens

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Background

During leptospirosis outbreaks and epidemics typing is essential to identify potential clusters and transmission pathways. Currently this requires difficult and time consuming culturing. Hence most human leptospirosis cases are only identified at serovar/serogroup level, neither allowing for reliable species assignment. An existing MLST scheme was modified to allow for direct typing of pathogenic Leptospira from patient samples and to enable species determination for surveillance purposes (1).

Methods

A previously published assay was modified by designing nested primers. The novel assay was applied to 44 clinical samples obtained from patients diagnosed in the UK and the Lao PDR. Samples were known to be positive for pathogenic Leptospira spp. and comprised various specimen types (serum, whole blood, buffy coat, urine). All obtained sequences were included as concatenated or single allelic sequences in maximum likelihood phylogenetic analysis to determine Leptospira species.

Results

The modified assay allowed for amplification of alleles directly from a variety of clinical samples. At least one allele was amplified in 22 samples (50%) and could be used for phylogenetic inference. The most frequently detected species in clinical samples was L. interrogans (UK: 10/14; Lao PDR: 7/8) in both countries. In contrast, all other species were distinctly associated with the country (UK: L. kirschneri, L. santarosai, L. weilii; Lao PDR: L. borgpetersenii).

Conclusion

The improved assay will be of use during epidemics and outbreaks by enabling rapid identification of leptospira species and MLST types. Further, it allows for species determination to support surveillance without the need of growing fastidious isolates.

Keywords: MLST, Leptospira, Leptospirosis, Bacterial Typing, Serovar, Serogroup

ABSTRACT ID: 211

PRESENTED BY: Sabrina Weiss (sabrinanweiss@gmail.com)

A 6.4 SMS as a promising data collection tool for repeated measurements of consumption and incidence – Results from epidemiological studies on drinking water and acute gastroenteritis in 2012

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Background

Due to the limited knowledge on drinking water related acute gastrointestinal illness (AGI), a one-year study on tap water consumption and AGI was conducted in the municipality Ale in Sweden, starting in February 2012. The main data collection method was monthly SMS (short message system) questionnaires.

Methods

Participants were recruited to the SMS survey by telephone interviews. During the SMS survey, participants received SMS questionnaires once a month, on various days of the week, during the year. Twenty-four hours prior to each SMS questionnaire a pre-reminder SMS was sent out. The first SMS question was on tap water consumption (24h-recall) and the second on AGI within the last 28 days. If the participants reported AGI, subsequent questions on AGI in the last 14 days, symptoms of the last AGI event, duration of illness, and number of episodes with diarrhoea were sent out. Each participant received a scratch card (approx. value 1€) as reimbursement for each completed SMS questionnaire.

Results

The response rate in the telephone interviews was 44 % out of which 67 % confirmed their interest in participating in the SMS survey. Among the SMS survey participants 76 % completed at least ten out of the twelve SMS questionnaires during the year. The average consumption of cold tap water in the study was ca. 1 l/day, the incidence of self-diagnosed AGI was 0.73 per person-year and the incidence of AGI with vomiting or ≥ 3 episodes of diarrhoea was 0.39 per person-year.

Conclusion

Due to the high response rate and because most citizens can use it, we believe that SMS is a promising tool for collecting data on consumption and illness in epidemiological surveys or outbreak investigations.

Keywords: Drinking water, drinking, acute gastroenteritis, data collection

ABSTRACT ID: 70

PRESENTED BY: Melle Säve-Söderbergh (jonas.toljander@slv.se)

A 6.5 Field epidemiology teaching by telephone. A low-tech but highly appreciated method.

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Background

Since 2013, the Academic Collaborative Centre on Public Health ('AMPHI') organizes three-monthly teaching sessions by telephone. AMPHI is based at the Radboud university medical centre in Nijmegen, The Netherlands and nine Infectious Disease departments of Regional Public Health Services (RPHS) are connected. The teaching sessions have been developed to increase knowledge and skills of medical doctors and nurses working at those RPHS with regards to applied infectious disease epidemiology and research methodology. This Abstract describes this teaching method, and an evaluation that was conducted.

Methods

Contact persons from the RPHSs in the network receive the PowerPoint presentation in advance. When the teaching session starts, all attendants from each RPHS gather in their conference room and dial into the teleconference. Sessions are 'broadcasted' from AMPHI. The presentation is given by the AMPHI epidemiologist (methodological sessions) and/or one of the infectious disease experts from the region (research projects). This method of teaching has been evaluated anonymously using an online questionnaire.

Results

Examples of topics that have been covered include: 'How to write a research proposal'; 'From research objectives to data collection'; 'Analysis of regional surveillance data' and 'Medical Ethical Guidelines and Rules'. Usually between 30-40 participants attend the sessions. The evaluation showed that attendants appreciate the method of teaching, as it easily fits into their busy work schedule and helps them refresh their skills and knowledge, with enough opportunity to ask questions.

Conclusion

The advantages of teaching by telephone (no travel time, easily accessible) are more important than the disadvantage that persons cannot see each other. These teaching sessions fit well into the mission of AMPHI to strengthen the connection between the RPHS's and the university.

Keywords: field epidemiology; Public Health Education; education; research methodology.

ABSTRACT ID: 229

PRESENTED BY: Alma Tostmann (alma.tostmann@radboudumc.nl)

A 6.6 Intensive monitoring of young families by interactive smartphone application reveals high incidence and transmission of (viral) gastroenteritis.

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Background

Viral gastroenteritis is common among young children who are considered key drivers of transmission. As most episodes remain undetected by healthcare, their occurrence and transmission are difficult to quantify. We used a novel smartphone monitoring tool to determine incidence, prevalence and transmission of acute gastroenteritis by major enteric viruses among young families.

Methods

Between January-March 2016, 305 households with a child aged < 24 months were enrolled. Parents daily record gastrointestinal symptoms for each household-member for 10 consecutive weeks using an interactive diary-application. Automated symptom-complex recognition detects gastroenteritis episodes and subsequently activates an App-based personalised stool specimen request and disease questionnaire. Samples are mailed and analysed by rtPCR for presence of rotavirus, norovirus, adenovirus and astrovirus.

Results

With 83% of follow-up weeks completed, the App detected 349 episodes with an overall acute gastroenteritis incidence rate of 173/100 person-years, being highest for household-members aged < 24 months (334/100 person-years). Of 349 episodes detected, 284 are household index episodes and 19 are secondary, occurring within 2 weeks of the index case (secondary attack rate: 9%). 51/125 index case stool specimens analysed thus far are confirmed viral infections (41%), dominated by norovirus (n=41, 33%), followed by astrovirus (4%), adenovirus (3%) and rotavirus (0%). Secondary gastroenteritis attack rates were highest for norovirus index cases (n=8, 89%). Furthermore, asymptomatic viral infections were detected in 30 of 125 (24%) household-members tested pair-wise with an index case.

Conclusion

Monitoring young families through mHealth technology, the acute gastroenteritis incidence during winter/early spring appears higher than previously estimated and carries a high within-household transmission rate, both symptomatic and asymptomatic. Norovirus is the dominant pathogen, although the unusual 2016 rotavirus season observed in the Netherlands should be noted.

Keywords: viral gastroenteritis, incidence, mHealth, children, household, transmission

ABSTRACT ID: 322

PRESENTED BY: Franke Quee (f.a.quee@umcutrecht.nl)

Track 7: Tuberculosis and other respiratory diseases (excluding viruses) (1)

Moderator: Iro Evlampidou, EPIET Alumni Network/Médecins Sans Frontières

A 7.1 Evaluation of latent tuberculosis infection surveillance in Peel region, Ontario

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Background

Surveillance of latent tuberculosis infection (LTBI) in Peel region, where half the population is foreign-born and at high risk, is conducted to provide information to prevent the progression of LTBI to active tuberculosis. Using the ECDC framework, an evaluation of LTBI surveillance was performed to assess data quality in the electronic reportable diseases system (iPHIS) and the system's usefulness in informing program decisions.

Methods

LTBI data in iPHIS from 2010 to 2014 were reviewed. Completeness was assessed based on the proportion of records with 'unknown' or missing responses for key variables. Validity of risk factors and treatment completion were assessed by comparing selected data fields to paper-based charts and by telephone interview, respectively. Usefulness was evaluated through semi-structured interviews with health department stakeholders.

Results

Of 6,576 records reviewed, 51% had risk factors listed as 'unknown'. Preliminary results reveal 29% of responses for risk factors did not match the paper-based charts. Treatment completion rates documented in iPHIS (20%) were lower than data obtained from the telephone survey (50%) and the Canadian benchmark (80%). Stakeholder interviews provided direction for improving usefulness of the data.

Conclusion

This evaluation identified opportunities for changes to LTBI documentation and case management to improve the quality of data collected, including standardization of processes for data entry of risk factor data and active follow up of LTBI clients to capture treatment completion data. The feasibility of electronic medical record alerts for community clinicians to report treatment completion to public health is also being explored. Improved data quality will contribute to better understanding characteristics of Peel LTBI cases which, in turn, can be used to design targeted interventions to reduce the progression of LTBI to active tuberculosis.

Keywords: Latent Tuberculosis/epidemiology, Latent Tuberculosis/transmission, Tuberculosis/prevention & control, Tuberculosis/epidemiology

ABSTRACT ID: 348

PRESENTED BY: Jo Ann Majerovich (joann.majerovich@peelregion.ca)

A 7.2 Risk factors for pneumonia in an area of intensive animal farming in the Netherlands

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Background

Previous research conducted in 2009 found a significant positive association between living close to poultry and goat farms and pneumonia in humans. However, as this result might have been affected by the Q-fever epidemic that ended in 2010, the aim of this study was to re-test this association, now that the Q-fever incidence has fallen below 0.5/100.000.

Methods

In 2014/15, as part of the "Livestock Farming and Neighbouring Residents' Health" project, 2494 adults (aged 20-72 years) living in a livestock-dense area in the Netherlands completed a questionnaire on respiratory health, lifestyle and other items. We retrieved additional information from electronic medical records (EMR) for 2426/2494 (97%) participants. The outcome was self-reported, physician-diagnosed pneumonia or pneumonia recorded in the EMR in the previous three years. We used livestock license data to determine exposure to livestock, including distance between residence and closest farm (at 500m intervals), and the number of animals (cattle, goats, horses, pigs, poultry, sheep) close to the home. We quantified associations between livestock exposures and pneumonia using odds ratios adjusted for participants' demographics, behaviors and comorbidities (aOR).

Results

The three-year cumulative attack rate was 186/2426 (7.7%). Residents within 2000m of a farm with at least 50 goats had an increased risk of pneumonia, which increased the closer they lived to the farm (2000m aOR 1.9, 95% CI 1.4-2.6; 500m aOR 3.7, 95% CI 1.6-8.6). We found no significant associations between exposure to other farm animals and pneumonia.

Conclusion

Living close to goat farms is still a risk factor for pneumonia. We recommend identifying causes of pneumonia by using molecular diagnostics on cases exposed to farms, and investigating the role of non-infectious agents such as dust or endotoxins.

Keywords: livestock, environmental exposure, human, pneumonia

ABSTRACT ID: 230

PRESENTED BY: Gudrun Freidl (gudrun.freidl@rivm.nl)

A 7.3 A higher prevalence of Pneumocystis pneumonia is observed in non-HIV patients, particularly those with cancer, in Northern Ireland, July 2011 – July 2012.

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Background

Since 2011, clinicians in Northern Ireland (NI) have reported concerns of an increase in Pneumocystis pneumonia (PCP) in non-HIV patients. We describe the epidemiology of PCP in order to inform preventive measures in these groups.

Methods

From July 2011 to July 2012information on demographics, clinical severity (including 30 day all-cause mortality) and clinical features for all hospital inpatients in NI aged ≥18 years with P. jirovecii confirmed in any respiratory tract sample (upper and lower). We defined PCP or P. jirovecii colonisation according to clinical symptoms and radiological findings. We statistically described PCP and P. jirovecii colonisation and calculated the adjusted median unbiased estimate (AMUE) of the odds ratio (OR) using multivariable exact logistic regression, adjusting a priori for age and sex.

Results

36/49 (73%) of P. jirovecii detections were PCP; median age 65 years (range 24-86) and 78% male. 28/36 (78%) were in non-HIV patients, of which 18 (64%) had cancer. 29/36 (81%) had 3 or more aetiological causes of immunosuppression. 30 day all-cause mortality for cancer patients was 42% compared with 13% for HIV patients (P-value=0.21). The odds of PCP increased with exposure to chemotherapy (AMUE OR 8.73; 95% confidence interval (CI) 0.84, ∞), immunosuppressive drugs (AMUE OR 12.1; 95% CI 1.94, ∞) and an HIV diagnosis (AMUE OR 16.2; 95% CI 1.71, ∞).

Conclusion

We observed the greatest burden of PCP in cancer patients. Exposure to chemotherapy and immunosuppressive treatment were identified as independent risk factors. We recommend increasing clinician awareness of PCP risk in non-HIV patients, and promoting the consideration of prophylaxis on a case by case basis. We propose further research to characterise cancer patients who may benefit from prophylaxis.

Keywords: Pneumocystis jiroveci, Pneumonia Pneumocystis, antibiotic prophylaxis, public health surveillance

ABSTRACT ID: 45

PRESENTED BY: Lynsey Patterson (lynsey.patterson@hscni.net)

A 7.4 Social determinants and risk factors for tuberculosis; need for harmonisation of definitions?

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Background

In most countries of the European Union (EU), tuberculosis (TB) rates are declining. However this trend may mask high TB rates in some populations associated with specific socioeconomic status and risk factors. In 2014, the Wolfheze Working Group has conducted a survey among all 53 countries of the WHO European Region, with the objective of investigating which social determinants and risk factors for TB are collected in the national TB surveillance systems. Following the results of this survey, ECDC conducted a follow-up study in the EU/EEA MS to document the definitions of social determinants and risk factors of TB as used by the national surveillance systems.

Methods

A semi-structured questionnaire was sent to TB surveillance operational contact points of 31 EU/EEA Member States. The answers were grouped by concepts and evaluated using descriptive analysis.

Results

Twenty-seven of 31 (87%) countries responded, and information on 21 different social determinants was collected by at least one country. Seventeen (63%) countries collected data on homelessness, and 16 (59%) on employment status, while information on living in urban/rural settings was collected by 14 (52%) countries. Regarding potential risk factors for TB; 22 countries (81%) collected data on known TB contacts and 15 on diabetes (56%). About half of the countries, 14 (52%), collected data on the use of alcohol and illicit drugs. Definitions of risk factors varied from physicians' assessment to using ICD-10 codes.

Conclusion

Clear objectives and standardised definitions need to be determined before considering implementation of supranational data collection on social determinants and risk factors for TB. The feasibility of harmonization of definitions will be discussed during the European TB Surveillance Network annual meeting in June 2016.

Keywords: Tuberculosis, social determinants, risk factors, European Union, surveillance

ABSTRACT ID: 330

PRESENTED BY: Vahur Hollo (vahur.hollo@ecdc.europa.eu)

A 7.5 What are surveillance data telling us about paediatric tuberculosis in the European Union and European Economic Area? An analysis of surveillance data from 2007 to 2014

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Background

Despite the constant decrease of tuberculosis (TB) notifications in the European Union (EU) and European Economic Area (EEA), the proportion of children with TB has been stable at around 4%. Challenges are that clinical diagnosis is not standardised in this age group, and the traditional and molecular laboratory diagnostic methods lack sensitivity in children.

The objectives of this study were to describe the burden of TB in children in the EU/EEA during 2007-2014 and to identify gaps in diagnosis and treatment.

Methods

Paediatric TB cases (age<15) grouped by laboratory confirmation and by availability of drug susceptibility testing (DST) results were compared by gender, origin, treatment history, site of disease, drug resistance pattern and treatment outcome.

Results

Among 17,132 notified paediatric TB cases reported by 26 EU/EEA countries, 3,731 (21.8%) were laboratory-confirmed and among these, DST results were available for 3,026 (81.1%) cases. Pulmonary site was reported for 8,564 (50.0%) and extrapulmonary for 8,435 (49.2%) cases. In ages between 5 and 12, the extrapulmonary cases were more frequently reported. The majority of paediatric TB cases with DST (N=2,650; 87.6%) were drug sensitive, 230 (7.6%) mono-resistant TB, 56 (1.9%) poly-resistant, 82 (2.7%) multi-drug resistant (MDR) TB and 8 (0.3%) extensively drug-resistant. Treatment success rate after 12 months of treatment among laboratory not-confirmed cases was 91.6% (N=10,914) and among laboratory-confirmed 83.4% (N=2,215). Treatment success rate after 24 months for MDR-TB cases was 77.1% (N=51).

Conclusion

Confirming the diagnosis of paediatric TB seems to pose a significant challenge despite the availability of modern laboratory techniques. To prevent treating children with miss-diagnosed TB more efforts in collection of a high quality sample for laboratory diagnosis may be employed.

Keywords: Europe, epidemiology, tuberculosis, paediatric tuberculosis, laboratory diagnosis, treatment outcome

ABSTRACT ID: 202

PRESENTED BY: Csaba Ködmön (csaba.kodmon@ecdc.europa.eu)

A 7.6 Using whole genome sequencing and social network analysis to investigate extensive transmission and high positivity of latent tuberculosis in an educational institution, South West England, 2015

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Background

In March 2015, a student living in South West England was diagnosed with sputum smear positive tuberculosis (TB). An earlier case diagnosed after leaving England in 2014 had epidemiological links to the same educational institution. Microbiological typing confirmed the same Beijing strain and indistinguishable 24 loci variable number tandem repeat profiles in contacts of these cases. An incident control team was established and screening undertaken for latent tuberculosis (LTBI) and active disease.

Methods

Students and staff were defined as high or low risk depending on whether they had shared a class with an infectious case. We used the T-SPOT.TB blood test to screen for LTBI and collected epidemiological data including potential symptoms and risk factors for TB. Further microbiological characterisation was undertaken using whole genome sequencing. We calculated LTBI positivity rates and estimated relative risks by classes shared. A network analysis was constructed to further understand the potential transmission network.

Results

Data were available for 1378 staff and students who were screened. Ten active cases were identified. We observed an LBTI positivity rate of 39.1% in the high risk group and 8.2% in the low risk group. The relative risk of LBTI in the high risk group was 4.8 (95% confidence interval 3.7 to 6.2) compared to the low risk group. Whole genome sequencing showed zero single nucleotide polymorphisms differences between the samples. The network analysis supported the epidemiological findings and identified sub-groups at high risk of LTBI.

Conclusion

Extensive transmission occurred within the educational institution, possibly associated with a single infectious case with a high bacterial load. We advocated enhanced epidemiological and microbiological techniques to direct the implementation of screening and describe complex TB incidents.

Keywords: Tuberculosis, latent tuberculosis infection, screening, whole genome sequencing, social network analysis

ABSTRACT ID: 273

PRESENTED BY: Simon Packer (simonpacker@nhs.net)

Track 8: Vaccine preventable diseases (1)

Moderator: Sabrina Bacci,ECDC, Expert Vaccine-preventable Diseases

A 8.1 Tackling meningococcal disease in England: the need for rapid vaccine coverage estimates to estimate effectiveness of the newly introduced MenB and MenACWY vaccines

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Background

Meningococcal disease is responsible for significant morbidity and mortality especially in young children and adolescents. In England, two new meningococcal (Men) immunisation programmes were implemented in summer 2015: a MenB programme at 2, 4 and 12 months delivered through general practice (GP) and a MenACWY conjugate vaccine programme targeting 13-18 year-olds through schools and GPs, in response to a national MenW outbreak. This study assessed early vaccine coverage of the GP delivered programmes in England to inform early vaccine impact and effectiveness.

Methods

MenB and MenACWY immunisation status of eligible patients recorded in approximately 95% of GP systems in England, to the end of January 2016, were automatically accessed using a web-based sentinel surveillance system. We estimated vaccine coverage and interpreted trends in meningococcal disease in light of these results.

Results

MenB coverage for the first routine cohort (born 03/07/2015-02/08/2015) was 94.0% for dose one and 84.8% for the second when evaluated at six months of age. For the MenW immunisation programme, coverage for 17-18 year-olds was 35.2% to end of March 2016. Compared with the previous epidemiological year, MenB and MenW cases have increased overall. However reductions in cases have been observed in vaccine-eligible cohorts for the respective meningococcal capsular groups within six months of the campaign.

Conclusion

High MenB vaccine coverage suggests the vaccine has been well accepted. MenACWY coverage in the oldest catch-up cohort is lower, but the routine programme is expected to perform better, in line with other school programmes. Vaccine effectiveness for both programmes will be assessed at the end of the current epidemiological year. Rapid availability of robust, age-specific vaccine coverage estimates across England will play a critical role in the analysis.

Keywords: Vaccination, Coverage, Meningococcal Infections, Meningococcal type B conjugate vaccine, Meningococcal Meningitis Serogroup W135, England

ABSTRACT ID: 184

PRESENTED BY: Bhavita Vishram (bhavita.vishram@phe.gov.uk)

A 8.2 Impact of vaccination rate on rotavirus disease incidence – Federal State of Brandenburg, Germany, 2007-2011

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Background

Since the approval of rotavirus vaccines for infants in 2006, rotavirus incidence has decreased markedly among children in Brandenburg. Brandenburg is the only State in Germany with rotavirus vaccine uptake (VU) data at population level in all 18 administrative districts (AD). We aim to quantify the impact of VU on rotavirus incidence in young children, and to describe VU at AD level to inform local authorities to address vaccination acceptance in districts with low uptake.

Methods

We described overall rotavirus notification rates from 2007 to 2011 at State and AD level in 5 age groups and rotavirus VU rates at State and AD level. Using Spearman correlation we quantified the impact of VU on rotavirus incidence at AD level, stratifying by age group.

Results

Overall VU increased from 0.4 to 61.4%, with a range of 37.7 to 72.6% between ADs in 2011. After an overall peak in 2009 of 3,023 rotavirus cases per 100,000 among children under 5, the rotavirus incidence rate decreased in all age groups: from 4,030 to 1,417/106 in <1-year-old, 5,897 to 2,497/106 in 1-year-old, 2,651 to 1,691/106 in 2-years-old, 1,525 to 1,060/106 in 3-years-old and 952 to 648/106 in 4-years-old. At AD level rotavirus incidence was significantly associated with VU in < 1–years-old (-0.57), 1-years-old (-0.47) and 2-years-old (-0.32) (all $p<0.003$), but not in older age groups.

Conclusion

VU in Brandenburg is comparable with that of other former East German States (estimated from vaccination sales and prescriptions). Analysis at district level identified areas where VU should be enhanced. Furthermore, analysis suggested efficacy of the vaccination in children

Keywords: rotavirus infections, vaccine uptake, prevention, administrative district level, local variation

ABSTRACT ID: 225

PRESENTED BY: Claudia Siffczyk (claudia.siffczyk@lavg.brandenburg.de)

A 8.3 Reasons for measles vaccination gaps among preschool children – A survey of social medical assistants in South-West Germany, 2015

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Background
WHO recommends two doses of measles containing vaccine for ›95% of the population to eliminate measles. In Baden-Wuerttemberg, social medical assistants (SMA) in 44 counties check vaccination records during school entry examination (SEE) and counsel parents on vaccinations. We adopted a "Guide to Tailoring Immunization Programmes (TIP)" in the WHO European Region to identify reasons for incomplete measles vaccination at preschool age in order to recommend specific interventions for different counties.

Methods
We designed a questionnaire for SMA on their perceived reasons of vaccination gaps among preschool children. We used an equidistant scale from 0 (never) to 4 (always) points for answers. The questionnaire was distributed and returned during two general meetings for SMA. We calculated frequencies and means. We stratified by counties reporting higher (over 90.2%) and lower (below 87.2%) two-dose measles vaccination coverage in the SEE 2013/14. We tested significance using Chi2-test.

Results
Of the 128 participants, 107 SMA returned questionnaires. Main reasons for measles vaccination gaps were: parents´ fear of side effects (2.4/4), health damages due to vaccine compounds (2.0/4) and excessive stress on the immune system (1.7/4), followed by measles being regarded as a harmless (1.9/4) and rare (1.6/4) disease. A significant difference was observed in the frequency of SMA reporting vaccination hesitant doctors in their county: 100% SMA of counties with low vaccination coverage in contrast to 87% SMA of counties with high coverage (p=0.026).

Conclusion
To increase measles vaccination coverage in Baden-Wuerttemberg we recommend informing parents of young children on risks of measles and addressing concerns about vaccination safety. Educational and motivational campaigns aimed at GPs are necessary to increase immunization rates among patients and to achieve higher population immunity for measles.

Keywords: measles, vaccination, children, WHO

ABSTRACT ID: 80

PRESENTED BY: Dorothee Lohr (dorothee.lohr@rps.bwl.de)

A 8.4 Who escaped the measles epidemic? A case-control study among unvaccinated orthodox Protestants in The Netherlands.

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Background
In The Netherlands measles epidemics periodically occur among unvaccinated orthodox Protestants, a socially clustered minority living mainly in the so-called Bible Belt. In the 2013/2014 epidemic (2700 reported cases) 17% was ›14 years. Given that measles provides lifelong immunity, these individuals must have escaped the previous epidemic in 1999/2000. This study investigated risk factors for 'escaping the 1999/2000 measles epidemic' and thus for persisting susceptibility and increased risk of complications when acquiring measles at older age.

Methods
A case control study was performed among unvaccinated orthodox Protestants born in 1988-1998, who had measles in 2013/2014 (cases) or in 1999/2000 (controls). Cases were recruited via Public Health Services; controls via orthodox Protestant media, secondary schools and social networks. Univariate and multivariate logistic regression was used to determine the association between demographic, geographical and religion-related variables and 'escaping the 1999/2000 epidemic'.

Results
In total, 203 cases and 563 controls were included. Due to skewed age distribution, analysis was stratified in two age-groups: those born in 1996-1998 and those born in 1988-1995 (respectively pre-school and school-aged in 1999/2000). Risk factors for 'escaping the 1999/2000 epidemic' for children born in 1996-1998 were: membership of less conservative churches (OR=4.28, 95%CI 2.33-7.88), absence of older siblings (OR=3.47, 95%CI 1.96-6.17) and residency outside the Bible Belt (OR=2.13, 95%CI 1.21-3.73). Highest risk for those born in 1988-1995 was the combination of residency outside the Bible Belt and attending a non-orthodox Protestant primary school (OR=9.28, 95%CI 2.70-31.86).

Conclusion
Unvaccinated orthodox Protestants of less conservative churches, who lived outside the Bible Belt or attended a non-orthodox Protestant school should be informed about their risks of acquiring measles at an older age to make an informed choice about vaccination.

Keywords: Measles, Immunity, Protestantism, Measles-Mumps-Rubella Vaccine, Religion and Medicine.

ABSTRACT ID: 210

PRESENTED BY: Anne de Munter (AdeMunter@ggdgelderlandzuid.nl)

A 8.5 Impact of pneumococcal conjugate vaccines on pneumococcal disease related hospitalizations in Spain, 2007-2012

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Background

In 2010, the 7-valent (PCV7) pneumococcal vaccine was superseded by the new 13-valent vaccine (PCV13) in Spain. Since 2006 the region of Madrid included these vaccines in the infant vaccination program (coverage >95%), while it remained optional in the rest of the country (coverage <60%). We described and compared the changes in pneumococcal disease hospitalization rates after the change from PCV7 to PCV13 vaccine in Spain.

Methods

We compared Period 1 (2007-2009), when PCV7 was available, with Period 2 (2010-2012) after PCV13 was introduced. We calculated hospitalization rates (HRs) and hospitalization rate ratios (HRRs) for each period by region, age-group and clinical presentation, using Poisson regression. Analysis is restricted to culture-confirmed cases.

Results

Of the 126,950 hospitalizations recorded in the National Registry of Hospitalizations, 76,789 (61%) were males (mean age 74 years). Most common clinical manifestations were: pneumonia (122,395 hospitalizations; 96%), septicemia (5,966 hospitalizations; 5%) and meningitis (2,870 hospitalizations; 2%). In Period 2, pneumonia HR reduction was significant in every age group ($p<0.001$), while septicemia hospitalizations increased in adults > 64 years (HRR: 1.17; 95%CI: 1.09-1.25). Meningitis hospitalizations decreased, mainly in children < 5 years (HRR:0.61; 95%CI: 0.51-0.74). Regions with known high vaccine coverage showed higher reductions in HRR for all clinical presentations. Adults > 64 years presented high mortality rates, especially for septicemia (35.0% and 30.0% in Period 1 and Period 2, respectively).

Conclusion

Introduction of PCV13 appeared to reduce pneumococcal-related hospitalizations, especially in children < 5 years. We observed a significant decline in pneumococcal HRs, even in regions without an integrated vaccination program. We recommend evaluating the recent introduction of PCV13 into the national infant immunization schedule in early 2016.

Keywords: Pneumococcal vaccine, pneumonia, meningitis

ABSTRACT ID: 43

PRESENTED BY: Leonidas Georgalis (leonidasgeorgalis@gmail.com)

Moderated Poster Session B
Tuesday, 29 November
15:30-16:30

Track 9: Antimicrobial resistance and healthcare associated infections (2)

Moderator: Alma Tostmann, EPIET Alumni Network/ Radboud University Medical Centre, Netherlands

B 9.1 External quality assessment (EQA) for Neisseria gonorrhoeae antimicrobial susceptibility among 26 European laboratories, 2015.

Sabrina Weiss (1,2), G. Spiteri (3), F. Tripodo (1), S. Seaton (4), E. Fagan (4), M. Cole (1) on behalf of the EURO-GASP network participants.

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Background

In October 2015, an EQA scheme for antimicrobial susceptibility testing in Neisseria gonorrhoeae was distributed to 27 laboratories in 25 participating countries as part of the European gonococcal antimicrobial susceptibility programme (Euro-GASP). Performance and inter-laboratory comparability were analysed to deploy resources and training where necessary.

Methods

Ten gonococcal isolates were selected by Public Health England (PHE) and distributed by the United Kingdom National External Quality Assessment Service (UK-NEQAS). Isolates chosen were representative of a range of different antimicrobial susceptibility profiles and selected from well characterised and recently isolated clinical strains. Participating laboratories were requested to test the panel using local methodology and breakpoints against a range of antimicrobial agents. Results were submitted to UK-NEQAS who issued individual laboratory reports. PHE decoded and further analysed the results based on the categories of susceptibility and the minimum inhibitory concentrations (MICs) assigned.

Results

Twenty-six laboratories (24 countries) returned EQA results. The majority of laboratories used E-tests and the European Committee on Antimicrobial Susceptibility Testing (EUCAST) breakpoints. Susceptibility category concordance showed a slight decrease to those of previous distributions (91.5% and >94% since 2010, respectively). Highest levels were seen with spectinomycin (100%) and lowest with azithromycin (76%). Most susceptibility category concordance discrepancies were attributable to strains that were on or close to the breakpoint. Overall 84.8% and 94.9% of the reported MICs were within one and two doubling dilutions of the modal MIC, respectively.

Conclusion

The inter – and intra-laboratory concordances were demonstrating comparability between different testing methodologies and allowing for confidence in Euro-GASP decentralised testing. Five centres should receive further guidance to help bring them into line with the recommended target of 95% of MICs within two dilutions of the modal MICs.

Keywords: EQA, Neisseria gonorrhoeae, Antibiotic Resistance, EUCAST, E-test

ABSTRACT ID: 215

PRESENTED BY: Sabrina Weiss (sabrinanweiss@gmail.com)

B 9.2 Surveillance of device-associated infection in Intensive Care Units in the region of Madrid (Spain), 2015

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4. Quality Indicator Control Group, INCLIMECC Network, Spain.

Background

Most patients admitted to Intensive Care Units (ICUs) are exposed to some kind of medical device during their hospital stay. Healthcare-associated infection (HAI) control in ICUs has been traditionally focused on device-associated infections since they are potentially modifiable risk factors and are associated with a high morbidity and mortality rate.

Methods

Infection surveillance (INCLIMECC network) of patients admitted for more than 48 hours to the ICU of 6 public hospitals in Madrid, from January-December 2015. HAI are defined using the Centers for Disease Control and Prevention and the National Healthcare Safety Network criteria.

Results

1,596 patients were included (average age 62.48 years ±16.577); 62.22% were males and 37.78% females. The median length of stay was 5 days (4 days in non infected patients, 20 days in infected patients). 80.33% of the patients needed a urinary catheter with a catheter-associated urinary tract infection rate of 4.78‰ catheter-days, higher than ENVIN-HELICS registry national data for the same period (Standardized Infection Ratio –SIR – 1.32). Mechanical ventilation was needed in 45.74% of the patients, with a ventilator-associated pneumonia rate of 9.50‰ ventilator-days, higher than national data (SIR 1.65). The percentage of patients with a central line was 57.95%, with a central line-associated bloodstream infection rate of 3.87‰ central line-days, higher than national data (SIR 1.41).

Conclusion

An HAI surveillance system with regular feedback to healthcare workers is key to improve the quality of care. Our region shows higher rates that national data obtained using the same methodology. An intervention including evidence-based preventive strategies focused on addressing safety culture, designating team leaders at each institution to collaborate with infection control personnel will be implemented in the second semester of this year.

Keywords: intensive care unit, healthcare-associated infection, surveillance, incidence, patient safety

ABSTRACT ID: 350

PRESENTED BY: Ángela Lourdes Rincón Carlavilla (angelalourdes.rincon@salud.madrid.org)

B 9.3 UK Field Epidemiology Training Programme masterclasses: development of a process for identifying and prioritising individual and group learning needs

Hannah Evans (1,2,3,5), N. Bundle (1,4,5)

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5. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden

Background

A learning needs assessment (LNA) is important for planning education and training. Within the UK Field Epidemiology Training Programme (FETP), masterclasses are delivered to meet training needs outside of core modules. The LNA for the 2015/16 FETP masterclass programme aimed to address both individual and group learning needs. We describe the prioritisation process developed to analyse survey responses from trainees.

Methods

We identified 17 preliminary topics covering software, analytics, statistics and microbiology identified by two cohorts of FETP, UK-based EPIET and EUPHEM fellows. We developed an online questionnaire for fellows to rank their top-ten topics and indicate, using a Likert scale, whether a masterclass on each topic would benefit them. Fellow's preferences about content and masterclass delivery method (tele/videoconference) were captured using categories and open-ended questions. To prioritise learning needs, we aggregated individual ranking and Likert responses, compared them at group level and identified differences between cohorts. We discussed LNA results with each presenter to tailor masterclass content.

Results

15/16 (94%) fellows completed the questionnaire, eight of whom identified themselves as cohort 2014. Our prioritisation process had four stages. We produced cohort-specific and combined topic shortlists from ranked scores and Likert responses and checking their agreement, removing topics where disagreement arose, e.g. an indication of high rank but of limited benefit. We timetabled remaining topics according to rank, biasing towards the needs of the cohort in their final year of training. Our final shortlist had eight topics, with preferable delivery via monthly 90-minute teleconferences.

Conclusion

This prioritisation process is an equitable way of identifying and balancing individual and group learning needs to maximise learning benefits. We recommend this approach to training programmes in other settings.

Keywords: Needs Assessment, Learning, Education, Staff Development

ABSTRACT ID: 133

PRESENTED BY: Hannah Evans (hannah.evans@phe.gov.uk)

B 9.4 Dutch-German cross-border epidemiology of multi drug resistance: Major differences for MRSA and Carbapenem-resistant Gram-negative organism (CRMO)

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Background

Multidrug-resistant organisms (MDRO) are a major cause of higher morbidity and mortality of healthcare-associated infections (HCAI). Multidrug-resistant Gram-negative bacteria are emerging at both sides of the border.

Methods

Within the EurSafety Health-net a network practicing comparable infection prevention and control has been established. Between 2012 and 2014, 41 acute care hospitals (about 80% in DE) collected data on the MRSA screening rate, the MRSA incidence, the nosocomial MRSA incidence density and the MRSA blood cultures / 1,000 patient days (MRSAB incidence density). Additionally, in 2013 and 2014 the numbers of CRMO per 100 inpatients were assessed.

Results

From 2012 to 2014 the average MRSA screening rate was 17-times higher in German (49.9%) than in Dutch (2.9%) hospitals. The MRSA incidence was 10-times higher in hospitals on the German (1.09 MRSA cases/100 inpatients) than on the Dutch (0.11) side of the border. The nosocomial MRSA incidence density was 14-times higher in German hospitals (0.14 nosocomial MRSA cases/1,000 patient days compared to 0.01). The MRSAB-incidence density was comparable (0.03 to 0.02).

From 2013 to 2014, the number of CRMO cases/100 admissions was 8-times higher in German hospitals (0.042 compared to 0.005).

Conclusion

Despite the higher MRSA – and CRMO-incidence at admission to hospital on the German side, the MRSA blood culture incidence density in patients is comparable on both sides of the border. This reflects the success of concerted prevention and infection control standards. As this study demonstrates cross-border discrepancies as well as similarities, additionally to infection prevention and control measures, differences in healthcare systems, such as the number of patients admitted to hospitals or antimicrobial prescribing practice may influence the epidemiology and should be investigated in further international studies.

Keywords: Carbapenems; Infection Control;Methicillin-Resistant Staphylococcus Aureus; Drug Resistance, Multiple

ABSTRACT ID: 62

PRESENTED BY: Annette Jurke (annette.jurke@lzg.nrw.de)

B 9.5 Poor adherence to guidelines for preventing central line-associated bloodstream infections (CLABSI): Results of a worldwide survey

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Background

Central line-associated bloodstream infection (CLABSI) are a cause of increased morbidity and mortality, and largely preventable. We documented attitudes and practices in intensive care units (ICUs) in 2015 worldwide to assess compliance with CLABSI prevention guidelines.

Methods

Between June and October 2015, we posted an online questionnaire, available in 10 different languages through ICU societies' websites and mailing lists to medical doctors and nurses working in ICUs worldwide. We investigated practices related to central line (CL) insertion, maintenance and measurement of CLABSI-related data. We computed weighted estimates and standard error (SE) for high, middle and low-income countries using country population as a weight. Countries completing at least 10 complete questionnaires were included in the analysis.

Results

95 countries provided 3,407 responses. No low income, 14 middle income (MIC) and 27 high income (HIC) countries provided 10 or more responses, totaling 3,250 responses analyzed. 80% in MIC (SE=1.5) and 81% in HIC (SE=1.0) reported availability of written clinical guidelines for CLABSI prevention in their ICU; 23% in MIC (SE=1.7) and 62% in HIC (SE=1.4) reported compliance to the following recommendations for CL insertion: hand hygiene, full barrier precaution, chlorhexidine >0.5%, no topic or systemic antimicrobial prophylaxis. 60% in MIC (SE=2.0) and 73% in HIC (SE=1.2) reported daily assessment for the need of a central line. Although 94% considered CLABSI measurement key to quality improvement, only 21% could report their CLABSI rate. Variation in reported practices between countries was high.

Conclusion

Despite selection and response bias likely leading to overestimating appropriate CLABSI prevention practices, this study has identified areas for improvement at CL insertion and maintenance. Priorities for intervention differ between countries and should be addressed locally.

Keywords: Healthcare associated infections; central line-associated bloodstream infections; prevention; surveillance; Intensive care units

ABSTRACT ID: 128

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

B 9.6 Should microbiological screening in neonates be applied for prediction and prevention of sepsis with gram-negative bacteria? A systematic review applying a new evidence-based medicine framework

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Background

A new guidance for the assessment of complex public health questions dealing with diverse study types was developed by the Framework for Rating Evidence in Public Health (PRECEPT). Our research question centres on microbiological colonisation screening of neonatal body surfaces for gram-negative bacteria to predict and prevent neonatal sepsis. This is routinely conducted at neonatal intensive care units despite weak evidence and potential harms through unnecessary barrier precautions impairing mother-child-bonding. We aimed to pilot and validate the application of PRECEPT to this research question.

Methods

We developed a protocol for a systematic review according the PRECEPT guidance. Two authors searched independently for prognostic accuracy studies addressing routine microbiological screening in EMBASE and Medline. We extracted data from identified studies accompanied by a risk of bias analysis using the Quality-Assessment-of-Diagnostic-Accuracy-Studies (QUADAS) tool, meta-analysis and assessment quality of evidence using GRADE (Grading of Recommendations Assessment, Development and Evaluation) approach.

Results

The protocol included 12 components and a combination of 22 defined search terms for database searches. We identified 3258 publications, of which by 01/05/2016 nine were eligible and reported data to calculate sensitivity and specificity as well as number needed to screen to prevent one case of sepsis. Since positive and negative predictive values critically depend on prevalence, pooling by meta-analytic methods was not feasible. Furthermore, confounding and loss-to-follow-up are not captured by using the QUADAS tool.

Conclusion

The PRECEPT framework served to identify relevant studies and to assess their quality of evidence. We recommend additional analyses to capture confounding and loss-to-follow-up by using complementary prognostic studies tools. Further analysis will be used to evaluate the preventive potential of systematic routine screening in order to formulate evidence-based recommendations.

Keywords: “Sepsis”, “Infant, Newborn”, “Sensitivity and Specificity”, “Predictive Value of Tests”, “Review”, “Gram-Negative Bacteria”

ABSTRACT ID: 141

PRESENTED BY: Sebastian Haller (HallerS@rki.de)

Track 10: Burden of disease (1)

Moderator: Edoardo Colzani, ECDC, Expert Science-based Prevention and Guidance for Infectious Diseases

B 10.1 Retrospective mortality and morbidity study following measles outbreak in two health zones of Katanga Province – Democratic Republic Congo (DRC) 2015-16

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Background

Measles is endemic in DRC with outbreaks every 2-3 years. MSF-France led vaccination campaigns and case management during a measles outbreak in 4 health zones in Katanga province in 2015. In two affected zones (Malemba-Nkulu and Mukanga), MSF interventions started 3-5 months after outbreak onset. We aimed to retrospectively estimate crude mortality rates (CMR), attack rates (AR), overall specific (SMR) and age specific (ASMR) mortality rates in order to assess the effect of the interventions on the course of the outbreak.

Methods

We conducted a retrospective household survey in December 2015 using two-stage cluster sampling with 50 randomly selected clusters at the first stage in each health zone. We collected data on demographics and health status of household members, cause of illness or death and vaccination status. We estimated AR, CMR and ASMR per 10.000 persons/day over the recall period (year 2015).

Results

We surveyed 1739 and 1750 households, with a mean size of 6.4 and 6.1 members. At the outbreak onset in January 2015, CMR was around 0.6 in both zones. At the outbreak peak, CMR increased to 1.3 in Malemba-Nkulu in June, and to 2.1 in Mukanga in July. The overall measles ARs over the recall period were 17.9 and 18.6, with significant differences between ^{3}5 years (AR 13.4) age groups. The SMR was 0.41 and 0.42. Among children – Nkulu) vs. 1.23 (Mukanga).

Conclusion

CMR and SMR increased notably in both health zones during the outbreak. Children under five were most affected, despite mass vaccination campaigns and measles case management. More rapid interventions need to be implemented in such outbreaks in order to reduce mortality rates.

Keywords: Democratic Republic of Congo, retrospective study, crude mortality rate, measles specific mortality rate

ABSTRACT ID: 255

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

B 10.2 Estimation of cytomegalovirus seroprevalence in the German adult population

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Background

While cytomegalovirus (CMV) infections are usually asymptomatic in immunocompetent hosts, they can be life-threatening in immunocompromised individuals. CMV is the leading cause of congenital infections worldwide and can result in hearing loss and neurodevelopmental delay in the child. Representative epidemiological data on the population susceptibility to CMV are essential to develop public health recommendations. We report the first CMV seroprevalence data from a nationwide, representative survey in German adults.

Methods

Data on CMV serostatus, measured by a multiplex assay, were available for 6,552 participants (17-79 years) of the German National Health Interview and Examination Survey 1998, which comprised a representative sample of the adult German population. Seroprevalence was calculated and weighted binomial regression was used to identify factors associated with CMV seroprevalence.

Results

Overall CMV seroprevalence was 51.0% (95%CI: 48.7-53.3%) in men, and 62.3% (95%CI: 59.8-64.6%) in women and increased with age: from 30.2% (95%CI: 25.3-35.6%, 20-29 years) to 63.7% (95%CI: 55.6-71.1%, 70-79 years) in men and from 44.3% (95%CI: 36.7-50.1%, 20-29 years) to 77.6% (95%CI: 70.8-83.2%, 70-79 years) in women. CMV seroprevalence in women of childbearing age (17-45 years) was 50.8% (95%CI: 47.5-54.1%). Preliminary multivariable analysis indicated that CMV seroprevalence was positively associated with age, country of origin other than Germany and number of siblings grown up with in both, men and women; number of sex partners in men; and number of household members in women.

Conclusion

Our results indicate that half the women of childbearing age were susceptible for primary CMV infection during pregnancy with a risk of neurological impairment of their child. CMV screening during pregnancy and informing seronegative women about CMV risk reduction measures could prevent congenital CMV infections with its serious consequences.

Keywords: Cytomegalovirus, seroprevalence, congenital infections, pregnancy

ABSTRACT ID: 144

PRESENTED BY: Raskit Lachmann (LachmannR@rki.de)

B 10.3 Decrease in rotavirus incidence among young children in the Netherlands, 2015-2016

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Background

Rotavirus is the most common cause of diarrhoea in young children. In 2014, a marked decrease in rotavirus circulation was reported in the Netherlands despite the absence of rotavirus vaccination. In 2015, the rotavirus incidence was high as usual. In 2016, however, the number of rotavirus notifications was low again. The aim of this study was to quantify the 2015 and 2016 rotavirus notifications and to determine whether rotavirus circulation genuinely decreased in 2016.

Methods

We used weekly collected data on (i) rotavirus notifications from virological surveillance and (ii) all-cause gastroenteritis consultations in We compared January-April, the usual rotavirus season in the Netherlands, in 2015 and 2016 with the same period in 2006-2013. We calculated Incidence-Rate Ratios (IRR) using negative binominal regression.

Results

The number of rotavirus notifications in 2015 (n=1,044) did not differ (IRR 1.0, 95%CI 0.9-1.2, p=0.833) from the numbers in 2006-2013 (range: 345-1,280). However, it was lower in 2016 (n=275, IRR 0.5, 95%CI 0.4-0.6, p<0.001). The 2015 gastroenteritis consultation rate did not differ (205/100,000 person-weeks, IRR 0.9, 95%CI 0.7-1.0, p=0.084) from the rate in 2006-2013 (range: 160 to 321/100,000 person-weeks). It was lower in 2016 (137/100,000 person-weeks, IRR 0.6, 95%CI 0.5-0.7, p<0.001).

Conclusion

There was a genuine decrease of rotavirus infections in 2016 in the Netherlands. The 2014 and 2016 decreases and the 2015 increase in rotavirus notifications possibly indicate a shift from annual to biennial increased rotavirus incidences. Reasons may include shrinking birth cohorts and mild winters. Further studies on the role of vaccination in neighbouring countries and circulating rotavirus genotypes in the Netherlands are required to assess the need for and impact of rotavirus vaccination.

Keywords: Rotavirus, child, epidemiology, gastroenteritis, trends

ABSTRACT ID: 244

PRESENTED BY: Roan Pijnacker (roan.pijnacker@rivm.nl)

B 10.4 Economic burden of varicella in children in Hungary, 2011-2015

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4. Merck & Co., Inc., Kenilworth, New Jersey, U.S.A.

Background

Although live-attenuated varicella-zoster virus (VZV) vaccines are safe and effective in preventing varicella and routine childhood immunisation programs are effective in dramatically reducing varicella associated morbidity and mortality, varicella vaccine is not included in the National Immunisation Program (NIP) in Hungary. This study documents the clinical and economic burden associated with varicella in Hungary.

Methods

This was a multicentre retrospective chart review study of varicella patients aged 1-12 years between 2011 and 2015. Healthcare resource utilisation (HCRU) associated with varicella, respective unit costs, and work loss were used to estimate direct and indirect costs. All costs are presented in 2015 Hungarian Forints (HUF) / Euros (€).

Results

156 children with varicella (75 outpatients, 81 inpatients), with a mean age of 4.4 (SD: 2.0) and 3.7 (SD: 2.1) years, respectively, were included. One or more complications were experienced by 12.0% of outpatients and 92.6% of inpatients, the most common being dehydration, skin and soft tissue infections, pneumonia, keratoconjunctivitis, and cerebellitis. HCRU estimates (outpatient: inpatients) included use of over-the-counter (OTC) medications (96.0%: 53.1%), prescription medications (9.3%:70.4%), tests/procedures (4.0%: 97.5%), and consultation with allied health professionals (2.7%: 30.9%). The average duration of hospital stay (inpatients) was 3.6 (95% CI: 3.2 , 4.1) days. The total combined direct and indirect cost per varicella case was 228,146.7 HUF (€ 736.0) (inpatients) and 49,790.6 HUF (€ 106.6) (outpatients). The overall annual cost of varicella in Hungary for children aged 1-15 years in 2015 was estimated at 1,903,332,524.3 HUF (€ 6,139,980.4).

Conclusion

Varicella is associated with substantial clinical burden and utlization of health care resources in Hungary; this burden could be reduced through the routine vaccination of all healthy children against varicella.

Keywords: Varicella, Chickenpox, Cost of Illness, Costs and Cost Analysis, Hungary, Retrospective Studies

ABSTRACT ID: 375

PRESENTED BY: Zsófia Mészner (meszner.zsofia@nefi.hu)

B 10.5 Measles importation into EU/EEA countries, 2011–2015

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Background

In Europe, measles is targeted for elimination. Imported cases through international travel constitute a constant threat to achieving this goal and maintaining it where the disease has been eliminated (at least 36 months without endemic transmission). The objective of this study was to describe the epidemiology of imported measles cases and estimate the risk of measles importation in the EU/EEA.

Methods

Measles surveillance in the EU/EEA is coordinated by the European Centre for Disease Prevention and Control. We retrieved measles surveillance data for 2011–2015 and obtained tourism data from Eurostat. An imported case of measles was defined as one for which the reported country of infection differed from the reporting country or as a case reported as imported. We described the main characteristics of imported measles cases, estimated the risk for measles importation by travel destination (number of cases reported/number of nights spent abroad) and adjusted associations between demographics and other potential confounders, and importation using logistic regression.

Results

During 2011–2015, 29 EU/EEA countries reported 62 108 measles cases, of which 1 837 (3%) were imported. Of 1 549 imported cases with known country of infection, 820 (53%) were associated with travel within the EU/EEA. The overall risk associated with travel abroad was 0.05 cases/million nights and the highest risk was observed with travel to Asia (0.36). Case categories more likely to be reported as imported were males (OR 1.2, 95%CI 1.1-1.3), people aged above 30 years (OR 2.3, 95%CI 1.8-2.9) compared to cases aged below one year, and people residing in countries with eliminated transmission (OR 3.4, 95%CI 3.0.1-4.0) compared to countries with endemic transmission.

Conclusion

To achieve and maintain measles elimination, high vaccination coverage is essential.

Keywords: Measles; Surveillance; Travel; Disease Elimination; Europe

ABSTRACT ID: 209

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

B 10.6 Late breaker: Hepatitis A virus infections and outbreaks in asylum seekers arriving to Germany, September 2015 to March 2016.

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Background

Conflicts particularly in the Middle-East led to a large influx of refugees into the EU, culminating in the 2nd half of 2015. Parallel to peaking numbers of refugees arriving in Germany, notified hepatitis A cases increased substantially. Most refugees originate from HAV endemic areas and experienced serious living conditions while fleeing to Europe and are thus potentially exposed to HAV. To refine prevention measures, we analysed HAV transmission among asylum seekers in Germany.

Methods

We assessed hepatitis A cases with clinical symptoms and laboratory confirmation and outbreaks (2 or more cases with an epidemiological link) notified to the RKI between September 2015 and March 2016. Cases with disease onset <30 days and ≥30 days after arrival in Germany were counted as imported and autochthonous, respectively. To verify chains of transmission, we applied molecular surveillance.

Results

In total, 699 hepatitis A cases were notified, of which 278 (40%) occurred in asylum seekers. Among the latter, 83% of cases occurred in persons aged <20 years and 35% in children aged 5-9 years.

Up to 47% of HAV infections in asylum seekers were apparently autochthonous cases.

Among asylum seekers, 52 outbreaks of hepatitis A were notified. Cluster sizes included up to 8 cases with a median of 2 cases (IQR: 2-3 cases). Obtained sequences clustered with HAV strains from Middle East, Turkey, Pakistan and West Africa.

Conclusion

Hepatitis A in asylum seekers is a substantial public health issue. However, outbreaks of hepatitis A were small and effectively controlled using rigorous hygiene measures, case isolation, and post-exposure prophylaxis. Nonetheless, hepatitis A immunisation of under-aged asylum seekers should be considered. The risk of HAV transmission into the residential population remained low.

Keywords: hepatitis A; hepatitis A virus; epidemiology; asylum seeker; refugee; migration

ABSTRACT ID: 721

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Track 11: Food- and waterborne diseases and zoonoses (2)

Moderator: Therese Westrell, ECDC, Expert Food- and Waterborne Diseases

B 11.1 Cancelled

B 11.2 Major shift in Shiga Toxin-Producing Escherichia coli serogroups causing Hemolytic and Uremic Syndrome in children in France, 1996-2015.

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Background

In children, the leading cause of Hemolytic Uremic Syndrome (HUS) is Shiga Toxin-Producing Escherichia coli (STEC) infection, which has an important outbreak potential. In France, since 1996, STEC infection surveillance relies on enhanced HUS surveillance in children aged <15 years. This study presents the results of this surveillance since 1996.

Methods

Children aged <15 years presenting microangiopathic hemolytic anemia and acute renal failure fulfill the HUS case definition. Cases are notified by a voluntary nationwide network of 31 pediatric nephrology units located in public hospitals. Two national reference laboratories perform microbiological STEC confirmation. Notification rates (NR) in cases/100000 persons-year in children aged respectively <15 and <3 years are provided, with the distributions of STEC serogroups evidenced in stools.

Results

In 1996-2015, mean HUS NR was 0.85/100000 persons-year (2.6 in children aged <3 years), representing a mean of 103 cases/year. In 2011, HUS NR peaked to 1.32 (3.7 in children aged <3 years), and finally decreased to 0.94 (3.1 in children aged <3 years) in 2015. Five foodborne outbreaks were identified (two STEC O157, two O26 and one O104), leading to control measures. Among STEC serogroups, O157 decreased from 68% in 1996-2005 to 23% in 2015. STEC O26 was globally stable, varying between 5% in 2006 and 20% in 2009. STEC O80 was first evidenced in 2005, and increased from 10% in 2010 to 27% in 2015.

Conclusion

No important changes in HUS notification rates were noted, while a major shift in serogroups was observed: O157 has declined while O80 emerged to become the most frequent in 2015. Investigations of STEC O80 reservoirs and sources of infection are needed to target prevention and control measures of this severe infection.

Keywords: HUS, surveillance, STEC O80

ABSTRACT ID: 301

PRESENTED BY: Mathias Bruyand (Mathias.BRUYAND@santepubliquefrance.fr)

B 11.3 Multiple epidemiological, environmental and genomic investigations moved us closer to the source of a recurrent seasonal outbreak of STEC O55:H7 in Dorset, England, 2014-15

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Background

A recurrent outbreak due to shiga-toxin producing Escherichia coli (STEC) serotype O55:H7, shiga-toxin 2a in Dorset, England was identified in July 2014. Previously undetected in England, cases had occurred in Ireland in 2012-14. A multi-agency team investigated to estimate the outbreak's extent and identify the source.

Methods

We established enhanced surveillance at three Dorset laboratories. A case was defined as having STEC-O55:H7 confirmed by serology (O55 antibodies) or culture and sequencing (isolates from stool within five single nucleotide polymorphisms (SNP) of the outbreak strain). We collected 14-day exposure histories, tested contacts and later pets, sampled the environment and considered flooding, migratory birds and livestock.

Results

Twenty-eight of thirty-one identified cases were linked to six epidemiological clusters, including a nursery. Microbiological surveillance identified one case. Twenty-one cases were symptomatic with haemolytic uraemic syndrome (HUS) or bloody diarrhoea. HUS was more common (13/31; 42%) than for STEC-O157 (172/3323; 5%, p<0.0001). Nine cases were primary, resident within two areas of Dorset, onset July-November 2014 and May-September 2015. Flooding occurred 1-11 days before onset of five primaries

In one area. We identified no common food exposures. Six of nine Irish isolates were within ten SNPs of the outbreak strain. Cases reported no links to Ireland nor lived near Ireland-UK cattle movements. Gulls seasonally migrate from Ireland. All 134 environmental samples, including bird droppings, were negative. We isolated the outbreak strain from two cats' faeces.

Conclusion

Extensive investigations including international collaboration confirmed infection to be less widespread than feared and transmission to be epizootic or from environmental contamination local to Dorset. Cats are a potential vector but the source remains unidentified. Our methods have application for other emerging pathogens with suspected environmental aetiology.

Keywords: Shiga-Toxigenic Escherichia coli, Hemolytic-Uremic Syndrome, Disease Outbreaks, Communicable Diseases, Emerging, Zoonoses

ABSTRACT ID: 93

PRESENTED BY: Nick Bundle (nick.bundle@phe.gov.uk)

B 11.4 Cancelled

B 11.5 Causes, sources and consultation needs in food – and waterborne outbreaks, Finland 2010-2015

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Background

An online Finnish food – and waterborne outbreak (FWO) registry was introduced in 2010. FWO registry is maintained by National Institute for Health and Welfare (THL) and Finnish Food Safety Authority Evira. Notifications and investigation reports are transferred electronically from municipal authorities to THL and Evira. At THL, notifications are monitored in real time in order to detect large outbreaks affecting more than one municipality simultaneously and to ensure rapid control measures. THL supports municipal authorities in local investigations and coordinates investigations of widespread outbreaks. We describe outbreak notifications and investigation reports in order to identify causes, sources and realized consultations.

Methods

Notification of suspected outbreaks to FWO registry is mandatory and involves clusters with › 5 non –family members with similar symptoms or one person with a suspicion of a serious illness, i.e. botulism. Investigation reports are classified by THL and Evira. Number of notifications and consultations, and causes and sources of outbreaks per year were calculated from the FWO registry, 2010-2015.

Results

In 2010-2015, 429 (52-88/per year) suspected outbreaks were notified to the FWO registry; 249 (58%) were classified as foodborne and 32 (7%) as waterborne outbreaks. Norovirus was the most commonly reported (30%, 86/281) cause. In 38% (106/281) outbreaks, the cause remained unknown. Outbreaks affecting several municipalities and observed via FWO registry were caused by Cryptosporidium parvum, Yersinia pseudotuberculosis, Salmonella Enteritidis, Listeria monocytogenes and unidentified pathogen linked to raw beetroot. THL acted as consultant in 130/429 (30%) notifications.

Conclusion

FWO registry enables real time outbreak monitoring and fast consultation and control measures. Two thirds of suspected outbreaks were classified as FWO outbreaks. Microbiological investigation practices for outbreaks with unknown cause should be evaluated.

Keywords: foodborne outbreak, waterborne outbreak, outbreak registry, evaluation

ABSTRACT ID: 241

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Track 12: HIV, sexually transmitted infections and viral hepatitis (2)

Moderator: Sybille Rehmet, ECDC, Head of Continuous Professional Development Programme

B 12.1 Impact of hepatitis B vaccination strategy, vaccine coverage and HBsAg prevalence on acute hepatitis B notification rates in EU/EEA countries, 2006-2012

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Background

Prevention strategies tackling hepatitis B virus (HBV) in European Union (EU)/European Economic Area (EEA) countries are centred around universal or targeted vaccination programmes. National differences exist in the type of strategy implemented and the coverage achieved.

Methods

The European Centre for Disease Prevention and Control have implemented an enhanced surveillance programme for HBV across EU/EEA countries. Using univariate and multivariate Poisson regression analysis, we evaluated the impact of HBV vaccination strategies, HBsAg prevalence and vaccination coverage data from the World Health Organization, on the acute HBV notification rates between 2006-2012. Results were expressed as incidence rates ratios (IRR) with 95% confidence intervals (CI).

Results

During the study period, the EU/EEA notification rate decreased from 1.6 per 100,000 population in 2006 to 0.7 in 2012. Multivariate analysis showed that countries starting their HBV vaccination programme before/during 1995, had significantly lower acute HBV notification rates (IRR 0.48; 95%CI 0.47 – 0.50; p‹0.01), as did countries with a HBV catch-up vaccination campaign (IRR 0.80; 95%CI 0.76 – 0.83; p‹0.01) and countries achieving HBV vaccination coverage ≥95% (IRR 0.61; 95%CI 0.58-0.67; p‹0.01). Countries with a Background HBsAg prevalence of ≥1% among the general population showed a higher acute HBV notification rate (IRR 1.07; 95%CI 1.03 – 1.08; p=0.03). At EU level, the acute HBV rate decreased by 11% for each 1% increase in vaccine coverage (IRR 0.89; 95%CI 0.85-0.92; p‹0.01).

Conclusion

These results provide statistical evidence that universal HBV vaccination strategies implemented with high coverage have contributed towards the reduction in acute HBV notifications across the EU/EEA countries. Ending transmission of HBV in Europe will require high vaccine coverage through universal programmes in all countries, supported, where appropriate, by catch-up vaccination campaigns.

Keywords: Hepatitis B, surveillance, public health policy, epidemiology, vaccination

ABSTRACT ID: 333

PRESENTED BY: Erika Duffell (Erika.duffell@ecdc.europa.eu)

B 12.2 Bloodborne disease prevalence in the blood supply, Georgia, 2012-2014

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Background

Georgia is embarking on an unprecedented Hepatitis C elimination program. Preliminary data from a nationwide seroprevalence survey showed high prevalence in the general population (7% vs. 0.2 – 2% Europe). Blood transfusion is a source of bloodborne disease transmission and to eliminate disease transmission from donated blood, the "Safe Blood" program was launched in 1997. Blood donors are paid or volunteers. Testing is ELISA-based with up to a six month window period and blood product recipients are not tracked.

Methods

retrospective data review was implemented. From 2012 – 2014, data were collected from 2 of the 3 largest blood banks and compared to "Safe Blood" data. Blood testing panels for all donors include HIV, HBV, HCV, and syphilis by immunoassay.

Results

From 2012-2014, 23,666 (80%) donated only once out of 29,640 donors with 38,650 blood donations. At least one bloodborne infection was detected in 1299 (4.4%) donors. One donation donors were two times more likely to be infected than ≥2 donations (RR=2.0; 95% CI 1.6-2.3). HCV prevalence was higher among one donation (2.6% vs 1.5%), while HBV and HIV were higher among ≥ 2 donations (0.8% vs 0.2%;0.7% vs 0.2%). Within the window period of infections among the ≥ 2 donations were 25 persons.

Conclusion

A 6-month window periodgreatly increases risk for bloodborne infections and the risk increases three fold as at least three blood products are derived from one blood donation. Bloodborne infections among cadre donors increased during the three years and coinfections increased among volunteers. Given these trends and Georgia's HCV elimination aspirations, the window period must be reduced by improving testing and launch a trace-back system for all blood products

Keywords: blood-borne disease, HCV, HBV, HIV, blood banks

ABSTRACT ID: 106

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B 12.3 Molecular epidemiology of Neisseria gonorrhoeae in Budapest, Hungary, 2012-2014

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Background

Gonorrhoea is still a global public health problem. The Euro-GASP survey in 2009-2010 revealed that there were prevalent genogroups of Neisseria gonorrhoeae (NG) (e.g. G1407, G225, G387) in Europe and among these G1407 and G225 were associated with antibiotic resistance. We aimed to investigate the clonality of Hungarian NG isolates and associations between genogroups, antimicrobial resistance and epidemiological variables.

Methods

Non-duplicate NG isolates from patients visited any of six sentinel Dermatology and Venereology clinics in Budapest, Hungary in 2012-2014 were included. Isolates were typed by NG multi-antigen sequence typing (NG-MAST) and genogroups (GG) based on sequence similarity of porB and tbpB allelles were defined. We tested associations between genogroups, antimicrobial susceptibilities and patient characteristics (gender, age, sexual behaviours), and expressed results as odds ratio (OR).

Results

We investigated 114 isolates from corresponding patients (median age 30 years, range 14-61y; males 82%). Of these, 43% were men having contact with sexworkers and 11% were men having sex with men. Of the 50 identified sequence types 16 were newly described and 7 were unique. Eighty-five isolates could be assigned to eight main GGs, with G1407, G387, G225 and G5333 being the most prevalent. G1407 was significantly associated with decreased susceptibility to cefixime (OR:12.5;$p<0.0001$) and azithromycin (OR:8.85;$p=0.001$). All isolates belonging to G1407, G225 and G5333 were resistant to ciprofloxacin ($p<0.0001$) and were associated with men having contact with sexworker (OR:2.46;$p<0.05$).

Conclusion

Among the isolates analysed we found association between the main European genogroups, antibiotic resistance, and men having contact with sexworker. Sexworkers likely serve as a reservoir of important NG genogroups in Hungary, thus their regular screening is recommended in order to prevent spread of gonorrhoea.

Keywords: Neisseria gonorrhoeae, molecular epidemiology, antibiotic resistance, genogroup

ABSTRACT ID: 104

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B 12.4 Risks of infections among Finnish international travellers 1995-2015, Finland

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Background

Annually Finns make 7.5 million overnight international trips and infection afterwards is the most common health problem reported. We estimated the risk of travel-related sexually transmitted infections (STIs) and food – and water-borne diseases (FWDs) and assessed the trends among Finnish travellers to help targeting travel advice for infection prevention.

Methods

We used data on STIs (gonorrhoea and syphilis) and FWDs (hepatitis A, shigellosis, salmonellosis and campylobacteriosis) notified to the Finnish infectious disease register as numerator and annual overnight travel statistics derived from surveys of Statistics Finland as denominator. We calculated overall risks per 100,000 travellers between 2012-2015 and trends in risks using negative binomial regression between 2000-2011 when yearly statistics were comparable (survey method changed in 2012).

Results

A total of 2,306 travel-related STIs and 70,929 FWDs were notified (26% and 53% of total, respectively). Most common destinations were Thailand (gonorrhoea, salmonellosis, campylobacteriosis), Russia (syphilis, hepatitis A), and Egypt (shigellosis). World regions with highest risk between 2012-2015 were Asia-Oceania for gonorrhoea (11.0; 95%CI, 9.5-12.8), syphilis (1.4; 95%CI, 0.9-2.1), salmonellosis (157.2; 95%CI, 151.1-163.5), and campylobacteriosis (135.0; 95%CI, 129.4-140.9), and Africa for hepatitis A (4.5; 95%CI, 2.5-7.9), and shigellosis (34.7; 95%CI, 28.3-42.5). Between 2000-2011 trends increased for campylobacteriosis to all regions, except Africa. For other FWDs, trends declined among travellers to Africa, Asia-Oceania, Russia and Baltic countries and European regions and similarly for STIs among travellers to Russia and Baltic countries.

Conclusion

Combining data of infectious disease register and travel statistics can provide country-specific risks of contracting infections abroad and trends in risk. Our findings could improve national travel advice for health care professionals and international travellers.

Keywords: travel, communicable diseases, sexually transmitted diseases, foodborne diseases, waterborne diseases

ABSTRACT ID: 112

PRESENTED BY: Viktor Zöldi (viktor.zoldi@thl.fi)

B 12.5 Comparative Analysis of Molecular Epidemiologic Surveillance of HIV-1 Infection in Two Regions of Spain, 2003-2015

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Background

HIV-1 genetic forms have implications for transmission, treatment outcomes, immune response and vaccine design. We analyzed trends in non – B subtypes (Non-Bs) in two regions in Spain in order to explore implications for prevention strategies.

Methods

Between 2003-2015, we collected all HIV-1 subtyping data from Galicia and Basque Country regions. Representativeness of the regional data was assessed by comparison with the National HIV Surveillance System. In each region and for each subtype, we described country of origin of the patients, transmission route and their changes over time.

Results

Genetic forms from 3051 HIV-1 infections were analyzed and found representative in terms of age, sex, year of diagnosis, transmission route and country of origin. We detected an increase in Non-Bs from 14.7% and 15.0% in 2003, to 37.3% and 42.4% in 2015 in Galicia and Basque Country, respectively. Half of Non-Bs infections occurred in Spanish individuals; the most frequent Non-Bs were subtype F1 (27%), subtype C (14.3%) and CRF02_AG (12.3%). The latter was more frequent in Basque Country ($p<0.001$) and associated with individuals of Sub-Saharan African origin. Since 2010, a decrease in subtype G and BG recombinants in Galicia has been associated with the decrease in injection drug users ($p=0.001$). Subtype F increased 22% in Galicia since 2010 and 18% in Basque Country since 2014, related to two transmission clusters among men who have sex with men ($p<0.001$%).

Conclusion

Non-Bs HIV-1 infections are increasing in these regions over time. Increasing HIV variability has implications for transmissibility and prevention strategies. Moreover, genetic form surveillance provides information on the strains in circulation in a given region and time, and could be used to tailor prevention measures and treatment strategies.

Keywords: HIV-1, Non-B genetic forms, MSM

ABSTRACT ID: 164

PRESENTED BY: Leonidas Georgalis (lgeorgalis@isciii.es)

Track 13: Influenza and other respiratory viruses(2)

Moderator: Svetla Tsolova, ECDC, Senior Expert Monitoring and Evaluation

B 13.1 Factors associated with parental acceptance of seasonal influenza vaccination for their children – A telephone survey in the adult population in Germany

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Background

In Germany, the Standing Committee on Vaccinations is currently assessing the evidence related to the potential introduction of universal childhood influenza vaccination. To inform the modelling of vaccination impact and future communication activities, we aimed to assess among parents the acceptance of such strategy and possible modifiers.

Methods

In May 2015, we conducted a telephone survey in households in Germany using random-digit dialing. We interviewed parents with children <18 years and descriptively analysed responses. We calculated the proportion of parents who would ummunize thier child for three hypothetical scenarios and compared these using McNemar's test: (1) hearing about the influenza vaccination recommendation through the media, (2) being recommended by a physician, or (3) being informed about the availability of the vaccine as a nasal spray. We used univariable and multivariable logistic regression to identify factors associated with vaccination acceptance.

Results

Of 2,030 persons answering the phone, 518 (response 26%) completed the questionnaire. Participants (74% female; mean age 41.3 years) had on average 1.6 children with a mean age of 8.9 years. In scenario 1, 52% of parents would immunize their child, compared to 64% in scenario 2 (p<0.01) and 44% in scenario 3 (p=0.20). Factors associated with vaccination acceptance in scenario 1 were previous influenza vaccination of the child (adjusted odds ratio [aOR] 4.3, 95% confidence interval [CI] 2.1-9.0) or parent (aOR 8.1, 95% CI 2.4-26.9), perceived severity of influenza (aOR 5.0, 95% CI 2.2-11.4) and living in Eastern Germany (aOR 2.3, 95% CI 1.2-4.7).

Conclusion

If seasonal influenza vaccination for children was recommended, more than half of the parents would potentially agree to immunize their child. Involving physicians in future information campaigns might further increase this proportion.

Keywords: influenza, vaccination, children, acceptance, telephone survey

ABSTRACT ID: 140

PRESENTED BY: Lena Boes (BoesL@rki.de)

B 13.2 Influenza vaccine effectiveness (VE) estimates from the I-MOVE multicentre case control study in Europe, 2015-16: Feasibility of representative clade-specific VE

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Background

In the eighth I-MOVE (Influenza – Monitoring Vaccine Effectiveness in Europe) season, we undertook a multicentre case-control study based on sentinel practitioner surveillance networks in eleven European Union (EU) countries to measure interim 2015/16 influenza vaccine effectiveness (VE) against medically-attended influenza-like illness (ILI) laboratory-confirmed as influenza. This season seven study sites participated in a pilot study to assess feasibility of providing clade-specific VE by randomly selecting specimens for genetic characterisation. The main circulating virus at mid-season was A(H1N1)pdm09, with sub-clade 6B.1 emergence.

Methods

Practitioners systematically selected ILI patients to swab within eight days of symptom onset.

We compared first influenza A(H1N1)pdm09 and then sub-clade 6B.1 positive patients to influenza-negative patients among those meeting the EU ILI case definition. Using logistic regression we calculated adjusted (age, sex, onset time, chronic conditions, study sites) VE by influenza subtype/clade, overall and by age group. We weighted the clade-specific VE analysis using the reciprocal of the fraction of samples characterised and used robust standard errors.

Results

We included 3323 ILI patients in the A(H1N1)pdm09 interim analysis, with 981 cases. VE against A(H1N1)pdm09 was 32.5% (95%CI: 4.3-52.4) overall and 31.6% (95%CI: – 11.9-58.2) among 15-59 year olds. Among countries included in pilot study analyses and within the period with available genetic analysis results, VE against A(H1N1)pdm09 was 47.3% (95%CI: 9.6-69.3) (N=2066; cases=584) and 46.2% (95%CI: – 70.5-83.0) against sub-clade 6B.1 (N=1610; cases=128). End-of-season results will be available in June.

Conclusion

Interim results suggest moderate VE against A(H1N1)pdm09 and sub-clade 6B.1, however similar time periods for analysis are needed before drawing conclusions. End-of-season results will allow stratification by age and VE for other influenza types/subtypes/clades. Providing early clade-specific VE from a representative sample of cases is feasible.

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

ABSTRACT ID: 272

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

B 13.3 Vaccination status does not impact the clinical outcome of influenza-confirmed cases admitted to intensive care units reported by ten EU countries, 2010–2016

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Background

Fatal outcomes related to influenza infection are important indicators for the severity of seasonal epidemics and targeted by vaccination strategies. Our aim was to investigate the impact of the vaccination status on fatal outcome in influenza-confirmed cases admitted to intensive care units (ICU) over six influenza seasons.

Methods

The European Centre for Disease Prevention and Control collects case-based data on hospitalised confirmed cases of influenza from EU/EEA Member States on a weekly basis. We analysed demographics, risk factors and vaccination status of cases admitted to ICU's reported from week 44/2010 to week 16/2016. To test the association between study variables and outcome, uni – and multivariable logistic regression models were applied.

Results

Of 15,290 influenza-confirmed cases reported to be admitted to ICU over six influenza seasons, 2,395 cases reported from ten countries and with information on age, outcome, pre-existing conditions, complications and vaccination status were included in the analysis. Of those, 651 died. Twenty-one percent of the cases were vaccinated, but vaccination was found not to influence outcome in neither the uni – nor the multivariable analysis. Independent factors associated with increased likelihood of fatal outcome were age (adjusted odds ratio (aOR) 1.02; 95% confidence interval (CI) 1.01–1.03), HIV infection (aOR 2.01; 95%CI 1.37–2.96), kidney (aOR 2.18; 95%CI 1.68–6.24) and liver disease (aOR 3.23; 95%CI 1.68–6.24) and infection with A(H1N1)pdm09 (aOR 1.37; 95%CI 1.06–1.76).

Conclusion

We found no association between the vaccination status and the clinical disease progression among influenza-confirmed cases admitted to ICU, but age, HIV infection, chronic kidney and liver disease as well as infection with A(H1N1)pdm09 were identified as risk factors for fatal outcome in patients admitted to ICU.

Keywords: Influenza, severity, intensive care units, surveillance

ABSTRACT ID: 85

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B 13.4 Epidemiological profile of influenza outbreaks in institutional settings

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Background

A congregate environment in institutions aids the spread of influenza viruses that might result in significant morbidity and mortality among residents.

Methods

We examined the patterns of occurrence and clinical outcomes of influenza outbreaks that occurred in Slovenian institutions between January 2011 and May 2015. The reported outbreak duration, attack rates, hospitalization rates, and case fatality rates among residents were calculated by viral aetiology, time to notification, and institution type and size.

Results

The attack rates for the 41 influenza outbreaks ranged 3.1–40.0% with an unadjusted mean of 20.6%. The median number of cases in each influenza outbreak was 37 (range: 6–158) and a median of 199 individuals (range: 25–574) was at–risk of influenza. The median influenza outbreak duration was 13 days (range: 2–49 days). Median time to notification was 10 days after the index case (range: 2–201). Outbreaks reported within the first week after the symptoms onset in the index case were associated with significantly shorter duration and lower case fatality rates.

Conclusion

Rapid reporting of influenza outbreaks to public health authorities prompts early implementation of infection control practices which lead to shorter outbreak duration and better clinical outcomes in those under care.

Keywords: Epidemiology, Influenza, outbreaks, institutions

ABSTRACT ID: 117

PRESENTED BY: Maja Subelj (maja.subelj@nijz.si)

B 13.5 Influenza Vaccine effectiveness against hospitalised laboratory confirmed influenza among elderly in Europe: results from the I-MOVE+ network

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Background

Elderly have a high risk of complications from seasonal influenza. European Union (EU) countries recommend yearly vaccination for them. We conducted a multicentre test negative case control study in 23 hospitals of 10 EU countries to measure 2015-16 influenza vaccine effectiveness (IVE) against hospitalised laboratory confirmed influenza among adults aged ≥65 years.

Methods

We screened patients admitted for motives compatible with recent influenza infection. We included patients swabbed for influenza virus presence within seven days after onset of symptoms compatible with a severe acute respiratory infection. We collected information on demographics, vaccination, disease course and underlying conditions. Cases were patients RT-PCR positive for influenza and controls those negative for any influenza virus. Using logistic regression we measured IVE by influenza subtype adjusted for onset week, study site, and other potential confounders.

Results

As of February 26th 2016, we had recruited 748 patients: 513 controls (260 vaccinated, 51%), 235 positive for any influenza (96 vaccinated, 41%) and 182 positive for A(H1N1)pdm09 (73 vaccinated, 40%). Study site, onset week and age-adjusted IVE was 41% (95% CI: 14;60) against any influenza and 51% (95%CI: 23;68) against A(H1N1)pdm09.

Conclusion

Mid-season IVE estimates against hospitalised influenza among ≥65 years are moderate. The mid-season sample size did not allow adjustment for other potential confounders than age or stratification. At the time of Abstract submission, influenza was still circulating in Europe. With a larger end of season sample size, the I-MOVE+ hospital network will provide adjusted IVE stratified by age group, chronic conditions, time since vaccination and previous year vaccination. Despite its moderate effectiveness, annual vaccination remains the best prophylactic tool against seasonal influenza.

Keywords: Influenza vaccine, Effectiveness, Case control studies, Hospitalisation

ABSTRACT ID: 205

PRESENTED BY: Marc Rondy (m.rondy@epiconcept.fr)

B 13.6 Influenza vaccination and infection rates among health care workers: Results of a survey from a German university hospital, 2014 / 2015

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2. Institute for Hygiene and Microbiology, University of Würzburg, Germany
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Background

Seasonal influenza causes potentially severe infections in hospitalized patients. Nosocomial transmission can be reduced by annual vaccination of health care workers (HCW), which is recommended by the German standing commission on immunization. Vaccination rates among HCW are known to be generally low. The 2014/2015 influenza season lead to high HCW dropout rates at the University Hospital of Würzburg (UKW).

The aim of this survey was to analyze acute respiratory infections, influenza vaccination rates and attitudes towards vaccination among HCW of the UKW in the influenza season 2014/2015.

Methods

A retrospective cross-sectional study was conducted using anonymized questionnaires provided for hospital staff. Questions addressed socio-demographic characteristics, information on influenza vaccination, respiratory symptoms and reasons for vaccine refusal.

Results

677 HCW replied to the questionnaire (response rate 31%). The overall self-reported vaccination rate was 55%. Uptake was significantly higher in physicians (72%) than in nursing staff (45%), and in males (67%) compared to females (51%) ($p < 0.05$). Most vaccinations were administered directly on the wards. Self-reported lost work-time due to adverse events after vaccination was low (0.6%). Vaccine uptake was highest in the pediatric clinic (70%) and lowest in the surgery department (37%).

Doubts about effectiveness and indication were the most relevant reasons for vaccine refusal.

Acute respiratory infection was reported by 24% of the participants. Laboratory testing was rare (5%) and five of nine tested individuals had a laboratory confirmed influenza infection.

Conclusion

Future measures to promote vaccination should focus especially on nursing staff and departments with a low uptake rate. Educational activities should emphasize scientific evidence for the benefits of vaccination in health care settings. Administering vaccines on wards was a successful strategy and should be further supported.

Keywords: Seasonal Influenza, Nosocomial infection, Vaccination, Health care workers, Vaccine refusal

ABSTRACT ID: 383

PRESENTED BY: Nina Katharina Stock (marc.hagemeister@yahoo.de)

Track 14: Vaccine preventable diseases (2)

Moderator: Katharina Alpers, Robert Koch Institute, Germany

B 14.1 Cross-sectional studies: Impact of vaccination program on brucellosis seroprevalence in sheep and goats, Lankaran economic region, Azerbaijan, 2016.

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2. Agricultural Competitiveness Improvement Project World Bank
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Background

Brucellosis is endemic in animals and humans in Azerbaijan. In May 2007, Azerbaijan initiated its first annual vaccination (Rev-1) campaign against brucellosis in female sheep and goats. In November 2015, Azerbaijan started cross-sectional seroprevalence studies of brucellosis in cattle and sheep and goats conducted by "Agricultural Competitiveness Improvement Project World Bank". We analyzed sero-survey data in Lankaran region to evaluate impact of vaccination.

Methods

In January 2016, a cross-sectional cluster study in 5(71%) of 7 districts of region was conducted. Sample size was calculated for each district for 95% confidence level at 4029 samples; five villages per district, 30-40 households per villages and 2-5 samples per households were included using probability proportional to size(PPS) methodology. Random selection of female sheep and goats (over24 month's age) was done regardless of vaccination and migration status. Sera were screened by the Rose-Bengal Test and all positives confirmed by ELISA. We analyzed sero-survey data by vaccinated and migration status.

Results

Among a total sample of 4029, total vaccinated 430 (11%), migratory animals 900 (22.3%), which of them vaccinated 125 (13.9%). Seropositive samples among vaccinated animals versus unvaccinated (2 (0.5%) vs. 82 (2.3%), RR=0.2; 95%CI 0.05-0.8). Seropositive samples among migrated animals versus unmigrated (60 (6.7%) vs. 24 (0.8%), RR=8.7; 95%CI 5-14). Seropositive samples among migratory animals vaccinated versus unvaccinated (2 (1.6%) vs. 58 (7.5%), RR=0.21; 95%CI 0.05-0.86).

Conclusion

The study showed low (11%) total vaccination coverage among randomly selected animals regardless of vaccination and migration status, the effectiveness of vaccination in the protection, and a high prevalence among the migratory animals. We recommend scaling up the studies in other regions of Azerbaijan, enhancing surveillance for migratory animals and number of carried out vaccination.

Keywords: brucellosis, vaccination, Rev-1, Azerbaijan, sheep, goats

ABSTRACT ID: 101

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B 14.2 Impact of the introduction of the rotavirus vaccine in reducing health inequalities in GP gastrointestinal consultation rates in children under 5 in Wales

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Background

Rotavirus accounts for an estimated 25% of acute gastroenteritis general practitioner (GP) consultations in children aged ‹5 years in England and in Wales. A socio-economic gradient exists for this illnes, which is more pronounced for hospitalised cases. Routine immunisation with Rotarix™ rotavirus vaccine began in Wales in July 2013. Uptake of 2 doses by first birthday increased quickly and was 93% for the last quarter of 2015. We investigated the change in GP gastroenteritis consultation rates in children ‹5 and associated health inequalities.

Methods

We conducted an ecological longitudinal study. All GP registered children ‹5 were included. We compared the mean annual incidence for gastroenteritis consultations in the pre (2011-13) and post vaccination period (2014-15) for the different age groups and how this varied by quintile of deprivation

Results

Mean annual incidence for consultations in the children aged ‹1 decreased by 12.5%, from 166(95% Cl:163.5-169.1) to 145 (95% Cl: 142.2-148.6) per 1,000 and by 25.3% in children aged 1 to ‹2 from 125 (95% CI: 122.2-126.8) to 93 (95%CI: 90.6-95.4) per 1,000. Other age groups did not show major changes between periods. Decreases were greatest in practices located in the most deprived quintile of area: from 190 (95%CI: 183.9-196.8) to 157 (95%CI: 149.5-164.1) consultations per 1,000 in children aged ‹1 and from 136 (95%CI: 130.5-140.8) to 92 (95%Ci: 86.8-97.5) in children aged 1to ‹2.

Conclusion

GP consultations rates for gastrointestinal declined in children ‹2 years following introduction of rotavirus vaccine. While practices from more deprived areas had higher rates, they also saw a greater decline in the post vaccination period, suggesting that rotavirus vaccine has reduced inequalities in gastrointestinal illness in children.

Keywords: Rotavirus, gastroenteritis, vaccine, GP consultations, Wales, children

ABSTRACT ID: 216

PRESENTED BY: Joana Vaz (joanamvaz@gmail.com)

B 14.3 **Cancelled**

B 14.4 **Cancelled**

B 14.5 Epidemiological Pattern of Measles Case-Based Surveillance Data; Oyo state, Nigeria, 2008-2014.

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Background

Case-based surveillance is crucial in the elimination process of measles in Nigeria. In September, 2015, we analysed the measles case-based surveillance data in Oyo State, Nigeria to determine the epidemiological distribution of the illness, between 2008 and 2014.

Methods

We conducted a secondary data analysis of measles case-based surveillance records from the Oyo State Ministry of Health, between 2008 and 2014. A suspected case was defined as any person with fever (>38oC) and maculo-papular rash, and cough, and/or conjunctivitis, and/or coryza; while a laboratory confirmed case was any suspected case with laboratory confirmation of positive measles IgM. We calculated frequencies, proportions, incidence and performed tests of association using Epi info version 7.

Results

During the review period, 2,592 suspected cases were investigated and 568(21.9%) were positive for measles IgM. The annual incidence of confirmed measles cases per 100,000 population was consistently 2 cases per 100,000). The highest proportion of confirmed measles cases occurred among the age group of < 5years [(359/568), (63%)] and rural dwellers [(333/568), (59%)].The case fatality rate (CFR) was 0.9% (5/568). 35% (200/568) and 48% (273/568) unvaccinated and vaccinated persons were positive for measles IgM respectively, while unknown vaccination status (in 2011) accounted for 17% (95/568) of positive measles IgM. Region of residence was found not to be associated with positive measles IgM (P=0.7250).

Conclusion

The major burden of confirmed measles cases lies in the rural areas, predominantly among children < 5 years who had zero and at least one measles vaccine dose (in 2011). We recommended that Supplemental Immunization Activities should target children < 5 years who live in the rural areas of Oyo state.

Keywords: Case-based surveillance, Measles, Immunization, Nigeria

ABSTRACT ID: 41

PRESENTED BY: Maureen Anyanwu (maureenanyanwu23@yahoo.com)

Track 15: Novel methods in epidemiology (2)

Moderator: Sandra Dudareva-Vizule, EPIET Alumni Network/ Dept. for Infectious Disease Epidemiology at RKI

B 15.1 Inference and forecast of H7N9 influenza in China

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Background

The recent emergence of A (H7N9) avian influenza poses a significant challenge to public health in China and around the world; however, partial observation of H7N9 infections make analysis of the transmission potential both among poultry populations and spillover to humans difficult.

Methods

Here, using the combination of a simple epidemic model and data assimilation method, we are able to infer key epidemiological parameters and to produce accurate forecasts of the peak timing and magnitude of human cases.

Results

Our findings indicate a high outbreak attack rate (33%) among poultry but a low rate of chicken-to-human spillover transmission. In addition, accurate forecasts of the timing and magnitude of human H7N9 cases are generated.

Conclusion

This work demonstrates that transmission dynamics within an avian reservoir can be estimated and that real-time forecast of spillover avian influenza in humans is possible.

Keywords: H7N9 subtype, avian influenza, Bayesian analysis, forecasting

ABSTRACT ID: 314

PRESENTED BY: Ruiyun Li (rl2817@cumc.columbia.edu)

B 15.2 An outbreak of Salmonella Enteritidis PT 8 of a unique MLVA profile but two different SNP clusters by Whole Genome Sequencing

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11. NHS Ayrshire and Arran Health Protection Team, Ayr, Scotland,
12. Greater Glasgow and Clyde Health Protection Team, Glasgow, Scotland
13. NHS Forth Valley Health Protection Team, Stirling, Scotland
14. NHS Fife Health Protection Team, Fife, Scotland
15. NHS Lanarkshire Health Protection Team, Bothwell, Scotland

Background

In December 2015 Scotland launched an investigation into an outbreak of S. Enteritidis PT8 with an unusual MLVA profile, which evolved via the issuing of an EPIS alert into a larger multi-country outbreak.

Methods

Information on food exposures prior to symptom onset was obtained from cases via interviews conducted by the NHS Board Health Protection Teams or local Environmental Health Officers.

Isolates from Scotland were sent to the Scottish Salmonella Reference service for phenotyping and MLVA, and subsequently to Public Health England for WGS.

Extensive food supply chain investigations in particular for the egg supply chain were undertaken by Food Standards Scotland and Food Standards Agency in England.

Results

WGS analysis revealed that whilst the isolates had a common MLVA profile, they formed two distinct single nucleotide polymorphism (SNP) clusters. The two clusters had no more than five SNP intra cluster variability and were separated by 75 SNPs. Based on a case definition of an isolate WGS profile falling into either of the two WGS clusters (within 5 SNP difference) and a symptom onset date on or after 1 July 2015, 66 cases were identified across UK, Netherlands and Finland. Twenty-six of these were resident in Scotland. Fourteen of the 26 cases in Scotland belonged to one cluster and 12 to the other.

Food exposure information was available for 24 of the cases in Scotland, 16 of which reported eating food from Chinese/Indian style takeaways, and in particular egg containing dishes.

Conclusion

The outbreak was unusual in that although cases in Scotland shared a common MLVA profile, the isolates fell into two distinct WGS clusters, with some isolates from other countries also falling into these two clusters.

Keywords: Salmonella Outbreak Whole Genome Sequencing

ABSTRACT ID: 221

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B 15.3 Dynamic modelling of hepatitis B vaccination to children in Sweden

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Background

During 2009-2013, about 100 cases of acute, and between 1,200-1,500 cases of chronic, hepatitis B were reported annually in Sweden. The aims of this study were to investigate how burden of disease would be affected by introducing a general hepatitis B-vaccination in the national childhood vaccination program and to assess the cost-effectiveness (CE) of such a vaccination program.

Methods

We developed a dynamic transmission model to simulate hepatitis B epidemiology in Sweden. The model included the following health states: susceptible, vaccinated, ill with acute/chronic hepatitis B, suffering from sequelae, and dead. At start the model was populated with an average Swedish birth cohort, all assumed to be susceptible. Age specific rates governed the dynamic flow between the states, calibrated to reproduce the yearly incidence as observed in Swedish surveillance data. Since sequelae (liver cirrhosis and liver cancer) do not occur until many years after infection, the time horizon was set to 50 years, with a delay of 20 years to progress from the health state chronic hepatitis B to sequelae. To each state in the model, corresponding averaged costs and health effects were applied. Costs included health care and medications, production losses when persons were prevented from working, and vaccine. Health effects were measured in quality-adjusted life years.

Results

Results show that vaccination of children in Sweden does not have a sufficient effect on the burden of disease to justify its costs. This is a consequence of the low spread of infection in the general population – almost all spread takes place in risk groups.

Conclusion

However, vaccinating children may be an effective strategy in order to vaccinate risk groups before they are subject to infection.

Keywords: Hepatitis B, vaccination, dynamic modeling, cost effectiveness, health economic evaluation

ABSTRACT ID: 324

PRESENTED BY: Ellen Wolff (ellen.wolff@folkhalsomyndigheten.se)

B 15.4 Domestically acquired salmonellosis in Finland, 2011-2015: One Health approach

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Background

In Finland, 15-20% of human Salmonella infections are considered domestically acquired. Despite a decrease among imported infections, the rate of domestic infections remained relatively stable during 2011-2015. Our objectives were to describe and compare Salmonella enterica serovars Typhimurium (ST) and Enteritidis (SE) isolates of human and non-human origin in order to identify potential sources of sporadic human domestic cases.

Methods

A dataset of 428 ST and 286 SE human clinical isolates, and 252 ST and 103 SE non-human isolates (food, wildlife, food-producing animals, and feed/farm-environment) were characterized by multiple-locus variable number tandem repeat analysis (MLVA). Human isolates were obtained through surveillance of gastroenteritis from clinical microbiological laboratories, while non-human isolates were selected from veterinary strain collection of surveillance programs and diagnostic activities at Finnish Food Safety Authority.

Results

Two-hundred-and-thirty-three ST MLVA profiles were detected, 126 among human and 133 among non-human isolates. The five profiles most common among humans accounted for 52%. Amongst these, ST MLVA profile 3-16-NA-NA-0311 was also detected in food (2%, 1/45), wildlife (10%, 6/59), food-producing animals (5%, 5/92), and feed/farm-environment (2%, 1/56). Ninenty-four SE MLVA profiles were detected, 83 among human and 33 among non-human isolates. The five profiles most common among humans accounted for 49%. These profiles also accounted for 73% (43/59) of food isolates, and were from imported food. One-hundred ST (43%, 183/428) and 62 SE (57%, 143/252) MLVA profiles were only detected among human isolates.

Conclusion

The most common human SE MLVA profiles identified in Finland were prevalent among isolates from imported food. Comparison of Salmonella MLVA profiles of human and non-human origin enables the identification of potential sources and could lead to prompt and targeted interventions to improve control strategies.

Keywords: surveillance, Salmonella Typhimurium, Salmonella Enteritidis, MLVA

ABSTRACT ID: 340

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B 15.5 Real-time visualization of contact tracing information to aid timely decision making in outbreak control

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Background

Contact tracing (CT) can provide accurate information on relevant parameters of the ongoing outbreak, which is needed by outbreak investigators to control an emerging infectious disease outbreak. However, crude CT data are difficult to interpret. We present a method to obtain key outbreak parameters from CT data in real-time.

Methods

Exposure type specific attack rates (AR) and the reproduction number R(t) are estimated from CT data by maximum likelihood estimation to account for censored data. To get a real-time overview of the outbreak, the ARs and R(t) over time are visualized together with the case-contact network and epicurve.

Results

We demonstrated the added value of the analysis of CT data by applying it to a smallpox outbreak in the Netherlands, analysed as if it was May 30th 1951. By this date, 52 smallpox cases were identified, 22 contacts were in follow-up and 174 contacts were discarded, as their incubation period was over. These ARs reflect, in the context of CT, the specificity of the contact definition; a higher value indicates a relatively efficient CT. In this outbreak, the AR among household contacts was relatively low compared to other exposure types, 18.2% [95% CI: 10.6 – 27.9%], indicating this contact definition could be made more specific to facilitate more efficient CT. The visualization depicts the evolution of R(t) over time which allows the evaluation of the effectiveness of interventions; the R(t) decreased around the time of implementing control measures which is consistent with effectiveness of these interventions.

Conclusion

Our method facilitates the analysis of CT data by quickly turning it into accessible information, helping public health professionals to make real-time decisions to more effectively and efficiently control infectious disease outbreaks.

Keywords: Contact Tracing, Infectious Disease Outbreaks, Basic Reproduction Number, Real-time Systems, Maximum Likelihood Estimates

ABSTRACT ID: 118

PRESENTED BY: Loes Soetens (loes.soetens@rivm.nl)

B 15.6 Will routine PFGE-genotyping replace questionnaires on food consumption for investigating Listeria monocytogenes cases in Baden-Wuerttemberg, Germany?

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Background

To identify sources of infection and prevent further cases, the State Health Office recommends local health officers to interview every notified Listeria monocytogenes (Lm) case in Baden-Wuerttemberg on food consumption by questionnaires. However, the data on exposures often is of poor quality due to old age and comorbidities of patients and long incubation periods. Since 2010, Lm isolates have been routinely PFGE-genotyped. PFGE-patterns of Listeria isolates from food items can be compared to those from human cases.

Methods

We evaluated how PFGE-typing and food questionnaires contributed to identifying the source of infection. We defined a cluster as two or more isolates with the same PFGE-pattern, and a "linked-food" as a food item with the same PFGE-pattern as cluster cases and consumed by at least two cases in that cluster. We assessed the number and characteristics of PFGE-typed isolates as well as the number of questionnaires received between 2010 and 2015 and linked food items.

Results

Of 432 reported cases, 116 (27%) completed a food questionnaire and 290/432 (67%) had isolates genotyped. 194/290 were grouped into 43 clusters of 2-37 cases (median 2 cases per cluster).For 12/43 (28%) clusters at least two food questionnaires were available; but in only 4/43 clusters, accounting for 17/290 cases, a linked food was identified.

Conclusion

In the past, clusters of Lm infections were only identified by PFGE-genotyping and not through analysis of questionnaires. In order to match apparently isolated cases to clusters, all human Lm isolates should be routinely genotyped. Food questionnaires only helped explain a small percentage of clusters identified by PFGE, but they might be needed to prioritize food isolates for PFGE and to match them with PFGE patterns of clusters.

Keywords: Listeria monocytogenes, PFGE-genotyping, questionnaires, food items

ABSTRACT ID: 289

PRESENTED BY: Dorothee Lohr (dorothee.lohr@rps.bwl.de)

Track 16: Tuberculosis and other respiratory diseases (excluding viruses) (2)

Moderator: Helen Maguire, TB expert & former EPIET coordinator

B 16.1 Outbreak of Mycobacterium tuberculosis infection among substance users and homeless in three regions of Quebec, Canada, 2003-2015

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Background

In Quebec, approximately 200 active tuberculosis infections are reported each year. Since 2003, a cluster of a specific genotypic profile has been observed. In order to guide interventions, we investigated this outbreak by describing case characteristics including geographic distribution.

Methods

All tuberculosis cases residing in Quebec with the genotype of interest or epidemiologically linked to these cases were included. Descriptive analysis of retrospective data from routine investigations conducted by Public Health was performed. Variables included sociodemographic and clinical characteristics, risk factors, and places attended by cases during their period of communicability. We conducted a spatial analysis to identify potential transmission sites using ArcGIS 10.2.1.

Results

Between 2003 and 2015, there were 33 confirmed cases for this outbreak in three contiguous regions of Quebec: Montréal, Montérégie, and Laval. Age varied between 1 and 69 years (median 35), and 54% were men. In most cases, the site of infection was pulmonary (91%). The median duration of contagiousness was 4 months (max 1.5 year). Two profiles were observed: 27 cases displaying risk factors (drug use (n=25), homelessness (n=12), HIV infection (n=9), mental health disorders (n=6)), and 6 members of their families without risk factors. Locations attended by vulnerable cases were concentrated in downtown Montreal and included crack houses visited by several cases. Public health orders and court orders were issued for one quarter of the cases because of compliance or isolation issues.

Conclusion

This outbreak affects highly vulnerable persons and has spread to members of their families. Awareness should be raised among clinicians serving this population and among community organizations, especially those tackling addictions and homelessness. Stronger collaboration for outreach prevention and screening in selected locations is also needed.

Keywords: Tuberculosis, outbreak, vulnerable population, surveillance, substance users.

ABSTRACT ID: 155

PRESENTED BY: Josephine Aho (josephine.aho@phac-aspc.gc.ca)

B 16.2 Evaluation of the national tuberculosis surveillance system in Ireland before and after incorporation into a web-based system

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2. Health Protection Surveillance Centre, Dublin, Ireland

Background

In 2011, the Irish tuberculosis (TB) enhanced surveillance system was integrated into the secure web-based national Computerised Infectious Disease Reporting system (CIDR). The aim of this evaluation was to assess the completeness, timeliness, simplicity, usefulness and flexibility of the system before and after integration into CIDR.

Methods

We estimated the completeness of 19 core and 26 enhanced variables in each system and compared them using Chi-square test. We calculated median time intervals between onset-diagnosis-notification for both systems and compared them using Wilcoxon Rank-Sum test. We evaluated the simplicity, flexibility and usefulness using an online questionnaire which was sent to all public health staff involved in TB surveillance. We used Likert scale for all questions and conducted descriptive analysis.

Results

Overall, there were 4007 TB notifications before (2002-2010) and 1776 after (2011-2015) CIDR's introduction. There was no significant difference in completeness for most demographic variables. Dates and diagnosis related variables were more complete in the old system while variables on drug susceptibility and patient outcome were more complete on CIDR ($p<0.05$). Median time intervals between onset-diagnosis-notification significantly increased in CIDR compared to the previous system ($p<0.05$). Twenty-four people responded to the survey (88.9% response rate). Compared to the old system 37.5% of respondents felt CIDR is simpler, 41.7% found it more useful and 29% more flexible.

Conclusion

Following the introduction of CIDR, the completeness of most variables and timeliness of TB data decreased. Stakeholder feedback showed increased satisfaction in relation to simplicity, usefulness and flexibility of CIDR compared to the older system, but additional qualitative studies should be undertaken to further investigate this. Reasons for the decrease in completeness and timeliness need to be explored in order to make improvements.

Keywords: Tuberculosis, Surveillance, Evaluation, Statistics

ABSTRACT ID: 95

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

B 16.3 Questioning the usefulness of the latent tuberculosis infection (LTBI) surveillance in children in France, 2010 – 2014

Georgios Theocharopoulos (1, 2), D. Antoine (2).

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

Background

Children with latent tuberculosis infection (LTBI) have increased risk of developing active TB, but treatment can prevent progression to TB. In 2003, LTBI in children became mandatorily notifiable in France to trigger investigations for active TB cases and improve LTBI detection and early treatment. We analysed surveillance data to identify possible areas of improvement in surveillance.

Methods

Cases were children <15 years old, with a positive skin test (following injection of 5U tuberculin) and no evidence of active TB. We described LTBI cases notified between 2010 – 2014 and calculated the ratio of LTBIs in children to pulmonary active TB cases, to identify trends in TB transmission.

Results

During 2010-2014, 3,862 LTBI cases were notified (634 cases in 2010 and 867 in 2014 compared to 440-485 cases/year during 2004-2006 and 600-633 cases/year during 2007-2009). Median age was 8 years (inter-quartile-range: 3-11). Of cases, 67% (2478/3476) were foreign-born or of foreign-born parents; 87% (2920/3347) were detected through active case finding. The overall ratio of LTBI in children/pulmonary active TB cases was 21/100 and increased from 17/100 in 2010 to 25/100 in 2014.

Conclusion

Reported LTBI cases in children increased, possibly due to improved reporting or case investigation practices. The ratio of LTBI/pulmonary TB was consistent with literature data for France and its increase in 2010-2014 might be attributed to increase of reported LTBIs and decrease of reported pulmonary TB cases during that period. Reported LTBI cases were largely detected through active case finding, suggesting that only a fraction of LTBIs was detected through surveillance. The LTBI notification system alone may not be sufficient to detect all LTBI cases and we recommend an evaluation of its public health usefulness.

Keywords: Latent Tuberculosis, Surveillance

ABSTRACT ID: 158

PRESENTED BY: Georgios Theocharopoulos (theocharopoulos1@yahoo.com)

B 16.4 Extensively drug-resistant tuberculosis exposure in an aircraft, Germany, July 2013 – a contact investigation

Maria an der Heiden (1), Barbara Hauer (1), Lena Fiebig (1), Gisela Glaser-Paschke(2), Markus Stemmler (3), Claudia Simon (4), Sabine Rüsch-Gerdes (5), Andreas Gilsdorf (1), Walter Haas (1)

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4. Landesamt für Gesundheit und Soziales, Berlin, Germany
5. Former Head of the National Reference Center for Mycobacteria, Borstel, Germany

Background

In July 2013, a passenger died of infectious extensively drug-resistant tuberculosis (XDR-TB) in an aircraft after a 3-hours flight. As initial information indicated that the patient moved about the aircraft coughing blood we aimed to contact and inform all passengers and crew members and to test them for new TB-infection.

Methods

A contact investigation comprising all passengers and crew members was carried out in cooperation with national and international health authorities in charge. Two-stage testing before and after 8 weeks post-exposure was suggested. Both, interferon gamma release assays and tuberculin skin test (TST) were accepted methods. The TST cut-off was >10mm; for differentiation between conversion and boosting, conversion was defined as an increase of skin induration >5mm.

Results

Overall, 162 contact persons from 17 countries were included in the investigation (155 passengers, 7 crew members): 130 (80%) persons were informed about the exposure and 112 (69%) were tested at least once for TB-infection. In 61 (54%) of the tested persons an initial and a following test were performed, of these one passenger who sat next to the area where the patient died had a test conversion (first TST: 2mm, second TST: 14mm; Bacillus Calmette–Guérin (BCG) – vaccinated; second test was performed 6 months after the flight, no other exposures were recalled). So far, no secondary active TB-cases have been reported.

Conclusion

The majority of contact persons could be informed about the XDR-TB exposure and tested for TB infection, but only in half of them it was possible to assess recently acquired TB-infection. Timely testing and interpretation of test results were challenging. Reliable tests allowing for the detection of a new TB-infection by a single test are urgently needed.

Keywords: Extensively Drug-Resistant Tuberculosis, XDR-TB, Contact Tracing, Interferon-gamma Release Assay, Tuberculin Test

ABSTRACT ID: 257

PRESENTED BY: Maria an der Heiden (anderheidenma@rki.de)

B 16.5 Late breaker: Results from one year tuberculosis screening in 13327 adult refugees by the public health authority of Mannheim, Germany

Nadja Oster (1), A.Kuhn (1), K. Menninger (1), A. Dettling (1), R. Helble (1), F. Karpa (1, 2), P. Schaefer (1)

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2. MDA Berufskolleg, SRH Fachschulen

Background

Examination for tuberculosis is mandatory for immigrants attending German refugee camps. These data show the TB results in adult refugees in Mannheim between July 2015 and June 2016.

Methods

All refugees were examined physically. Non-pregnant adults underwent chest x-ray followed by computer tomography in suspicious cases. In cases with radiological evidence for TB microbiological confirmation was tried to achieve by microscopy, culture and PCR. Pregnant women underwent IFN gamma-release assay instead of x-ray.

Results

From July 1st, 2015 to June 30th, 2016 the Mannheim public health authority examined 13327 adult refugees. 46 cases (prevalence 0,35%) of active tuberculosis in adult refugees were reported in Mannheim during this period. 41 were pulmonary cases of which 28 were infectious. Two were cases of MDR tuberculosis. 10 infectious cases were diagnosed by other ways than mandatory examination. In TB cases diagnosed in mandatory examination suspicion of TB was always determined radiologically, not clinically. The prevalence for bacteriologically confirmed tuberculosis was 0.54% among refugees from Subsahara Africa and 0.14% for immigrants from the Middle East. Of the 347 pregnant women examined 81 (prevalence 23%) showed latent TB infection.

Conclusion

Prevalence of bacteriologically confirmed tuberculosis was 44fold higher among refugees than among the average German population (0.008%). 10 of 28 infectious TB cases were not detected in mandatory examination partly due to delay of the examination. For mandatory examinations during migration waves priorisation according to the TB risk in the country of origin and implementing radiological before physical examination could be strategies for a more rational TB screening. High prevalence of latent TB infection in pregnant women indicate a high overall prevalence of latent TB infection in the refugee population.

Keywords: tuberculosis, refugees, burden of illness, Germany, diagnosis

ABSTRACT ID: 732

PRESENTED BY: Nadja Oster (nadja.oster@mannheim.de)

MODERATED POSTER SESSION C
WEDNESDAY, 30 NOVEMBER
15:30-16:30

Track 17: Antimicrobial resistance and healthcare associated infections (3)

Moderator: Barbara Albiger, ECDC, Expert Microbiology

C 17.1 Evaluation of the microbiological surveillance system for antifungal drug resistance in Spain, 2014-2015

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Background

Antifungal drug resistance has emerged worldwide in the last years representing a possible public health threat. To assess the level of antifungal drug resistance in Spain a surveillance system was established at the Mycology Reference laboratory in June 2014. Our aim was to evaluate this system and if required, to provide recommendations for improvement.

Methods

We followed the updated CDC guidelines for evaluating Public Health surveillance systems. We appraised the simplicity of the system analysing its structure and ease of operation, the representativeness through the population coverage of the participating hospitals and the data quality, calculating the completeness of data reported and validity (proportion of cases complying with case definition). We analysed the existing database organised with the epidemiological and microbiological data gathered from the questionnaires sent electronically by the participants.

Results

The evaluation reveals that the system is simple and the data flow is clearly defined. The population covered by the participating hospitals was 11.8% of the Spanish population. The completeness was 84.6%, although no information about the total number of strains analysed in each hospital was available and therefore the level of antifungal resistance in Spain could not be assessed. The validity assessment showed that 38.7% of the isolates did not match the case definition and consequently were not further analysed.

Conclusion

The current system is simple, presents good completeness but low validity. It lacks representativeness as the coverage is low. We recommend switching to a sentinel system and to further investigate the reason for the high number of received isolates not matching the case definition, in order to provide advice to the participating hospitals.

Keywords: Evaluation, Antifungal drug resistance, Surveillance, Spain

ABSTRACT ID: 46

PRESENTED BY: Fátima Amaro (fatima.f.amaro@gmail.com)

C 17.2 Establishing Electronically Assisted Surveillance of Surgical Site Infections in Norway, a 10-year Project

Hege Line Løwer

Norwegian Institute of Public Health

Background

During recent years, there has been an increased attention given to healthcare-associated infections (HAIs) as an important aspect of patient safety by politicians, patients and healthcare providers as well as public reporting of quality indicators. In order to obtain better and more reliable surveillance data, the Norwegian Surveillance System for Antibiotic Consumption and Healthcare-Associated Infections (NOIS) was introduced by regulation in Norway in 2005. Surgical site infections (SSIs) comprised the first module in the new system.

Methods

One of the objectives when implementing NOIS-SSI was to utilize as much of the existing data in hospital information systems as possible, in order to limit the burden on hospital staff and ensure good data quality. Infection control computer programs were developed by the hospitals in collaboration with different IT-providers and a national database was established.

Results

In 2005, 28 hospitals submitted about 2,300 procedures to the national database. In 2015, 58 hospitals submitted over 30,000 procedures. There are now three major suppliers of ICMs in Norway and several smaller in-house systems. The systems utilize data extracted from different sources. Some systems are integrated in the work flow, and some are “stand-alone” systems. Efforts have been made to assist case identification by tagging potential infections on the basis of microbiology or pharmacy data, but none have yet been successfully implemented. Data is uploaded to the national data base through a web-tool.

Conclusion

Encouraging the development of computer tools for surveillance in the hospitals has resulted in systems that greatly reduce the burden of data collection on hospital staff, improve data quality and pave the way for more comprehensive surveillance.

Keywords: electronic health records, surgical wound infection, epidemiological surveillance, medical informatics

ABSTRACT ID: 271

PRESENTED BY: Hege Line Løwer (hege.line.lower@fhi.no)

C 17.3

Validation of an electronic nationwide surveillance system for periprosthetic joint infections following total hip arthroplasty in Denmark

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5. Representatives from the Capital Region of Denmark, Region Zealand, Region of Southern Denmark, Central Denmark Region, North Denmark Region

Background

Periprosthetic joint infections (PJI) after total hip arthroplasty (THA) have high morbidity and are often used as indicators in infection control. We compared an algorithm based on administrative and microbiological data from the Danish Hospital-Acquired Infections database (HAIBA) to identify PJI against an algorithm from Gundtoft et al., which also accounts for clinical information.

Methods

The algorithm for HAIBA used data from the Danish National Patient Registry (DNPR) and the Danish Microbiology Database. We defined an (early) PJI as a reoperation between 3-90 days after primary THA implantation, in which at least two positive biopsies with the same microorganism were identified. The algorithm of Gundtoft et al. uses the Danish Hip Arthroplasty Registry (DHR) to define index operations and identifies PJI using microbiological, prescription, biochemistry data and clinical findings from medical records.

An extract from Gundtoft et al. with THA performed in 2010-2011 in selected hospitals was compared with data from HAIBA for the same period and hospitals. Sensitivity and specificity were calculated with 95% Confidence Intervals (95% CI) and discrepancies were described.

Results

Among 9788 THA performed, 44 led to a PJI in both algorithms and 9715 did not. The sensitivity was 95.7% (44/46, 95% CI 90.8-100%), the specificity was 99.7% (9715/9742, 95% CI 99.6-99.8%). The majority of discrepant cases was due to differences in index operation registrations in DNPR and DHR.

Conclusion

The algorithm developed for HAIBA closely approaches an algorithm using clinical data and is applicable to monitor PJI after THA. This is an important improvement in infection control allowing all hospitals in Denmark to follow their trends and giving insight in the burden of these infections on a regional and national level.

Keywords: Hospital-acquired infections, periprosthetic joint infection, surveillance, Denmark,

ABSTRACT ID: 305

PRESENTED BY: Manon Chaine (gub@ssi.dk)

C 17.4

Vulnerable babies most at risk during a multicentre outbreak of Bacillus cereus bacteraemia associated with Total Parenteral Nutrition (TPN) in England, May-June 2014

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4. Statistics, Modelling and Economics Department, National Infection Service, Public Health England
5. National Infection Service, Public Health England

Background

A Public-Health-England-led investigation into a bacteraemia outbreak among babies in 11 English hospitals confirmed 19 cases of a single strain of B. cereus with onset 28/05/14 to 16/06/14. A rapid case-control study identified TPN from company X as the likely source. 81 potentially contaminated batches were identified and recalled; three tested, and the outbreak strain identified. We conducted a cohort study among recipients of recalled batches to test our hypothesis that particular ingredients, allowing for case characteristics, may have been risk factors for illness.

Methods

Company X provided ingredient details for each of the X-TPN batches. We identified all babies exposed to X-TPN at English hospitals after 26/05/14 and excluded those without recorded batch numbers; cases were defined as having B. cereus fAFLP type Bc.44 isolated from a sterile site. We used a structured questionnaire completed by clinicians to collect information on babies' clinical characteristics, indicators of vulnerability e.g. premature birth, and batches received. We calculated "postmenstrual age" as days between mother's last menstrual period and receipt of X-TPN. We compared the risk of bacteraemia among those exposed and unexposed to various ingredients, and with different characteristics, calculating adjusted odds ratios (aORs) and 95% CIs using logistic regression.

Results

84 patients received ≥ 1 unit of X-TPN; 16 cases and 50 non-cases were included in the study. No ingredients were associated with illness. Each additional week of post-menstrual age reduced the odds of illness by 15% (aOR=0.85, 95% CI=0.77-0.95).

Conclusion

Our study highlights the vulnerability of the youngest, most premature infants receiving X-TPN. TPN cannot be sterilised or tested for contamination prior to administration; so rapidly reporting potential contamination and recalling product is vital to prevent similar incidents.

Keywords: bacteremia, cohort studies, disease outbreaks, infant, newborn, infant, premature

ABSTRACT ID: 68

PRESENTED BY: Kirsty Hewitt (kirsty.hewitt@phe.gov.uk)

C 17.5 Outbreak of Q fever among patients and staff of a psychiatric hospital, South-West Germany, 2015

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2. European Programme for Intervention Epidemiology Training (EPIET), ECDC, Stockholm, Sweden
3. Q fever Consulting Laboratory, Stuttgart, Germany
4. Local Health Office Rottweil County, Baden-Wuerttemberg, Germany

Background

In July 2015, Q fever pneumonia occurred in three patients and one staff of one sheltered accommodation of a psychiatric hospital. About 60% of infections of C. burnetii occur without symptoms, but underlying diseases increase the risk of chronic infections. Therefore we conducted a retrospective cohort study to detect undiagnosed cases and identify the source of infection.

Methods

We defined the cohort as persons living or working in this accommodation between 15th May and 31st July 2015. Serological tests and questionnaires on symptoms, underlying diseases and exposures were offered. Cases were those with a positive test for Phase2-IgM-antibodies against C. burnetii (Elisa Virion-Serion). We excluded persons with former, chronic or unclear infections. We calculated attack rates (AR). As a sheep herd had grazed and lambed nearby, veterinarians tested three ewes serologically for antibodies against C. burnetii using complement fixation.

Results

79/100 residents and 27 staff responded. 34/106 (32%) participants reported cardiac diseases, diabetes and/or immunosuppression. We identified three symptomatic and three asymptomatic cases in addition to the four initial cases. AR was 11.6% (8/69) for residents and 8.0% (2/25) for staff, the median age for cases was 60.5 years, and 50% were female. A ewe, which lambed two weeks before the onset of the first human case, was tested positive.

Conclusion

Onset of diseases was compatible with a point source from lambing of the infected ewe, which was followed by strong winds blowing towards the building. We recommended expanding the investigation to known risk groups for developing a chronic outcome in the whole hospital complex. To prevent further outbreaks in endemic regions only vaccinated or negatively tested sheep flocks should graze in proximity to hospitals or maternity clinics.

Keywords: Q fever, psychiatric hospital, sheep, heart diseases

ABSTRACT ID: 79

PRESENTED BY: Dorothee Lohr (dorothee.lohr@rps.bwl.de)

C 17.6 Sentinel surveillance for acute diarrhea and Shigella antimicrobial resistance (AMR) patterns, in Georgia, 2015

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2. US CDC-Georgia Country Office Georgia, National Center for Disease Control and Public Health South Caucasus Field Epidemiology and Laboratory Training Program,Tbilisi, Georgia

Background

Since 2010, the increasing number of infectious diarrhea with unknown etiology (IDUE) has been a public health problem in Georgia. In 2014, the incidence of IDUE was 683 per 100,000, Salmonellosis and Shigellosis incidence were 7.9 and 18.8 respectively.

Methods

In 2015, we started sentinel-site, laboratory-based bacterial diarrheal disease surveillance to enhancepathogen isolation, identify AMR patterns and strengthen outbreak response. Three main regional hospitals were included; stool samples were collected from diarrhea patients, cultured and serotyped. AMR testing was done using disc diffusion method. Positive cases were investigated by epidemiologists.

Results

A total of 867 specimens were collected. Fourteen Salmonella (7 from group ”B”, 3-group ”C”, 2 S.arizonae, S.typimurium, S.paratypi B) and 105 Shigella sonnei culture-confirmed cases were identified. Six outbreak were detected. AMR testing was conducted on 91 S. sonnei isolates. All were resistant to at list one antibiotic, 17% were multidrug resistant.The AMR profile included Streptomycin 96% (26/27), Trimethoprim-sulphamethoxazole 78% (56/72), Ampicillin 62.5 (25/40), Tetracycline 56%(32/57), and Ceftriaxone 40%(36/91). Ceftriaxone is the first-line treatment for children with diarrhea in Georgia. All strains were susceptible to Ciprofloxacin, except 2, which hade intermediate susceptibility.

Conclusion

Improving stool submission and laboratory capacity at regional level is essential for early detection and control of outbreaks. The prevalence of Shigella in Georgia is much higher than previously estimated. S. sonnei is becoming more resistant to treatment with antibiotics, including Ciprofloxacin.

Recommendation: Strive to obtain stool cultures from patients suspected of having enteric infection and promote AMR testing isolates for susceptibility is required for clinicians. Revise antimicrobial therapy protocols against Shigellosis in children. Health Care agencies must take appropriate measures to improve AMR testing and promote antibiotic stewardship.

Keywords: Sentinel surveillance, Shigella spp., Antimicrobial resistance

ABSTRACT ID: 269

PRESENTED BY: Eka Khabazi (ekakhabazi@gmail.com)

Track 18: Food- and waterborne diseases and zoonoses (3)

Moderator: Florian Burckhardt, EPIET Alumni Network

C 18.1 Waterborne acute gastroenteritis outbreak in a South West city, February 2016, France

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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 Landes, Mont de Marsan, France
3. French Institute of Public Health Surveillance, Department of environmental health, Saint-Maurice, France

Background

In February 2016, an acute gastroenteritis (AGE) outbreak in a district of a French city was reported to the local health authorities as well as complains linked to the tap water (smell and color). Epidemiological and environmental investigations were carried out to describe the outbreak, determine the source of contamination and adapt control measures.

Methods

Beside the description of the persons who complained for AGE at the local health authorities, a cohort study was conducted in the district to collect AGE symptoms and water consumption data. Microbiological analyses were performed on stool samples of AGE cases and on samples from the drinking water network. Retrospectively, health insurance reimbursements of AGE drugs from different villages of the area, connected or not to the same drinking water supply, were analyzed and compared.

Results

In the district, 170 cases of AGE were identified between the 10 and the 15 February. The cohort study, highlighted a significant relation between tap water consumption and AGE. Drug reimbursement data confirmed an epidemic episode of AGE only in this city. Different enteric viruses were isolated from cases' stool samples, but no fecal coliforms neither viruses were found in the tap water. No dysfunction was reported in the municipal water supply network. A wastewater treatment plant located on the district, was checked, but no dysfunction was found.

Conclusion

Investigations strongly validated the hypothesis of a waterborne outbreak: complains about tap water; AGE cases living in the same district, more likely tap water drinkers, with different virus detected in their stools. The municipality will implement a reactive complaint register. to take care quickly of the complaints of the inhabitants for AGE or tap water bad quality.

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

ABSTRACT ID: 75

PRESENTED BY: Martine Charron (martine.charron@ars.sante.fr)

C 18.2 Water cooler talk: Use of qualitative data in the investigation of a large norovirus outbreak

Lara Utsi (1), H. McAuslane (2)

1. Field Epidemiology Service, Public Health England, Leeds, United Kingdom
2. Yorkshire and the Humber Health Protection Team, Public Health England, Leeds, United Kingdom

Background

In July 2015, the local Health Protection Team was notified of 180 call centre employees with diarrhoea and vomiting. We investigated to describe the extent of this large outbreak, assess possible sources and implement control measures.

Methods

We defined cases as individuals working between 17 and 22 July who developed symptoms of diarrhoea and/or vomiting. An online questionnaire, which included open questions due to limited prior information, was e-mailed to all employees working on the premises over this time period. We compared exposure information from cases with non-symptomatic persons by calculating relative risks (RR) and 95% confidence intervals (CI). Open text responses were coded into thematic groupings. Cases were asked to submit faecal samples for microbiological testing.

Results

898 individuals completed the questionnaire, of which 220 were cases. 60.9% of cases reported both vomiting and diarrhoea. Workers on the first floor (88.6% of cases) were 3.4 times (95% CI: 2.3-4.9) more likely to report illness than those working elsewhere. Drinking from the first floor water cooler (73.2% of cases) was independently associated with illness (RR=2.6, 95% CI: 2.1-3.5). Respondents provided 459 statements describing inadequate cleaning, poor hand hygiene and mixing of clean and dirty cups at the water cooler. We implemented control measures including improved cleaning, hand-hygiene training and demarcation of clean cups at the water cooler. PCR confirmed norovirus in 3 out of 6 faecal specimens.

Conclusion

Qualitative data supported epidemiological evidence in suggesting that this large outbreak arose through contamination at a water cooler and first floor workspaces, identifying key issues for intervention. The use of qualitative data and thematic analysis can supplement classical epidemiological investigations, informing public health action where limited exposure information is available.

Keywords: Infectious Disease Outbreak, Cohort Study, Questionnaire Design, Gastroenteritis, Norovirus

ABSTRACT ID: 97

PRESENTED BY: Lara Utsi (lara.utsi@phe.gov.uk)

C 18.3 A norovirus outbreak with person-to-person transmission at an international sports tournament, Slovenia, July 2015

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2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden

Background

The Slovenian National Institute of Public Health (NIJZ) advises inclusion of public health authorities (PHA) in event planning to timely detect and contain outbreaks. On 4 July 2015, a paediatrician notified NIJZ of eight hospitalised children with acute gastroenteritis, related to a youth handball tournament (1-6 July 2015; 70 teams; 18 countries; 2000 participants; 4 courts).

Methods

We defined cases as participants with onset of vomiting, diarrhoea, nausea or stomach cramps between 1-8 July. We conducted a cohort study among participants restricting analysis to cases with symptoms onset 48 hours after the first reported case to exclude secondary transmission. Exposures were considered associated with illness if they explained at least 50% of cases and the association was statistically significant ($p<0.05$). Stool specimens were tested for bacteria, parasites, and viruses.

Results

All teams responded, 39 (56%) reported individual level data (n=1223) with 157 (13%) cases. The outbreak started on 2 July, peaked on 3 July (60 cases) and last case occurred on 8 July. Teams playing first-day matches at court X had 5.3 (95%CI: 1.3-21.3) times the risk to report ill participants. Most participants stayed in dormitories with shared bathrooms; no dormitory or caterer was associated with illness. Teams shared water bottles. Cases' samples tested positive for Norovirus GI (3/3) and Campylobacter jejuni (1/3); an asymptomatic kitchen staff tested positive for Rotavirus (1/12). PHA were not included in event planning, delaying access to the organizer and other stakeholders by 6 hours.

Conclusion

No common source was identified; results suggest initial norovirus introduction at court X with subsequent person-to-person transmission. Mandatory PHA involvement in planning mass gatherings in Slovenia would improve rapid detection and timely implementation of control measures.

Keywords: Norovirus, Gastroenteritis, Disease Outbreaks, Sports, Policy

ABSTRACT ID: 363

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

C 18.4 Genotyping of Bacillus anthracis strains in Azerbaijan by single nucleotide polymorphisms (SNP)

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2. National Center for Disease Control and Public Health of GeorgiaTbilisi, Georgia
3. South Caucasus Field Epidemiology Laboratory Training Program Tbilisi, Georgia

Background

Anthrax is endemic for the Republic of Azerbaijan and occurs among animals and humans. The majority of human cases are recorded at the Apsheron Peninsula, including the capity Baku and the bordering regions (Gakh and Shamkir). Currently very little is known about the genetic diversity of Bacillus anthracis in Azerbaijan; therefore we phylogenetically characterized 12 Bacillus anthracis isolates to place them into a global phylogeographic context.

Methods

Fifteen cultures of Bacillus anthracis have been studied from the collection of the Museum of the Republican Anti-Plague Station, collected from humans during the past 15 years. Final confirmation was performed by PCR. DNAs extracted from obtained Bacillus anthracis cultures were screened across canonical Single Nucleotide Polymorphisms (SNPs) to provide further genetic differentiation at the Central Reference Laboratory of the Richard Lugar Centre (NCDC, Tbilisi, Georgia). Georgian reference strains were taken as controls and Azerbaijan lineages were compared to Georgian.

Results

Twelve of 15 (80%) cultures were tested. From this analysis we discovered two populations of Bacillus anthracis that belong to different genetic groups defined by canonical SNPs (A. Branch 008/009 (Transeurasia) and A. Branch 013/015 groups (Australian 94)) across the country. Nine isolates belonged to the A. Branch 008/009 clade and three isolates belonged to the A. Branch 013/015 clade.

Conclusion

Application of SNP-analysis to determine genotype of Bacillus anthracis strains, lineage and origin of circulating and re-emerging strains in Azerbaijan is important for detection and timely response. The phylogenetic lineage highlights migratory routes. Future Anthrax outbreak investigations should use this data within the unified concept of One Health in Azerbaijan.

Keywords: Azerbaijan, B. anthracis, genotyping, SNP.

ABSTRACT ID: 270

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C 18.5 Surveillance systems for hepatitis E vary across EU/EEA countries, as of 2015

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Background

Hepatitis E virus (HEV) is one of the most common causes of acute hepatitis world-wide. HEV is currently not under EU-wide surveillance and populations under surveillance, case definitions and reporting systems, are nationally defined. The aim of this study was to document surveillance systems and reporting practices for HEV across EU/EEA.

Methods

A standardised questionnaire was developed and sent to all EU/EEA countries. Questions were related to surveillance systems, case definitions and reporting details. Data were extracted and summarised.

Results

A total of 29 (94%) out of 31 countries responded to the survey. Twenty (69%) reported HEV-specific surveillance systems, a further five (17%) have HEV embedded in general viral hepatitis surveillance systems, four reported no related monitoring. There was variation in case definitions reported to be used with three countries having additional case definitions for chronic cases. Of the 20 countries with HEV-specific surveillance, nine (45%) used a case classification to distinguish between possible, probable, and confirmed cases. Five (25%) countries relied on transfer of data from laboratories, three (15%) relied on clinician-reporting, nine (45%) used both laboratory and clinician reporting, and three (15%) countries did not provide this information. The majority (80%) of reporting was case-based, with two (10%) countries receiving aggregate data, and one country receiving both case-based and aggregate data. In most countries (55%), real-time or daily data-reporting was available. More than 70% of the surveillance systems collected a unique patient identifier, the date of HEV notification, and the patient's sex and date of birth.

Conclusion

Data on hepatitis E infections are regularly collected in most of the EU/EEA countries with a variability in the applied case definitions and data collection schemes that hinder comparability.

Keywords: Hepatitis E virus, Europe, surveillance systems, data collection

ABSTRACT ID: 52

PRESENTED BY: Cornelia Adlhoch (cornelia.adlhoch@ecdc.europa.eu)

Track 19: Novel methods in epidemiology (3)

Moderator: Isabel Oliver, Public Health England

C 19.1 The International Health Regulations (2005) in Malawi: Assessment of the status of implementation in 2015

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Background

Malawi, as party to the International Health Regulations (IHR) 2005, is required to develop, strengthen and maintain the capacities to detect, assess, notify and report public health events. In 2015, with support from the Norwegian Institute of Public Health, we conducted a joint assessment of these capacities to determine the status of implementation and establish a baseline for measuring progress towards full IHR implementation.

Methods

From March to August 2015, we conducted a mixed-methods cross-sectional assessment using the adapted WHO IHR assessment protocol. We conducted seventy-five semi-structured interviews with a purposive sample of informants from central, district, health facilities and laboratories. A national tabletop exercise was held to identify areas for improvement in preparedness and response to a fictional emerging zoonotic event. We convened two multi-sectoral stakeholder meetings to discuss the current capacity to implement IHR and identify actions for improvement.

Results

There are structures, guidelines and protocols in existence in Malawi that provide a good foundation for fulfilling the IHR requirements, although many are not fully implemented or operational. The IHR requirements are not integrated into national legislation and the IHR National Focal Point functions must be strengthened. Multi-sectoral collaboration and the adoption of an all-hazards approach to event preparedness and response are not formalized. Improving training opportunities, increasing laboratory capacity and reinforcing the Integrated Disease Surveillance and Response strategy will be necessary to improve surveillance, preparedness and response capacity.

Conclusion

The assessment demonstrated that Malawi does not yet have the core capacities to fulfill the IHR requirements. A prioritized action plan has been developed to address gaps. Multi-sectoral collaboration and support from partners is essential for strengthening existing structures and fostering support for implementing the IHR.

Keywords: Surveillance; Outbreaks; Global health; Public health; Africa

ABSTRACT ID: 283

PRESENTED BY: Ambonishe Mwalwimba (ambonishe@yahoo.com)

C 19.2 Integrating additional information on asylum seekers into the German routine surveillance system for infectious diseases, Sep-Dec 2015

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Background

In 2015 more than 450.000 persons were seeking asylum in Germany. To assess the epidemiological situation of infectious diseases among asylum seekers (AS), since week 40/2015 additional information on country of birth, date of entry and mass accommodation is collected for notified infections among AS. We evaluated the implementation of the additional information into the routine surveillance system.

Methods

We extracted all cases of infectious diseases transmitted to Robert Koch Institute between week 40-53/2015. We evaluated the simplicity and flexibility of the system and data completeness. Data was defined as incomplete if information could not be investigated by local health authorities (LHA). We compared data completeness using chi-square test.

Results

Among 98,620 cases of infectious diseases we identified 4,873 (4.9%) asylum seekers. Data transmission was implemented in all 16 federal states within 3 weeks either by integrating the new variables into the software (SW 52%), using standardized free text (FT 42%), other means (6%). Completeness for country of birth was 68% (SW 84%; FT 57%; $p<0.001$), date of entry 24% (each method) and mass accommodation 89% (SW 93%; FT 88%; $p<0.001$). Comparing data completeness between non-asylum seekers (NAS) and AS, it was not different for the variables sex (each 99%) and hospitalization (NAS 76%; AS 75%). Complete information on onset date (NAS 77%; AS 45%; $p<0.001$) and country of exposure (NAS 54%; AS 42%; $p<0.001$) were more likely to be complete for NAS.

Conclusion

Rather than establishing a new surveillance for AS the German surveillance system could simply and flexibly be adapted with satisfactory data completeness. Data completeness could be improved by avoiding free text; however investigations by LHA might be difficult due to language barriers.

Keywords: Population surveillance, refugees, evaluation, Germany

ABSTRACT ID: 373

PRESENTED BY: Michaela Diercke (dierckem@rki.de)

C 19.3 Studybugs: A novel system for studying infectious disease in children

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Background

Community-based surveillance and public health research are often resource-intensive and challenging to reach high coverage; surveillance in the community often relies on a self-selected sample. We created a novel system for community-based surveillance and research in school-aged children in the United Kingdom (UK) to overcome these constraints.

Methods

We built a free online attendance system for schools, "Studybugs", which provides parents with an app to report their child's absence from school due to illness. Symptom and disease information is prompted for and free text is coded into anonymised data, which are made freely available in real time. A messaging function within the app can elicit more information. We piloted the system between January 2015 and March 2016 in selected parts of Sussex, UK.

Results

During the pilot, 24 schools used Studybugs, ranging in size from 40 to 2,200 pupils of ages 3 to 19. Uptake at each school averaged 70% of families and around 5% of the pilot area population was registered with Studybugs. 25,000 reports were collected on 73 symptoms and diseases, showing trends over time and space. Studybugs is now being used for a public health research project on childhood asthma, with targeted interventions delivered via the app.

Conclusion

The pilot shows Studybugs can provide community-based data on burden of disease with high coverage and representativity. A wider rollout of Studybugs across the UK and beyond would enhance existing infectious disease surveillance, including use for outbreak detection, and provide a powerful platform for epidemiological research focussing on school-aged children.

Keywords: Public Health Surveillance, research, child, online systems

ABSTRACT ID: 306

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C 19.4 Evaluation of an Adverse Event Following Immunization reporting system for a meningococcal vaccination campaign in Nigeria: 2015

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Background

An Adverse Event Following Immunization (AEFI) is an untoward medical incident that occurs after an immunization and is believed to be caused by the vaccination. The introduction of new vaccines in the national immunization program in Nigeria highlights the need for an efficient and effective surveillance system for AEFIs. We evaluated this system to assess its key attributes and determine its effectiveness in detecting AEFI cases.

Methods

We conducted key informant interviews with stakeholders at the National Primary Health Care Development Agency to obtain information on the operations of the system. We analyzed AEFI data for the meningococcal A conjugate vaccination campaign held in 2014 from four states. We evaluated the key attributes using the National Field Guide for AEFI Surveillance. Mild and serious AEFIs were defined as medical incidents posing no potential risks and posing potential risks to the health of vaccine recipients respectively.

Results

Key stakeholders described the system as useful. It was however reported that AEFI surveillance trainings were not cascaded from national and state level stakeholders to health facility workers. Stakeholders indicated that training and supervision will improve reporting and investigation of AEFIs. A total of 1,274 AEFIs were reported from the four states. The system detected 1,111 (87%) mild, 66 (5%) serious AEFIs while 97 (8%) cases were unclassified. Children aged 15 years and below accounted for 702(57%) cases. Cross River State reported 483(37.9%) cases, Oyo and Kogi States each reported 376(29.5%) cases while Imo State reported 39(3.1%) cases. Timeliness of reporting and investigating serious AEFI cases were 83% and 62% respectively.

Conclusion

Regular training and supervision of all surveillance staff will ensure timely reporting and investigation of AEFIs.

Keywords: Adverse events following immunization, surveillance system, evaluation, Nigeria

ABSTRACT ID: 88

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C 19.5 Late breaker: An international Salmonella Braenderup outbreak investigation using whole genome sequencing, March - June 2016

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Background

Salmonella Braenderup is the 8th most common nontyphoidal Salmonella infection in England and Wales. Salmonella isolates submitted to the PHE Gastrointestinal Bacterial Reference Unit (GBRU) are routinely whole genome sequenced (WGS). A novel cluster of genetically closely related S. Braenderup cases reported from different geographical locations within Great Britain (GB) was identified by GBRU, in March 2016. By April, European countries including Netherlands, Switzerland and Denmark also reported increases.

Methods

A total of 51 isolates; England (45), Wales (2), Scotland (1), Jersey (1) and Switzerland (2) were WGS and subjected to Single Nucleotide Polymorphism (SNP) analysis to confirm genetic relatedness. To generate a hypothesis for a potential food vehicle of infection, twenty trawling questionnaires were administered to randomly selected GB cases to identify common exposures which were investigated further using a targeted questionnaire on specific food items and shopping locations. Other European cases were not further investigated to generate hypothesis.

Results

Descriptive analysis of GB cases revealed 27 female (59%) and 19 male (41%) with an age range <1 to 97 years old. No particular food item was identified from further investigating common exposures. A phylogenetic tree indicated that all 51 cases were part of a discrete genetic cluster at the 5-SNP level, with most isolates identical at the core genome level, with over 50 SNPs from the nearest S. Braenderup cluster.

Conclusion

Analysis of WGS data allowed rapid confirmation of an international outbreak of S. Braenderup, however this outbreak could not be further investigated due to lack of hypothesis and resources. Although WGS is a great tool for detection of outbreaks and defining cluster cases, epidemiological data is also required to identify the source of an outbreak.

Keywords: Salmonella Braenderup, Whole Genome Sequencing (WGS), Single Nucleotide Polymorphism (SNP)

ABSTRACT ID: 742

PRESENTED BY: Baharak Afshar (Baharak.Afshar@phe.gov.uk)

C 19.6 Cancelled

Track 20: Burden of disease (2)

Moderator: Alessandro Cassini, ECDC, Expert Antimicrobial Resistance and Healthcare-associated Infections

C 20.1 Down but more deprived – differing social gradients in the burden of measles between outbreak and non-outbreak periods in London and South-East England, 2010-15

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Background

Measles incidence fell sharply in England from 3.8 in 2012 to 0.17 per 100,000 in 2015. Evidence about health inequalities in measles disease is equivocal and limited. We aimed to quantify inequalities in measles risk in London and South-East England and determine whether the relationship between area deprivation and measles risk changes between outbreak and non-outbreak periods.

Methods

We used geographies designed for small area statistics (mean population 1,620) as the unit of analysis (n=10,064). Within each area we calculated odds of measles (outcome) for quintiles of the composite area-level English index of multiple deprivation (IMD, main exposure). We used mixed effects ordinal logistic regression to adjust for age, population, ethnicity, rurality and MMR vaccine coverage. We defined outbreak (2010-12) and non-outbreak (2013-15) periods, comparing them via an interaction with IMD. We calculated odds ratios (OR) relative to the least deprived IMD quintile in each period. Finally, we used biologically plausible IMD components (distance to general practice, adult English skills and overcrowding) as main exposures to assess their contribution to the overall effect.

Results

Crude odds of measles increased linearly with deprivation. After adjustment, no association remained in the outbreak period but in the non-outbreak period odds of measles were seven times higher in the most deprived than least deprived IMD quintile (aOR 7.3; 95% CI: 4.2-13). Only one component, overcrowding, produced a similar effect (non-outbreak: aOR 8.8; 95% CI: 3.2-24).

Conclusion

A social gradient in measles risk was only observed during the non-outbreak period with measles cases concentrated in more deprived neighbourhoods. Overcrowding accounts for much of the association with the composite IMD. This contributes new evidence about health inequalities with relevance for measles prevention and control.

Keywords: Socioeconomic Factors, Measles, Healthcare Inequalities, London, Measles-Mumps-Rubella Vaccine, Logistic Models

ABSTRACT ID: 92

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C 20.2 Salmonella Napoli infection in Italy, 2011-2015: a current and specific Italian public health concern.

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Background

Human infections by Salmonella serovar Napoli are uncommon in Europe. Since 2000 S.Napoli was reported as 5th serovar from human infections in Italy. We analysed 2011-2015 surveillance data and compared genetic similarities among human/environmental/animal/food isolates to identify possible common source.

Methods

We collected data from the national voluntary laboratory-based surveillance system for human/environmental isolates, and from the veterinary surveillance system for animal/food isolates. Factors associated with human S.Napoli infection were evaluated by multiple logistic regression model (S.Napoli isolates versus other serovars).

We characterised S.Napoli isolates (120 human, 47 environmental, 11 animal and 4 food strains) by Pulsed-Field Gel Electrophoresis (PFGE), and analysed genetic relatedness (BioNumerics 7.5).

Results

S.Napoli was the fourth serovar (4.7%) among 21,132 human isolates. We observed seasonality from June to October (81% of all human isolates, OR 5.7, 95%CI 4.7-7.0). Cases (median age 6.0 years, range 0-96 years, 8.9% younger than 1 year old, 57% male) more likely occurred in North (OR 1.9, 95%CI 1.6-2.4) and South (OR 2.1, CI 1.2-3.5) than in Central Italy.

S.Napoli was the seventh serotype (3.8%) among 1,920 environmental isolates (82% surface water), while it was 1.0% among 9,533 animal/food isolates.

Despite high genetic variability among strains, we observed clustering (80% similarity) by PFGE patterns in the three main geographical areas.

Conclusion

Most reported S.Napoli cases were from human and environmental samples, and transmission to human less likely occurs by food of animal origin. The high genetic strain variability of isolates did not allow the identification of source(s) of transmission. We recommend national surveillance systems improvement to increase reporting of cases and molecular characterisation of isolates. We suggest a prospective case-control study indicating specific risk factors allowing targeted microbiological investigations.

Keywords: Salmonella Infections/epidemiology, Salmonella Infections/microbiology, Humans, Animals, Environment, S. Napoli.

ABSTRACT ID: 136

PRESENTED BY: Michela Sabbatucci (michela.sabbatucci@iss.it)

C 20.3 Cryptosporidium infections in Sweden in 2014 – understanding the regional differences in reported incidence

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Background

Cryptosporidium surveillance has revealed substantial differences in disease incidence in different regions in Sweden. While microscopy with modified Ziehl-Neelsen staining (mZN) is the gold standard diagnosing Cryptosporidium, PCR-based methods are also increasingly used. We aimed to evaluate how Cryptosporidium diagnostics is currently performed in Sweden, and combined this with county-specific reported Cryptosporidium data in order to identify reasons for the observed differences in its incidence.

Methods

An on-line questionnaire regarding the screening strategies and laboratory methods was submitted to all 26 clinical microbiology laboratories in Sweden. These results were compared to the data on Cryptosporidium infections reported in 2014 to the SmiNet2 database at the Public Health Agency of Sweden.

Results

A total of 404 Cryptosporidium infections were diagnosed in Sweden in 2014. The highest incidence of Cryptosporidium was noted in Halland, Jönköping and Uppsala counties (34.44, 21.20 and 14.90 per 100.000 inhabitance, respectively), whereas the incidence varied between 0 and 3.94 in the remaining 18 counties. A total of 20 laboratories in 15 counties performed Cryptosporidium testing in 2014; 18 laboratories used mZN staining and five PCR. Laboratories in Halland, Jönköping and Uppsala counties screened the biggest number of stool samples (approximately 5000 samples each; two with multiplex PCR and one with microscopy), whereas 23 laboratories in the remaining 18 counties either performed a small number of mZN stainings annually (range: 20 – 1200 samples; data missing for 3 laboratories) or referred samples elsewhere for Cryptosporidium testing (n=6).

Conclusion

Cryptosporidium infection is significantly underdiagnosed in Sweden, especially where a selective testing criteria is used or when samples are referred elsewhere for testing. Further guidance for Cryptosporidium screening is required to improve surveillance in Sweden.

Keywords: cryptosporidium, Incidence, surveillance, screening, diagnosis

ABSTRACT ID: 252

PRESENTED BY: Heli Harvala (heli.simmonds@hotmail.com)

C 20.4 Hepatitis E virus seroprevalence among the general population in a livestock-dense area in the Netherlands

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Background

Recent serological studies indicate that hepatitis E virus (HEV) is endemic in industrialized countries. Although the exact source and route of infection is unknown, zoonotic transmission from pigs to humans through food or the environment has been suggested. This is supported by the high prevalence of HEV among domestic pigs and wild boars and frequent detection of HEV in pork products.

Methods

We performed a cross-sectional population-based serological survey among 2,494 non-farming adults from the general population in a livestock-dense area in the south of the Netherlands. Participants completed risk factor questionnaires and blood samples of 2,422 subjects (median age 58 years, range 20-72) were tested for anti-HEV IgG using an enzyme immune assay (Wantai). The aim of this study is to determine the HEV seroprevalence and to assess whether seropositivity in adults was associated with living in the vicinity of pig farms.

Results

The average seroprevalence of HEV was 28.7% (95%CI: 26.9-30.5). Determinants associated with an increased risk for HEV seropositivity were age, male gender and low level of education. A high number of pigs within 1,000 meters of the residential address was not a risk factor for seropositivity. Seronegative participants lived closer to pig farms than seropositive participants.

Conclusion

This study confirmed the high HEV seroprevalence in the general population of the Netherlands, but presence of antibodies was not associated with residential proximity to pig farms. Our findings support the assumption of a cumulative lifetime exposure to HEV in the Netherlands and cannot refute the notion that transmission is primarily food-borne.

Keywords: Hepatitis E virus, environmental exposure, livestock, seroprevalence, zoonoses

ABSTRACT ID: 175

PRESENTED BY: Rianne van Gageldonk-Lafeber (rianne.van.gageldonk@RIVM.nl)

C 20.5 Retrospective analysis and economic burden of national hospitalizations for herpes zoster in Italy, 2001-2012

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Background

Herpes zoster (HZ) is a painful infectious disease caused by the reactivation of varicella-zoster virus. It mainly affects the elderly, and frequent complications include post-herpetic-neuralgia (PHN) and ophthalmic complications (OC). Considering the upcoming introduction of HZ vaccination programme nationwide, we assessed the burden of hospitalization for HZ, its complications and direct costs related to hospitalized cases in Italy.

Methods

We conducted a retrospective study on 2001-2012 data from the National Italian Hospital Discharge Registry, where HZ is identified by ICD9-CM codes 053.xx as main or secondary diagnosis. We described number of cases and mean length of hospital stay (mLoS), comorbidities, and hospitalization rates for HZ /100,000 Italian residents by year. We estimated total cost and average cost per admission.

Results

A total of 44,948 discharges reported HZ as main diagnosis (54% female, 82% ≥50 years old, 7.8 days mLoS); 43,613 reported HZ as secondary diagnosis (55.6% female, 85.7% ≥50 years old, 13.5 days mLoS). Annual rates decreased from 9.6 in 2001 to 3.9/100,000 in 2012 for HZ as main diagnosis, and from 1.4 and 1.6 in 2001 to 0.8/100.000 and 0.6/100.000 in 2012 for PHN and ophthalmic complications, respectively. The proportion of immunocompromised patients increased from 8.9% to 11.2%. For the period, the total cost was about 121M€; the average cost per case with HZ as main diagnosis decreased from 2,886€ to 2,551€. HZ as secondary diagnosis was associated with higher average cost (3,918€ in 2012).

Conclusion

Data on HZ epidemiology and cost in Italy are still limited. Despite the decreasing case numbers, our study confirmed a considerable disease and economic burden of HZ in elderly and immunocompromised patients, supporting the introduction of vaccination programmes for these categories.

Keywords: Herpes zoster, Post-herpetic neuralgia, Direct cost, Hospitalization, Herpes zoster vaccination

ABSTRACT ID: 132

PRESENTED BY: Iulia Adelina Turiac (adelinaiulia@yahoo.co.uk)

C 20.6 Evaluation of the German surveillance system for hepatitis B regarding timeliness and completeness

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Background

In Germany, cases of acute, laboratory-confirmed hepatitis B are mandatorily notified to the local health authority (LHA) from where they are forwarded to the state agency and the Robert Koch Institute (RKI). An amendment to the law in March 2013 aimed at decreasing time for notification. We evaluated hepatitis B surveillance from 2005-2014 regarding completeness and timeliness to detect weak spots and suggest improvements.

Methods

We included all cases of acute hepatitis B notified to RKI 2005-2014. Timeliness was defined as the delay between date of notification to LHA and date of transmission to RKI. We defined completeness as the proportion of notifications with information regarding selected surveillance variables. Timeliness and completeness were calculated and compared by year of notification using x^2 – and Wilcoxon rank-sum test. As only laboratory-confirmed cases with HBV-specific clinical symptoms fulfill the reference case definition (RCD) by RKI and are reported in national statistics, we furthermore calculated the proportion of RCD-cases on all hepatitis-B-notifications.

Results

From 2005-2014, a total of 20,580 acute hepatitis-B-cases were notified to RKI. Median reporting delay from 2005-2014 was 10.4 days (95%CI 6.3-19.6 days), improving from 2010-2014 (10.7 vs. 2.4 days, $p<0.001$). Concurrently, completeness of information regarding any clinical symptoms, previous vaccinations and probable routes of transmission decreased from 2010-2014 (99.8% vs. 81.7%, $p<0.001$; 76.6% vs. 60.1%, $p<0.001$; and 26.7% vs. 18.7%, $p<0.001$, respectively). The proportion of RCD-cases was 42.3% from 2005-2014, decreasing continuously from 50.1% in 2005 to 31.7% in 2014.

Conclusion

Improved timeliness for hepatitis-B-notifications was accompanied by a decrease in completeness of information and the proportion of RCD-cases. We recommend to identify and to eliminate reasons for low completeness in order to improve quality of hepatitis-B-surveillance data.

Keywords: hepatitis B, surveillance, evaluation, timeliness, completeness

ABSTRACT ID: 123

PRESENTED BY: Lena Boes (BoesL@rki.de)

Track 21: Vaccine preventable diseases (3)

Moderator: Robert Whittaker, ECDC, Scientific Officer Vaccine-Preventable Diseases

C 21.1 Assessment of different serological assays for anti-HBs testing; results from a quality assessment program in 2013

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Background

Post-vaccination testing after hepatitis B vaccination is indispensable to evaluate long-term immunological protection and necessary for correct clinical management of specific risk groups. Using a threshold level of antibodies against hepatitis B surface antigen (anti-HBs) to define serological protection, implies reproducible and valid measurements of different diagnostic assays. In this study we assess the performance of different currently used anti-HBs assays.

Methods

In 2013, 42 laboratories participated in an external quality assessment program with a set of six pooled anti-HBs serum samples which represented anti-HBs results around the cutoff values 10 IU/l and 100 IU/l. Laboratories used either Axsym (Abbott Laboratories), Architect (Abbott Laboratories), Access (Beckman-Coulter), ADVIA Centaur anti-HBs2 (Siemens Healthcare Diagnostics), Elecsys, Modular or Cobas (Roche Diagnostics) or Vidas Total Quick (Biomerieux) for anti-HBs titre quantification. We analysed covariance using mixed-model repeated measures. For the assessment of sensitivity/specificity and agreement a true positive or true negative result was defined as an anti-HBs titre respectively above or below the cutoff value by ≥ 4 of 6 assays.

Results

Different anti-HBs assays were associated with statistically significant ($P < 0.05$) differences in anti-HBs titres in all dilutions. Sensitivity and specificity ranged respectively from 64% – 100% and 95% – 100%. Agreement between different assays around an anti-HBs titre cutoff value 10 IU/l ranged from 93%-100% and was 44% for a cutoff value of 100 IU/l.

Conclusion

Around cutoff value 10 IU/l use of the Access assay may result in false-negative results. Concerning the cutoff value of 100 IU/l, a sample being classified below or above this cutoff relied heavily on the specific assay used, with both the Architect and the Access resulting in false-negative results.

Keywords: Hepatitis B, Serology, Prevention & Control, Analysis

ABSTRACT ID: 228

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C 21.2 Description of Hepatitis A outbreaks and subsequent public health actions in England, 2011-2015

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Background

In developed countries, the most common mode of Hepatitis A virus (HAV) transmission is from person to person. We described HAV outbreaks that occurred in England from April 2011 to April 2015 and the public health actions taken in response to inform the revision of public health guidance on HAV management.

Methods

We defined an outbreak as any situation i) with >1 HAV laboratory-confirmed epidemiologically linked cases with at least one case occurring outside the household of the primary case or ii) any school child not linked to an identified HAV case for whom we assumed transmission in school. The local health protection teams completed a questionnaire describing these outbreaks in terms of place, time, person, HAV genotype and public health actions taken.

Results

We collected information on 19 HAV outbreaks. Median age of primary and secondary cases was 9.5 years (range: 2-52, n=16), and 9.5 (range: 0-58, n=39), respectively. Thirteen (68%) outbreaks occurred in an educational setting (school/nursery), four in households, one in a care home and one during a choir trip. Genotype was obtained in 10 outbreaks: three were genotype 1A, seven genotype 1B. Oral fluid test (OFT) to identify asymptomatic cases was used in 3/19 outbreaks. Vaccination beyond household contacts was done in 16 outbreaks (14 schools/nurseries, one care home, and one choir trip contacts), the definition of a contact varied according to the setting.

Conclusion

Children and school/nursery settings play an important role in the spread of HAV in England. In view of the potential unknown transmission of virus from asymptomatic cases in children, OFT should be used to determine the real extent of HAV community outbreaks and provide evidence for extended vaccination.

Keywords: Hepatitis A, outbreak, vaccination, oral fluid test

ABSTRACT ID: 53

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

C 21.3 Measles virus infection by the vaccine strain in Athens, 2015: the importance of genotyping

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Background

Infections from the measles vaccine strain have been reported worldwide. We report a case of infection by the measles vaccine strain in a two year old boy who was admitted to hospital with fever, cough, conjunctivitis and maculopapular rash and was treated to the ICU with Respiratory Distress Syndrome until his full recovery after 30 days. The boy was vaccinated ten days before the onset of symptoms with the live, attenuated vaccine against measles, rubella, mumps and varicella zoster virus Priorix – Tetra®.

Methods

Serum, whole blood and bronchial secretions samples were collected from the patient. The serum was tested for the presence of IgM antibodies using the Enzygnost ® Anti-Measles IgM kit. The bronchial secretions and the whole blood were tested for detection of varicella zoster virus, Epstein-Barr virus, cytomegalovirus and measles virus with Real-time PCR. Nested PCR and sequencing for measles genotyping were applied in the bronchial secretions sample.

Results

The serum was found positive for the detection of IgM antibodies against measles virus. The whole blood was negative for all the viruses tested, whereas the bronchial secretions sample was positive for the detection of measles virus and negative for the rest. The virus genotype was determined as vaccine strain, genotype A, MVs/HongKong.CHN/51.15 [A-Vaccine].

Conclusion

The measles vaccine-associated infection is rare and indistinguishable from the wild-type. Genotyping is a useful tool in the identification of the virus and, thus, the exclusion of a wild type infection. This is important for public health, as during measles outbreaks the vaccine is provided in order to control the spread of the infection, a vaccine reaction may be falsely classified as a wild-type case.

Keywords: measles, vaccine strain, genotyping, Greece

ABSTRACT ID: 110

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C 21.4 Genotype distribution of noroviruses associated with sporadic gastroenteritis in Europe

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Background

Noroviruses are a leading cause of acute gastroenteritis worldwide. Molecular diagnostic techniques have improved detection and reporting of norovirus outbreaks; however, there is limited information on the strain epidemiology of norovirus associated with sporadic gastroenteritis and its evolution over the past decades.

Methods

We conducted a systematic literature review of all publications indexed in PubMed in all languages up to January 2016 describing genotypic distribution of noroviruses associated with sporadic gastroenteritis in Europe. The relative frequencies of polymerase and capsid genotypes were calculated independently by setting, country and age-group.

Results

Genotypic data was obtained for 4873 norovirus strains selected for genotyping from 34 studies in 13 European countries, conducted between 1993 and 2013. Only 2.5% strains (122) were tested among adults. The most predominant genotypes were capsid-based GII.4 (44.4%) and GII.3 (15.9%) and polymerase-based GII.P4 (56.6%) and GII.P21 (10%). During the periods 1993-2000, 2000-2006, 2006-2011 & 2011-2013, capsid genotype GII.4 has constantly predominated (relative frequencies: 48.1%; 37.5%; 43.7%; 66.6%) whereas GII.3 has decreased (25.6%; 29.2%; 13.3%; 10%). Likewise, polymerase GII.P4 increased (41.5%; 48%; 70%; 74%) while polymerase GII.P21 distribution fluctuated (1.4%; 21.8%; 12%; 0%).

Conclusion

Capsid genotypes GII.4 and polymerase genotype GII.P4 predominate in sporadic cases tested mostly among children, whereas capsid genotype GII.3 appears to be decreasing. These results are comparable to genotype distribution data derived from outbreak reporting. The recent emergence of a novel GII.17 strain in Asia emphasizes the importance of continued monitoring of circulating norovirus strains.

Keywords: Diarrhea; Gastroenteritis, Genotype; Molecular epidemiology; Norovirus

ABSTRACT ID: 193

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C 21.5 A survey of European National Reference Laboratory capacity for pertussis PCR and serology diagnostics, 2015

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Background

The European Pertussis Laboratory Network (EUpert-Labnet) is a consortium of laboratory and epidemiological experts set up to perform a range of pertussis activities for laboratory surveillance of whooping cough in EU/EEA countries, including a survey to map laboratory capacity.

Methods

A questionnaire was sent to the ECDC Operational Contact Points for Pertussis Epidemiology and Microbiology in 29 EU/EEA countries. The questionnaire contained questions on laboratory practices for all countries and more detailed questions for the countries with a pertussis national reference laboratory (NRL).

Results

Completed questionnaires were received from 26 (89%) of 29 countries. Twenty-one countries had a designated pertussis NRL. Countries reported a wide range of PCR and serology methods for laboratory confirmation of pertussis infection. For Bordetella PCR, 19/21 centres used the recommended IS481 as the Bordetella pertussis target, either alone (n=3), or with at least one other target, including the single copy target pertussis toxin promoter (ptxP) (n=15). For serological confirmation using ELISA, 19/21 laboratories used the recommended purified pertussis toxin (PT) as the coating antigen and 16 used WHO or FDA reference sera for the standardisation of results. For reporting of serologically confirmed pertussis, there was variation in the cut-off values used to define recent infection.

Conclusion

The number of laboratories following the recommended ECDC guidelines for pertussis serology has increased from 13/20 (65%) in 2010 to 19/21 (90%) in 2015. The number of laboratories following the recommended ECDC guidelines for PCR has increased from 9/18 (50%) in 2010 to 19/21 (90%) in 2015. Continuing harmonisation at the European level is essential to ensure collection of comparable data on pertussis in Europe.

Keywords: whooping cough,Bordetella pertussis,Polymerase Chain Reaction,serology,Surveys and Questionnaires

ABSTRACT ID: 220

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C 21.6 The compliance rate to the National Immunization Program Schedule in Romania – defining causes and means of improvement

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Background

Low immunization levels in Romania present a threat for an increase in the incidence and prevalence of the vaccine-preventable diseases. The aim of this study is to identify the causes of the negative attitudes and behaviours that lead to vaccine hesitancy between parents in our country.

Methods

We designed a cross-sectional study and applied in the general population a survey that included questions regarding the knowledge on immunisation schedule. The study included 600 participants from Romania, aged between 18 and 75 years, with a median age of 40 years. Data has been analysed using Epi Info 7.1.5.2.

Results

Out of the 600 participants included in the study, the knowledge about the components of the National Immunization Program Schedule was different for each of the vaccines included: BCG 69.83% (95%CI: 65.96%-73.45%), DTP 74.33% (95%CI: 70.60%-77.75%), hepatitis B 83.17% (95%CI: 79.88%-86.02%), poliomyelitis 82.17% (95%CI: 78.81%-85.10%), rubella 71.83% (95%CI: 68.02%-75.36%) and measles 79.17% (95%CI: 75.65%-82.30%). Regarding the benefits of vaccination, 95.33% (95%CI: 93.23%-96.82%) are aware of it and 44.17% (95%CI: 40.16%-48.25%) of the participants think that vaccines imply risks that outgrow the positive effects. Regarding the immunization coverage, 92.58% (95%CI: 89.87%-94.63%) of the participants' children were vaccinated according to the immunisation schedule. Between the alternatives that parents consider to be equivalent to vaccination, the most frequently stated were homeopathy, healthy diet, regular exercise and good personal hygiene.

Conclusion

Findings from this study represent a call for the implementation of better educational and communication strategies, in order to provide better knowledge on immunization. A significant percent of the population is still guided by wrong beliefs and perceptions on vaccines, resulting in low vaccination coverage in our country

Keywords: Immunization, Primary prevention, Patient adherence, Community surveys

ABSTRACT ID: 374

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Track 22: Emerging and vector-borne diseases (2)

Moderator: Wim Van Bortel, ECDC, Senior Expert Vector-borne Diseases

C 22.1 French armed forces health surveillance tool (OSEA): an information system for outbreak detection

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Background

The French armed forces deploy 300,000 military personnel all around the world. The broad range of location and movement of the staff increases their exposure to infectious hazards. In 2001, we implemented the weekly surveillance of 60 health events (including 45 epidemic-prone events) in 400 military medical treatment facilities (MMTF). To insure an early and sensitive detection of outbreaks, we developed OSEA, a web-based tool allowing real-time reporting and automated analyses nested in the French armed forces health service secured network.

Methods

After preliminary stages of procurement procedure, to build detailed specifications and tool functionalities, we conducted a needs assessment during regular meetings between French military epidemiologists and EpiConcept IT experts. Based on the conclusions, we developed a data model and a highly scalable analysis module in an iterative and incremental approach (AGILE method) for outbreak detection for the health events under surveillance.

Results

Based on the data collected at the MMTF level, R-based outbreak detection algorithms are run every night. The Farrington method is used when ≥3 years of historical data are available; EARS C2 method is used otherwise. Besides time-series based detection, a real-time automated analysis of cases occurrence in time and place suggest clusters. When an alarm is triggered, its validation requires further investigation by an epidemiologist.

Conclusion

At the time of Abstract submission, software developments are still ongoing. We will measure the agreement between outbreaks detected by OSEA and those detected with former system using historical data as well as prospective outbreak detection based on simulated data. OSEA should improve infectious disease outbreaks detection and management in the French armed forces.

Keywords: Health surveillance, information system, Outbreak detection

ABSTRACT ID: 212

PRESENTED BY: Gabriel Bedubourg (gabrielbedubourg@hotmail.fr)

C 22.2 Imported infectious diseases among newly arrived Eritrean refugees in Switzerland

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Background

A quarter of refugees arriving in Switzerland in 2015 originated from Eritrea. Yet, data on health status of Eritrean immigrants in Europe is scarce. We report preliminary data from screening for selected infectious diseases among asymptomatic newly arrived Eritrean refugees in Switzerland.

Methods

The study started in January 2016 with recruitment still on-going. Asymptomatic Eritrean refugees aged ≥16 years who arrived in Switzerland in 2015 are recruited via cantonal refugee registries. Screening comprises 2 stool samples for protozoa and helminths, serology for HIV, hepatitis B and C, syphilis and schistosomiasis, circulating cathodic antigen (CCA) in urine and malaria PCR in blood. We anticipate having enrolled ≥150 participants by November 2016.

Results

At submission of the Abstract 37 participants (32 male, 5 female), median age 21 years (inter-quartile range: 18-28), were enrolled. Fourteen (38%) had ≥1 pathogenic parasite in stool: (5 Schistosoma mansoni, 5 Giardia lamblia, 4 Hymenolepis nana, 3 others); 17 (46%) had positive CCA test in urine, indicating active schistosomiasis infection. Among those with schistosomiasis, 45% had level D peri-portal fibrosis according to WHO ultrasound classification. Four (11%) had positive PCR for Plasmodium vivax. All had negative serology for HIV, hepatitis B and C and syphilis.

Conclusion

More than one out of three asymptomatic Eritrean refugees had at least one pathogenic parasite detected in stool examinations, nearly half had evidence of active schistosomiasis, often with substantial pathological lesions – none was aware of it. And 1 out of 9 had a Plasmodium vivax infection.

Routine screening for stool-parasites, schistosomiasis using CCA and malaria using PCR may be considered in refugees arriving from Eritrea to prevent long term sequelae from untreated schistosomiasis or relapsing malaria episodes.

Keywords: Refugees, parasites, Screening, Infection

ABSTRACT ID: 203

PRESENTED BY: Afona Chernet (afona.chernet@unibas.ch)

C 22.3 Lyme borreliosis in Finland: Register-based insight into epidemiology, 1995-2014

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Background

The incidence and nationwide distribution of Lyme borreliosis (LB) has not been comprehensively assessed in Finland. We aimed to investigate the epidemiology of LB by analyzing three different disease registries in which LB cases are reported.

Methods

Data from the Finnish National Infectious Diseases Register (NIDR, 1995-2014) and National Hospital Discharge Register (Hilmo,1996-2014), representing disseminated LB, and the Register for Primary Health Care Visits (Avohilmo, 2011-2014), representative of erythema migrans, were reviewed. A case definition of an LB case included either a laboratory confirmation (NIDR) or a diagnosis with the ICD-10 code A69.2 (Hilmo, Avohilmo).

Results

A total of 21 051 and 10 402 LB cases were identified in NIDR and Hilmo. The NIDR-based incidence increased from 7 per 100 000 population in 1995 to 31/100 000 in 2014. In Avohilmo, 11 793 cases were identified; the incidence increased from 44/100 000 in 2011 to 61/100 000 in 2014. LB incidence increased significantly in most (72%) hospital care districts over time ($p<0.05$). Cases were predominantly females (54% in NIDR, 56% in Hilmo and 60% in Avohilmo) and a bimodal age distribution of LB cases was observed in all registries with peaks occurring in age-groups 5-9 and 60+ years. LB cases in NIDR and Hilmo were reported throughout the year with a peak in September; over 50% of cases were reported in August –November. Most LB cases in Avohilmo (75%) occurred in June –September with the peak in July.

Conclusion

The incidence of LB has considerably increased over time and the geographical distribution has expanded in Finland. Our results inform health care practitioners, public health risk and disease burden assessments as well as the public.

Keywords: Lyme borreliosos, epidemiology, surveillance, Finland, register

ABSTRACT ID: 246

PRESENTED BY: Jussi Sane (jussi.sane@thl.fi)

C 22.4 Exposure to wild birds was associated with sporadic psittacosis notifications in Sweden, 2014-2016

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Background

Professional and domestic exposures to birds are the most commonly reported sources of psittacosis. However, in 2013, an outbreak investigation in Sweden indicated an association with exposure to wild birds. We conducted a case-control study to identify current risk factors for sporadic psittacosis to inform preventive measures.

Methods

We individually matched (on sex, age and postal-code) psittacosis cases reported between December 2014 and April 2016 to controls randomly selected from the population register. Cases and controls completed a self-administered questionnaire investigating exposures to wild and domestic birds and use of protective measures. We estimated adjusted matched Odds Ratios (amOR), using conditional logistic regression.

Results

Thirty (94%) cases and 77 (50%) controls completed the questionnaire. The median age of cases was 67 years (inter-quartile-range 50-71). Of all cases, 26 (81%) were male; 29 (97%) were hospitalized; 26 (87%) reported exposure to wild birds, 10 (33%) to domestic birds/poultry and 3 (10%) reported professional exposure. Compared with controls, cases were more likely to be exposed to wild (amOR: 16 CI:1.3-198; 87% cases exposed) or domestic birds (amOR: 8.5; CI 1.5-47; 33% cases exposed). Cleaning bird-tables contaminated by wild bird faeces (amOR: 12 CI: 1.0-134; 21% cases exposed) were associated with the disease. Two (20%) cases used gloves to clean-up bird-tables. Neither cases nor controls used respiratory protections when removing wild bird faeces from surfaces.

Conclusion

Exposure to wild birds was the most common risk factor for sporadic psittacosis in Sweden with exposure to wild bird faeces by cleaning bird-tables being a likely route of transmission. We recommend using bird-tables that reduce accumulation of bird faeces and cleaning surfaces in well ventilated areas. We also recommend wetting contaminated areas before cleaning.

Keywords: Psittacosis, prevention, zoonosis, risk-factors

ABSTRACT ID: 259

PRESENTED BY: Fanny Chereau (fanny.chereau@free.fr)

C 22.5 Piloting feasibility of a newly-developed dashboard tool to support real time analysis of surveillance data in Tonkolili District, Sierra Leone, 2016

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4. Public Health France

Background

As part of strengthening surveillance of infectious diseases following the 2014-15 Ebola outbreak, the District Health Management Team (DHMT) in Tonkolili District, Sierra Leone, weekly collated paper-based surveillance data from Peripheral Health Units (PHU). As this team lacked tools to analyse the data and produce reports, we developed an open source interactive dashboard software to allow real time data analysis by time (week, year), place (chiefdom, PHU) and person (<5, >5 years). We piloted the tool to assess feasibility, initial acceptability and usefulness.

Methods

We delivered training to the DHMT and practical exercises covering three main areas: checking reporting completeness, weekly data analysis by time/place/person and export of figures and maps. The trained DHMT staff completed an anonymous questionnaire to collect information on their perceptions on ease of use of the tool and its appropriateness for surveillance needs.

Results

All eight trained DHMT staff reported that the tool was appropriate for their needs, seven considered it easy to use and six felt confident using it by themselves. All participants stated that practical exercises allowed them to practice data analysis and discover other potential uses of the tool such as detection of outbreaks, planning interventions and quality checking following data entry.

Conclusion

The pilot indicated that the dashboard tool was easy to use, acceptable and useful, suggesting that it could support the DHMT on core surveillance activities and planning public health responses. We recommend that the use of the tool be monitored over time to assess its usefulness under real field conditions.

Keywords: Surveillance, Communicable Diseases, Software tools, Sierra Leone

ABSTRACT ID: 278

PRESENTED BY: Silvia Funke (sifu@ssi.dk)

C 22.6 First insights into the variability of *Borrelia recurrentis* genomes

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Background

Borrelia recurrentis is the causative agent of louse-borne relapsing fever, endemic to the Horn of Africa. Current migrations brought new attention to the disease with 42 cases reported in 2015 in Germany. So far only one reference sequence genome is available. This hindered the development of specific molecular diagnostic and typing tools. We aimed to examine the genome variability of six strains and the possibility to identify new targets for typing.

Methods

Diagnosis of the cases was based on microscopy, culture, DNA directly isolated from patient blood and typed using flaB, glpQ and multi spacer typing to distinguish closely related relapsing fever Borrelia species. From 38 available blood samples, 21 could be cultured and only 9 gave meaningful density. Out of those, just 4 isolates from migrants from Somalia and Ethiopia yielded sufficient DNA for sequencing. Whole genome sequencing was performed on those isolates, and two historical strains from Ethiopia. Read mapping and de novo assembly was performed using CLC Genomics Workbench software.

Results

The genomes of all B. recurrentis were highly homologous, 16-27 identified SNPs were evenly distributed on the chromosome and plasmids, compared to the available reference genome. Migrant strains were identical, thus no geospatial pattern could be identified.

Conclusion

These preliminary results underline the low variability possibly due to the adaptation to their vector-host cycle and the limited targets available for discriminating typing methods. Strain discrimination even at this high resolution is unfeasible due to the high genome conservation. Hence, we recommend development of a common algorithm for identification and characterization of closely related Borrelia species at European level for timely diagnostic, prevention and control measures.

Keywords: Relapsing fever, Borrelia recurrentis, whole genome sequencing, genome variability, molecular typing Methods

ABSTRACT ID: 150

PRESENTED BY: Durdica Marosevic (djurdjica.marosevic@gmail.com)

Track 23: Vaccine effectiveness

Moderator: Kari Johansen, ECDC, Expert Vaccine-preventable Diseases

C 23.1 Vaccine effectiveness of 10-valent pneumococcal conjugate vaccine against invasive pneumococcal disease: indirect cohort design

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Background

Vaccine effectiveness (VE) data of the 10-valent pneumococcal conjugate vaccine (PCV10) in Europe are scarce and cross-protection of PCV10 against serotype 19A is debated. In 2011, PCV10 replaced PCV7 that was introduced in the Dutch National Immunization Program in 2006. We estimated VE of PCV10 against vaccine-type and vaccine-related invasive pneumococcal disease (IPD) using nationwide surveillance data.

Methods

We included cases with a positive cerebrospinal fluid or blood culture for Streptococcus pneumoniae up to March 2016 who were eligible for PCV10 vaccination, aged ≥2 months, and had known serotype and vaccination status obtained by linkage to the national vaccination register. Vaccine doses received ≥14 days before IPD diagnosis were included. VE of PCV10 was estimated for ≥1 dose and ≥2 doses (compared with 0 doses) using the indirect cohort method.

Results

The analysis included 133 IPD cases aged 2-54 months of which nine vaccine-type cases (1x14, 1x19F, 2x23F, 5x7F) and 40 vaccine-related cases (6x6C, 25x19A, 3x23A, 6x23B). VE for ≥2 doses for vaccine-type IPD was 87% (95% confidence interval: 33 to 97) and for serotype 7F was 92% (35 to 99). VE for ≥2 doses for vaccine-related IPD was 28% (-223 to 84) and for serotype 19A was 57% (-99 to 91). VE estimates for ≥1 doses were slightly lower.

Conclusion

VE of PCV10 against vaccine-type IPD was high (87%), showing that PCV10 protects well against vaccine-type IPD. VE estimates against vaccine-related IPD and serotype 19A were not statistically significant. Therefore, cross-protection of PCV10 against vaccine-related IPD including serotype 19A cannot be concluded.

Keywords: vaccination, invasive pneumococcal disease, program effectiveness,

ABSTRACT ID: 206

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C 23.2 Effectiveness of acellular pertussis vaccination in children twenty years after its introduction in Italy

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Background

In Italy, acellular pertussis vaccines replaced whole cell vaccines in 1995. Since 1999, National Vaccination Plan has recommended routine use of acellular vaccines in infants with the 2+1 schedule at 3-5-12 months, and a booster dose at 5-6 years. Since 2012, a booster for teens was also recommended. This study aimed at estimating acellular vaccines effectiveness (VE) in preventing pertussis of any severity and severe hospitalized cases in children ≤12 years in Apulia region (≈4,000,000 inhabitans), Italy.

Methods

A population-based retrospective study was conducted by linking mandatory notifications and hospital registrations for pertussis to obtain cases occurred between 2008-2013. VE for 3 and 4 doses was estimated using the screening method, where the proportion of the population vaccinated (PPV) was the vaccination coverage in children aged 1-4 years and 7-12 years, and the proportion of cases vaccinated (PCV) among notified or hospitalized cases was the proportion of subjects vaccinated ≥30 days before the disease onset or the hospital admission, respectively.

Results

Seventy-three cases aged 1-4 years (79% hospitalized) and 78 cases aged 7-12 years (77% hospitalized) were recorded during 2008-2013 and included in VE estimation. PPV was 96.7% among children aged 1-4 years and 90% among those aged 7-12 years. PCV was 72.6% and 64.1% in the two groups, respectively. Three-dose VE against pertussis of any severity and severe hospitalized disease was 88.7% (95%CI: 80.9-93.3%) and 88.9% (95%CI: 79.6%-93.8%), respectively. Four-dose VE against pertussis of any severity and severe hospitalizations was 81.8% (95%CI: 70.6%-88.7%) and 81.3% (95%CI: 67.7%-89.2%), respectively.

Conclusion

Acellular pertussis vaccines showed good effectiveness within the first years of life, protection partially waned as age increased. Improving booster uptake at 5-6 years visit is strongly recommended.

Keywords: Acellular pertussis vaccination, Vaccine effectiveness, Children, Notification, Hospitalization

ABSTRACT ID: 318

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C 23.3 Cancelled

C 23.4 A cross-sectional survey on completion of screening and immunisations and availability of preventive care services for asylum seekers in Finland

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Background

Health monitoring of asylum seekers is complex. Finland received ›32 000 applications for asylum in 2015. Nationally recommended screening tests are scheduled individually based on country of origin and results of a health interview and should be conducted within 3 months of arrival. Children and mothers should have access to pre-school child health clinics, school health services and antenatal care, respectively. Our aim was to evaluate adherence to national recommendations.

Methods

In March 2016, we conducted a cross-sectional survey of all asylum seeker centres in Finland. The web-based 31-item-questionnaire covering issues such as screening, immunisation and preventive care was sent to centre managers and nurses. Respondents answered with data or best estimates according to the situation of the reply date.

Results

152 out of 223 reception centres (68%) responded to the survey. 3353 (14%, range by region 4-31%) of asylum seekers had not had their first health interview. Recommended chest x-rays of 5557 (22%, range by region 4-41%) and blood tests of 6608 (27%, range by region 4-51%) asylum seekers had not been taken and required vaccinations had not been given to 4687 (19%, range by region 4-33%) asylum seekers. Antenatal care was not available for asylum seekers of one (‹1%) reception centre, well-baby clinics of four (2.6%) and school health services of 21 (14%) reception centres.

Conclusion

Gaps in screening, immunisation and access to preventive care may increase a risk for epidemics among asylum seekers and the population as a whole. Screening and immunisation efforts should be concentrated to the regions lagging behind.

Keywords: Refugees, mass screening, immunisation, preventive health services

ABSTRACT ID: 243

PRESENTED BY: Karolina Tuomisto (karolina.tuomisto@thl.fi)

C 23.5 Has the universal varicella vaccination introduction impacted on measles dynamics? A pilot experience in Apulia region, Italy, 2001-2014

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Background

In Italy, plans to add new vaccinations into the National Immunization Schedule raised concerns about possible negative effects on vaccination coverage (VC) of existing vaccination programmes. We aimed at demonstrating that the introduction of Universal Varicella Vaccination (UVV) since 2006 has favourably impacted on VC and incidence of measles in Apulia.

Methods

VC for measles in children aged ‹ 24 months for the period 2001-2014 were obtained from the Regional Immunization Registry. Incidence was estimated by matching Mandatory Notifications and Hospital Discharges, identifying measles cases as IC9 code 055.x. VC and incidence in the "measles-mumps-rubella vaccine period" (2001-2005), before UVV introduction, "1-dose monovalent varicella vaccine period" (2006-2008, a shot at 13-15 months), and "2-dose combined measles-mumps-rubella-varicella vaccine period" (2009-2014, first dose to toddlers, second dose at 5-6 years, and catch up at 11-12 years) were compared. Overall and stratified by age incidence rate ratios (IRRs) with 95% Confidence Interval (95%CI) were calculated using Poisson regression.

Results

VC for 1-dose measles vaccine was 85.8% in birth cohorts 1999-2004 (MMR period), 92.4% in cohorts 2005-2008 (1-dose V period), and 90.3% in cohorts 2009-2012 (2-dose MMRV period). Incidence of measles declined from 34 (N=1,374) in 2001-2005 to 2 x100,000 (N=80 cases/year) in 2006-2008 (IRR=0.06, 95%CI=0.05-0.07). The most significant reduction in the number of cases was recorded among the age groups ‹ 35 years, particularly between 5-9 years. No difference resulted when comparing 1-dose V and 2-dose MMRV periods.

Conclusion

In our large regional experience, VC and incidence of measles were not influenced by the simultaneous implementation of UVV. A wider vaccines offer has not hampered the achievement of important goals such as measles control, conversely MMRV use has increased vaccination coverage.

Keywords: Universal Varicella Vaccination, Measles, Vaccination coverage, Incidence, Children

ABSTRACT ID: 323

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C 23.6 Late breaker: Effectiveness of the 2015/16 tetravalent live and trivalent inactivated influenza vaccines against A(H1N1)pdm09 in children and adolescents in Germany

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Background

Since 2007 the health authorities of the German federal states Saxony-Anhalt and Lower Saxony perform a similar influenza virologic surveillance. During the influenza season 2015/16 we estimated the effectiveness (VE) of the tetravalent live attenuated influenza vaccine (LAIV4) and trivalent inactivated influenza vaccines (TIV) in preventing laboratory-confirmed A(H1N1)pdm09 cases among children in a pooled analysis.

Methods

From week 40/2015 to 19/2016, sentinel paediatricians systematically swabbed ARI (acute respiratory illness) patients for testing of influenza viruses by PCR. We compared A(H1N1)pdm09 cases and influenza-negative controls. We estimated vaccine type specific VE against laboratory-confirmed A(H1N1)pdm09 among 2-17-year-old children, stratified by age group (2-6; 7-17 years). We used multivariable logistic regression to calculate VE (1-OR) and to adjust estimates for age, sex, month of illness, study site and underlying chronic diseases.

Results

Of 1,888 included patients (mean age 5.4 years, 52% males), 17% (n = 320) were positive for A(H1N1)pdm09. Among children aged 2-17 years the adjusted VE for TIV was 90% (95% CI: 57-98%) and for LAIV4 12% (95% CI: -95-60%). LAIV4 VE in 2-6-year-old children was -13% (95% CI: -178-54) and TIV VE 91% (95% CI: 33-99). In children aged 7-17 years VE estimates for LAIV4 and TIV were 68% (95% CI: -169-96) and 87% (95% CI: 0-98) respectively.

Conclusion

Our study indicates no preventive effect of LAIV4 and a high preventive effect of TIV against A(H1N1)pdm09 2015/16 among 2-6-year-old children. Similar results in the United States were reported by the Centers for Disease Control and Prevention (CDC). We inform stakeholders and health professionals to discuss influenza vaccine recommendations for the coming season. Further studies are needed to explain potential causes of the observed low LAIV4 VE.

Keywords: Influenza; Human; Influenza Vaccines; Respiratory Tract Infections; Case-Control Studies; prevention & control; surveillance

ABSTRACT ID: 700

PRESENTED BY:
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Track 24: Late Breakers

Moderator: Sergio Brusin, ECDC, Senior Expert Communicable Diseases/Group Leader Response and Emergency Operations

C 24.1 Swimming event in an urban canal in the Netherlands, June 2016; prospective study to assess infection risks.

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Background

Swimming events in city canals are gaining popularity in the Netherlands. Canal water is typically not official swimming water but is often used for swimming events. Despite previous studies, knowledge about the risk of infection in canal swimming events is limited. Our study aimed to prospectively determine the risks of infections during an urban swimming event, the Singel Swim Utrecht 2016 (SSU).

Methods

We sent online questionnaires to 270 participants of the SSU, including questions on gastrointestinal symptoms. Participants were requested to forward the questionnaire to 3 relatives, i.e. non-exposed. We analysed water specimens from the venue and stool specimens of participants with gastrointestinal illness (AGI). AGI was defined as diarrhea, nausea, vomiting or stomachache within seven days after the event. AGI in participants as compared with non-exposed, as well as risk factors for AGI in participants, was assessed using binomial regression models.

Results

One-hundred sixty SSU participants (59%) and 40 non-exposed relatives (5%) returned the questionnaires. Eleven percent of the participants (n=17) and 3% of non-exposed (n=1) reported AGI (aRR 4.25 CI 0.58-31). Norovirus genotype-II was detected in 2 of 6 water specimens and in none of the stool specimens. In 1 of 3 stool specimens, rotavirus was detected.

Conclusion

We conclude that there was no significant higher risk for participants of the SSU to develop AGI. Limitation of our study was the small number of non-exposed controls. We could not identify a risk factor which would lead to a greater risk of AGI. Although we did not detect an outbreak during this event, viral pathogens are present in water and therefore we recommend to inform participants about the health risks of swimming in open water.

Keywords: swimming, gastrointestinal diseases/epidemiology, prospective studies, water pollution

ABSTRACT ID: 703

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C 24.2 Large cyclosporiasis outbreak in the UK linked with travel to Mexico, 2016: a case of "déjà vu"

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Background

Beginning in June 2016, the United Kingdom (UK) experienced a large outbreak of cyclosporiasis. A previous outbreak with 79 cases in 2015 occurred in UK travellers to Mexico. The aim of this investigation was to characterise the outbreak in order to support local investigations in Mexico, provide travel advice and raise awareness to support timely case detection and treatment.

Methods

UK laboratories and public health teams were alert for Cyclospora due to the 2015 outbreak and detected cyclosporiasis cases despite it not being a notifiable disease. Demographics, clinical presentation, travel history and food/water exposures were collected for laboratory-diagnosed cases using a questionnaire. Descriptive analyses were undertaken.

Results

430 UK cases were reported from 1 June to 23 September 2016 (median age 46 years, 54% female), of whom 322 (75%) were known to have travelled to Mexico (mainly to Riviera Maya), staying in 33 different hotels. Food and water exposure analysis is ongoing to identify potential sources of infection. Other countries were notified via the European Early Warning and Response System and WHO's Event Information Site. Information was shared with the Mexican authorities and the travel industry to assist local investigations.

Conclusion

This is the second year that a large cyclosporiasis outbreak has occurred in UK travellers returning from Mexico. Investigations are ongoing and the UK will continue to work with Mexico to identify potential sources of infection. The travel industry, health professionals and travellers will be informed to minimise the risks of future outbreaks. Healthcare providers should ask patients with gastrointestinal symptoms about recent travel history and consider Cyclospora testing. Increased awareness and laboratory testing capacity is necessary to support timely case detection and treatment.

Keywords: cyclosporiasis, Cyclospora, diarrhoea, gastrointestinal infection, travel, outbreak Abstract ID: 740

PRESENTED BY: Diogo Marques (diogo.marques@nhs.net)

C 24.3 Initial findings from a gap analysis on securing diphtheria diagnostic capacity in the EU/EEA

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Background

Diagnosis of diphtheria poses a major challenge in countries with low disease incidence and this was highlighted by a fatal case in an unvaccinated child in Spain in 2015, where not only diagnosis but procurement of diphtheria antitoxin was problematic.

Methods

ECDC therefore, commissioned a gap analysis amongst 30 EU/EEA Member States (MS) where a questionnaire collecting information on surveillance systems, laboratory diagnostics, policies and guidelines, training and the impact of ceasing diagnostic activities was distributed.

Results were analysed against three minimal standards to determine the extent of the 'gap':

- Microbiological and epidemiological surveillance – systems in place for all three potentially toxigenic species (Corynebacterium diphtheriae, C. ulcerans and C. pseudotuberculosis), with close collaborations between microbiology and epidemiology;
- Laboratory diagnostic capacity - at least one laboratory reaching the defined 'reference' level in each MS. Defined as having one or more methods for primary culture and biochemical identification, plus toxigenicity determined by PCR or Elek;
- Expertise in laboratory diagnostics - at least one laboratory staff member who received training in or more recently than 2013.

Results

Responses were received from all 30 MS; 19 met the criteria for diphtheria surveillance; 24 reached reference laboratory standards and 11 fulfilled training requirements. Only six MS met all three standards.

Conclusion

The analysis confirmed gaps in diagnostic capacity across the EU. Areas for action included availability of accurate and specialised laboratory diagnostics and ensuring countries had surveillance for all three diphtheria-causing organisms, particularly given the increase in toxigenic C. ulcerans isolates amongst MS since 2013. Microbiologists must have sufficient skills and resources for the microbiological diagnosis of diphtheria. Maintaining this expertise in the face of low disease incidence is a key challenge for diphtheria surveillance.

Keywords: Diphtheria, Microbiology, Laboratories, European Union
Abstract ID: 735

PRESENTED BY: Vicky Head (vicky.head@phe.gov.uk, vicky.head@nhs.net)

C 24.4 First autochthonous cases of tick-borne encephalitis detected in the Netherlands, July 2016

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Background

Until recently, tick-borne encephalitis virus (TBEV) was thought to be absent in the Netherlands. No autochthonous human cases had been diagnosed yet, and imported tick-borne encephalitis (TBE) is considered rare.

Methods

In June 2016, the National Institute of Public Health and the Environment found that Ixodes ricinus ticks collected in national park “Sallandse Heuvelrug” were RT-PCR positive for TBEV-Eu. On 30 June, this signal was reported through the weekly Communicable Disease Threats Report and (Lab)Inf@ct, an instant mailing service for medical professionals in infectious diseases, providing information for action. This mailing contained information on clinical aspects of TBE and available diagnostic methods.

Results

In July 2016, 5 days after the mailings were released, the first autochthonous case of TBE was diagnosed, 9 days later, a second case in another region was detected. Both male patients had illness onset in June. They were hospitalised with neurological symptoms and positive for TBEV-specific IgM and IgG and TBEV neutralising antibodies in serum. Both had a recent tick bite most likely acquired in a national park, the first in ”Utrechtse Heuvelrug”, the second in ”Sallandse Heuvelrug”. A tick collected from the first patient tested TBEV-positive in qRT-PCR. Interestingly, this TBEV was genetically distinct from the TBEV previously found in Dutch ticks.

Conclusion

Dutch human tick-borne encephalitis cases were diagnosed shortly after national awareness was raised on TBEV-presence in ticks. TBE should now also be considered in patients with compatible symptoms without recent travel history. Ongoing research focuses on the geographic spread of TBEV in the Netherlands through serological screening of wildlife and tick collection. A sero-epidemiological study is initiated to quantify the risk for infection in high-risk groups such as forestry workers.

Keywords: European tick-borne encephalitis, awareness, emerging infectious diseases, awareness, Netherlands Abstract ID: 728

PRESENTED BY: Barbara Schimmer (barbara.schimmer@rivm.nl)

C 24.5 Investigation of a national measles outbreak linked to a single imported case in Ireland, April-September 2016.

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Background

Measles incidence has declined in Ireland in recent years, but the European elimination target (<1 case per million) has never been reached. In April 2016, a case of measles was confirmed in an adult who travelled within Ireland while infectious. Cases subsequently arose in five of the eight public health regions around the country.

Methods

A national outbreak control team was convened. Extensive contact tracing was undertaken for each case. A variety of samples were used to confirm or rule out measles: primarily oral fluid samples, serum, or throat swabs. Laboratory confirmation was defined as measles virus detection on PCR testing, or measles-specific IgM. Genotyping was performed for the primary case, and for subsequent cases where epidemiological links were uncertain.

Results

There were 41 confirmed cases between April and September 2016. All sequenced cases were genotype B3 and were identical. Vaccination status was known for 34 cases, of whom 31 (91%) were unvaccinated. Eight cases (20%) were aged <12 months. Median age was 8 years (range 3 months to 40 years). Nine cases (22%) were nosocomial, and three cases (7%) were infected on separate international flights. Eighteen cases (45%) were known to have been hospitalised. The primary case was a child who was hospitalised after return from travel to another European country, but whose diagnosis was unrecognised by clinicians. The child was diagnosed retrospectively as measles PCR-positive on a stored throat swab.

Conclusion

This was a protracted, complex outbreak linked to a single imported case, with multiple routes of transmission and a high rate of hospitalisation. This outbreak demonstrated that Ireland remains at risk of measles outbreaks since vaccination rates are suboptimal and elimination targets are not achieved.

Keywords: Measles, Measles-mumps-rubella vaccine, Disease outbreaks, Ireland Abstract ID: 705

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C 24.6 Measles outbreak in England derails achieving elimination targets

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Background
Following a successful MMR catch-up campaign in 2013, measles incidence in England was at historically low levels with interruption of endemic transmission for the subsequent two years. Since February 2016 a national increase in a measles was observed affecting mainly older teenagers and young adults.

Methods
All suspected measles cases in England are notified to local Health Protection Teams and recorded on a web based management tool, HPZone. Oral fluid kits are posted to suspected cases for self-sampling and submitted to the National Reference Laboratory (NRL) for IgM,IgG and /or PCR testing. Results from these and other samples sent to the NRL and local laboratories are reconciled with HPZone data.

Results
Between 1st February and 31st August 2016, 463 (23%) of 2006 suspected cases were confirmed in England. The majority of cases were identified in London (57%, 266) and the South West (20%, 91) in 15 to 24 year olds (158, 34%). Peak activity occurred in July (n=119) with 43 (9%) cases reported during the summer (mid-June to end August) linked to music and arts festivals. The majority of cases were unvaccinated with only 4% reporting at least one dose of a measles containing vaccine. The reported hospitalisation rate was 38% reflecting the age distribution of cases with 10% reporting complications.

Conclusion
Despite current high MMR immunisation coverage in the routine childhood programme and several MMR catch-up campaigns there remains a pool of susceptibles among older teenagers and young adults in England. Any elimination strategy has to target this group in order to be successful.

Keywords: measles, outbreak, England, susceptible population

ABSTRACT ID: 730

PRESENTED BY: Antoaneta Bukasa (antoaneta.bukasa@phe.gov.uk)

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