ESCAIDE

ABSTRACT BOOK

European Scientific Conference on Applied Infectious Disease Epidemiology 2017

Stockholm Waterfront Congress Centre
6-8 November 2017
Stockholm, Sweden

ecdc
EUROPEAN CENTRE FOR
DISEASE PREVENTION
AND CONTROL

www.escaide.eu

ESCAIDE is organised by the European Centre for Disease Prevention and Control, ECDC, in collaboration EAN (EPIET Alumni Network) and TEPHINET Europe (Training Programmes in Epidemiology and Public Health Interventions NETwork).

The ECDC works in three key strategic areas: it provides evidence for effective and efficient decision-making, it strengthens public health systems, and it supports the response to public health threats. ECDC coordinates the EPIET/EUPHEM fellowship programme and works with TEPHINET and EAN to make ESCAIDE an even more successful event! Find out more at ecdc.europa.eu

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It is my pleasure to welcome to you to ESCAIDE 2017!

Over the past ten years, ESCAIDE has become the place to be for the latest on infectious disease epidemiology! It is the meeting place for leading seniors, mid-career professionals, bright and enthusiastic students and early career experts. We are honoured to host you and many others from over 50 different countries and encourage you to be an active participant at ESCAIDE!

Take every opportunity to:

- share scientific knowledge and experience;
- discuss and debate scientific advances and current public health challenges;
- strengthen and expand your network in Europe and globally;
- be curious, open-minded and use the opportunities to further your professional development

To further engage you in peer discussions and inspire you, the ESCAIDE Scientific Committee has put together a set of plenary sessions with leading experts in the field. We will kick-off by looking at the past, present and future of disease elimination and discuss critical success factors (Plenary A). We will debate if and how we can achieve better outcomes by working together (Plenary B), improve seasonal influenza surveillance (Plenary C) and share views on how to effectively advocate for science in times of fake news (Plenary D). The programme will close with a session on the Public Health Event of the year, during which we will discuss the complexities and cross-sector impact of the multi-country outbreak of Salmonella Enteritidis.

The parallel and poster sessions' programme this year covers a variety of infectious diseases and topics in surveillance, outbreak investigations, public health microbiology and many other fields, related to infectious disease epidemiology. These sessions are the heart of ESCAIDE and we are very proud of the high quality of submitted abstracts. Special thanks to all of you who submitted their work, to all reviewers, moderators and the Scientific Committee!

This year's ESCAIDE is hosting a Reception, which is a wonderful social event, a career compass seminar, the Eurosurveillance seminar, a training on evidence-based methods in public health, a workshop with INTEGRATE, many interesting information stands and our annual BarCamp. Do not miss these opportunities to socialise, expand your professional network, learn more and discuss current topics, proposed by peers, in a very relaxed setting.

Thank you for being part of ESCAIDE and let's make this year's Conference the best one yet!

Prof. Mike Catchpole
Chair, ESCAIDE Scientific Committee

Scientific Committee

Mike Catchpole

Chief Scientist, Chair of ESCAIDE Scientific Committee, ECDC

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 a 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.

Aileen Kitching

Consultant in Public Health Medicine in the Health Service Executive in Ireland, President of the EPIET Alumni Network (EAN)

Aileen is a consultant in Public Health Medicine in the Health Service Executive in Ireland, where her portfolio includes HIV/STIs, health inequalities and health information for health service planning. Having a background in clinical medicine (hospital & general practice in Ireland, Scotland and Australia; Médecins Sans Frontières (MSF) in Liberia), she undertook the EPIET Programme (2007-2009) at the Health Protection Agency (HPA) in London. During 2009-2015, Aileen completed her specialisation in public health medicine with a main focus on communicable disease control (surveillance and outbreak response) at the local, regional and national level in the UK (at HPA/Public Health England). Internationally, she has worked in the Outbreak Response Unit at the National Institute for Communicable Diseases in South Africa, and as a consultant with WHO in the Philippines (Typhoon Haiyan, 2014) and Sierra Leone (Ebola response, 2015). She was elected President of the Board of the EPIET Alumni Network (EAN) in 2015.

Fehminaz Temel

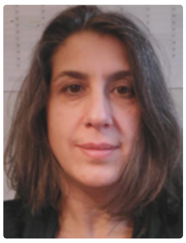
Head of the Field Epidemiology Unit and Director of the Turkish Field Epidemiology Training Programme in the Public Health Institute of Turkey, member of Training Programs in Epidemiology and Public Health Interventions Network Europe, Public Health Institute

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

Thea Kølsen Fischer

Head Surveillance and Research Unit and all Danish WHO National Reference Laboratories for viruses, Statens Serum Institut (SSI), Denmark

Thea is a public health virologist heading the Virology Surveillance and Research Unit and all Danish WHO National Reference Laboratories for viruses at SSI. Thea is a Professor in Global Health and Infectious Diseases and her research has focused on global high-incidence viruses such as influenza, enteroviruses and rotavirus combining epidemiology, molecular profiling and vaccinology. She specialised in epidemiology and laboratory outbreak management as an EIS Officer at CDC. Thea is a member of the ECDC National Microbiology Focal Points forum.



Helena de Carvalho Gomes

Head of the Scientific Advice Coordination Section, Scientific Advice Coordination Section, 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 represented the National Association of Statutory Health Insurance Physicians at the German Federal Joint Committee as a member of the subcommittee on prevention. 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.

Osamah Hamouda

Head of the Department of Infectious Disease Epidemiology at the Robert Koch Institute, Robert Koch Institute

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 from 2003 and head of the HIV/AIDS, STI and Bloodborne Infections Unit since 1995. He studied medicine at the Free University, Berlin and completed his postgraduate 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.

Aura Timen

Head of the National Coordination Centre for Outbreak Management of the Dutch National Institute for Public Health and Environment and a member of the ECDC Advisory Forum on behalf of EUPHA, National Coordination Centre for Outbreak Management, National Institute for Public Health and the Environment

Aura is the Head of the National Coordination Centre for Outbreak Management of the Dutch National Institute for Public Health and Environment and a member of the ECDC Advisory Forum on behalf of EUPHA. Prior to this role, Aura worked for the Delfland Municipal Public Health Service as a physician in social medicine. She is a medical doctor by training, specializing in communicable disease control, with extensive research experience on crisis management in the Netherlands and abroad. Aura holds a PhD in outbreak management from the Radboud University Nijmegen, The Netherlands.

Marion Muehlen

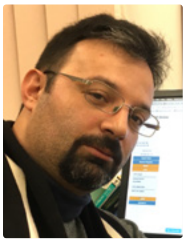
Head of the EPIET programme in the Public Health Training section at ECDC, Public Health Training section, ECDC

Marion currently heads the EPIET programme in the Public Health Training section at ECDC. 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 becoming an EPIET fellow, 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 based at the Robert Koch Institute, Germany, and later at Public Health England 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.

Karl Ekdahl

Head of the Public Health Capacity and Communication Unit, Public Health Capacity and Communication Unit, ECDC

Karl is the Head of the Public Health Capacity and Communication Unit at ECDC. He was the first expert to join the European Centre for Disease Prevention and Control in 2005. Within ECDC, he has been Strategic Adviser to the Director (2005-2007), and Head of the Health Communication Unit (2007-2010). From February to April 2010, Karl was the Centre's Acting Director. Karl is a medical doctor and a specialist in infectious diseases. He has a PhD in Infectious Diseases from Lund University in Sweden, a Diploma in Tropical Medicine and Hygiene from Prince Mahidol University, Bangkok, Thailand, and a Master's Degree in Epidemiology from the London School of Hygiene and Tropical Medicine. In 1999 he became Associate Professor and in 2007 Adjunct Professor in Infectious Disease Epidemiology, at the Karolinska Institute in Stockholm.



João André Nogueira Custódio Carriço

Researcher in the Molecular Microbiology and Infection Unit, Medical University of Lisbon

João is currently working as a Researcher in the Molecular Microbiology and Infection Unit at the Instituto de Medicina Molecular in the Faculty of Medicine, University of Lisbon, and teaches at the Instituto Superior Técnico, University of Lisbon. He studied Applied Chemistry, Biotechnology and did his PhD on Microbial typing and data analysis methodologies. João's research interests are in Bioinformatics and the development of novel analysis and visualization methodologies with special focus on microbiology, molecular epidemiology and microbial typing methods.

Christopher Barbara

Chairman of the Pathology Department, Mater Dei Hospital, Malta

Christopher is the Chairman of the Pathology Department at Mater Dei Hospital in Malta. He received his medical training in both Malta and the United Kingdom. Furthermore, he is a Consultant Virologist and Head of the Virology Unit in the Department of Pathology. Christopher also lectures in Microbiology at the University of Malta and is a member of various National Health Committees related to Pathology and Infectious Diseases. He is the National Microbiology Focal Point for Malta at ECDC.

Abstract Reviewers

The Scientific Committee warmly thanks everyone who participated in the reviewing of the abstracts submitted for ESCAIDE 2017.

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Richard Goering
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J Todd Weber

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. In order to achieve this mission, ECDC works in partnership with national health protection bodies across Europe to strengthen and develop continent-wide disease surveillance and early warning systems. By working with experts throughout Europe, ECDC pools Europe's health knowledge to develop authoritative scientific opinions about the risks posed by current and emerging infectious diseases.

Within the field of its mission, the Centre shall:

- search for, collect, collate, evaluate and disseminate relevant scientific and technical data;
- provide scientific opinions and scientific and technical assistance including training;
- provide timely information to the Commission, the Member States, Community agencies and international organisations active within the field of public health;
- coordinate the European networking of bodies operating in the fields within the Centre's mission, including networks that emerge from public health activities supported by the Commission and operating the dedicated surveillance networks;
- exchange information, expertise and best practices, and facilitate the development and implementation of joint actions.

www.ecdc.europa.eu

Public Health Training Section – ECDC

The ECDC Fellowship Programme is a two-year competency based training with two paths: the field epidemiology path (EPIET) and the public health microbiology path (EUPHEM).

After the two-year training, EPIET and EUPHEM graduates are considered experts in applying epidemiological or microbiological methods to provide evidence to guide public health interventions for communicable disease prevention and control.

Both curriculum paths provide training and practical experience using the 'learning by doing' approach in acknowledged training sites across European Union (EU) and European Economic Area (EEA) Member States.

www.ecdc.europa.eu/en/epiet-euphem

Training Network Strengthening (TNS) Group - ECDC

Training Network Strengthening (TNS) Group

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.

www.ecdc.europa.eu/en/training

EPIET Alumni Network (EAN)

The EPIET Alumni Network (EAN) was created in 2000 to help develop and maintain a network of European public health epidemiologists that have participated in the European Programme for Intervention Epidemiology Training (EPIET); it now also includes alumni from the European Programme for Public Health Microbiology Training (EUPHEM) and the EU/EFTA/EEA Field Epidemiology Training Programmes (FETP). As well as alumni of training programmes, the EAN also has some 'external' members who, through their work, meet similar objectives to the EAN. The EAN is an association, run by a voluntary advisory board of six elected members.

www.epietalumni.net

Training Programs in Epidemiology and Public Health Interventions Network

First incorporated in 1997, Training Programs in Epidemiology and Public Health Interventions Network (TEPHINET) is a global network of field epidemiology training programs (FETPs), trainees, and graduates. Currently, TEPHINET comprises 69 programs actively training field epidemiologists in more than 100 countries. TEPHINET member programs include those with laboratory and veterinary education components. Overall, TEPHINET comprises more than 10,000 trainees and 6,500 graduates who play a critical role in improving global health security by strengthening country capacity to detect and respond to disease outbreaks. With a secretariat based in Atlanta, Georgia, USA, and a global Advisory Board, TEPHINET is the only global network of FETPs and spans multiple regional FETP networks, sub-regional programs, and national programs.

Mission
To empower and mobilize a competent field epidemiology workforce for all people through standardized training, experiential learning, training program quality improvement, mentoring, and knowledge exchanges in order to connect epidemiologists better, faster, and with quality across the globe.

Vision
All people are protected by a field epidemiology workforce capable of detecting and responding to health threats.

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

Information Stands

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

ERS

ERS is an international organisation that brings together physicians, healthcare professionals, scientists and other experts working in respiratory medicine. We are one of the leading medical organisations in the respiratory field, with a growing membership representing over 140 countries.

Our mission is to promote lung health in order to alleviate suffering from disease and drive standards for respiratory medicine globally. Science, education and advocacy are at the core of everything we do.

One in eight people in Europe die due to lung diseases – this means one person every minute. It includes well known diseases like asthma and lung cancer and other less known like Chronic Obstructive Pulmonary Disease (COPD), which is now the third most common cause of death.

The European Respiratory Society (ESR) is involved in promoting scientific research and providing access to high-quality educational resources. It also plays a key role in advocacy – raising awareness of lung disease amongst the public and politicians.

The latest ERS Vision instalment focuses on the value of broader public health initiatives for respiratory health – at a time where personalised and targeted approaches are taking the lead in healthcare.

www.ersnet.org

ESCAIDE App

AppInConf is a modern and exciting company that expands rapidly. With solid experience, we offer our customers the best solutions in the mobile market. We want to increase the value and enhance the experience of the conference using our apps and digital solutions. It's not just technology; it is relationship building and dialogue with the participants.

www.appinconf.com

IMI_DRIVE

At the Innovative Medicines Initiative (IMI), we are working to improve health by speeding up the development of, and patient access to, innovative medicines, particularly in areas where there is an unmet medical or social need. We do this by facilitating collaboration between the key players involved in healthcare research, including universities, research centres, the pharmaceutical and other industries, small and medium-sized enterprises (SMEs), patient organisations, and medicines regulators. IMI is the world's biggest public-private partnership (PPP) in the life sciences. It is a partnership between the European Union (represented by the European Commission) and the European pharmaceutical industry (represented by EFPIA, the European Federation of Pharmaceutical Industries and Associations). Through the IMI2 programme, we have a €3.3 billion budget for the period 2014-2020.

www.imi.europa.eu/

中美新发和再发传染病合作项目
CHINA–US COLLABORATIVE PROGRAM ON EMERGING AND RE–EMERGING INFECTIOUS DISEASES

China-U.S. Collaborative Program on Emerging and Re-emerging Infectious Diseases

As the most populous country in the world with many national borders, China is uniquely vulnerable to the emergence and spread of new infectious diseases. In 2005, following the SARS outbreak in China, the China Ministry of Health (MOH) and the U.S. Department of Health and Human Services (HHS) signed a Memorandum of Understanding to establish the China-U.S. Collaborative Program on Emerging and Re-emerging Infectious Diseases (EID Program). In June 2015, the third five-year version of this MOU expanded the collaboration to include additional health threats and efforts to increase global health security in other countries including those in Africa. China's National Health and Family Planning Commission (formerly the Ministry of Health) has recognized how this collaboration has "achieved remarkable results in responding to emerging and re-emerging infectious diseases over the past few years." International Emerging Infections Program

- Assessing whether Zika virus is circulating in Southern China in collaboration with Guangdong CDC, Yunnan Institute of Parasitic Diseases, and China CDC. This is part of a GDD Network project that will also generate information on the benefits of new diagnostic tools.
- Collaboration with China CDC to better understand the gaps in receiving appropriate post-exposure prophylaxis for suspected rabies cases.
- Surveillance to better detect and monitor trends in Salmonella Typhi and Paratyphi in high priority provinces in the southern region of China.
- Identifying influencing factors in the extremely low seasonal influenza vaccination rate among Chinese pregnant women in a joint effort with the Chinese Center for Health Education.
- Strengthening the national infectious disease laboratory system, including adopting internationally recognized laboratory assessment tools.
- Building capacity to enhance healthcare-associated infection (HAI) detection and surveillance, including comprehensive tuberculosis control and better understanding of anti-microbial resistance in healthcare settings in collaboration with local hospitals.

Invited Speaker Biographies

Plenary Session A: Key Note Address Infectious Disease Elimination – Opportunities and Challenges: Past, Present and Future Perspectives

Dr. Donato Greco

Senior Research Fellow, International Prevention Research Institute, Lion, France

Donato Greco is a medical doctor specialised in communicable disease, hygiene and public health, epidemiology and medical biostatistics. He has been working for 32 years in the National Institute of Health (ISS) of Italy where he directed the Laboratory of epidemiology and biostatistics. He then became Director General of Department of Disease Prevention in the Ministry of Health for four years. As Director he was in charge of the Influenza Pandemic preparedness. As National Epidemiologist at ISS he investigated many epidemics in Italy and in several other countries, including a severe Ebola outbreak. He has intensive collaborations with WHO (former Director of the WHO Collaboration Centre for Communicable Disease, member of the Regional Polio Certification committee for 28 years and member of the IHR roster) and with the European Union as expert evaluator of research projects, expert on communicable diseases of the TAIEX plan for the EU accession countries and consultant for the European Centre for Disease Prevention and Control (2015-16). Donato is participating in two large EU FP7 research projects on communication and communicable diseases. He is following some Uganda based IDRC (Canadian research agency) research projects. From 2012 Donato is a senior research fellow of IPRI Lyon. He is the author of more than 150 scientific publications and has been teaching epidemiological methods in ISS and Italian universities for many years. He is Grand Official of the Italian Republic and has been awarded the Italian Gold Medal for Public Health.

Plenary Session B: Working together for better outcomes

Dr. Christiana Nöstlinger

Clinical/Health Psychologist & Behavioral Scientist, Department of Public Health, Institute of Tropical Medicine Antwerp, Belgium

Christiana Nöstlinger, PhD, is a clinical/health psychologist and behavioral scientist working at the Institute of Tropical Medicine (Antwerp, Belgium) at the department of Public Health. Currently, she also holds a professorship in Clinical and Health Psychology at the University of Vienna (Austria). She has been involved in HIV-related behavioral research since 1990 after completing a postdoctoral fellowship at the HIV Center for Clinical and Behavioral Research at Columbia University (New York). She has lived and worked in various European countries.

Her main expertise lies in the field of social and behavioral science with an emphasis on sexual health behavior and its contextual components. She is an expert for HIV prevention and (sexual) health promotion, including the systematic development of behavior change interventions and evaluation for vulnerable populations such as adolescents and young people, men having sex with men (MSM), and migrants.

She was the principal investigator of several large scale public health projects, for instance Eurosupport IV, V and VI, focusing on the psychosocial and prevention needs of people living with HIV. Eurosupport VI was conducted in ten European countries to develop and evaluate a computer-assisted behavioral counseling intervention for people living with HIV to improve their sexual health. She participated in other European public health projects, such as Sialon II, i.e. a bio-behavioral study to build capacity in combining targeted HIV prevention with surveillance among MSM, where she led the work-package on prevention. She also led the evaluation work-package of the EU project “Quality Action” on the use of quality improvement tools in HIV prevention (with 45 partners in 26 European countries). She has also worked in low-resource settings in the area of intervention development and evaluation for young people living with HIV in Kenya and Uganda. Within an interdisciplinary team, she currently heads the social science component of the Belgian “Be-PrEP-ared” study, a PrEP demonstration project among MSM me at high risk of HIV infection. She is also the director of the Flemish program for HIV prevention and sexual health promotion for sub-Saharan African migrants adopting a community-based and participatory approach.

She has published extensively on all the above-mentioned topics and teaches on behavioral theories and health promotion models, and on qualitative and mixed methods in international health.

Plenary Session B: Working together for better outcomes (continued)

Dr Juliet Bedford

Founder and Director of Anthrologica

Juliet Bedford is the Founder and Director of Anthrologica. Anthrologica is an international research organisation specialising in applied anthropology in global health and conducting formative and operational research at the interface between the provision and uptake of health services (www.anthrologica.com). Juliet has over fifteen years technical experience in developing contexts, fragile states and emergency settings and has worked intensively across Africa, South and Southeast Asia. She holds a Doctorate in Anthropology from the University of Oxford, where she is a Research Associate at the Institute of Social and Cultural Anthropology, and is an Adjunct Professor at the College of Global Public Health at New York University.

Prof Frederik Liljeros

Professor of Sociology, Stockholm University, Sweden

Fredrik Liljeros is a professor of sociology at Stockholm University. Liljeros did his posdoc the Swedish Institute for Diseases Control. His research is about different types of contact patterns and their significance for different types of diffusion processes, contagious infections as well as social institutions. The research has been carried out with researchers from different disciplines MDs, mathematicians, physicists and criminologists in world leading Journal's for interdisciplinary research such AS Nature, PNAS and Physical Review Letters.

Invited Speaker Biographies

Plenary Session C: Seasonal influenza surveillance – can we do with less than the ‘full Monty’?

Prof. Lone Simonsen

Professor, Global Health & Infectious Disease Epidemiology, University of Copenhagen, Denmark

Lone Simonsen is currently a Marie Curie Visiting Professor of Historic Epidemiology at the U. Copenhagen. She also is a Research Professor in Global Health at George Washington U (GWU), DC since 2007 and a senior fellow with the Fogarty Center at the National Institute of Health. She holds a PhD in population genetics from U. Massachusetts, Amherst and later trained in infectious disease epidemiology at the Centers for Disease Control and Prevention (CDCs EIS program) in Atlanta. She is an elected member of the Danish Royal Academy of Sciences and Letters, and of the American Epidemiological Society AES.

Over the past 25 years Simonsen has worked at the CDC, the WHO and NIH researching many topics including unsafe medical injections and hepatitis, global patterns of HIV/AIDS, TB drug resistance, SARS, pandemic influenza, e-health data, surveillance systems, “big data” and vaccine program evaluation (influenza, pneumococcus, rota). Before moving to academia in 2007, she was a senior epidemiologist at the NIH-NIAID where she advised leadership on vaccine program effectiveness and adverse events and emerging infectious disease events. She has published ~170 well-cited peer-reviewed papers, book chapters, commentaries and letters, in collaboration with her extensive global research network. Her research currently focuses on historic epidemiology (smallpox, cholera), and modeling patterns and burden of historic and contemporary pandemics/emerging infectious diseases (ebola, zika), investigating drivers of epidemiological transitions and childhood mortality reductions in 19th century Europe, 20th century latin america and 21th century Africa. On a Gates grant she also develops methodology and evaluates impact of pneumococcal PCV vaccine programs in low and middle income countries with colleagues at Yale SPH. She is a frequent speaker at national and international meetings.She served on an influenza expert panel for the Council of Foreign Relations, presented at the President’s Council of Advisors on Science andTechnology Policy, led a WHO multi-country modeling collaboration, served on several WHO expert panels: She co-hosted Historic Epidemiology meetings in Copenhagen in 2010 in 2014 and a NIH Ebola modeling meeting in 2015 and was a keynote speaker at the 2016 ISIRV influenza meeting at the Instite Pasteurs.

Dr. Anders Tegnell

State epidemiologist, Public Health Agency of Sweden

Dr Tegnell is the state epidemiologist in Sweden and the head of the department of Monitoring and evaluation at NPA. The responsibility includes AMR issues and HIV prevention and the general surveillance and control of communicable diseases at national level.

Before the position he was responsible for a department of the National Board of Health and Welfare dealing with knowledge management, developing guidelines and recommendations in all of the Boards areas of responsibility. The National Board of Health and Welfare is a government agency under the Ministry of Health and Social Affairs, with a very wide range of activities and many different duties within the fields of social services, health and medical services, environmental health, communicable disease prevention and epidemiology.

In the past he has been responsible for the development of the Swedish preparedness plan for a flu pandemic, for the Swedish national vaccination-programme and the work with AMR and HAI with focus on regulatory issues and supervision.

He has published around 60 articles in scientific journals.

Plenary Session D: Science Advocacy in times of alternatives facts and fake news

Xavier Prats Monné

Director-General, Health and Food Safety (DG SANTE)

Xavier Prats Monné is the Director-General for Health and Food Safety of the European Commission (EC) since September 2015. He is responsible for EU policies and programmes in health and food safety, including the promotion of public health, the assessment of national healthcare systems' performance, pharmaceutical legislation, animal health and welfare, as well as the strengthening of Europe's capacity to deal with crisis situations in human health and the food sector. He previously served as Director-General for education and culture, responsible for the Erasmus+ and Marie Curie programmes and representing the EC on the Governing Board of the European Institute of Innovation and Technology (EIT). From 2007 to 2010, he was Director for employment policy and one of the five founding members of the Impact Assessment Board, reporting to the President of the European Commission.

He holds degrees in Social Anthropology from the Universidad Complutense (Madrid, Spain); in Development Cooperation from the International Centre for Advanced Mediterranean Agronomic Studies (CIHEAM; Paris, France); and in European Studies from the College of Europe (Bruges, Belgium), where he graduated first of the Class of 1981-82 and served as assistant professor. He completed his primary and secondary education (Maturità Scientifica) at the Istituto Massimo of Rome, Italy. He is from Spain, fluent in Spanish, English, French, Italian and Catalan.

Dr. Kåre Mølbak

Vice-President, Statens Serum Institut; Director, Division of Infectious Diseases Preparedness , Denmark

After training in clinical infectious diseases, Kåre Mølbak held research positions in connection with the Bandim health research project in Guinea Bissau and at several departments at Statens Serum Institut, Denmark. At the present position, he is Vice-President of Statens Serum Institut and the director of the Division of Infectious Diseases Preparedness. This division include public health reference laboratories, surveillance and control activities. Personal areas of interest are control of infections, vaccines as well as the emerging problems of zoonotic infections and antimicrobial resistance.

Kåre Mølbak has published more than 300 peer reviewed papers, mainly on the epidemiology of infectious diseases.

Invited Speaker Biographies

Plenary Session E: Public health event 2017

Dr. John Besser

U.S. Centers for Disease Control and Prevention (CDC)

John Besser has been the Deputy Chief of the Enteric Diseases Laboratory Branch at the U.S. Centers for Disease Control and Prevention (CDC) since July 2009, where he has been involved in national and global programs to detect, characterize, and track bacterial enteric diseases. As part of his responsibilities, he leads a research team tasked with developing metagenomic and other advanced molecular methods for foodborne disease surveillance. Prior to CDC, John led the infectious disease laboratory at the Minnesota Department of Health for 19 years. John received his MS and PhD degrees from the University of Minnesota.

Ettore Severi

ECDC, Sweden

Ettore Severi joined the FWD group in ECDC in January 2013 as expert in outbreak response. He's a pharmacist by training, gained an MsC in epidemiology at the London School of Hygiene and Tropical Medicine and is an alumnus of the European Programme for Intervention Epidemiology and Training (EPIET, cohort 2010). As a pharmacist he worked in the private sector in Italy and with Médecins Sans Frontières in Malawi, Zambia and Kenya until 2008. After the MsC (2009) he worked in the Epidemiology Unit of the South-East & London regional office of the Health Protection Agency. His main research interests include outbreak response, epidemic intelligence and the prevention and control of hepatitis A in Europe.

Plenary Session Abstracts

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Plenary Session Abstracts

PLENARY SESSION A
DAY 1, MONDAY 6 NOVEMBER
9:15-10:30

Plenary Session A: Keynote address

Chair: Prof. Mike Catchpole, ECDC

Infectious Disease Elimination – Opportunities and Challenges: Past, Present and Future Perspectives

Presented by

Dr Donato Greco

Affiliation

Senior Research Fellow, International Prevention Research Institute Lion, France

Abstract

The eradication of infectious disease remains the vision for those responsible for the control and prevention of a group of diseases that continue to represent a major cause of preventable morbidity and mortality on a global scale. Following the successful elimination of smallpox, a number of other infectious diseases have been the subject of elimination programmes. To date, however, the initial promise offered by the success with smallpox has not been realised for other infections, although we are nearing success for a few.

This presentation reviews the history of infectious disease elimination efforts, and considers the factors that contribute to or present barriers to such efforts. These factors include the inherent adaptability of pathogens, as well as environmental and public health system factors. Success and failures are discussed focusing on the new capacities to day available both in technology and in the epidemiological workforce. The growing legion of field epidemiologist and public health practitioners married with new lab and communication technologies can realize the vision of eliminating infectious diseases and pursue a successful role in the near future.

Keywords: Disease eradication, diseases elimination, disease control.

PLENARY SESSION B
DAY 1, MONDAY 6 NOVEMBER
17:00-18:30

Plenary Session B: Working together for better outcomes

Chairs: Dr. Helena de Carvalho Gomes & Prof. Karl Ekdahl, ECDC

Working together for better outcomes

Presented by

Prof. Christiana Nöstlinger

Affiliation

Institute of Tropical Medicine, Department of Public Health, Antwerp, Belgium

University of Vienna, Faculty of Psychology, Vienna, Austria

Abstract

To resolve real-world problems in public health, different forms of collaboration between disciplines are needed. Most public health problems are complex, influenced by multi-level factors and require interventions that cut across these different levels, as proposed by socio-ecological models or health promotion frameworks focusing on an inter-sectoral approach (e.g. the Ottawa Charter).

This key-note delivers the conceptual framework for understanding multi-, inter- and transdisciplinary approaches in public health and infectious diseases. HIV serves as an example for a typical public health problem not confined to single academic disciplines.

The presentation touches on some of the challenges that interdisciplinary research in the HIV field has encountered (e.g. the contribution of social sciences, different conceptualization of evidence and respective evaluation standards and indicators, missing funding opportunities). Examples stem from recent collaboration in inter- and transdisciplinary projects, such as community-based epidemiological research among sub-Saharan migrants living in Belgium to assess HIV prevalence, and an ongoing PrEP demonstration project.

Five questions are being elaborated as a guiding framework to define whether and how multiple disciplines should be employed in public health research. Lessons drawn from the research examples show challenges as well as emerging opportunities and solutions, borrowing from “team science” as a way forward to solve complex public health problems.

PLENARY SESSION C
DAY 2, TUESDAY 7 NOVEMBER
9:00-10:30

Plenary Session C: Seasonal influenza surveillance – can we do with less than the 'full Monty'?

Chairs: Prof. Thea Kølsen Fischer, SSI, Denmark & Dr. Aura Timen, RIVM, The Netherlands

Influenza Surveillance: Why, how, notable successes, dramatic failures – and the anticipation of a wonderful "Big Data" future

Presented by

Prof. Lone Simonsen

Affiliation

Research Professor, Dept Global Health, George Washington University, Washington DC, USA

Abstract

Influenza is the poster child of surveillance systems. The key reason was always to be on the outlook for the next pandemic -- inspired by the deadly 1918 "Spanish influenza". With the availability of influenza vaccine since the 1960s, surveillance components track the seasonal burden of influenza: mild influenza-like illness (ILI) and hospitalizations and mortality). Adding mathematical modeling to the mix the data can be used to track or even forecast the peak and impact of seasonal influenza, the circulating strain subtype and its match with influenza vaccine strains.

I will discuss the long and century-long distinguished history and evolution of influenza surveillance systems from the "fax" era and to the recent excitement of "Big Data". These newer data are "syndromic" in nature, and include 1) ICD-coded diagnoses from record-level electronic health or claims records and 2) algorithms based on internet search activities, twitter and media reports. I will demonstrate how large-volume medical claims data can show influenza dissemination patterns with unprecedented spatio-temporal resolution, and then discuss the current barriers to the use of such electronic health (e-health) data. Then I will review the rise and fall of Google Flu Trends -- a system based on non-health internet searches that was received by public health with enormous expectations.

Despite recent setbacks and tough barriers, it is only a matter of time before "Big Data" are well integrated in influenza surveillance worldwide. "Hybrid solutions" of big data streams combined with traditional surveillance systems and e-health data for validation seems to be the way forward. This is about time as influenza surveillance has been sort of stuck in the 20th century fax era and left behind by other fields such as finance and weather tracking. A new generation of influenza surveillance systems will be here soon -- bringing rapid, flexible and deeply granular local- and global tracking, the timely evaluation of severity, the effectiveness of interventions/vaccines. This is needed for a more robust public health response to seasonal influenza as well as future pandemics.

PLENARY SESSION D
DAY 3, WEDNESDAY 8 NOVEMBER
9:00-10:30

Plenary Session D: Science Advocacy in times of alternatives facts and fake news

Chair: Dr. Osamah Hamouda, RKI, Germany

How to bridge the gap between a rational approach and an emotional approach? Experiences from the HPV-vaccination crisis in Denmark.

Presented by:

Dr. Kåre Mølbak

Affiliation

Statens Serum Institut, Copenhagen, Denmark. E-mail krm@ssi.dk

Abstract

Vaccination against human papillomavirus (HPV) was introduced in the Danish Childhood Vaccination Programme in 2009. The vaccine was well received, and 80% of girls in birth cohorts 1999 and 2000 became fully vaccinated. From 2013 an increase in suspected adverse reactions following immunization was reported, including mainly unexplained medical symptoms that otherwise also are commonly seen in young women. No study have showed an increased risk of having these symptoms among vaccinated individuals. Nonetheless, the safety concerns created considerable attention by written media, television, websites and social media. The content of this "infostorm" penetrated into the health care system, and health care workers began to share concerns over the safety of the vaccine. As these events unfolded, the vaccine uptake declined dramatically, and only 32% of birth cohort 2003 is fully vaccinated (as of 4/9-2017).

Efforts to counterbalance the crisis included research addressing vaccine safety and explaining the lifeworld of "the vaccinated girls". Furthermore, a mixed-methods approach was used to inform a campaign to convince hesitant parents to vaccinate their daughters. This campaign was implemented on Facebook and a designated website, 2017. At the present, vaccination rates are increasing, but it will take time to regain confidence.

The bridge the gap between the rational approach and the emotional approach (narratives and anecdotes) requires that scientists from various disciplines understand why this gap was created. We need to be aware of the difference between facts and opinions, between good and bad science, and understand how "fake news" can amplify. We also need to spend time on the social media, to show empathy, and recognize that research may lead to unplanned findings.

PLENARY SESSION E
DAY 3, WEDNESDAY 8 NOVEMBER
17:00-18:30

Plenary Session E: Public health event 2017

Chairs: Dr. Denis Coulombier, ECDC

Whole Genome Sequencing for Foodborne Disease Surveillance in North America

Presented by:

Dr. John Besser

Affiliation

U.S. Center for Disease Control and Prevention (CDC)

Abstract

For over 21 years molecular-based foodborne disease surveillance in North America has played a key role in detecting unrecognized problems in a wide range of food commodities. The ensuing investigations triggered interventions that have prevented millions of illnesses and saved billions of dollars of associated healthcare and lost productivity costs. Based on data from the U.S., Europe, and Australia, it appears likely that the implementation of whole genome sequencing (WGS) will substantially increase these benefits. Strategies that evolved over two decades to overcome laboratory, epidemiology, regulatory, and cultural barriers will be described, along with challenges and opportunities that have emerged with the implementation of WGS technology. Finally, the presentation will take a brief peek into a future that includes culture-independent diagnostic tests (CIDT) and metagenomics.

One Health EU-level perspective of Salmonella Enteritidis multi-country outbreak linked to contaminated eggs

Presented by:

Ettore Severi, ECDC

Affiliation

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

Abstract

In 2016, two countries reported through Epidemic Intelligence Information System for food- and waterborne diseases (EPIS-FWD) unusual increases of Salmonella Enteritidis cases with MLVA type 2-9-7-3-2: United Kingdom in January and the Netherlands in August. Cases with the same MLVA type were reported from other European Union/European Economic Area (EU/EEA) countries. Cross-border investigations were initiated to identify the source so that measures could be taken by Competent Authorities to stop the outbreak.

A probable case was S. Enteritidis positive with MLVA type 2-9-7-3-2 or 2-9-6-3-2 and symptom onset after 1 May 2016. A confirmed case was characterized by whole genome sequencing (WGS). Patient interviews, epidemiological studies and food/environmental testing was performed. Food trace-back and forward data were collected from Rapid Alert System for Food and Feed (RASFF).

Patient interviews suggested exposure outside home. Norway found the first WGS link to eggs. Dutch investigations revealed a common link to one Polish egg packing centre. Of 48 farms, 18 had 82 Salmonella positive flocks. Four MLVA types and four WGS types were identified in 10 farm isolates. Five outbreak-associated MLVA types represented 3962 cases in the European Surveillance System. Over 600 consignments with 97 million eggs were distributed to 18 EU/EEA and 30 million eggs to 12 third countries during the withdrawal period. As of 5 May 2017, 13 EU/EEA countries have reported 230 confirmed and 245 probable cases. Of these, 41 reported travel history to another EU country. Two patients have died.

The outbreak underlines the importance of cross-sectorial investigations both at national and EU level. WGS was crucial to narrow down the investigations for source identification. RASFF system was effective for coordinating targeted control measures.

Parallel Session Abstracts

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PARALLEL SESSION PROGRAMME
DAY 1, MONDAY, 6 NOVEMBER
11:00-12:40

Parallel Session 1: Antimicrobial resistance and healthcare-associated infections

O1.1 Travel to Asia associated with colonization with extended-spectrum beta-lactamase-producing Enterobacteriaceae upon hospital admission, Norway, 2014-2016

Laura Espenhain (1,2), S. B. Jørgensen (3), M. Sunde (4), T. M. Leegaard (3), M. M. Lelek (3), M. Steinbakk (1)

1. Department of Antibiotic Resistance and Infection Prevention, Norwegian Institute of Public Health
2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden
3. Department of Clinical Microbiology and Infection Control, Akershus university hospital
4. Department of Molecular Biology, Norwegian Institute of Public Health

Background

The prevalence of extended-spectrum beta-lactamase (ESBL)-producing Enterobacteriaceae has been increasing in Europe and ESBL has been seen in hospital outbreaks in Norway. We aimed to estimate the prevalence of fecal carriage of ESBL-producing Enterobacteriaceae in non-Intensive Care Unit (non-ICU) patients upon hospital admission and identify factors associated with carriage to guide screening recommendations.

Methods

Between October 2014 and December 2016, we recruited non-ICU patients admitted to five non-psychiatric departments for adults and one acute-care department for children at a Norwegian university hospital. Upon admission, rectal swabs or stool samples were collected for screening for ESBL-producing Enterobacteriaceae. Isolates were characterized by phenotypic methods. Patients or parents of children completed a questionnaire covering possible risk factors for ESBL colonization. We calculated prevalence and adjusted prevalence ratios (aPR) using binomial regression.

Results

Of 746 patients, 50 (6.7%) were colonized with ESBL-producing Enterobacteriaceae; 92% (46/50) with Escherichia coli and 14% (7/50) with Klebsiella pneumoniae. 43 (86%) patients had isolates with co-resistance to ciprofloxacin. Prevalence of ESBL was higher among travelers to Asia (15/39; prevalence=38% compared with non-travelers to Asia (35/707; prevalence=5.0%; aPR=7.7; 95%CI 4.6-13; p<0.001). Previous hospitalization in Norway (aPR=0.81; 95%CI 0.45-1.5; p=0.47) or antimicrobial treatment 12 months prior to admission (aPR=1.4; 95%CI 0.85-2.3 p=0.18) was not associated with ESBL colonization.

Conclusion

The observed prevalence of ESBL colonization upon admission was lower than that reported in similar studies in Germany (9.5%) and the Netherlands (8.2%), but comparable with previous studies in Norway and Sweden. Consistent with other studies, travel to Asia was associated with ESBL colonization and needs to be included in the screening recommendations.

Keywords: Cross-Sectional Studies, Prevalence, beta-Lactam Resistance, Hospitals University

ABSTRACT ID: 828

PRESENTED BY: Laura Espenhain (laes@fhi.no)

O1.2 Need for standardisation of antimicrobial policy and surveillance for Neisseria gonorrhoeae in Northern Ireland, 2015

Anna Maisa (1,2), L. Patterson (2), S. Quah (3), M. Cole (4), N. Irvine (2)

1. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
2. Public Health Agency, Health Protection Service Northern Ireland, Belfast, Northern Ireland
3. Genito-Urinary Medicine, Royal Victoria Hospital, Belfast, Northern Ireland
4. Antimicrobial Resistance and Healthcare Associated Infections Reference Unit, Public Health England (PHE), Colindale, England

Background

In Northern Ireland (NI), disease notification data indicated a 3-fold increase in gonococcal infections between 2010 (n=206) and 2015 (n=619). Since 2015, NI has participated in a Europe-wide sentinel surveillance system (Euro-GASP) to monitor the emerging antimicrobial resistance of Neisseria gonorrhoeae to first-line treatment with ceftriaxone and azithromycin. We compared routine laboratory and sentinel surveillance antimicrobial susceptibility data from 2015 to identify deviations in order to inform testing and surveillance policy.

Methods

Antimicrobial susceptibility of sentinel isolates was performed at the Public Health England reference laboratory using the agar dilution technique. Minimum inhibitory concentrations (MIC) were interpreted using European Committee on Antimicrobial Susceptibility Testing (EUCAST) breakpoints. Routine antimicrobial susceptibility data was reported from local laboratories in NI using Etest and EUCAST breakpoints, however, antibiotic susceptibility testing panels varied across different laboratories.

Results

Of the 36 sentinel isolates, all were susceptible to ceftriaxone, 14% (5/36) were resistant to azithromycin and 39% (14/36) were on the breakpoint of azithromycin resistance (MIC 0.5 mg/L). Of the azithromycin resistant isolates, 80% (4/5) had a MIC of 1 mg/L. From routine laboratory surveillance, antimicrobial susceptibility data was reported for 35% (221/626) of confirmed cases of gonococcal infection. Ceftriaxone resistance was found in 0.5% (1/207). All 41 isolates tested for azithromycin were susceptible.

Conclusion

These findings highlight the deviation between the sentinel and routine laboratory surveillance data on gonococcal antimicrobial resistance. The extent of azithromycin resistance in the sentinel isolates is of concern. We recommend standardising local laboratory testing panels in NI and continuing the sentinel scheme using reference laboratory methodology to both complement routine laboratory surveillance and allow comparison with other European countries.

Keywords: Neisseria gonorrhoeae, Sexually Transmitted Diseases, Antimicrobial Resistance, Sentinel Surveillance

ABSTRACT ID: 775

PRESENTED BY: Anna Maisa (anna.maisa@gmail.com)

01.3 A comparative analysis of prophylactic antimicrobial use in Ireland (HALT study 2013 and 2016)

Meera Tandan (1), R O' Connor (2), K Burns (3, 4), H Murphy (3), S Hennessy (3), F Roche (3), S Donlon (3), M Cormican (5), A Vellinga (1, 5)

1. Discipline of General Practice, School of Medicine, National University of Ireland (NUI) Galway, Ireland
2. Discipline of pharmacology, School of Medicine, National University of Ireland (NUI) Galway, Ireland
3. Health Protection Surveillance Centre (HPSC), Dublin, Ireland
4. Department of Clinical Microbiology, Royal College of Surgeons in Ireland (RCSI), Dublin, Ireland
5. Discipline of Bacteriology, School of Medicine, National University of Ireland (NUI) Galway, Ireland

Background

There are concerns regarding the extent of inappropriate antimicrobial prophylaxis. This study explores the use and factors associated with antimicrobial prophylaxis in long-term care facilities (LTCFs) in Ireland.

Methods

The data are from the HALT point prevalence survey on health care-associated infections (HCAI) and antimicrobial use in LTCFs (2013 and 2016) in Ireland. In 2013, 9,318 residents recorded from 190 LTCFs and 10,044 residents from 224 LTCFs in 2016. Details were collected regarding the facility and the residents. Information on age, gender, antimicrobial, and indication were collected with respect to residents meeting the surveillance definition for a HCAI and/or prescribed an antimicrobial.

Results

Of the 10% residents on antimicrobials, 40% of the indication was prophylaxis. Among the antimicrobials prescribed for urinary tract infections (UTIs), 62% were prophylactic and of the antimicrobials for skin/wound infections, 20% was prophylaxis. The only change between 2013 and 2016 was an increase in the proportion of prophylaxis prescribing for respiratory infections (RTIs) from 16% to 26%. Nitrofurantoin and trimethoprim were the main prophylactic agents for UTIs (more than 95%), tetracycline for skin/wound prophylaxis (71%) and macrolides for RTIs prophylaxis (81%). Nearly 80% of prophylaxis had no end date. Of the prophylaxis prescription, more than 50% in intellectual disability facilities and around 40% in nursing homes. Enteral vancomycin prophylaxis for skin/wound and multiple types of prophylaxis for UTI were recorded. Prophylaxis was more often recorded for females, residents living in LTCFs for >1 year and residents with a urinary catheter.

Conclusion

Even though guidelines only support prophylaxis in specific circumstances and generally for a limited duration, the high prevalence of prophylaxis and lack of improvement point to key opportunities for education and antimicrobial stewardship.

Keywords: Antimicrobials, Prophylactic, long-term care facilities, HALT, surveillance

ABSTRACT ID: 955

PRESENTED BY: Meera Tandan (m.tandan1@nuigalway.ie)

01.4 Development of a novel application for visualising infectious disease data in hospital settings

Catherine M. Smith (1), Z. Kozlakidis (1, 2), D. Frampton (2), E. Nastouli (3), P. G. Coen (4), D. Pillay(2), A.C. Hayward (1)

1. Farr Institute of Health Informatics Research, UCL, London, UK
2. Division of Infection, Medical School, UCL, London, UK
3. Department of Clinical Virology, University College London Hospitals NHS Foundation Trust, London, UK
4. Infection Control office, University College London Hospitals NHS Foundation Trust, London, UK

Background

Whole genome sequencing, and other molecular methods, can be used to identify potential chains of transmission of infections in hospitals. However, integrating this information with epidemiological data to guide control measures is challenging. We aimed to produce an interactive application for visualisation of hospital infection data for use by infection control teams and researchers.

Methods

We developed this application using Shiny, the web application framework for R. The minimum data set required to run the application comprises admission and sample dates and the ward on which the sample was taken. Optional additional data are dates of patient ward transfers, descriptive patient characteristics including genetically defined clusters, and genetic distances between infections. We demonstrate this application with a case study of 242 influenza samples from a UK hospital (September 2012 to March 2014), which were sequenced as part of the ICONIC project.

Results

The application presents two data visualisations: One displays epidemic curves of the numbers of cases of the infection over time, both overall and separately for each ward. Interactive options allow the user to change graph scales and display subsets of the data. The second visualisation is a schematic representation of hospital wards that shows patient locations on a given date. It then highlights epidemiological and genetic links between patients.

Code for the tool is open-source, and available at www.github.com/cathsmith57/HospMap.

Conclusion

This novel application produces visual displays to aid interpretation of complex epidemiological and genomic data in hospital settings. Advantages include its flexibility for use in any setting with similar data on any pathogen. A challenge is integration with existing hospital systems to facilitate data import.

Keywords: Infection control, Cross infection, Influenza human, Disease outbreaks, Molecular epidemiology

ABSTRACT ID: 988

PRESENTED BY: Catherine Smith (catherine.smith.13@ucl.ac.uk)

O1.5 Late breaker: Determinants for prolonged carriage of ESBL/pAmpC-producing Escherichia coli and Klebsiella pneumoniae in the general population

Cornelia C.H. Wielders (1), E. van Duijkeren (1), C.M. Dierikx (1), A.H.A.M. van Hoek(1), P.D. Hengeveld (1), C. Veenman (1), A. Florijn (1), A. Lotterman (1), L.A.M. Smit (2), J.T. van Dissel (1), C.B.M. Maassen (1), S.C. de Greeff (1)

1. Centre for Infectious Disease Control (CIb), National Institute for Public Health and the Environment (RIVM), Bilthoven, the Netherlands
2. Institute for Risk Assessment Sciences (IRAS), Utrecht University, Utrecht, the Netherlands

Background

This longitudinal study aimed to investigate determinants of prolonged carriage of extended-spectrum β-lactamase and pAmpC β-lactamase-producing Escherichia coli and Klebsiella pneumoniae (ESBL-E/K) in the Dutch community.

Methods

Following a cross-sectional study among 2,432 adults (aged 20–72 years), a subset of ESBL-E/K positive (n=76) and negative (n=249) individuals provided four to five additional monthly faecal samples with questionnaires. ESBL-E/K was cultured using selective enrichment/culture and up to five colonies were characterized by phylogenetic group analysis and MLST. ESBL/pAmpC-genes were analysed using PCR and sequencing. Plasmids were characterized and subtyped. Prolonged carriage was defined as ≥4 positive samples. Determinants were analysed using univariate and multiple logistic regression analysis.

Results

In total, 1,896 samples from the 325 participants were included. Of the initially ESBL-E/K positive participants, 25/76 (32.9%) remained positive in all subsequent samples and carriage extended for >8 months (median 242 days). Fifty-one (67.1%) tested ESBL-E/K negative at some time point during the follow-up of which 31 (40.8%) stayed negative throughout the longitudinal study. Prolonged carriers often harboured the same ESBL-gene and plasmid and often, but not always, in similar bacterial strains, which is indicative of horizontal and clonal spread of ESBL-genes. Of the 249 initially ESBL-E/K negative participants, the majority (n=218; 87.6%) tested continuously negative, while 31 (12.4%) participants acquired an ESBL-E/K during the course of the study. Prolonged carriage was detected in 36 individuals and E. coli phylogenetic group B2 (OR: 11.2; 95%CI: 2.0-64.1), group D (OR: 10.4; 95%CI: 2.7-39.3), and travel to Asia, Latin America or Africa (OR: 3.5; 95%CI: 1.1-11.2) were associated determinants.

Conclusion

Sampling frequency and procedures (multiple colony selection) need to be taken into account to study the (molecular) epidemiology of ESBL-E/K.

Keywords: antimicrobial drug resistance, β-lactam resistance, ESBL, AmpC β-lactamases, carriage, longitudinal study

ABSTRACT ID: 1366

PRESENTED BY: Lieke Wielders (lieke.wielders@rivm.nl)

Parallel Session 2: Influenza and other respiratory viruses (1)

O2.1 Implementation of a surveillance system for Severe Acute Respiratory Infections (SARI) in Dutch pediatric intensive care units: Results from respiratory season 2016/17

G.S. Freidl (1,2), C.N.M. Brouwer (3), M. de Jong (4), M. de Neef (5), D. Markhorst (6), E. Roodbol (4), D. Tibboel (4), B. Timmers-Raaijmakers (7), G. Vos (8), Wim van der Hoek (1), Anne Teirlinck (1)

1. Centre for Infectious Disease Control, National Institute for Public Health and the Environment (RIVM), Bilthoven, The Netherlands
2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
3. Leiden University Medical Center, Pediatric Intensive Care Unit, Leiden, The Netherlands
4. Sophia Children's Hospital, Erasmus Medical Center, Rotterdam, The Netherlands
5. Emma Children's Hospital, Academic Medical Center, Amsterdam, The Netherlands
6. Vrije Universiteit Medical Center, Amsterdam, the Netherlands
7. Wilhelmina Children's Hospital, Pediatric Intensive Care, University Medical Center Utrecht, Utrecht, The Netherlands
8. Maastricht University Medical Center, Maastricht, The Netherlands

Background

During the 2009 influenza pandemic, insight into the epidemiology of severe cases was lacking, which hampered targeted provision of vaccine to high-risk groups. In response, the World Health Organization encouraged countries to implement surveillance for Severe Acute Respiratory Infections (SARI). We established a SARI surveillance system in Dutch pediatric intensive care units (PICU) to monitor SARI and provide early warning of serious respiratory infections.

Methods

Between week 42, 2016 and week 20, 2017, PICUs reported aggregated data weekly using an online platform. Reported data comprised number of patients on PICU, total number of SARI cases and number of newly admitted SARI cases by age group. For newly admitted SARI cases, PICUs also reported laboratory results.

Results

Six of eight PICUs in Dutch hospitals participated, covering ~75% of the pediatric population. SARI burden in PICUs was highest in week 50, accounting for 49% of admissions (24/49). SARI incidence peaked in week 49 at 39 cases (1.4 per 100.000 children <18 years). The cumulative seasonal incidence was 11.8 cases per 100.000 (n=321), and 81% of SARI cases were 0-1 years old. Laboratory results were available for 254/321 SARI cases (79%). Respiratory syncytial virus (RSV) was identified earliest, and most often (64%), followed by rhino/enterovirus (25%), other respiratory viruses (20%) and influenza (7%).

Conclusion

PICU surveillance meets the objective to clarify the epidemiology of SARI in the Dutch pediatric population. Most pediatric SARI cases in 2016/17 were caused by RSV, corroborating the observation that the early start of the respiratory illness season in primary care was mainly attributable to RSV rather than influenza. Surveillance results can be useful for capacity planning on PICUs, and public health communications about respiratory virus circulation.

Keywords: syndromic surveillance, severe acute respiratory infections, pediatric intensive care units, implementation

ABSTRACT ID: 820

PRESENTED BY: Gudrun Freidl (gudrun.freidl@rivm.nl)

O2.2 Novel insights into French (2013-2015) influenza (A) virus quasi-species in human specimens using Next Generation Sequencing (NGS): A toolbox to accurately predict intra and inter-seasonal evolution?

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Background

Predicting which influenza strains will predominate six months ahead of the upcoming season remains a considerable challenge for matching vaccine composition. Although rare, vaccine mismatch for A(H3N2) virus occurred in the 2014-2015 influenza season resulting in low vaccine effectiveness. Current understanding of the quasi-species structure and predictive value in virus evolution is limited. Ultra-deep sequencing (NGS) allows the finest resolution insights into the composition of genetically distinct quasi-species. The objective of this study was to assess whether viral quasi-species offer predictive value regarding emergence of antigenically distinct influenza viruses within and between subsequent seasons.

Methods

Clinical specimens from the primary care surveillance systems (Seasons:2013-2014&2014-2015), tested positive for influenza A(H3N2) by the National Influenza Center, were selected based on their occurrence during the pre-defined early-peak-end periods of the respective epidemic periods. NGS (Illumina) was performed targeting the HA gene. Sequences were assembled and three different algorithms were used to call minority variants (Qiagen CLC,ViVAN,Lofreq*) at a threshold value between 0.5 and 0.05%. Variants occurring in all three algorithms were selected for intra and inter-seasonal trend analyses based on SNP divergence and translational changes.

Results

Minority variants were retrieved from 163/219 samples (mean coverage:978, range:1-2276). A total of 441 unique SNPs, translating into 213 translational changes were identified in all quasi-species variant algorithms. Differential trends were observed among the different quasi-species both intra and inter-seasonal indicating possibly predictive temporal trends. Results are preliminary.

Conclusion

Initial results indicate that in-depth NGS-analyses provides data about quasi-species variants that potentially allow to more accurately predict trends of viral evolution. Development of NGS bioinformatics-pipelines integrated into surveillance systems can be used to augment more accurately informed definitions of the vaccine composition earlier in time.

Keywords: Influenza, High-Throughput Nucleotide Sequencing, algorithms epidemics, vaccines

ABSTRACT ID: 951

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

O2.3 Human protection measures during the epidemic of highly pathogenic avian influenza A(H5N8) virus infection in birds in the EU/EEA, 2016/17

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Background

During the winter 2016/2017, Europe faced a large epidemic of highly pathogenic avian influenza A(H5N8) virus infection with more than 8 million affected birds in 24 EU/EEA countries. Public health risk assessment and recommended measures require careful consideration to minimise risk to the population and ensure optimal public health response. We sought to improve understanding of these processes across EU/EEA countries.

Methods

We circulated an online questionnaire to national influenza experts in all EU/EEA countries in relation to risk assessment processes and public health recommendations during the ongoing outbreaks. Final data were extracted following further countries' responses and analysed descriptively.

Results

Twenty-two countries participated. Of these, eighteen performed a national risk assessment for A(H5N8) and all determined an overall low or very low risk to the general public. In most countries, occupational safety guidelines were available for cullers (20), farmers (20), veterinarians (21) or persons directly exposed (17) to sick birds. Goggles, masks, gloves and body suits were recommended as personal protective measures for people handling sick wild birds or poultry in outbreak situations. Influenza-like illness, acute respiratory infections and conjunctivitis were criteria used to determine the need for follow-up and testing among exposed persons. Antiviral pre- and/or post-exposure prophylaxis was recommended in six countries. Most countries (14) recommended vaccination of occupationally exposed persons against seasonal influenza. Animal and public health laboratories collaborated in 15 countries.

Conclusion

The level of recommended personal protection was high for exposed persons although the overall risk was considered low, with no evidence of bird to human transmission. Mode of antiviral prophylaxis varied across countries, with most not recommending such.

Keywords: Avian influenza, public health protection measures, vaccination, antiviral prophylaxis, occupational safety

ABSTRACT ID: 806

PRESENTED BY: Cornelia Adlhoch (cornelia.adlhoch@ecdc.europa.eu)

O2.4 Effect of influenza activity on the incidence and severity of invasive group A streptococcal disease: a retrospective study in England, 2008-2016

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Background

During 2016, an increase in invasive Group A streptococcal (iGAS) infections concurrent to a late influenza season was observed. This retrospective study aimed to assess the impact of influenza on development of iGAS infection and fatal outcome in order to inform prevention strategies.

Methods

Laboratory confirmed influenza and iGAS infections between 2008/2009 and 2015/2016 iGAS seasons (37th to 36th week) were extracted from the English laboratory surveillance system and combined using a unique patient identifier. Co-infection (influenza and iGAS) was defined as dual laboratory diagnosis within 15 days. All-cause case fatality rate (CFR) was calculated within one week of iGAS diagnosis.

Results

Overall, 44,429 influenza and 11,124 iGAS infections were identified. Co-infections were observed in 106 (0.2%) cases, 54.3% of which were female and with a median age 33.3 years. An increase in co-infections was observed during 2015/2016 (1.8%; 40/2,237) compared to previous seasons (0.2%; p=0.0001 to 0.8%; p=0.04), with the exception of the 2010/2011 season (2.0%; 24/1,193). Influenza A/iGAS co-infections were the most common (62.3%; 66/106) followed by influenza B (36.8%; 39/106). The CFR was significantly higher in patients whose iGAS infection was associated with influenza (22.6% vs 13.5%; p=0.006). During the 2015/2016 season, the CFR in patients with co-infection was higher still at 27.5% (11/40), particularly in children ≤6 years (38.4% vs 22.2% in adults; p=0.01).

Conclusion

The study confirmed the increase of iGAS/influenza co-infections in the 2015/2016 season, similar to that seen in 2010/2011, both dominated by influenza A(H1N1)pdm09. Given the severe impact of co-infections, particularly in young children, further investigation is needed to clarify whether influenza strain or seasonality could be key factors in coinfections, helping inform decisions in vaccine policy and contact management.

Keywords: Group A streptococcus, Streptococcus pyogenes, influenza virus, surveillance, coinfections

ABSTRACT ID: 928

PRESENTED BY: Laura Bubba (laura.bubba@phe.gov.uk)

O2.5 Views from the general public on communication and information dissemination during a pandemic; results and experiences from the 2016 Irish citizen consultation

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Background

Communicating well with the general public is important to disseminate information properly during a pandemic outbreak. We collected public views of how to communicate in order to help create successful policies.

Methods

As part of the ASSET project, funded through FP7, we held citizen consultations simultaneously in eight European countries, following a design created to facilitate this multi-site consultation. Each country had approximately 50 participants, representing demographics of the country and participants were given a unique anonymous ID to facilitate stratification of results by gender, age. In Ireland 51 people participated. A short film introduced each topic, followed by a set of questions that were discussed in groups. We then asked participants to fill out questionnaires. The topics were: Personal freedom and public health safety; Communication between citizens and public health authorities; Transparency in public health; and Access to knowledge. The final session was an open session on policy recommendations.

Results

Findings from the 25 questions show at times diverging views from the Irish and the overall data: for example, General Practitioners were most trusted source of information overall whereas in Ireland it was European health authorities. Overall, the opinion was that public health interests should infringe on individual freedom in an emergency, however the Irish consultation didn't support mandatory vaccination for healthcare workers. 73% preferred clear one-way communication from health authorities as their source of information during a pandemic and transparency was key to build trust.

Conclusion

The results showed great enthusiasm among citizens to be included in policy development when possible. The difference in age in preferred information source and the evolving social media communications channels makes a continuous dialogue especially valuable for devising effective policy.

Keywords: Communication, Information dissemination, Public Health, Emergency, Vaccination, Europe

ABSTRACT ID: 990

PRESENTED BY: Rebecca Moore (moorerm@tcd.ie)

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

O3.1 A cluster of hepatitis C virus infection in a hematology ward – next generation sequencing analysis reveals close relationship among viral variants

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Background

On 18/12/2015 a suspected HCV outbreak in a county hospital was reported to local public health department, with 5 cases diagnosed among patients of hematology ward. We investigated the outbreak to determine its extent and identify transmission routes.

Methods

We defined the case as a previously undiagnosed HCV infected patient, hospitalized in the hematology ward between 1st August and 31st October. We selected the exposure period based on HCV incubation time. We attempted to screen all patients hospitalized during exposure period and collected exposure data from medical records. Relative risks were calculated from Poisson regression. Next-generation sequencing (NGS) analysis of hypervariable region 1 (HVR1) was used to search for relationship of HCV variants.

Results

Of 129 people eligible for screening, 34 died before being reached, 17 refused or could not be contacted, and 78 were tested. HCV infection was confirmed in 11 (14%) patients, of whom in seven HVR1 amplification was feasible. NGS analysis revealed predominating viral variant sequence similarity of 98.3% -100.0%, whereas similarity to control sequences from acute cases ranged from 76.0% to 82.3%. The infection risk increased by 5.8% (95% 3.0-8.7%) per day of hospital stay. No specific procedure or date was associated with infection. However, minor procedures (e.g. i.v. line flushing, injections) were not fully documented. Multidose vials of fraxiparine and saline were used.

Conclusion

Our results indicate a close relationship of the virus in the hematology ward patients suggesting a common source of infection, despite inconclusive exposure analysis. Plausible transmission route includes breaches in minor procedures. As HCV outbreak investigations inevitably rely on medical documentation, we recommend that at least those minor procedures, which were previously linked to transmission, be documented in detail.

Keywords: HCV, Hepatitis C, Healthcare Associated Infections, Infection Transmission, Molecular Epidemiology

ABSTRACT ID: 962

PRESENTED BY: Magdalena Rosinska (mrosinska@pzh.gov.pl)

O3.2 A national hepatitis C screening guideline – a step toward elimination

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Background

Treatment advances have shifted the paradigm of hepatitis C virus (HCV) towards elimination. The WHO aims to eliminate HCV as a public health threat by 2030, stating that national testing policies and increased investments screening services are needed. In Ireland, we developed a national screening guideline to improve the identification of undiagnosed infections and progress the goal of elimination.

Methods

A Guideline Development Group (GDG) consisting of key stakeholders developed the guideline. Recommendations were adapted from existing high quality guidelines where appropriate. Where existing recommendations did not exist or were insufficient, systematic literature reviews were undertaken to provide an evidence base. In formulating recommendations the GDG considered: the quality of available evidence, local epidemiology, national policy, balance of benefits and harms, cost-effectiveness, budget impact, health equity, acceptability, and the feasibility of implementation.

Results

The guideline makes 26 recommendations spanning who and how to screen, promotion of screening, and linkage to care. In addition to traditional risk groups, screening is recommended for: migrants from a country with a HCV prevalence >2%; men who have sex with men; and non-injecting drug users. Birth-cohort screening could not be recommended the absence of a comprehensive health technology assessment. A comprehensive implementation plan and a monitoring and evaluation framework are included.

Conclusion

While a number of recommendations reiterate current practice, implementation of others will require novel approaches and multisectoral commitment. Linkage to care and treatment will be key to the success of the guideline. A national treatment programme aims to provide treatment to all persons infected with HCV in the coming years. Implementation of this guideline, in conjunction with expansion of treatment access will advance Ireland toward the goal of HCV-elimination by 2030.

Keywords: hepatitis C, screening, prevention and control

ABSTRACT ID: 1058

PRESENTED BY: Eve Robinson (eveprobinson@gmail.com)

O3.3 A cross-sectional sero-survey on preoperative HBV vaccination policy in Poland

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3. Department of Computer Science and Education Quality Research, Pomeranian Medical University, Szczecin, Poland

Background

Study objective was to evaluate a two-dose preoperative HBV vaccination policy, which has been widely accepted in Poland in the last twenty years, by an assessment of the proportion of patients who don't present a protective level of anti-HBs (<10.0 mIU/ml) after receiving a second dose.

Methods

Consecutive patients from surgical/gynecologic wards of 12 randomly selected hospitals in West Pomerania, Poland, hospitalized between 2010-2013, vaccinated against HBV with a two-dose regimen, were asked to complete an anonymous questionnaire. Serum samples were assayed for anti-HBs with the use of third-generation testing methods. A ROC curve was determined to compare sensitivity versus specificity across a range of values for the ability to predict a protection against HBV infection.

Results

There were 193 patients, 58.5% women, median age 52 years. Almost a half (46.0%) were operated on within 0-60 days after taking the second vaccine dose, 16.2% – 61-180 days after, 37.8% >180 days after. Anti-HBs titer was <10.0 mIU/ml in 49.2% of participants; none of them were aware of this fact. Age ≤52 years (OR=1.89) and having surgery more than 37.5 days after HBV vaccination (OR=2.70) were associated with greater odds of being protected. For the time frame between the second dose implementation and surgery >37.5 days-60 days, a sensitivity of 80% and specificity of 41% for obtaining protection against HBV infection was found; there was an apparent peek on the ROC curve between 38-60 day.

Conclusion

Current recommendations regarding a preoperative policy with a 2-dose vaccination schedule in Poland should be revised; the best time to perform surgery after the implementation of the second dose of vaccine in the context of patient protection against HBV infection would be 38-60 days.

Keywords: preoperative, vaccination, HBV, schedule, anti-HBs, protection

ABSTRACT ID: 1064

PRESENTED BY: Maria Ganczak (ganczak2@wp.pl)

O3.4 Syphilis outbreak investigation in northern Manitoba, Canada: Use of enhanced surveillance and social network data to inform public health action.

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4. Northern Regional Health Authority, Manitoba, Canada

Background

In response to a syphilis outbreak in northern Manitoba, enhanced surveillance using a social network informed questionnaire was implemented in late 2015. Analysis was conducted to better understand the outbreak in order to implement data informed public health actions.

Methods

An enhanced surveillance syphilis investigation form was created and used to gather information on cases and their reported sexual contacts. This included social network questions including how individuals with syphilis had met new sexual partners in general and where specifically they met each identified sexual contact. Social network analysis included looking at connections between cases and contacts and between cases and locations.

Results

From January 1, 2013 to August 31, 2016, 148 infectious cases of syphilis were identified. Females made up 41.1% (60) of the cases and one congenital case of syphilis was also reported. Enhanced data was available for 72.6% of the cases. The majority of social networks (components) are heterosexual in nature and include individuals from more than one community. 48.1% (51) of individuals met new sexual partners through house parties, 38.7% (41) through friends/family, 22.6% (24) at hotels/bars and 16% (17) through social media.

Conclusion

This is primarily a heterosexual outbreak, raising the concern of congenital syphilis. Policy changes to prenatal screening practices were implemented. Communication between communities/health regions is critical given that sexual networks are not restricted by geographic boundaries. People are meeting new sexual partners through house parties and existing friend networks. A poster was developed to relay key messages and dissemination of the poster informed by social network location data. Enhanced surveillance and social network analysis allowed for region specific data informed actions.

Keywords: Syphilis, Outbreak, Social Network Analysis,

ABSTRACT ID: 1088

PRESENTED BY: Tammy Stuart Chester (tammy.stuartchester@canada.ca)

O3.5 Estimating the annual burden of chlamydia, gonorrhoea, hepatitis B and syphilis to advise prioritisation of prevention and control strategies, Slovenia, 2011-2015

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

Background

Sexually transmitted infections (STI) and their complications have a significant impact on population health. Reported incidence underestimates true number of cases, and does not provide insight into burden of sequelae. The objective of this study was to estimate the burden in disability-adjusted life years (DALYs) of chlamydia, gonorrhoea, hepatitis B and syphilis in Slovenia, in order to prioritise public health interventions.

Methods

We used surveillance notifications to estimate the 2011-2015 age- and sex-specific mean annual incidence of selected acute symptomatic STI per 100.000 population. Multiplication factors were derived from published literature and Slovenian estimates for chlamydia and applied to account for underestimation of cases. We estimated DALYs with 95% uncertainty intervals (UI), using the Burden of Communicable Diseases in Europe toolkit from ECDC.

Results

Chlamydia had the highest estimated burden at 9.81 DALYs per 100.000 population per year (95% UI: 5.53-16.87). Hepatitis B accounted for 1.09 DALYs per 100.000 population (95% UI: 0.77-1.52) while the estimated burden of both gonorrhoea and syphilis was 0.05 (95% UI: 0.04-0.06) DALYs per 100.000 per year. For all STI, sequelae were the main component of the overall burden. The burden of chlamydia was higher in women <34 years old (37.52 DALYs per 100.000 stratum-specific population (UI: 16.41-73.06)) compared to all other women (4.77 DALYs per 100.000 stratum-specific population (UI: 2.07-9.82)).

Conclusion

STI, particularly chlamydia, and their sequelae represent a substantial health burden in Slovenia. Both primary prevention measures and treatment of diagnosed cases are critical in reducing the burden of all STI. In addition, we advise offering testing for chlamydia to all sexually active women <34 years old seeking primary care, to provide for early diagnosis and timely treatment to prevent sequelae.

Keywords: Burden of disease, sexually transmitted infections, chlamydia, gonorrhoea, syphilis, hepatitis B, prevention

ABSTRACT ID: 864

PRESENTED BY: Sanja Vuzem (sanja.vuzem@nijz.si)

PARALLEL SESSION PROGRAMME
DAY 1, MONDAY, 6 NOVEMBER
14:30-15:30

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

O4.1 Analyzing emerging trends of Zika apprehension in high epidemic setting

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2. Department of Social and Behavioral Sciences, School of Public Health, Rennes, France

Background

During the last decade, French Guiana has been affected by major dengue fever outbreaks. Although this arbovirus has been a focus of many awareness campaigns, very little information is available about beliefs, attitudes and behaviors regarding vector-borne diseases among the population of French Guiana. In late 2015, population faced the emergence of Zika virus that led to an outbreak in the following year. The aim of the study was to assess and characterize perceptions, knowledge and behaviors in the context of zika emergence.

Methods

A cross-sectional phone survey was conducted among the general population with a total of 1129 individuals interviewed. The sample was based on a random cluster, stratified on municipalities with a proportional allocation. A multiple correspondence analysis associated with a hierarchical cluster analysis was performed to identify groups regarding the level of risk perception and knowledge.

Results

Population seemed aware of zika infection with more than 80% that properly identified zika as a vector borne disease and 79% who knew that zika can be transmitted from mother to child. The infection appeared as a new health threat, more dreadful than dengue fever and chikungunya disease, with women more worried than men whatever their level of knowledge. Experience was associated with the level of knowledge and risk perceptions were associated with behaviors.

Conclusion

Findings suggested that women well assimilated prevention and information messages and understood the risk associated with zika infection. These results have implications for the development of multifaceted infection control programs, including strategies for prevention and awareness, helping the population to develop an accurate perception of the threat they are facing.

Keywords: Zika, Emergence, Risk Perceptions, Knowledge, French Guiana

ABSTRACT ID: 959

PRESENTED BY: Camille Fritzell (camillefritzell@gmail.com)

O4.2 The impact of Ebola Treatment Centre caseload on fatality among suspected Ebola Virus Disease cases during the 2014/15 outbreak in Conakry, Guinea

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6. Clinical Sciences Department, Institute of Tropical Medicine, Antwerp, Belgium

Background

During the 2014/15 Ebola Virus Disease (EVD) outbreak, Ebola Treatment Centres (ETC) functioned as triage points for any ill person possibly suffering from EVD, on top of isolation of confirmed cases. Admitting many suspect EVD cases increased bed occupancy and workload in the ETC, delayed diagnosis and treatment and increased risk for nosocomial EVD infection. Following laboratory testing for viral RNA, suspect cases become either confirmed EVD cases who remain in the ETC, or non-cases to be discharged after testing EVD negative. Our objective was to investigate the influence of admission numbers on death of suspected EVD cases (EVD cases and non-cases), in the Conakry ETC.

Methods

Admission and medical records of EVD cases and non-cases between March 2014 and September 2015 were retrospectively analyzed. We measured the association between being admitted during an increased-caseload-week (≥20 admissions more than in previous week) or a high-caseload-week (≥50 admissions during the week) and death using logistic regression. We controlled for age, sex, origin and admission delay, and present adjusted odds ratios (OR) with 95% confidence intervals.

Results

In total, 377 (45.9%) of 822 EVD cases and 98 (6.4%) of 1,540 non-cases died. EVD cases admitted during an increased-caseload-week or high-caseload-week were not more likely to die (OR 0.94; 95%CI 0.70-1.26 and OR 1.08; 95%CI 0.82-1.43 respectively). However, non-cases were less likely to die when admitted during an increased-caseload-week (OR 0.31; 95%CI 0.17-0.58) or high-caseload-week (OR 0.61; 95%CI 0.38-0.96).

Conclusion

While EVD-case fatality was stable during busy admission weeks, the decreased fatality of non-cases might be explained by early admission of less severely ill contacts of EVD cases in outbreak intense weeks.

Keywords: Ebola Virus Disease, Ebola Virus, Guinea/epidemiology, Disease Outbreaks, RNA, Viral/analysis

ABSTRACT ID: 933

PRESENTED BY: Brecht Ingelbeen (brechtingelbeen@gmail.com)

O4.3 Urban yellow fever outbreak – Democratic Republic of the Congo (DRC), 2016: learning for future urban outbreaks

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Background

Between December 2015 and July 2016 a yellow fever (YF) outbreak affected urban areas of Angola and DRC, with 884 laboratory-confirmed cases (121 deaths) in Angola and 81 confirmed cases (16 deaths) in DRC. Due to increasing presence of its mosquito vector (Aedes ssp.), outbreaks will probably reoccur in cities. Our study objective was to describe the outbreak and thus facilitate early recognition and diagnosis of future cases.

Methods

We retrospectively analyzed characteristics and outcomes of 78 laboratory-confirmed YF cases in DRC using case investigation and hospital admission forms. Suspect cases presenting with jaundice within 2 weeks after acute fever onset were tested for YF by IgM serology or PCR for viral RNA.

Results

Seventy-three percent of confirmed cases (57/78) had travelled from Angola: 88% (50/57) men; median age 31.0 years (IQR 25.0 – 36.5). Nineteen percent (15/78) were infected locally in urban settings in Kinshasa (n=8), Kwango (n=4), and Kongo-Central (n=3) provinces. We identified one geographical cluster of three cases in the same Kinshasa neighborhood. All other cases were widespread. Median time from symptom onset to healthcare consultation was 6.5 days (IQR 5-9), to appearance of jaundice 8 days (IQR 7-11), to sample collection 9 days (IQR 7-14), and to hospitalization 16.5 days (IQR 10.5-25.5).

Conclusion

As jaundice appears late, most cases were only diagnosed and confirmed after two weeks, often too late for supportive care and prompt vector control. Local vector control was complicated because cases were not restricted to discrete neighborhoods. In areas with known local YF transmission, a wider suspect case definition without jaundice as essential criterion and improving access to primary care could facilitate earlier YF diagnosis, care and control.

Keywords: Yellow Fever, Yellow fever virus, Disease Outbreaks, RNA, Viral/analysis, Democratic Republic of the Congo/epidemiology

ABSTRACT ID: 832

PRESENTED BY: Brecht Ingelbeen (brechtingelbeen@gmail.com)

Parallel Session 5: Food- and waterborne diseases and zoonoses (1)

O5.1 An international outbreak of foodborne botulism associated with the consumption of dried roach (Rutilus rutilus), Germany and Spain, November-December 2016.

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2. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden
3. Chemisches und Veterinäruntersuchungsamt Stuttgart, Fellbach, Germany
4. National Centre of Epidemiology, Institute of Health Carlos III, Spain
5. CIBER Epidemiología y Salud Pública (CIBERESP), Institute of Health Carlos III, Spain
6. Biological Toxins (ZBS 3), Centre for Biological Threats and Special Pathogens, Robert Koch-Institut, Berlin, Germany
7. Department for Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany

Background

Early November 2016, two cases of foodborne botulism were notified almost simultaneously in two German states. We describe the epidemiological and laboratory investigations that followed.

Methods

Cases were persons hospitalized in the EU with clinical symptoms of foodborne botulism, 1/10/2016 through 31/12/2016. Local health authorities collected information on food consumption. Food safety authorities collected food samples and initiated traceback investigations. Serum, stool and food samples were tested by mouse bioassay (MBA) and/or PCR for the detection of botulinum neurotoxin (BoNT) or bont genes, confirmed by a reference laboratory. German authorities issued international warnings through European alert networks.

Results

Four additional cases were identified: two in Germany, two in Spain. All six were of Russian/Kazakh background. Age ranged from 37 to 55 years. Two were female. Two cases tested positive for BoNT/E (in serum), four for bont/E (in stool). Two cases were laboratory unconfirmed. All were hospitalised (1 to 21 days), four required ventilation, two received antitoxin, all recovered. All cases had consumed salt-cured, dried roach (Rutilus rutilus), purchased at five different retail locations. Presence of bont/E (PCR) was confirmed in two household fish samples. BoNT/E was confirmed (MBA) in one household and two retail fish samples. Traceback investigations identified the distributor of the implicated roach products in Europe. Precise product and batch numbers could not be determined due to missing labels at retail, prompting a multi-product EU-wide recall.

Conclusion

This is the first international outbreak of foodborne botulism in the EU. Dried roach was identified as the source of infection. Although additional cases were likely prevented by the recall, continued monitoring is required. Existing stringent food traceability and production standards for counter-sale fish products require enforcement.

Keywords: disease outbreaks, botulism, botulinum toxins, clostridium botulinum

ABSTRACT ID: 1003

PRESENTED BY: Christiane Wagner-Wiening (David.Hendrickx@rps.bwl.de)

O5.2 Ice cube outbreak caused by leaking air ventilation valve – evidence of a novel vehicle for viral gastroenteritis outbreaks

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2. University of Helsinki, Finland
3. Water and health and Viral infections, National institute for Health and Welfare, Helsinki, Finland

Background

A gastrointestinal outbreak was reported among 154 Christmas party visitors during 9th and 10th December, 2016. Two groups had buffé dinner in the same restaurant, a few cases were reported among a la carte diners.

Methods

A retrospective cohort study was undertaken among two dining groups and an inspection to restaurant. Faecal samples were tested for routine pathogens, water, ice and air ventilation device for indicator bacteria and/or norovirus and sapovirus.

Results

The main symptoms were diarrhea with fever, nausea and vomiting, also two cases of bloody diarrhea were reported. Among those 91 enrolled, 24 fulfilled the case definition. Three cases of norovirus genogroup I were detected in faecal samples, one of these cases also had sapovirus with a family member diagnosed with the same pathogens. Ice cubes in water or drinks (RR 6.5, 95 % CI 1.5-113.0) or both (RR 8.2, 95 % CI 1.7-145.5) was the only significant factor in a dose response manner. Ice cubes from three vending machines had high levels of heterotrophic bacteria. There was no breakage in the water pipe line system, nor construction works. A faulty air ventilation valve was identified in the same room space as the ice cube machines and was considered a likely cause of this outbreak. The air ventilation valve pipe was drawn to another space.

Conclusion

The likely source of this viral gastrointestinal outbreak by contaminated ice cubes was a leaking air ventilation valve in the ice cube preparation room space. Both leaking air ventilation valves and dried-up U-traps in floor drains may serve as routes of virus contamination in high hygiene spaces. This may represent a neglected route of transmission and warrants further studies.

Keywords: norovirus, disease outbreaks, public health surveillance, diarrhea, ice

ABSTRACT ID: 958

PRESENTED BY: Katri Jalava (katriyalava@gmail.com)

Parallel Session 6: Vaccine- preventable diseases (1)

O6.1 Addressing HPV vaccine hesitancy in Denmark, 2017

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4. Infectious Disease Preparedness, Statens Serum Institut, Copenhagen, Denmark

Background

Vaccination of 12-year-old girls against human papilloma virus (HPV) was included in the Danish vaccination program in 2009. Since 2014, increased public concerns about vaccine safety have resulted in a dramatic decrease in uptake.

In 2016, we initiated an investigation to better understand parents' and girls' knowledge, attitudes and decision patterns regarding HPV vaccination to design an information campaign.

Methods

We applied a mixed-methods approach: (1) a media analysis investigating online trends and mapping the media consumption of parents and daughters; (2) focus group interviews with mothers and double interviews with young girls looking into knowledge and risk perception; perceived credibility of national public health organizations, general practitioners, and others; household dynamics and message framing; and (3) a survey including a representative sample of 1,000 parents to validate conclusions from the focus group interviews.

Results

Mothers are primary decision makers regarding HPV vaccination of their daughters. Their primary source of information is online media, particularly Facebook. Thirty-four percent of survey respondents were vaccine hesitant. Hesitant parents indicated relatively high confidence in GPs, but less than half had discussed HPV-vaccination with them. The respondents had a lack of knowledge on several HPV-related facts.

Three main messages showed potential for convincing hesitant parents to vaccinate their daughters: 1) high prevalence of HPV infection in young women; 2) scientific consensus on HPV vaccine effectiveness; and 3) risk of cervical cancer versus risk of adverse events.

Conclusion

Based on these findings, the HPV vaccination information campaign is implemented on Facebook and a designated website. It focuses on presenting facts to parents including the three above-mentioned main messages. Material targeted at healthcare personnel is developed to prime them for evidence-based conversations with parents.

Keywords: vaccination, communication, public health, qualitative research, surveys

ABSTRACT ID: 773

PRESENTED BY: Stine Ulendorf Jacobsen (suja@sst.dk)

O6.2 Attitudes towards vaccinations among adults in the Swedish population 2016 – A cross-sectional survey

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2. Lund University, Department of Translational Medicine, Sweden

Background

The World Health Organization (WHO) promotes a life-course approach to immunizations. In Sweden, there is no adult National Immunization Program in place and attitudes to vaccination in the adult population has rarely been described. This study aimed to examine vaccine hesitancy and attitudes towards vaccinations among adults in the Swedish population and to evaluate the feasibility of a web-based survey panel for continuous monitoring of vaccine hesitancy and attitudes.

Methods

A web-based survey was sent to 4885 adults (16-85 years) who participated in an ongoing survey panel run by the Public Health Agency of Sweden. The survey included questions on: vaccinations received, vaccine safety, hesitancy and vaccination information channels. Feasibility of the web-based survey was evaluated in terms of response rate by background factors in comparison to the total population.

Results

3086 adults (80%) responded to the questionnaire. Preliminary analysis indicated 62% had received a vaccination within the last five years of which vaccinations for influenza (56%) and tick-borne encephalitis (42%) were most common. Nearly 25% of participants had hesitated before at least one vaccination. 555 adults (18%) had been recommended vaccination but declined. Based on their responses participants were categorized as vaccinator, uncertain or vaccination-refuser. Analysis is ongoing of the importance of background variables for vaccine decision and hesitancy as well as of the feasibility of the web-survey.

Conclusion

It is important to describe and address the adults who are feeling hesitant in order to prevent potential vaccine refusal. Recurring attitude surveys are an important tool to capture changes in attitudes and to tailor intervention concerning vaccine hesitancy. Results will be used to tailor communication interventions to adults according to attitudes and characteristics.

Keywords: attitudes, vaccines, immunization, vaccine hesitancy

ABSTRACT ID: 889

PRESENTED BY: Emma Byström (emma.bystrom@folkhalsomyndigheten.se)

O6.3 Assessing determinants of the intention to accept a pertussis cocooning vaccination: a survey among various health care workers

Olga Visser (1,2), M.E.J.L. Hulscher (3), L. Antonise-Kamp (1), R. Akkermans (1), J. van der Velden (1), R.A.C. Ruiter (4), J.L.A. Hautvast (1)

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Background

Many countries have reported a resurgence of pertussis in recent decades. Pertussis booster vaccination for Health care workers (HCW)has been recommended, but the uptake has remained low. A vaccination program designed to carefully target the barriers and facilitators of acceptance could ensure optimal uptake. Therefore, the aims of this study were to assess HCWs' intention to accept a pertussis vaccination and to examine and quantify the determinants that influence this intention.

Methods

In our study we targeted Dutch maternity assistants, midwives, and paediatric nurses specifically. We developed a 123-item questionnaire based on a literature review and the Reasoned Action Approach (a social cognitive model of behaviour). With this questionnaire we explored the determinants of HCWs' intention to accept pertussis cocooning vaccination and assessed the behavioural beliefs underlying HCWs' attitudes towards pertussis cocooning. We used correlation and regression analyses to assess univariate and multivariate associations in the study variables.

Results

Altogether, 486 maternity assistants, 320 midwives, and 200 paediatric nurses completed the questionnaire; 45%–63% reported their intentions to accept pertussis vaccination. Attitude, anticipated affect regarding non-acceptance, and decisional uncertainty were uniquely associated with the intention to accept a pertussis vaccination. Further, their general vaccination beliefs, agreement with a policy advice to vaccinate HCWs, the perceived cost-benefit ratio, and the perceived personal responsibility to prevent pertussis in patients explained their attitude towards pertussis cocooning vaccination.

Conclusion

About half of the participating HCWs reported their intentions to accept a pertussis cocooning vaccination. Attitude, anticipated affect regarding non-acceptance, and decisional uncertainty came forward as the most important determinants of intention. This study helps build the evidence base describing the determinants of the intention to accept a pertussis cocooning vaccination among HCWs.

Keywords: Bordetella Pertussis, Pertussis Vaccine, Health personnel, Vaccination, Vaccination refusal, Attitude

ABSTRACT ID: 799

PRESENTED BY: Olga Visser (ovisser@ggdru.n

PARALLEL SESSION PROGRAMME
DAY 2, TUESDAY, 7 NOVEMBER
11:00-12:40

Parallel Session 7: Evaluation of Surveillance

O7.1 A consolidated framework to understand and measure the added value of One Health surveillance for antimicrobial resistance based on the Canadian experience

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3. Royal Veterinary College, London, United Kingdom
4. Swiss Tropical and Public Health Institute, Basel, Switzerland
5. Public Health Agency of Canada, Guelph, Canada

Background

In order to detect rapidly the emergence of new resistant microorganisms and to inform decisions on the implementation of interventions, it is crucial to develop highly effective and efficient surveillance systems. Integration of human and animal components, in line with a "One Health" approach to surveillance, is broadly encouraged internationally, but evidence on the added value of these approaches is lacking. Building on existing evaluation frameworks for surveillance systems, the aim of this study was to develop specific framework and measurement tools focusing on the performances and added value of integration strategies for AMR surveillance systems.

Methods

The framework was developed based on the Canadian Integrated Program for Antimicrobial Resistance Surveillance (CIPARS)'s experience. Focus groups and interviews were conducted in 2016 and 2017 with CIPARS team members, end-users and international experts in order to identify and validate the framework components.

Results

The evaluation approach includes two phases. The first phase consists in the assessment of the level of integration of the surveillance system and proposes a new measurement tool to quantify the integration within each of four principal surveillance activities: data collection, analysis, interpretation and dissemination. The second phase provides an approach to measure the impact of the integration on the system's effectiveness and economic efficiency at different levels in terms of the surveillance system's outputs (information, team, network) and outcomes (policy changes, health and economic impacts).

Conclusion

This study presents an enhanced evaluation framework as a concrete and useful tool for public health decision-makers involved in the surveillance of AMR and other infectious diseases at the human-animal-ecosystem interface. Furthermore, an assessment of the performance will inform other countries in setting up more integrated AMR surveillance systems.

Keywords: One Health surveillance, integration, antimicrobial resistance, surveillance systems evaluation

ABSTRACT ID: 965

PRESENTED BY: Cécile Aenishaenslin (cecile.aenishaenslin@mcgill.ca)

O7.2 Capture-recapture finds maternal death cases missed in routine reporting from MSF projects

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3. Médecins Sans Frontières – Operational Centre Amsterdam (OCA), The Netherlands

Background

Maternal deaths are reported in a standardised surveillance tool (RH-Gynobs) used by all health facilities providing maternal health care in Médecins Sans Frontières projects globally. We hypothesised that maternal deaths are under-reported and conducted a capture-recapture study to determine the sensitivity of the RH-Gynobs tool for maternal mortality and estimate the true burden of maternal mortality during 2015.

Methods

We used two approaches. For 21 healthcare facilities where the RH-Gynobs tool contained only aggregate data (by site and month), we used modified two source capture-recapture methods. This data was disaggregated to create a line list which was compared to pooled data from inpatient mortality reports and monthly medical reports. This provided the most accurate estimate possible of the number of deaths and sensitivity of the RH-Gynobs tool.

For one site where the RH-Gynobs tool was underpinned with individual level data (the only tertiary site) standard three source capture-recapture log linear modelling was used.

Results

For 21 facilities reporting aggregate data, two-source capture-recapture methods estimated 129 deaths (95%CIs: 124-134) and RH-Gynobs tool sensitivity of 71.4% (95%CI: 68.8-74.3%). Analysis for the tertiary facility with individual data estimated 55 deaths (95%CI: 55-56) and sensitivity of 97.9% (95%CIs: 97.5-98.3%). For this facility log-linear modelling estimated 56 deaths (95%CIs: 56-57) (P=0.01, AIC=5.14) and RH-Gynobs tool sensitivity of 89.3% (95%CIs: 87.7%-89.3%).

Conclusion

Maternal deaths were underreported in the 21 health facilities reporting aggregate data. The aggregate nature of the data meant sensitivity may be overestimated. Where the RH-Gynobs tool was linked to individual data, sensitivity was higher and greater detail was available for surveillance. We recommend that future surveillance should link to individual level data which includes key indicators relevant to maternal health.

Keywords: Surveillance, Maternal mortality, Health facilities, Global health

ABSTRACT ID: 822

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

O7.3 Missing data and reporting delay in the European HIV Surveillance System: exploration of potential adjustment methodology

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2. National and Kapodistrian University of Athens, Athens, Greece
3. European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden

Background

Accurate case-based HIV surveillance data are key to estimate HIV burden and epidemic trends in Europe. Our aim was to explore the occurrence of missing data (MD) and reporting delay (RD) in the EU/EEA dataset and to identify statistical techniques that are or could be applied by countries to account for these quality issues.

Methods

Using data for 397,364 HIV diagnoses reported by 25 EU/EEA countries between 2000 and 2014, we explored the patterns of missingness and the RD distribution, by country and over time. Further, we conducted a literature review and a country consultation to identify existing adjustment techniques and assess their relevance for the studied dataset.

Results

Missingness level was the highest for CD4 count (43.5%), migration status (13.0%) and transmission category (12.2%) with patterns varying across countries. CD4 count was systematically missing for all or some years in 20 countries. The proportion of cases reported within 2 quarters of diagnosis varied from 45% to 100% across countries, with significant time trends and occasional peaks. Two countries routinely performed statistical adjustments. We identified and will present a range of multiple imputation techniques applicable for MD adjustment, either by country or in an overall, multilevel setting to account for systematically MD. We will present examples of RD adjustments, based on weighting or imputation techniques, and discuss their uses and limitations in context of HIV surveillance data.

Conclusion

The levels of missing information and of reporting delay require corrections to make data more informative for public health decision-making. Statistical techniques are available, but rarely used by the Member States. A tool to adjust HIV data using similar methodology is currently being developed to foster harmonisation at EU level.

Keywords: Disease Notification, Epidemiological Monitoring, Public Health Surveillance, HIV, Europe, Statistical Models

ABSTRACT ID: 961

PRESENTED BY: Magdalena Rosinska (mrosinska@pzh.gov.pl)

O7.4 Under-ascertainment of notifiable infectious diseases and organisms: evaluation using birth cohort data, Yorkshire, UK.

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M. Schweiger (3), J. Wright (2).

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3. Public Health England, Yorkshire and the Humber, Leeds, UK

Background

Statutory notification of infectious diseases (NOIDS) surveillance has not been comprehensively evaluated in England, since legislation was revised in 2010. We used data from a birth cohort study of 13,500 children born in Bradford (BiB), Yorkshire, England during 2007-2010, to evaluate the NOIDS surveillance system in terms of sensitivity and timeliness and make recommendations.

Methods

We interrogated primary and secondary care and laboratory information systems to retrieve diagnostic records of BiB participants and identify clinical diagnoses consistent with NOIDS (between 08/2007–04/2015) and laboratory-diagnosed notifiable organisms (10/2010–07/2015). We retrieved NOIDS notifications recorded by Public Health England (PHE) in Yorkshire and linked data using unique identifiers. We calculated the proportion of episodes of notifiable diseases/organisms recorded by PHE for each data source and for diseases from all sources combined (sensitivity), and estimated time from diagnosis to PHE record (timeliness).

Results

Overall sensitivity for clinically diagnosed notifiable diseases was 37% (114/310). 36% (82/227) of primary care-diagnosed episodes of notifiable diseases were recorded by PHE including: 32% (39/121) scarlet fever and 46% (12/26) measles. 34% (23/68) of hospital-diagnosed notifiable diseases were recorded by PHE including: 0% (0/4) acute encephalitis and 26% (10/38) acute meningitis. 90% (148/165) of episodes of notifiable organisms were present in the national PHE laboratory surveillance system and 56% (93/165) recorded by PHE in Yorkshire. Median time from diagnosis to PHE record was 2 (interquartile range 1-6), 1 (0-2) and 8 (3-16) days from primary care, secondary care and laboratory, respectively.

Conclusion

NOIDS surveillance in Yorkshire was timely but not sensitive. We recommend automating notification from clinical information systems, prioritising diseases requiring timely public health action, and undertaking regular quality assurance of existing automated laboratory notification processes.

Keywords: Public Health Surveillance, Disease Notification, United Kingdom, Sensitivity and specificity

ABSTRACT ID: 973

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

O7.5 Evaluation of acute flaccid paralysis surveillance system in Ebonyi State Nigeria, February 2017.

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3. Department of Community Medicine, Ahmadu Bello University, Zaria, Kaduna State, Nigeria

Background

Poliomyelitis is a highly infectious disease which causes irreversible paralysis especially in children less than five years of age. High quality acute flaccid paralysis (AFP) surveillance is essential to rapidly detect and respond to on-going polio transmission. We evaluated the Ebonyi state AFP surveillance system to assess its performance and key system attributes.

Methods

We interviewed key system players and also administered a semi-structured questionnaire on all disease surveillance and notification officers in the state. We analyzed the state AFP surveillance data from 2011-2015 and also reviewed relevant documents and reports.

Results

The AFP surveillance system in Ebonyi state is sensitive (all13 LGAs met the target for annualized non-polio AFP rate and percentage stool adequacy from 2011-2015), flexible (seamless transition from hard copy to electronic reporting) and acceptable to stakeholders (100% interview acceptance and completion rates).The system is not that simple as it involves multiple levels of reporting and requires a highly specialized lab test for case confirmation. There is timely investigation of reported cases but timeliness of LGA to state report is poor (progressively declined from 92% in 2012 to 65% in 2015). Furthermore, the surveillance system might not be representative as private and informal healthcare facilities are not adequately covered. The system is fairly stable but its heavy reliance on partners (WHO) for funding is a valid threat. Data quality is just average (completeness of reports from LGAs to state undulated around the 90% target between 2011 and 2015).

Conclusion

The AFP surveillance system in Ebonyi State is meeting its objectives so we recommend that it be continued. However, to enhance its performance, the government state should take full ownership and actively drive the process.

Keywords: Poliomyelitis, Surveillance System, Evaluation, Nigeria.

ABSTRACT ID: 1095

PRESENTED BY: **Izuchukwu Frank Obi (obifranko3@gmail.com)**

Parallel Session 8: Food- and water-borne diseases (2)

O8.1 Salmonella Enteritidis infections associated with non-retail eggs in the Netherlands, during a multi-country outbreak, 2015 – 2017

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3. The Netherlands Food and Consumer Product Safety Authority (NVWA), Utrecht, Netherlands
4. Municipal Health Service (GGD) Hollands Noorden, Alkmaar, Netherlands

Background

In August 2016, an increase in Salmonella Enteritidis cases with Multi-Locus Variable number tandem repeat Analysis (MLVA) profile 2-9-7-3-2 was observed in several EU countries including the Netherlands. We investigated the outbreak in the Netherlands, to identify the vehicle of infection.

Methods

Confirmed cases were infected individuals with S. Enteritidis sharing a common t5-level single nucleotide polymorphism (SNP) address based on whole genome sequencing (WGS); probable cases were those with MLVA profile 2-9-7-3-2/2-9-6-3-2. We compared cases reported since 1/08/2016 with controls selected randomly from population registries, frequency-matched on age, sex and municipality of residence. We collected information on food exposures using a structured questionnaire. We calculated odds ratios (OR) using logistic regression. Food trace-back investigations were performed based on identified food exposures of cases.

Results

From May 2015 to April 2017, 74 confirmed cases and 128 probable cases were reported in the Netherlands. Cases were more likely to have eaten in restaurants than controls (48% (n=41) vs 75% (n=49); OR 3.4, 95%CI 1.6-7.3). Trace-back investigations of foods that cases consumed at restaurants identified a common supplier for 19 restaurants that imported non-retail eggs from a Polish packing station. Of these eggs, 66 (13%) egg shell samples and 2 (<0.1%) egg contents (pools of ten eggs) tested positive for Salmonella spp., and were linked to human cases using WGS. After eggs originating from the implicated packing station were removed from the market, no additional cases occurred.

Conclusion

Environmental and laboratory evidence suggested that non-retail eggs were the likely vehicle of transmission. This outbreak highlights the importance of a coordinated collaboration between public health institutes and food authorities, and the potential of routine WGS in Salmonella surveillance and outbreak response.

Keywords: Salmonella, outbreaks, public health, epidemiology

ABSTRACT ID: 815

PRESENTED BY: Roan Pijnacker (roan.pijnacker@rivm.nl)

O8.2 Outbreak of Salmonella Bovismorbificans associated with raw ham products in the Netherlands, 2016-2017

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4. Netherlands Food and Consumer Product Safety Authority (NVWA), Utrecht, the Netherlands

Background

In January 2017, an increase was observed in reported Salmonella Bovismorbificans cases in the Netherlands since October 2016. A similar increase was observed concurrently in Belgium; an outbreak investigation was initiated to identify the source.

Methods

Cases were defined as persons with laboratory-confirmed S. Bovismorbificans infections, reported after October 2016, in the Netherlands. Human isolates were sequenced using whole-genome sequencing (WGS). We interviewed cases to identify exposures and then implemented a case-control study, including all cases from December 2016. Age-, gender- and municipality-matched controls were randomly selected from population registers. Adjusted odds ratios were calculated using logistic regression analysis. We traced back the distribution chain of suspected foods, and sampled them for microbiological analysis.

Results

From October 2016 to March 2017, 53 cases of S. Bovismorbificans were identified (typically 3-14 cases/year reported). Cases were 5 to 90 years old (median 65), 56% were female. Sequencing indicated all, including Belgian cases, had identical strains (<5 alleles difference). Twenty-four cases and 37 controls participated in the study. Cases were more likely to have consumed ham products than controls (aOR 13, 95% CI 2.0-77) and to have shopped at a supermarket chain (aOR 7, 95% CI 1.3-38). Trace-back investigations led to a Belgian meat producer: one ham sample from this producer tested positive for S. Bovismorbificans and matched the outbreak strain by WGS.

Conclusion

Trace-back investigations guided by the case-control study identified ham products from a specific producer as the source of this outbreak. This investigation illustrates the importance of laboratory surveillance for all Salmonella serotypes, including rare serotypes. Intensive collaboration among epidemiologists, microbiologists and food safety specialists, and the use of WGS were key factors in this investigation.

Keywords: salmonella salmonella enterica Disease Outbreaks Foodborne Diseases Case-Control Studies Sequence Analysis

ABSTRACT ID: 769

PRESENTED BY: Diederik Brandwagt (diederik.brandwagt@rivm.nl)

08.3 European-wide salmonellosis outbreak with a novel serovar (11:z41:e,n,z15) attributable to sesame products

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Background

In spring 2016, Greece reported an outbreak with a novel Salmonella serovar (antigenic formula 11:z41:e,n,z15) with epidemiological evidence for sesame products as vehicle. Additional cases were reported from Germany, Luxembourg, Czech Republic and the UK. In December 2016, a German case without any connection to Greece suggested the possibility that contaminated food might have been distributed outside of Greece. Outbreak investigations were intensified in the affected countries and on EU-level in order to identify the source and control the outbreak.

Methods

Outbreak cases were defined as laboratory-confirmed notifications of Salmonella with the antigenic formula 11:z41:e,n,z15. Cases exposed in Germany and in Luxembourg were interviewed focusing on consumption of sesame products. Suspicious food items were sampled and traced back in case of detection of Salmonella. Human and food isolates were sequenced.

Results

Between March 2016 and April 2017, 46 outbreak cases were notified (Greece: 22; Germany: 13; Czech Republic: 5; Luxembourg: 4; United Kingdom: 2). 7/9 patients interviewed regarding sesame products reported consumption of a particular brand of sesame spread. A specific lot of the product tested positive for the novel serovar. Trace back revealed that the spread was produced in Greece with sesame originating from Sudan. The serovar was also detected in sesame seed originating from Nigeria distributed via Greece to Germany and in sushi containing sesame in the UK. Whole genome sequencing revealed very close relatedness within the novel serovar.

Conclusion

Epidemiological and microbiological data confirm sesame as the common source of human cases. This outbreak highlights the benefits of an international outbreak investigation to identify the causative food vehicle enabling recall and an EU-wide food-chain analysis with the aim to disentangle the origin of the contamination.

Keywords: salmonellosis, salmonella, sesame, outbreak, foodborne

ABSTRACT ID: 1008

PRESENTED BY: Klaus Stark (starkk@rki.de)

08.4 National outbreak of Salmonella Give in Malta linked to a local food manufacturer, October 2016

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Background

Salmonella Give is a rare serotype across Europe. In Malta, an average of one case per 100,000 was reported annually from 2007-2015. On 15/10/2016, five cases of S. Give were detected. We investigated to identify the source and implement control measures.

Methods

We conducted a descriptive epidemiological investigation. Confirmed cases were defined as persons with laboratory-confirmed S. Give infection since 08/10/2016 and suspected cases as persons with gastroenteritis and epidemiologically linked to a confirmed case. Casualty physicians reported patients presenting with fever and gastroenteritis. Laboratories were alerted to report preliminary Salmonella results. We collected data on risk exposures from cases by telephone interviews, inspected implicated restaurants and conducted food trace-back investigations. Food and human samples were microbiologically analysed. Whole Genome Sequencing (WGS) was performed on positive human isolates.

Results

Thirty-three cases were reported with onset dates from 8-30th October (18 confirmed, 15 suspected). Eight confirmed cases required hospitalisation. Twelve (67%) confirmed and 14 (93%) suspected cases were linked to four restaurants. Eight sequenced human isolates belonged to the same distinct phylogenetic cluster. S. Give was isolated from ready-to-eat antipasti served by the restaurants which were supplied by the same local manufacturer. At the manufacturer, S. Give was identified in packaged bean dips, ham products and an asymptomatic food handler; inspections found inadequate separation between raw and ready-to-eat food during processing.

Conclusion

Multi-disciplinary investigations identified cross-contamination at the manufacturer as the likely source of infection. The severity of illness indicates a high virulence of this specific serotype. To prevent further cases, food products were recalled and the manufacturers' food safety practices reviewed. This outbreak highlights the importance of reinforcing adherence to food safety standards at manufacturing level.

Keywords: Salmonella, Malta, Food-borne diseases, Disease Outbreaks, Food-Contamination

ABSTRACT ID: 760

PRESENTED BY: Alastair Donachie (adonachie@hotmail.co.uk)

O8.5 Late breaker: Utilising genomic surveillance of Salmonella Enteritidis in the UK

Jacquelyn McCormick (1), Hassan Hartman (1), Amy Mikhail (1), Lesley Larkin (1), Tim Dallman (1)

1. Public Health England

Background

Public Health England deployed Whole Genome Sequencing (WGS) for routine surveillance of Salmonella since April 2014. We present three years of genomic surveillance of S. Enteritidis and consider the actionable interventions and their effect on Salmonella burden in England.

Methods

S. Enteritidis sequencing data from 1 April 2014 to 31 March 2017 were analysed according to their single linkage clustering groups at the 5-single nucleotide polymorphism (SNP) level.

Results

6105 cases of S. Enteritidis fell into 1680 distinct 5-SNP single linkage clusters. 1542 clusters had less than five cases. 17 clusters had 50 cases or more and represented one third of human cases of S. Enteritidis in England. Through epidemiological investigation the probable or suspected vehicle was identified for some of the clusters. These included 7 clusters linked/potentially linked to the egg industry, and 3 clusters were linked or potentially to other identified sources including poultry meat and reptile exposure. Additionally, 2 clusters linked to EU travel, 5 clusters linked to non-EU travel. Clusters associated with the egg industry or EU travel represented a restricted phylogeny lineage in the S. Enteritidis population distinct to other S. Enteritidis cases with non-EU travel in this study.

Conclusion

Routine genomic surveillance identified a significant burden of salmonellosis (~33% of human cases) is caused by a paucity of strain diversity (1% of 5-SNP clusters) in England. Of these, at least 50% are potentially associated with persistence of S. Enteritidis in the egg-laying industry. The effective implementation of EU Salmonella control legislation has significantly impacted the disease burden of poultry-associated S. Enteritidis. Through effective continued enforcement of existing EU legislation we could further decrease the burden of salmonellosis across the EU.

Keywords: Salmonella Enteritidis, Whole Genome Sequencing, Surveillance, Source attribution

ABSTRACT ID: 1438

PRESENTED BY: Jacquelyn McCormick (jacquelyn.mccormick@phe.gov.uk)

Parallel Session 9: Vaccine-preventable diseases (2)

O9.1 Impact of rotavirus vaccine introduction on gastrointestinal rates in children under 5 in Wales, a time series analysis

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Background

The rotavirus vaccine (Rotarix) was introduced in Wales in July 2013 and uptake is high (93% at first birthday). While reductions in hospital admissions for acute gastroenteritis have been shown, the impact on milder illness presenting to general practitioners (GPs) in Wales is not known. We calculated incidence reduction of GP consultations for gastroenteritis (GE) after vaccine introduction in children under 5s. We used time series analysis to estimate number of consultations prevented and proportion attributable to rotavirus.

Methods

National GP consultation incidences for GE (READ codes) per 100,000 were calculated within rotavirus season (weeks 3-29). Laboratory and GP weekly data on rotavirus and GE, respectively, were used to determine temporal trends, 26 and 52 weeks periodicity and vaccine effect using Poisson regression models. Using 2011-13 as pre-vaccine and 2014-15 as post-vaccine period, we excluded the vaccine term and post-vaccine data from the model to estimate GP consultations prevented after 2013. We used a linear regression model, including laboratory data, to estimate GP consultations attributable to rotavirus.

Results

Mean annual incidence of GP consultations for GE decreased by 12% (95% CI 0.10-0.13) in post-vaccine period in under 5s. Estimated number of consultations prevented was higher in 2015 (N=4406, 17% of expected) than 2014 (N=3298, 14%) for under 5s. This was similar in under 1s increasing from 15% (N=1477) to 25% (N=2556). The proportion of GP consultations attributable to rotavirus fell in the post-vaccine period, from 17% to 12% in under 5s.

Conclusion

Our results suggest an impact from rotavirus vaccination on the burden in primary care (2189 consultations per 100,000 avoided each year). This adds weight to the argument for introducting routine rotavirus vaccination throughout Europe.

Keywords: rotavirus, vaccine, Wales, gastroenteritis, hospital, GP

ABSTRACT ID: 851

PRESENTED BY: Christopher Williams

O9.2 Impact of rotavirus vaccination in the UK: a real effect or an ecological artefact?

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Background

The UK introduced rotavirus universal vaccination in July 2013 and a large decrease in AGE rates has been observed since. Following suggestions that this decrease may be a chance finding, we assessed whether the decrease persisted 3 years after vaccination and whether the impact was differential among different age groups.

Methods

We compared AGE rates before and after 1st July 2013 among all subjects registered in the Clinical Practice Research Datalink between July 2010 and June 2016. AGE episodes were defined using Read and ICD-10 codes with a 14 day disease free period. We calculated crude episode rates of AGE, stratified by age group, health care setting and calendar time.

Results

The GP consultation rates for any AGE episodes declined from 28 to 23 per 1,000 person-years, a 18% (95% CI: 17.5-18.6) reduction. The impact on AGE hospitalizations was minimal overall (1.7%, 95% CI 0.3–3.1), but significant in children <5; 29% (95% CI: 25.9-31.9) reduction. The observed reduction in AGE rates persisted in each individual year following 2013. Notably, the AGE peaks observed in the first months of every year pre-vaccination, typically attributed to rotavirus, disappeared entirely in the vaccine eligible age groups.

Conclusion

This ecological analysis confirms a significant decrease in AGE rates at both the GP and hospital level in the UK following the introduction of rotavirus vaccination. The fact the impact persists over 3 consecutive years and is largest in the vaccine eligible age groups, as well as the complete disappearance of the typical rotavirus peaks suggests that the decreased AGE rates are reflective of a real impact of rotavirus vaccination and not an ecological artefact.

Keywords: rotavirus, rotavirus vaccines, health impact assessment, program evaluation

ABSTRACT ID: 1062

PRESENTED BY: Margarita Riera (margarita.riera@p-95.com)

O9.3 Early impact of the rotavirus vaccination program in Norway

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2. Department of Infectious Diseases Epidemiology and Modelling, Norwegian Institute of Public Health
3. Department of Virology, Norwegian Institute of Public Health

Background

Norway introduced rotavirus immunisation for all children in October 2014 using a two-dose vaccine. A follow-up program was established to monitor vaccine uptake, safety and impact of rotavirus vaccination.

Methods

We monitor vaccine coverage through the national immunisation register SYSVAK. The program impact is measured by using data from the Norwegian Enhanced Paediatric Immunisation Surveillance (NorEPIS) network, the Norwegian Syndromic Surveillance System (NorSySS) and the National Rotavirus Reference Laboratory.

Results

Within two years after introduction, the vaccine coverage reached 92% for one dose and 88% for two doses. Among fully vaccinated children, 98% were immunised within the recommended upper age limits of 12 weeks for the first and 16 weeks for the second dose. The number of hospitalised all-cause gastroenteritis cases in children <5y enrolled through NorEPIS decreased by 35% and the number of rotavirus-confirmed cases by 86% in 2016 compared to the mean for 2014–2015. The post-introduction rotavirus proportion among hospitalised gastroenteritis cases decreased by 85% in vaccine-eligible children <24 months of age but a 59% reduction was also observed among children aged 3-5 years not eligible for vaccination. Among fully vaccinated gastroenteritis cases, 95% were negative for rotavirus. In primary care, a 26% reduction in the numbers of gastroenteritis-associated consultations in children <5y was also observed in 2016 compared with mean for 2006–2014. The number of reported rotavirus-positive tests decreased by 60% in 2016 compared with the mean for 2002–2014.

Conclusion

Norway has rapidly achieved a high national coverage after introduction of rotavirus immunisation despite the strict age limits for vaccine administration. Early post-introduction data demonstrate a reduction in the rotavirus burden likely attributable to the vaccination program.

Keywords: Rotavirus, Vaccination, Epidemiology, Program Evaluation

ABSTRACT ID: 1019

PRESENTED BY: Tone Bruun (tone.bruun@fhi.no)

O9.4

Decreased incidence of pertussis in young adults after the introduction of booster vaccination in military conscripts in Finland

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4. Turku University Hospital (TYKS), Turku, Finland

Background

In 2005, in Finland, the whole-cell pertussis vaccine was replaced by acellular given at 3–5–12 months, and boosters at 4 and 14-15 years of age. From July 2012, the military conscripts have been offered a pertussis booster dose. Conscription is mandatory for Finnish men, and > 95% was 19–21 years old when enrolled during 2012–2015. We aimed to describe the epidemiology of pertussis in Finland during 1995–2015, and examine the indirect effect of the booster in conscripts on pertussis incidence in the Finnish population.

Methods

We extracted laboratory confirmed notified pertussis cases from the National Infectious Diseases Register. We calculated annual incidence using as denominator population data and incidence rate ratios (IRR) using Poisson regression.

Results

The overall pertussis incidence peaked in 2004 (31/100,000) and was lowest in 2015 (3.0/100,000), with 66 reported cases in < 3 months infants in 2004 versus 6 in 2015. Among the 19- to 21-year-olds in the general population, incidence decreased from 49/100,000 in 2011 to 0.51/100,000 in 2015 (IRR=0.01; 95%CI, 0.00 0.16). Among the same age group, comparing the 3.5-year period before and after July 2012, incidence decreased from 33/100,000 to 5.3/100,000 (IRR=0.16; 95%CI, 0.06 0.40) in males and from 16/100,000 to 5.0/100,000 (IRR=0.31; 95%CI, 0.11 0.84) in females.

Conclusion

Implementation of the booster dose in the Finnish Defence Forces was followed by a significant decrease in pertussis incidence among the 19- to 21-year-old males and females, possibly reflecting herd immunity effect. Together with booster doses in adolescents, this has resulted in low incidence in the whole population including infants. Our results support the implementation of the booster dose for conscripts. We recommend continuing monitoring pertussis epidemiology to optimize pertussis vaccination strategies in Finland.

Keywords: pertussis, surveillance, respiratory infections, bacterial infections, vaccines

ABSTRACT ID: 764

PRESENTED BY: Viktor Zöldi (viktor.zoldi@gmail.com)

O9.5

Impact of pneumococcal conjugate vaccines on invasive disease caused by pneumococci non-susceptible to antimicrobials in European children under five years old: SpIDnet multicentre study (2011-2015)

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16. Scottish Haemophilus- Legionella- Meningococcus and Pneumococcus Reference Laboratory, Glasgow, United Kingdom.
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Background

The introduction of pneumococcal conjugate vaccines covering 7, 10 or 13 serotypes (PCV7/10/13) was followed by a decrease in vaccine serotypes and an increase in non-vaccine serotypes causing invasive pneumococcal disease (IPD). In this context, the increase in antimicrobial non-susceptibility of non-vaccine serotypes is of concern. The SpIDnet network collects antimicrobial non-susceptibility data on IPD cases from nine European sites. We measured the impact of PCV10/13 on incidence of IPD isolates non-susceptible to penicillin (IPD-PenNS) or erythromycin (IPD-EryNS) in children under five years-old.

Methods

We measured the incidence of culture-confirmed IPD-PenNS and IPD-EryNS defined as minimum inhibitory concentrations to benzylpenicillin >0.06mg/L and erythromycin >0.25mg/L, respectively. Pooling data from nine sites using random effects meta-analyses, we calculated pooled incidence rate ratio (IRR) between each of the five PCV10/13 years (2011-2015) and average incidence in PCV7 years. We computed percentage (%) change in incidence as (1-IRR)*100.

Results

Compared to PCV7 period, the % change in all-type IPD-PenNS incidence was -31% (95%CI: 12-46) in 2011, -43% (17-61) in 2013, and -10% (-8; 25) in 2015. Percentage change in vaccine-serotype IPD-PenNS incidence was -74% (27-91) in 2015. Non-vaccine serotype IPD-PenNS incidence increased each year and % change was +338% (171-608) in 2015. The % change for all-type and vaccine serotype IPD-EryNS incidence was -33% (5-53) and -86% (62-95) respectively; % change for non-vaccine IPD-EryNS was +269% (172; 402) in 2015.

Conclusion

After an initial decrease, all-type IPD-PenNS incidence stabilised in 2015 due to an increase in non-vaccine serotype IPD-PenNS incidence. All-type IPD-EryNS incidence decreased each year since PCV10/13 introduction; however non-vaccine IPD EryNS incidence increased. Continued long-term monitoring of IPD antimicrobial non-susceptibility is crucial to detect the emergence of non-vaccine non-susceptible serotypes.

Keywords: Invasive pneumococcal disease, pneumococcal conjugate vaccine, surveillance, Streptococcus pneumoniae, penicillin, erythromycin

ABSTRACT ID: 948

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

PARALLEL SESSION PROGRAMME
DAY 2, TUESDAY, 7 NOVEMBER
14:30-15:30

Parallel Session 10: Food- and water-borne diseases (3)

O10.1 Outbreaks of nephrocalcinosis due to vitamin D in infants, Morocco

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A. Tebaa, R. Soulaymani Bencheikh (3)

1. Field Epidemiology Training Program (FETP-Morocco)
2. Ecole Nationale de Santé Publique-Morocco
3. Centre Anti Poison et de Pharmacovigilance du Maroc

Background
In Morocco, several outbreaks were detected between 2012 and 2016 related to adverse drug reactions "ADR" due to vitamin D2 in infants. The total number of cases reported is 31 among which 2 were fatal. An investigation was conducted to identify the underlying causes in order to put in place control and prevention measures.

Methods
The outbreaks have been confirmed by performing the causality assessment of ADR reported. Following the first case of death, a brief report has been sent, by the Centre Anti Poison et de Pharmacovigilance du Maroc "CAPM" to the health authorities. The National Pharmacovigilance Technical Committee has been held to propose recommendations to be implemented. Following the second case of death, the National Pharmacovigilance Commission has been held to implement urgently the proposed actions.

Results
The Causality assessment showed a certain link between ADR reported and vitamin D2. The investigation revealed that the recommended dose is three times higher than the one recommended by international standards. The infants were administered adult formulation of vitamin D2 because the pediatric one was not available in the market. The age of infants ranged from 10 days to 6 months. The sex ratio was 3,3. All infants experienced symptoms of vitamin D2 overdose and explorations showed nephrocalcinosis in 67.7 % of the cases. The main measures implemented were the amendment of the dose recommended of vitamin D2 and the approval of the marketing authorization of the pediatric formulation of vitamin D2.

Conclusion
This outbreak allowed preventing the recurrence of similar cases of serious ADR related to vitamin D2. Reporting of health events, including ADR, should be strengthened to enable early warning and quick response to public health risks.

Keywords: Keywords: outbreaks, infants, nephrocalcinosis, vitamin D2, adverse drug reaction

ABSTRACT ID: 1023

PRESENTED BY: Loubna Alj (naloub20@yahoo.fr)

O10.2 Preventive Interventions to Address Severe Acute Malnutrition in Children in Bokoro District, Chad, 2016.

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3. Médecins Sans Frontières, Operational Centre Amsterdam, Amsterdam, The Netherlands

Background
Bokoro district, Chad, experiences recurring annual food shortages from June to October, causing high rates of severe acute malnutrition (SAM) in children <5 years. From June -September 2016, Médecins Sans Frontières conducted active case finding and treatment for SAM, and mass distributions of Plumpydoz targeting 27,105 children between 6-23 months. We conducted three cross-sectional surveys in April (baseline), August (hunger gap) and November (two months after the last distribution) to measure the impact of these preventive interventions on SAM and the under-5-years mortality rate (U5MR).

Methods
We conducted three two-stage cluster surveys, including 50 clusters in April and 40 in August and November, using sampling proportional to population size. We randomly selected 20 households per cluster using household lists or modified WHO-EPI sampling. In each household, we measured mid-upper-arm-circumference (MUAC) on children 6-59 months and recorded the number of deaths, by age, within three months preceding the survey. We calculated? the U5MR, global acute malnutrition (GAM; MUAC<125 mm and/or oedema) and SAM (MUAC<115 mm and/or oedema) prevalence among children 6-59 months.

Results
GAM prevalence was 5.8% (95%CI: 4.7-7.1) in April, 5.1% (95%CI: 3.7-7.0) in August and 11.0% (95%CI: 9.1-13.1) in November. SAM prevalence was 1.3% (95%CI: 0.8-1.9), 0.5% (95%CI: 0.2-1.1) and 0.9% (95%CI: 0.5-1.6) in April, August and November, respectively. The U5MR remained between 0.69-0.78 deaths/10,000 person-days in each survey.

Conclusion
SAM prevalence in Bokoro remained below 2% throughout the intervention. The increased GAM in November indicated deteriorating nutritional status after the distributions ended, due to ongoing food insecurity. Preventive activities only temporarily relieved the malnutrition burden. Longer term solutions to ensure food security are required to avoid recurrent nutritional crises in Bokoro.

Keywords: Malnutrition, Severe Acute Malnutrition, Child Mortality, Food insecurity

ABSTRACT ID: 794

PRESENTED BY: Patricia Ndumbi (patricia.ndumbi@gmail.com)

O10.3 Prevalence of Brucellosis in Sindh Pakistan

Dr. Om Parkash Suthar and Dr. Muhammad Athar Abbas

Background

Brucellosis is a bacterial disease caused by genus brucella. Bovine brucellosis affects cattle, sheep & goats, camels, equines, dogs and may also infects other animals. The disease in animals is characterized by abortion in last trimester and reproductive failure. All ages of cattle are susceptible and infection can last for many years. Infected males develop epididymitis, orchitis and testicular abscesses. In humans, brucellosis can be caused by B. abortus, B. melitensis, B.suis (biovars 1-4) and rarely B. canis. The major losses caused by brucellosis are; decreased milk production, weight loss, calf mortality, infertility and lameness.

Methods

The present study was aimed to determine the prevalence of brucellosis in cattle with reproductive disorders, randomly selected cattle, cross breed cattle and small ruminants (sheep and goat) in eight districts of Sindh by Milk Ring Test (MRT), Rose Bengal Plate Test (RBPT) and Indirect ELISA.

Results

A total of 4559 animals with reproductive disorders (4225 female and 334 male) were screened. The prevalence was found 25.16% in female cattle while 27.84% in male cattle. A total of 6390 randomly selected animals (6248 female and 142 male) were screened. The prevalence was found to be 10.57% in female cattle while 21.12% in male cattle. The 1002 samples were screened from cross breed cattle, the prevalence was 25.54%. A total of 1639 samples were screened from sheep and goat. The prevalence was found to be 14.46%.

Conclusion

It was concluded from the present study that brucellosis is endemic in Sindh, therefore the prevention of brucellosis with vaccination is best policy for the control of the disease.

Keywords: Brucellosis, Cattle, Sindh, MRT, RBPT, SAT, ELISA

ABSTRACT ID: 1040

PRESENTED BY: Om Parkash Suthar (omrajani2005@yahoo.com)

Parallel Session 11: HIV, sexually transmitted infections and viral hepatitis (2)

O11.1 Estimating HIV incidence and the undiagnosed HIV population in the EU/EEA, 2003-2015

Anastasia Pharris (1), Ard van Sighem (2), Chantal Quinten (1), Teymur Noori (1), Andrew J. Amato-Gauci (1), on behalf of ECDC HIV/AIDS Surveillance and Dublin Declaration Networks

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Background

Annually, about 30,000 people are newly diagnosed with HIV in the 31 countries of the European Union/European Economic Area (EU/EEA). To evaluate and direct public health prevention and testing efforts, we estimated the number of people living with undiagnosed HIV in the EU/EEA.

Methods

Annual data on human immunodeficiency virus (HIV) diagnoses in 2003-2015 were retrieved from the European Surveillance System database. HIV diagnoses were adjusted for reporting delay and stratified by presence of AIDS and CD4 cell count category at the time of diagnosis. Countries were grouped in United Nations-defined sub-regions. A back-calculation method based on the ECDC HIV Modelling Tool was used to estimate annual numbers of newly acquired HIV infections, the annual distribution of time between infection and diagnosis, and the number of people still undiagnosed by the end of 2015.

Results

In 2003-2015, there were reported 403,169 HIV diagnoses: 142,010 (35%) in Western, 121,624 (30%) in Northern, 27,662 (7%) in Eastern, and 111,873 (28%) in Southern Europe. In the EU/EEA, 120,100 (95% CI: 113,000-127,800) people were estimated to be living with undiagnosed HIV by the end of 2015, of whom 47% had a CD4 count ≥500 cells/mm3 and 31% <350 cells/mm3, with 28,000 (95% CI: 24,700-31,700) new infections in 2015. The estimated number of undiagnosed HIV infections was highest in Southern Europe, while incidence rates were highest and time to diagnosis shortest in Northern and Western Europe.

Conclusion

A substantial number of people in the EU/EEA are living with undiagnosed HIV. Estimates suggest that approximately half of them have been infected recently, however a significant proportion are estimated to have late stage infection, suggesting more efforts are needed to test and diagnose high-risk populations.

Keywords: HIV, modelling, surveillance, implementation science

ABSTRACT ID: 1017

PRESENTED BY: Anastasia Pharris (anastasia.pharris@ecdc.europa.eu)

O11.2 Transmitted drug resistance among newly HIV-1 infected in Denmark 2004-2016

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Background

Transmission of human immunodeficiency virus (HIV) harboring resistance mutations impairs the efficiency of antiretroviral therapy (ART). Surveillance of transmitted HIV drug resistance (TDR) is essential to inform treatment policy. The aims of this project were to describe TDR among newly diagnosed HIV-1 patients in Denmark and to identify active transmission networks.

Methods

HIV-1 POL sequences, clinical and epidemiological information was obtained from 1,789 treatment naïve HIV-patients in Denmark diagnosed between 2004-2016. Subtyping, resistance and surveillance mutations were identified using the online tools REGA 3.0, CPR (SDRM 2009) and HIVDB 8.2. Phylogenetic transmission clusters were identified using ClusterPicker and linked to age, country of infection and sexual risk group.

Results

TDR was identified in 222 patients (12.4%). The most common TDR was resistance to non-nucleoside reverse-transcriptase inhibitors (7.5%) followed by nucleoside reverse-transcriptase inhibitors (2.9%). A total of 197 transmission clusters were identified including 707 patients, hereof 37 transmission clusters including 86 patients which were associated with TDR. The male:female ratio of patients in TDR transmission clusters was 6:1. Most were between 30 and 40 years of age (38%). Sixty-six percent were MSM and 30% reported heterosexual infection. Sixty-three percent reported infection in Denmark while 24% had unknown country of infection. Eight patients in seven TDR transmission clusters were reported from 2015 indicating transmission may be ongoing.

Conclusion

Transmission of TDR occurred among newly diagnosed Danish HIV-1 patients. The larger fraction of patients in transmission clusters was MSM. TDR was not demonstrated at a higher frequency in patients belonging to transmission clusters. This emphasizes the importance of a national surveillance program in order to detect TDR occurrence by detecting and following up active transmission clusters.

Keywords: HIV-1, transmitted drug resistance, surveillance,

ABSTRACT ID: 829

PRESENTED BY: Andreas Petersen (aap@ssi.dk)

O11.3 HIV infections among people who inject drugs in Glasgow are strongly associated with cocaine injection and homelessness, 2011 – 2016

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4. Scottish Improvement Science Collaborating Centre, University of Dundee, Dundee, UK
5. School of Media, Society and Culture, University of West of Scotland, Paisley, UK

Background

An outbreak of HIV infection among people who inject drugs (PWID) was detected in Glasgow in 2015. We aimed to describe demographic and behavioural characteristics of PWID in Glasgow, and identify risk factors for HIV infection to prevent further transmission.

Methods

The Needle Exchange Surveillance Initiative (NESI) is a national, anonymous, repeat cross-sectional survey that collects data on injecting risk behaviours and blood-borne viruses (BBV) among PWID in Scotland. Trained interviewers administer a face-to-face questionnaire to individuals recruited from services that provide sterile injecting equipment. Participants also provide a blood spot sample for BBV testing, which is linked to the questionnaire via a unique identifier. Using data from NESI surveys undertaken in Glasgow in 2011-2016, we conducted multiple logistic regression analysis to measure the association between exposures and HIV infection. Variables with p-value <0.25 in univariable analysis were included in the multivariable analysis using a forward stepwise approach.

Results

2,453 participants were eligible for inclusion in the study. HIV prevalence among PWID in Glasgow increased from 0.11% (1/923) in 2011-12 to 2.5% (23/915) in 2015-16. For the 6 months preceding survey, 23% (557/2,447) reported homelessness; 76% (1,871/2,450) injected heroin, 16% injected cocaine, and 12% injected both. After adjusting for confounders, cocaine injection (adjusted odds ratio [AOR] 9.9, 95% CI 3.7-26.0) and homelessness (AOR 4.2, 95% CI 1.9-8.9) were independently associated with HIV infection among PWID in Glasgow.

Conclusion

HIV infection among PWID has increased substantially in Glasgow in recent years. Recent homelessness and cocaine injection are key risk factors. Enhanced harm reduction provision (e.g. greater evening availability) and expanded HIV testing and treatment among PWID are recommended to reduce HIV transmission amongst this vulnerable population.

Keywords: HIV infection, people who inject drugs, HIV outbreak, drug injection

ABSTRACT ID: 834

PRESENTED BY: Diogo Marques (diogo.marques@nhs.net)

Parallel Session 12: Tuberculosis and other respiratory diseases (excluding viruses)

O12.1 Surveillance of Mycobacterium tuberculosis (TB) cases attributable to relapse or reinfection in London, 2002-2015

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Background

Recurrence of TB in an individual can occur due to relapse of the same strain or reinfection by a different strain. The contribution of reinfection and relapse to TB incidence, and the factors associated with each are unknown. We aimed to quantify and describe cases attributable to relapse or reinfection, and identify associated risk factors in order to reduce recurrence.

Methods

We categorised recurrent TB cases from notifications in the London TB register (2002-2015) as relapse or reinfection using molecular and epidemiological information. Demographic, social and clinical factors associated with each outcome were determined using logistic regression in Stata 13.1 (2009-2015 only).

Results

Of 43,465 TB cases, 1.4% (618) were classified as relapse and 3.8% (1,637) as reinfection. Although the proportion with relapse decreased from 2002 (2.3%) to 2015 (1.3%), the proportion of reinfection remained around 4%. Relapse was commoner among recent migrants (<1 year, odds ratio (OR)=1.99, p=0.005), those with a social risk factor (OR=1.51, p=0.033) and those with central nervous system, spinal, miliary or disseminated TB (OR=1.75, p=0.001). Reinfection was commoner among long term migrants (>11 years, OR=1.67, p=<0.001), and those with a social risk factor (OR=1.96, p=<0.001) within specific areas in London.

Conclusion

A small and decreasing proportion of TB cases in London were attributable to relapse, while re-infection continues to account for 4% of patients per year. Patients with social risk factors were at increased risk of both relapse and reinfection. Characterising those with relapsed disease highlights vulnerable patients and factors associated with reinfection suggest groups where transmission is occurring. This will inform TB control programs to target appropriate treatment and interventions in order to reduce the risk of recurrence.

Keywords: TB recurrence, relapse, reinfection, social risk factors

ABSTRACT ID: 872

PRESENTED BY: Baharak Afshar (Baharak.Afshar@phe.gov.uk)

O12.2 Analysis of public health response to high influx of migrants to Finland in 2015-2016; using procurement data to evaluate coverage and timing of infectious disease screening

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National Institute for Health and Welfare, Department of Health Security

Background

In total 38,134 refugees applied for asylum in Finland during 2015-2016. The nine-fold increase in refugees was among the highest in Europe. Majority of the applicants were from Iraq (57%), Afghanistan (16%) and Somalia (6%). According to the national guidelines, pulmonary tuberculosis is screened within two weeks, and HIV, blood-borne hepatitis and syphilis within three months of arrival. We evaluated the effectiveness of the public health response to sudden increase of asylum applications by using screening test procurement data.

Methods

The two national private health service providers contracted for refugee health services report regularly to the Finnish Immigration Service on the number of services provided, including the number of chest X-rays (CXR), HBsAg, HIVAgAb and Trpa screenings. The number and timing of screening tests was compared to the number of asylum seekers originating from risk areas.

Results

In 2015-2016, altogether 10,873 CXR were provided and the coverage of pulmonary tuberculosis screening was 92%. The screening rate for HIV, hepatitis and syphilis was 63% with 22,900 tests provided. Half of the applicants had arrived by mid-September 2015 and 90% by December 2015. The average time interval from arrival to screening was 2 months for the CXR and 3 months for the blood screens. There was significant variation in the screening coverage and testing intervals between different regions.

Conclusion

The coverage of tuberculosis screening was good but it had delays in regard to the national guidelines. The regional differences in coverage and timing may demonstrate different levels of preparedness but may also reflect local policies and attitudes towards service provision. Health care system's preparedness including acceptance of national policies needs to be further developed to cope with increased cross-border mobility.

Keywords: Refugees, Mass Screening, Public Health

ABSTRACT ID: 1022

PRESENTED BY: Paula Tiittala (paula.tiittala@thl.fi)

O12.3 Late breaker: Ongoing invasive group A Streptococcus emm74 outbreak in a homeless population in Montréal, Québec, Canada

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6. National Microbiology Laboratory, Winnipeg, Canada

Background

In June 2017, Montréal Public Health detected an outbreak of invasive group A Streptococcus (iGAS) emm74 infections among homeless individuals. Few outbreaks of iGAS in homeless populations are reported and little evidence exists on managing such outbreaks. This investigation aims to describe the outbreak epidemiology and identify intervention strategies.

Methods

iGAS infection is a notifiable disease in Québec. Cases are routinely investigated and isolates are molecularly characterized. Upon outbreak detection, sentinel surveillance of non-invasive GAS infections was initiated. Emm sequence typing was done for invasive and non-invasive cases among homeless individuals or individuals who use services for the homeless in Montréal. Whole genome sequencing (WGS) was performed for emm74 invasive cases. Social network analysis examined links between cases and services.

Results

Between March and August 2017, among 19 iGAS cases in the target population, 13 had the outbreak sequence type emm74. Outbreak iGAS cases ranged in age from 35-75 years, 11 were male, common presentations included soft tissue infections (7) and septicemia (5), and 3 died. Among 21 non-invasive GAS cases, 12 were emm74. WGS analysis revealed that emm74 isolates were closely related, and phylogenetically linked to a strain that recently appeared in other Canadian provinces. Social network analysis illustrated complex relationships between cases and services for the homeless.

Conclusion

Epidemiological and WGS analysis confirmed an ongoing outbreak. The complex relationships between cases and services reflect the mobility of this population and make targeting a specific facility for intervention difficult. Interventions focused on raising awareness, facilitating rapid detection and treatment of cases, and reinforcing environmental infection prevention measures across services for the homeless. Effectiveness and feasibility of approaches such as mass screening and prophylaxis need to be explored.

Keywords: Streptococcus pyogenes, Infectious Disease Outbreak, Homeless Persons, Sequence Analysis, DNA

ABSTRACT ID: 1402

PRESENTED BY: **Karon Hammond-Collins (noemie.savard.ccsmtl@ssss.gouv.qc.ca)**

PARALLEL SESSION PROGRAMME
DAY 2, TUESDAY, 7 NOVEMBER
17:00-18:30

Parallel Session 13: Vaccine-preventable diseases (3)

O13.1 Acute flaccid paralysis surveillance- Kaduna State, Nigeria 2011 – 2015

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2. State Primary Health Care Agency, Kaduna, Nigeria
3. National Stop Transmission of Polio, Abuja, Nigeria

Background

Suboptimal Acute Flaccid Paralysis (AFP) surveillance results in delayed detection and response to polio outbreak. Increase AFP surveillance and quality is recommended to interrupt transmission of polio virus in Nigeria. Active surveillance of AFP is done in Nigeria. All AFP cases are to be detected, investigated and line listed with results sent to higher level weekly. We reviewed AFP 2011-2015 surveillance data to characterize cases of AFP in Kaduna State and evaluate some performance indicators.

Methods

We reviewed AFP linelist and extracted information on socio-demographics, date of onset, polio vaccination status, collection of stool specimen and laboratory results. Frequencies and proportions were calculated.

Results

We identified 1607 AFP cases, 884(55.2%) were males. Median age was 29 months (IQR: 20-44). AFP case identification increased from 178 in 2011 to 620 in 2015. Most (94.2%) AFP cases received at least 3 doses of OPV; 27(1.7%) had zero dose. In the period under review, 13 cases of Wild Polio Virus were reported in 2012 among children less than 5 years. There was increase in non-polio AFP rate (NPAFP) in children <15 years from 5.4 to 16.5 per 100,000 population while stool adequacy was between 89-93%. Proportion of Local Government Areas meeting the target for both indicators increased from 69.6 to 92%.

Conclusion

Kaduna State AFP surveillance system meets the target for both NPAFP rate and stool adequacy and can be relied upon to detect polio outbreak. We recommended the Kaduna State Primary Health Care Agency strengthen routine immunization (RI) to decrease proportion of children with zero dose of polio vaccine. State Task Group on Immunization has been set up which is tasked with improving RI coverage in the State.

Keywords: Acute flaccid paralysis, Kaduna State, Nigeria, Poliomyelitis, Surveillance

ABSTRACT ID: 774

PRESENTED BY: **Ummulkhulthum Bajoga (kumsiela@gmail.com)**

O13.2 Hygienic measures for a wild poliovirus type 2-shedder: balancing containment and intrusion in private life

Manon Haverkate (1), E. Duizer (1), J. Broekhuijsen (1), A. Jacobi (1), C. van der Weijden (2), H. Ruijs (1), A. Timen (1)

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2. Communicable Disease Control, Municipal Health Service Flevoland, Lelystad, the Netherlands

Background

After an accidental release of wild poliovirus type 2 (WPV2) at an IPV production plant in the Netherlands, an employee was found positive for poliovirus in stool samples. Despite being fully vaccinated, he continued shedding WPV2 until 29 days post-exposure. To comply with the WHO Global Action Plan (GAPIII), stringent hygienic measures had to be imposed ensuring no further transmission of WPV2 would take place. However, the public health threat was perceived low in a country with high vaccination coverage and good sewage systems. A delicate balance had to be found between the stringent GAPIII recommendations, the low public health threat, and the intrusion in daily life of the index and his household members.

Results

The index agreed to home isolation until stool cultures were negative for 3 consecutive days. In total, he spent 32 days in isolation. Practical challenges were encountered concerning, among others, the two household members, toilet use, collection, transportation and destruction of stools and final disinfection of the house. The household members were followed up by stool sampling every other day. They were allowed to leave the house for school and were instructed to avoid contact with unvaccinated persons and to refrain from defecating outside their house. Starting ten days post-exposure, a disposable toilet system was installed, ensuring all stools of the index were collected separately and transported safely to a certified destruction plant. The process was effectively supported by regular visits of public health officials.

Conclusion

The hygiene measures proved to be effective in preventing transmission, as the two household members remained negative for poliovirus in throat swabs and stool samples until 10 days after the last positive sample from the index.

Keywords: poliovirus, hygiene, patient isolation, toilet facilities

ABSTRACT ID: 891

PRESENTED BY: Manon Haverkate (manon.haverkate@rivm.nl)

O13.3 To vaccinate or not to vaccinate – results from a serosurvey for nine vaccine-preventable diseases among adult refugees in the Netherlands in 2016

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3. Department of Primary and Community Care, Radboud university medical centre, Nijmegen, the Netherlands

Background

Refugees are vulnerable to contracting infectious diseases due to overcrowding. Outbreaks occur among children and adults. In the Netherlands, refugee children are offered vaccination according to the National Immunization Program. As little is known about adult refugee seroprotection, we aimed to assess their immunity against vaccine-preventable diseases (VPD) to identify groups that might benefit from additional vaccinations.

Methods

In 2016, we invited adult refugees in three Dutch centres, from Syria, Iran, Iraq, Afghanistan, Eritrea and Ethiopia, to participate in a serosurvey for VPD. Participants completed questionnaires (demographics, vaccination history) and provided blood samples. We measured prevalence of antibodies to measles, mumps, rubella, varicella, diphtheria, tetanus and hepatitis A and B, comparing them by originating country and age groups using chi-squared tests. For polio, results are pending.

Results

We surveyed 622 refugees. The median age was 28 years (interquartile range: 23-35), 81% were male and 48% originated from Syria. Overall, seroprevalence was 88% for measles (range between countries: 83-93%), 91% for mumps (81-95%), 94% for rubella (84-98%), 96% for varicella (92-98%), 82% for diphtheria (65-88%), 98% for tetanus (86-100%), 84% (54-100%) for hepatitis A and 27% for hepatitis B (anti-HBs) (8-42%). Except for varicella and measles, seroprevalence differed between countries (p-values: <0.001-0.002). For measles and hepatitis A seroprevalence increased with age (p-values: 0.009 and <0.001).

Conclusion

Our results indicate insufficient protection against certain VPD. For all countries, measles seroprevalence was below the WHO-threshold of 95% required for elimination. In comparison, seroprevalence in the Dutch general population was 96% in 2006/07. Rubella seroprevalence was below 95% for Syria and Iraq. In outbreak situations, results of this study can help prioritizing vaccination of susceptible subgroups of adult refugees in Europe.

Keywords: serosurvey refugees vaccine-preventable diseases seroprotection

ABSTRACT ID: 861

PRESENTED BY: Gudrun Freidl (gudrun.freidl@rivm.nl)

O13.4 The Health Protection Response to the first onward transmission of toxigenic Corynebacterium diphtheriae within England in 30 years

David Edwards (1), A. Trindall (2), C. Pearson (2), C. Lester (1), D. Kent (1), M. Murphy (3), A. Itani (4), N. Brown (5), O. Sule (5), Iain Roddick (2), D. Zenner (5), M. Chand (6), N. Fry (6), J. Hoffmann (1), N. Iyanger (6), L. Kemp (4), J. White (6), B. Javid (6), I. Ramsay (6), D. Litt (6), A. Ahmed (1), G. Amirthalingam (6), C.S. Brown (6), S. Salimee (1), M. Reacher (2)

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2. PHE Field Epidemiology Service East, National Infections Service, Cambridge, UK
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5. PHE Microbiology Services, East of England, UK
6. PHE National Infection Service, London, UK

Background

A UK born female presented to her family doctor with sore throat, enlarged tonsils and two skin ulcers on her right foot three weeks after returning from Ghana. The case was fully immunised according to the routine UK immunisation schedule.

A swab from the ulcer which identified Corynebacterium diphtheriae at the local laboratory was confirmed as toxigenic by the Public Health England (PHE) reference laboratory.

Methods

PHE risk assessed the case and undertook contact tracing of household and healthcare contacts. Public health actions included organizing pre-antibiotic screening (nasopharyngeal and throat swabs), chemoprophylaxis and a booster diphtheria toxoid containing vaccine for identified contacts.

Results

The case was treated with clarithromycin and given a booster vaccination. Six close contacts (family and household) were initially identified: one (a female of uncertain immunisation status who had not recently travelled) screened positive for toxigenic C. diphtheriae and reported a history of mild coryzal symptoms. The isolate was confirmed to be the same type by MLST as that of the index case. The other close contact and seven excluded healthcare workers (HCW), screened negative for C. diphtheriae.

The index case and one close contact (HCW) had complete diphtheria immunisation, while the second case had unknown immunisation status and was likely to be unimmunised against diphtheria.

Conclusion

This is the first documented case of transmission of toxigenic diphtheria within the UK in 30 years, where diphtheria remains a rare disease due to an effective immunisation programme.

The main risk factors for toxigenic C. diphtheriae are travel to an endemic country, close contact with a diphtheria case and being unvaccinated. Infection can still occur in fully vaccinated individuals leading to transmission to individuals without up-to-date immunisation.

Keywords: Corynebacterium Diphtheriae, Diphtheria Toxin, Chemoprevention, Transmission

ABSTRACT ID: 952

PRESENTED BY: David Edwards (david.s.edwards@phe.gov.uk)

Parallel Session 14: Food- and waterborne diseases and zoonoses (4)

O14.1 Norovirus outbreak among staff working at a food processing company in Malta, February-March 2017

Alastair Donachie (1, 2), M. Borg (1), T. Melillo (1)

1. Infectious Disease Prevention and Control Unit (IDCU) – Health Promotion and Disease Prevention Directorate, Malta
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Background

On 03/03/2017, the Infectious Disease Prevention and Control Unit (IDCU) in Malta was notified about an outbreak of gastroenteritis affecting employees of a food processing company since 28/03/2017. We aimed to identify the source and implement control measures.

Methods

We inspected the company, identified all employees though Human Resources, and collected data on risk exposures using self-administered questionnaires. We defined cases as company employees with at least two episodes of vomiting or diarrhoea in 24 hours since 28/02/17. We calculated risk ratios (RR) and 95% confidence intervals (95%CI). Stool samples were collected and analysed.

Results

Of 514 employees, 272 (53%) responded; 55 (20%) met the case definition with onset dates from 28/02/2017- 04/03/2017. Five (9%) cases required hospitalisation. Fifty-three (96%) cases ate from the canteen from 27/02/2017 – 02/03/2017. Eating in the canteen was associated with illness (RR: 11; 95% CI: 2.7 – 43). No significant food exposures were identified. Eleven of 26 (42%) stool samples were positive for norovirus. Of these, 3 were food handlers in processing plants; 8 were canteen food handlers, of which 3 (38%) were asymptomatic. Environmental inspections identified deficiencies in food safety practices; food handlers preparing canteen food were also responsible for cleaning the toilets and premises of the company.

Conclusion

Environmental and epidemiological evidence suggest this point source outbreak occurred due to cross-contamination of canteen food and/or inadequate adherence to food hygiene practices. To prevent further cases, food processing was temporarily suspended, positive food handlers were excluded, the company's premises was disinfected and staff responsibilities revised. This outbreak highlights the potential role of asymptomatic food handlers in norovirus transmission and the importance of reinforcing adherence to personal hygiene and food safety practices.

Keywords: Norovirus, Malta, Disease Outbreaks, Cohort Studies

ABSTRACT ID: 761

PRESENTED BY: Alastair Donachie (adonachie@hotmail.co.uk)

O14.2 Ingredient-based analysis reveals potential vehicle for a large norovirus outbreak at a national chain of Mexican-themed restaurants in the UK, October 2016

Vicky Watts (1, 2), V Decraene (2), R Vivancos (2), J Sedgwick (3)

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3. On behalf of epidemiological investigations cell, Public Health England, London, UK

Background

In October 2016 a confirmed norovirus outbreak was investigated at 23 branches of a Mexican restaurant chain, coinciding with a new menu launch. Our retrospective staff cohort study suggested an association between salmon tostada or chicken wings and illness. Smaller customer studies suggested an association with chicken dishes. Due to these different conclusions we conducted investigations by ingredient and kitchen-section to identify the source to implement control measures and prevent further illness.

Methods

We reviewed recipes, interviewed chefs and inspected restaurants to identify common ingredients and preparation methods for dishes implicated by our study. Ingredient and kitchen preparation section exposures were assigned to respondents according to menu items consumed. We estimated the association between exposure and illness using a Poisson regression with robust errors to calculate adjusted risk ratios (aRR) and 95%-confidence intervals (95%-CI).

Results

The service-kitchen was divided into three sections. Over 70% of cases had consumed a dish prepared in the salad section (RR: 2.1; 95% CI: 1.3-3.4). Chipotle in adobo sauce (CAS) was common to most implicated dishes. Individuals who consumed CAS were twice as likely to develop symptoms (aRR:2.2; 95%-CI: 1.4-3.5). Restaurant inspections revealed two products labelled as CAS, including one introduced for the new menu from Mexico which the outbreak control team discovered had not undergone pasteurisation, heat treatment or microbial testing in the UK.

Conclusion

We believe the likely vehicle was a newly introduced ingredient common to multiple dishes and cross-contamination from that ingredient occurred within the salad kitchen-section; we suspect this to be uncooked CAS. We advised the company to dispose of the CAS and review risk assessments for uncooked products and the potential for cross-contamination within the service-kitchen.

Keywords: Norovirus, Disease Outbreak, Cohort Studies, Foodborne Diseases

ABSTRACT ID: 873

PRESENTED BY: Vicky Watts (vicky.watts@phe.gov.uk)

O14.3 The largest Campylobacter coli outbreak in Germany, associated with mincemeat consumption, May 2016

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7. Local Public Health Authority, Berlin Mitte, Germany

Background

Outbreaks of Campylobacter coli are rare in Germany and usually involve <5 cases. On 01/06/2016, the public health office of Märkisch-Oderland reported 11 C. coli cases, located in neighboring towns. We investigated the outbreak to identify the source of infection.

Methods

We defined cases as residents in Märkisch-Oderland with symptoms' onset between 23/05-27/05/2016 and with positive C. coli-culture or epidemiologically linked symptomatic persons. We compared cases with controls selected from the same area using random digit dialing. We interviewed cases and controls using a structured questionnaire on food consumption and calculated odds ratios (OR) with 95% confidence intervals (95%CI). The local food safety authorities collected food and environmental samples. The National Reference Center subtyped human isolates by pulsed-field gel electrophoreses (PFGE).

Results

Overall, 15 cases were identified (33% female, median age: 51 years; range: 4-69 years; 4 hospitalised); 12 had identical PFGE pattern. Cases were more likely to consume pork mincemeat compared to controls (9/10 cases vs 6/14 controls; OR=12, 95%CI=1.2-122), and to consume it raw (9/10 cases vs 0/14 controls; OR=∞, 95%CI=16 -∞). Seven cases, but none of the controls bought meat at the local butcher. Pork and environmental samples in the butchery tested negative.

Conclusion

This was the largest Campylobacter coli outbreak documented in Germany since 2001. Epidemiological evidence suggested raw mincemeat from a local butcher as the most likely vehicle of infection. The investigation highlights the need of close collaboration between food safety and public health authorities. Consumers should be advised about the risk of consuming raw pork. Improvements of food safety regulations are still required to reduce contamination of pork with Campylobacter coli.

Keywords: Campylobacter coli, Outbreak, Food-borne Diseases, Pork, Raw Mincemeat

ABSTRACT ID: 853

PRESENTED BY: Claudia Siffczyk (claudia.siffczyk@lavg.brandenburg.de)

O14.4 Outbreak of leptospirosis among Kayakers, France, 2016

Alexandra Septfons (1,2), M. Pivette (3), P. Bourhy (4), F. Ayral (5), A.Decors (6), H. Aranda Grau (7), C.Richomme(8), M.Le Guyader(9), B.Combes (10), C.Malhère (11), L.King (3), Y.Guillois (3)

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9. Univ Lyon, VetAgro Sup, Laboratoire des Leptospires, UsC 1233 RS2GP, F-69280, MARCY L'ETOILE, France
10. Entente for the Control of Zoonoses, Nancy, France
11. Directorate General for Food (DGAl), Paris, France

Background

In September 2016, a kayak club on the Vilaine river, Brittany, reported seven kayakers with symptoms compatible with leptospirosis since July 2016. Human and environmental investigations were performed to identify the outbreak source and guide control measures.

Methods

We asked kayak clubs, laboratories, hospitals and general practitioners to report cases with symptoms compatible with leptospirosis (fever, myalgia, arthralgia) or positive laboratory results in a 40km area adjacent to the river and requested further information using a standardized questionnaire.

A possible case was a person with symptoms compatible with leptospirosis between 1 June and 31 October 2016 and exposure to the river, and a confirmed case was a possible case with laboratory evidence.

Rodents were trapped near the river and PCR tested for leptospirosis.

Results

Eight confirmed and 6 possible cases were identified with symptom onset between 22 June and 15 September. Three cases were hospitalized. All cases practiced kayaking over a 30 km section of the Vilaine river. No other at-risk exposure was identified. Nine cases reported skin lesions, 50% wore integral swim suits and none were vaccinated.

L.kirschneri was the only species identified in 5 cases. 24% of the 38 trapped animals were positive for leptospirosis DNA, none being L. kirschneri.

An unusually dry summer period and an interruption of rodent control campaigns on the stretch of river concerned have been documented.

Conclusion

Access to the river was immediately forbidden after detection of the first cases. We informed the health professionals and all kayak clubs about leptospirosis risk and individual prevention measures including vaccination. We recommended enhanced rodent control and active surveillance of cases for the next season to rapidly identify areas of transmission.

Keywords: Leptospirosis, Outbreak

ABSTRACT ID: 1066

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

O14.5 Integration of context information to improve automated outbreak detection and the evaluation of an epidemic situation

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Background

The Robert Koch Institute collects case reports of more than 70 notifiable infectious diseases. This amounts to about 500.000 reported cases and 20.000 outbreaks every year. We provide an early warning service for infectious disease outbreaks to experts at the institute and local health agencies. This service is now being extended by context information to improve performance of the detection algorithms and interpretability of the epidemiological situation.

Methods

For the automated outbreak detection we use generalized linear models to compute expected and threshold values. The current model uses historic case counts, seasonal factors and trend as independent variables. The new model adds several independent variables related to weather, school holidays, demographics and neighbouring counties. Variables are also included in lagged variants. Finally, variable importance is computed and a variable selection method is applied. For the expert user several visualisations allowing to interpret the correlation between context and case counts are provided.

Results

The study of 30 infectious diseases showed that the context variables can help reveal potential sources of anomalies in case count time series. The inclusion of demographics and information of neighboring counties improved prediction accuracy for time series with few counts and large noise. An R package was developed that allows easy extraction and integration of contextual information for the detection of infectious disease outbreaks and visual analysis via an interactive dashboard representation.

Conclusion

Considering context helps to detect infectious disease outbreaks and better assess the epidemic situation. We have established a basis for a systematic evaluation of the contribution of external factors. Integration of further sources (e.g. syndromic surveillance data, internet searches, social media) may also improve timeliness of outbreak detection and allow short-term forecasts.

Keywords: Automatic Data Processing [L01.224.085], Public Health Informatics [L01.313.750], Disease Outbreaks [N06.850.290], Data Interpretation, Statistical [L01.313.500.750.190.380], Epidemics [N06.850.290.200]

ABSTRACT ID: 1025

PRESENTED BY: Alexander Ullrich (ullricha@rki.de)

Parallel Session 15: Late breakers (1)

O15.1 A rapid research needs appraisal methodology to inform research prioritise in response to (re-) emerging infectious disease outbreaks

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2. Cochrane Response
3. Evidence-Aid

Background

The evidence base for responses to epidemics of (re-) emerging pathogens is limited. The challenges and the limited window of opportunity to implement research, makes it important that during the earliest stages of an epidemic the priorities for research are rapidly and rigorously defined, ensuring the potential for a direct clinical and public health impact. Here we present a methodology for the rapid, systematic identification of gaps in evidence (≤5 days) in response to (re-) emerging epidemics, to inform research prioritise.

Methods

The protocol was developed in collaboration with Cochrane Response and Evidence-Aid. The protocol was optimised through use of pre-defined clinical research domains and minimal, data outcome tables. Moreover, through effective use of global time-zones and systematic review software, allowing simultaneous tasks 24-h a day without knowledge transfer loss. The protocol was piloted using a Lassa fever outbreak scenario (July 2017), with Cochrane Response teams in the UK, Canada and Singapore. The result of the pilot will be evaluated using an expert panel.

Results

1104 articles were identified and screened for inclusion. 111 articles met the inclusion criteria; 53 articles met the data extraction criteria. The data outcomes tables were submitted to the team in Oxford on day 5 of the pilot. Across the 8 clinical domains (Phenotype/natural history of disease; Risk factors; Immune response; Diagnostics; Drug therapy; Supportive care; Transmission; Prevention), 14 clinical research prioritise were identified. These will be evaluated against expert panel opinion and presented with the results.

Conclusion

These results shows that it is feasible to carry out a rapid, systematic research needs appraisal ≤ 5 days to inform clinical research prioritise early on in response to (re-) emerging infectious disease outbreaks globally.

Keywords: Emerging: Infectious diseases: Research prioritisation: Evidence base

ABSTRACT ID: 1433

PRESENTED BY: Louise Sigfrid (louise.sigfrid@gmail.com)

O15.2 How prepared are we for cross-border outbreaks? An exploratory analysis of cross-border response networks for outbreaks of highly resistant microorganisms in the Netherlands and Germany.

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2. Department of Organization Studies, Tilburg University, Tilburg, the Netherlands

Background

The emergence and spread of highly resistant microorganisms (HRMO) is a serious threat to transnational public health. Therefore, it is vital that cross-border outbreak response systems are constantly prepared for fast, rigorous, and efficient response. The present research aims to improve transnational collaboration by identifying, visualizing, and exploring two regional cross-border response networks that are likely to unfold during cross-border outbreaks of HRMO between the Netherlands and Germany.

Methods

Quantitative methods were used to empirically explore characteristics of two response networks during a cross-border outbreak of CPE (Carbapenem-resistant Enterobacteriaceae) in healthcare settings. 86 Dutch and German health professionals reflected on an online delivered, fictive but realistic, outbreak scenario (response rate 70%). Data were collected regarding outbreak control responsibilities, roles, and collaboration with partners. Network analysis techniques (i.a. density, centralization, and clique structures) were used to analyse collaborative structures during crisis response.

Results

Two relatively similar response networks were identified in which 37 stakeholders are involved in joint outbreak response. The networks are well integrated, with a small group of stakeholders acting as brokers by connecting most healthcare professionals. However, levels of trust are moderately low and cross-border prior working relationships are sparse. Within countries we see a centralized network structure with public health services and hospitals having a central position. Across national borders, several actors are beneficially positioned to coordinate transnational collaboration.

Conclusion

This comparative case research revealed two regional cross-border response networks. Given the characteristics of these networks, dual lead organization governance is most suited to facilitate transnational coordination during future outbreaks. Furthermore, networks identified in this study are not only crucial in times of outbreak containment, but should also be fostered during times of non crisis.

Keywords: cross-border outbreak management, highly resistant microorganisms, social network analysis, network coordination

ABSTRACT ID: 1412

PRESENTED BY: Jacklien Maessen (Jacklienmaessen@gmail.com)

O15.3 Hepatitis A outbreak disproportionately affecting men who have sex with men (MSM) in the European Union and European Economic Area (EU/EEA), 1st June 2016 – 31st May 2017.

Authors Patricia Ndumbi (1, 2), G. S. Freidl (1, 3), C. Williams (4), O. Mardh (5), C. Varela (2), A. Avellón (2), I. Friesema (3), H. Vennema (3), K. Beebeejaun (6), S. L. Ngui (6), M. Edelstein (6), A. Smith-Palmer(7), N. Murphy(8), J. Dean(9), M. Faber(10), J. Wenzel(11), M. Kontio(12), L. Müller(13), S. Midgley(13), L. Sundqvist(14), J. Ederth(14), A. Roque-Afonso(15), E. Couturier(16), S. Klamer(17), J. Rebolledo(17), V. Suin(17), S. W. Aberle(18), D. Schmid(19), R. de Sousa(20), G. F. Augusto(20), V. Alfonsi(21), M. Del Manso(21), A. Ciccaglione(21), K. Mellou(22), C. Hadjichristodoulou(23), A. Donachie(24), M. Borg (24), Maja Sočan(25), Mario Poljak(26), Ettore Severi(5, 28) and The European Hepatitis A outbreak team(28)

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27. Karolinska Institute, Stockholm, Sweden
28. Members of the hepatitis A outbreak investigation team are listed at the end of the manuscript.

Background

Between June 2016 and May 2017, 16 EU/EEA countries reported cases associated with a multi-country hepatitis A (HA) outbreak. Molecular analysis identified three co-circulating hepatitis A virus strains: VRD_521_2016, V16-25801 and RIVM-HAV16-090. We aimed to describe the characteristics of cases and compare exposures associated with the different outbreak strains.

Methods

Affected EU/EEA countries completed an enhanced surveillance questionnaire, including case characteristics and risk behaviour, for confirmed cases. Confirmed cases were defined as EU/EEA residents with symptom onset between June 2016 and May 2017 and laboratory-confirmed HAV strain ≥99.3% homologous to one of the three outbreak strains based on overlapping fragment at the VP1-2a region. We calculated the prevalence of exposures, and compared them between outbreak strains using logistic regression.

Results

1400 confirmed cases were reported from 16 countries. VRD_521_2016 accounted 56% of all cases. Of cases with available data, 93% (1283/1382) were male, 92% (361/393) were unvaccinated, 43% (83/195) reported travelling to Spain, 54% (429/797) were hospitalised, 43% (60/140) were HIV-positive and 84% (565/676) of males self-identified as MSM. Among cases with sexual exposure data, 36% (72/199) had sexual contact with ≥3 partners (54% anonymous), 30% (58/194) used dating apps for sex and 62% (82/133) reported inconsistent condom use. Case characteristics and sexual exposures did not significantly differ between strains.

Conclusion

We describe an outbreak of multiple HA virus strains within a cross-European population, particularly driven by sexual transmission between unvaccinated MSM engaging in high-risk behaviour. We recommend vaccination of susceptible MSM against HAV (particularly those engaging in high risk sexual behaviour), and raising awareness of preventive measures through information campaigns targeting the MSM population.

Keywords: hepatitis A, hepatitis A virus, men who have sex with men – MSM, vaccine-preventable diseases, vaccines and immunisation, sexually transmitted infections.

ABSTRACT ID: 1416

PRESENTED BY: Patricia Ndumbi (patricia.ndumbi@gmail.com)

O15.4 High levels of immunity for Hepatitis E Virus in urban population affected by an acute outbreak in Am Timan, Chad, 2016-2017

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Background

During a community-wide outbreak of Hepatitis E Virus (HEV) genotype 1e in Am Timan (Chad) in April 2017, we estimated the sero-prevalence of anti-HEV antibodies and estimated risk factors associated with recent HEV infection to understand the transmission dynamics of this disease.

Methods

We conducted a population-based serological survey in 384 households selected using simple random sampling. Household members answered a questionnaire about risk factors for HEV infection and provided blood samples. These were tested for HEV IgG and IgM antibodies using Enzyme-Immune-Assay (EIA). We calculated weighted prevalence estimates and prevalence ratios (PRs) for possible risk factors for infection using multivariate Cox regression.

Results

1529 persons in 241 households were included (response rate: 62.8%). The overall weighted prevalence for a recent and past HEV infection were 7.7% (95%CI: 6.2-9.6) and 59.6% (95%CI: 56.3-62.8) respectively. The highest prevalence of anti-HEV IgM antibodies was in children <5 years of age (12.6%; 95%CI: 8.7-17.9). The prevalence of past HEV infection increased from 23.5% (95%CI: 18.3-29.7) in children <5 years of age to 75.9% (95%CI: 72.1-79.2) in individuals ≥15 years of age. Risk factors for recent HEV infections included: sharing the sanitation facility (PR 1.72; 95%CI: 1.08-2.73), not systematically using soap for handwashing (PR 1.85; 95%CI: 1.30-2.63) and having animals sleeping inside the compound (PR 1.69; 95%CI: 1.15-2.50).

Conclusion

Our results suggest that the population of Am Timan was already highly immune for HEV prior to this outbreak. The identified risk factors suggest that household level transmission is contributing to the propagation of this infection during outbreaks. Control measures in future outbreaks should ensure safe water and improved access to sanitation and hygiene at household level.

Keywords: Hepatitis E virus, Chad, outbreak, sero-prevalence, Wantai ELISA

ABSTRACT ID: 1373

PRESENTED BY: Annick Lenglet

O15.5 Outbreak of measles linked to the current European B3 circulation, Wales 2017

Chris Williams(1), Jonny Currie(1), Meredid Bowley(2), Simon Cottrell(1), Llion Davies (1), Joanne McCarthy(1), Catherine Moore(1), Malorie Perry(1), Rhianwen Stiff (1), Giri Shankar (1)

1. Public Health Wales
2. Aneurin Bevan Gwent Public Health Team

Background

In May 2017, a confirmed case of measles in a high school in Newport, linked to a community with low vaccination coverage, led to an outbreak in the local authorities of Newport and Torfaen.

Methods

We defined used modified ECDC case definitions, for persons resident in outbreak areas. Dry throat swabs were sought from all cases, tested via PCR and genotyped. Contacts were identified through case investigation. We collected information on cases and contacts using a standardised form, constructing network diagrams using CytoscapeTM. We compared vaccination status in cases aged 2-18 years with immunisation registry information to calculate vaccine effectiveness using the screening method.

Results

There were 21 cases between May and August 2017; 33% were male, with mean age 11 years (10 months-29 years); 67% were school-aged.)17/21 were PCR-confirmed and genotyped B3 (indistinguishable from the Romanian outbreak strain). Networks showed initial transmission in the index's high school (4/5 earliest confirmed cases), then transmission in linked primary schools. Later were exposure episodes in six healthcare settings, two associated with three secondary cases in children below scheduled vaccination age, and a healthcare worker. 62% of cases were unvaccinated. Vaccine effectiveness was 96.0% for two doses and 92.8% for a single dose.

Conclusion

School transmission was addressed through early vaccination interventions in the affected schools, starting 11 days after rash onset of the first confirmed case, followed by interventions in all schools in the Newport area. Media interviews and social media were used to encourage vaccination and early isolation. Some early cases were not in immunisation registries or GP records. We recommend identification of other under-immunised school populations and earlier identification of cases in healthcare settings to avoid transmission.

Keywords: measles, outbreak, healthcare, immunisation

ABSTRACT ID: 1439

PRESENTED BY: Simon Cottrell (kitwilliams70@gmail.com)

PARALLEL SESSION PROGRAMME
DAY 3, WEDNESDAY, 8 NOVEMBER
11:00-12:40

Parallel Session 16: Emerging and vector-borne diseases (2)

O16.1 Population-based Borrelia burgdorferi seroprevalence and associated risk factors in Finland

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Background

Lyme borreliosis (LB) is the most common vector-borne disease in the Northern hemisphere and a major health concern since reported case numbers have steadily increased in Europe during the last two decades. The objectives of this study are to determine the Borrelia burgdorferi (BB) seroprevalence among the general Finnish population, and to identify risk factors and medical conditions associated with BB seropositive status to prioritise targeted interventions.

Methods

Two thousand sera from a nationwide health survey from 2011, representative of the adult population (aged ≥29), were tested by whole cell sonicate IgG screening ELISA. Positive specimens were confirmed by C6 peptide ELISA and recomBead IgG 2.0. Test results were linked to a general health questionnaire conducted in 2011 and the national hospital discharge registry by a unique identifier. A multivariable logistic regression model, adjusting for stratified cluster design taking into account sampling weights, was used to identify risk factors.

Results

The median age of the study population was 56 years (range 29-97) and the BB weighted seroprevalence was 3.9% (95% confidence interval (CI) 3.03-5.08). The weighted seroprevalence was significantly higher among males than females (adjusted odds ratio 1.91, 95%CI 1.21-3.04) and a significant age-related seroprevalence increase was observed. The seroprevalence was highest in Southern, Central, and Eastern regions. Chronic diseases (i.e. cancer, and pulmonary-, heart-, skin-, rheumatic-, and autoimmune diseases) were not associated with a BB seropositive status.

Conclusion

The first BB seroprevalence study in Finland showed a seroprevalence of 3.9% (95%CI 3.03-5.08). The results of this study can be used, together with previous data on LB incidence and spatial tick distribution, to target public health communication about preventive measures.

Keywords: Lyme borreliosis, Borrelia burgdorferi, seroprevalence, Finland

ABSTRACT ID: 881

PRESENTED BY: Janko van Beek (johannes.vanbeek@thl.fi)

O16.2 Urogenital schistosomiasis acquired in Southern Corsica: are we observing the early signs of endemicization?

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Background

Urogenital schistosomiasis, a tropical snail-borne disease, re-emerged in Europe in 2013 with 106 cases linked to exposure to the Cavu River in Southern Corsica. Subsequent detection of cases exposed to the river in 2015 and 2016 has raised the question of a possible endemicization of schistosomiasis in Corsica. We developed a human and snail surveillance system to detect and control schistosomal transmission.

Methods

From 2016, autochthonous urogenital schistosomiasis became a notifiable disease in France. A case was defined as a person with serological or parasitological evidence of schistosomiasis, with no history of travel outside of Corsica in a known endemic area. Patient specimens were genotyped and compared with the 2013 outbreak strain. Seasonal molecular surveillance of snails in the Cavu River was established for rapid detection of schistosomes.

Results

Four new cases were identified after the 2013 outbreak. In 2015, two cases reported exposure to the Cavu River the same year, while two other cases identified in 2017, reported exposure both in 2015 and 2016. Although no specimen was isolated from patients exposed only in 2015, specimens from a patient exposed in both 2015 and 2016 were closely related to the 2013 strain. Snail surveillance has not detected any Schistosoma-infected snails in the river in 2015-2016.

Conclusion

Corsica has all the necessary conditions for repeated transmission of urogenital schistosomiasis. One or more individuals infected in the 2013 outbreak is hypothesized as the source of the re-contamination of the Cavu River in 2015-2016. As a large proportion of persons infected with schistosomiasis remains asymptomatic, other recent cases may exist in the region. Therefore, schistosomiasis awareness and screening should be reinforced among healthcare providers to prevent endemicization in Corsica.

Keywords: Schistosomiasis, Corsica, parasitic diseases, bulinus, outbreaks, surveillance

ABSTRACT ID: 771

PRESENTED BY: Lauriane Ramalli (lauriane.ramalli@santepubliquefrance.fr)

O16.3 Extent of scabies cases reported to local public health authorities, Germany, 2016

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Background

According to the German Infection Protection Act, only community and institutional settings (IS) in which predominantly infants, children and young people are cared for (§33-IS, e.g. kindergartens, schools) have to notify local health authorities (LHA) about scabies cases. Other IS (non-§33-IS, e.g. nursing homes, homes for asylum seekers) might report scabies cases voluntarily to LHA. None of this information is communicated to state or national health authorities. We conducted a survey to assess the extent of notified scabies cases in Germany in 2016.

Methods

We invited all 378 German LHA via email to participate in the online survey in each quarter of 2016. The survey included questions about the IS where scabies cases occurred, the number of scabies cases and their contacts, and measures conducted by LHA.

Results

On average, 37% (30-44%) of LHA participated in the survey per quarter and 84% of these received scabies notifications. In total, 6,889 scabies cases occurring in 3,025 institutions (thereof 63% §33-IS) were reported. Individual §33-IS reported up to 50 cases (74% had single cases) and up to 40 contacts, and individual non-§33-IS reported up to 84 cases (43% had single cases) and up to 460 contacts. LHA spent over 430 working days in 2016 supporting IS where scabies cases occurred, mostly providing hygiene counselling. On average, LHA spent one hour supporting §33-IS and two hours for non-§33-IS.

Conclusion

These first nationwide scabies data collected from LHA show that scabies is a considerable problem in IS in Germany. Non-§33-IS reported higher numbers of scabies cases and contacts than §33-IS. These results support the extension of mandatory notification to non-§33-IS, aiming at earlier LHA counselling to prevent further scabies cases and outbreaks.

Keywords: Scabies, Germany, Survey, Communicable Disease, Community and Institutional Settings

ABSTRACT ID: 826

PRESENTED BY: Raskit Lachmann (LachmannR@rki.de)

O16.4 Disease burden of psittacosis in the Netherlands

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Background

Psittacosis (infection with Chlamydia psittaci) can have diverse presentations in humans, ranging from asymptomatic infection to severe systemic disease. Awareness of psittacosis and its presentations is low among clinicians and the general public. Therefore, underdiagnosis and thereby underestimation of the incidence and public health importance of psittacosis is very likely.

Methods

For estimation of psittacosis incidence, we performed a systematic review and meta-analysis of the proportion of community-acquired pneumonia (CAP) patients testing positive for C. psittaci. Secondly, we used the methodology developed for the Burden of communicable diseases in Europe (BCoDE) toolkit of the European Centre for Disease Prevention and Control (ECDC), to construct a model to estimate disease burden in Disability-Adjusted Life Years (DALYs) attributable to psittacosis. This model includes pneumonia, invasive illness and nonspecific febrile illness as presentations of acute psittacosis.

Results

C. psittaci was the causative pathogen in 1.03 percent (95% CI: 0.79-1.30) of all CAP cases from the included studies combined. According to our estimates, 4.4% (95% CI 1.6-8.2%) of all symptomatic psittacosis cases were notified in the Netherlands in 2012-2014. We estimated the disease burden caused by psittacosis in the Netherlands to have been 183.5 DALY (95% CI 145.9-226.7) per year over the period 2012-2014. This is comparable to the amount of DALYs estimated to be due to listeriosis or shigellosis in the same period in the Netherlands.

Conclusion

Our results highlight the public health importance of psittacosis and identify evidence gaps pertaining to the clinical presentations and prognosis of this disease.

Keywords: psittacosis, incidence, pneumonia, zoonoses

ABSTRACT ID: 845

PRESENTED BY: Brechje de Gier (brechje.de.gier@rivm.nl)

O16.5 Late breaker: Outbreak of Meningococcal Disease associated with a Funeral in Liberia, April 2017

Anne Perrocheau (1), J. Naiene (2), E. K. Dokubo (3), V. Katawera (2), J. Doedeh(4), M. Gbanyan (5), M. Fallah (6), J. A. Frimpong (7), K. Yealue (2), R. George (5), T. Nagbe (6), H. Kohar (6), M. Massaquoi (5), T. Nyenswah (6), M. Kromah (2), J. Sesay (2), N. Mahmoud (2), D. Allen (3), C. Kinkade (3), G. Gwesa (3), M. Reed (3), S. Friesen (3), D. Williams (3), D. Naidoo (1), O. Ronveaux (1), H. Djingaré (4), S. Minet Dubravka (2), C. Bozio (8), J. Patel (8), J. Vuong (8), X. Wang (8), L Fox (8), T Clark (8).

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Background

On 25 April 2017, the Liberian Ministry of Health reported a cluster of 14 unexplained illnesses, including eight deaths, in Sinoe County. Patient histories pointed to exposure at a funeral ceremony on 21-22 April. Predominant symptoms included abdominal pain, weakness, vomiting, diarrhoea, and confusion without fever.

Methods

A suspect case was defined as illness with onset on or after April 10, 2017 with two or more symptoms including headache, vomiting, mental confusion, and weakness, in a person who visited or lived in Sinoe County.

Results

Further investigation identified a total of 31 suspect cases, including 13 deaths in Sinoe, Montserrado and Grand-Bassa counties. On 27 April, a case-control study identified that attendance at the funeral wake and possibly consumption of three food and drink products there were associated with disease. Samples of food and beverages consumed during the funeral were negative for › 600 fungal and bacterial toxins; toxicological testing results were not consistent with an exposure that could explain the outbreak. The last case was reported on 7 May. On 6 May, oral swabs and serum from four dead patients tested positive for Neisseria meningitis serogroup C (NmC) by PCR. PCR testing of 24 additional patients identified a total of 13 patients positive for NmC. The outbreak was therefore classified as an outbreak of NmC septicaemia.

Conclusion

Questions remain regarding the large number of cases of septicaemia and mortality occurring over a short period of time in this outbreak.

We will describe the outbreak investigation, the clinical characteristics of the patients, and discuss how to prevent the recurrence of a cluster of deaths due to meningococcal septicaemia in Liberia.

Keywords: meningococcal disease, septicaemia, outbreak investigation, field epidemiology

ABSTRACT ID: 1385

PRESENTED BY: Anne Perrocheaua (perrocheaua@who.int)

Parallel Session 17: Influenza and other respiratory viruses (2)

O17.1 Feasibility of measuring influenza vaccine effectiveness by brand, I-MOVE primary-care multicentre case-control study in Europe, 2010-11 to 2016-17

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Background

The European Medicines Agency requests vaccine manufacturers to provide brand-specific influenza vaccine effectiveness (VE). To assess feasibility of measuring influenza brand-specific VE, we pooled seven seasons of the European I-MOVE primary care multicentre case-control studies (MCCS) (2010/11-2016/17).

Methods

Using a test-negative design, we calculated pooled-season VE (pVE), adjusting for age, sex, chronic conditions, onset time, study site and season. We measured brand-specific pVE against influenza $A(H_1N_1)pdm09$, $A(H_3N_2)$ and B for vaccines with highest coverage (Influvac, Fluarix and Vaxigrip). We included a study site in a given season if ≥1 influenza-like illness (ILI) patient was vaccinated with the specific vaccine. Persons vaccinated with other vaccines were excluded. In a sensitivity analysis, we weighted the analysis by number of ILI patients by age-group and season to correct for different sample sizes across seasons.

Results

We included ›10,000 ILI patients in each brand- and influenza type/subtype-specific analysis.

pVE for Influvac, Fluarix and Vaxigrip respectively was 43.7% (95% CI: 25.9-57.2), 74.1% (95%CI: 54.7-85.2) and 40.1% (95%CI: 24.3-52.6%) against influenza $A(H_1N_1)pdm09$; 26.2% (95% CI: 11.4-38.5), 28.6% (95% CI: -2.8-50.4) and 20.9% (95% CI: 6.4-33.2) against influenza $A(H_3N_2)$ and 46.1% (95%CI: 29.8-58.6), 57.1% (95%CI: 28.1-74.4) and 39.3% (95%CI: 22.5-52.4) against influenza B. In the sensitivity analysis for Influvac, Fluarix and Vaxigrip respectively, weighted pVE was 49.6%, 70.7% and 43.4% against $A(H_1N_1)pdm09$, 25.9%, 32.5% and 11.0% against $A(H_3N_2)$ and 47.0%, 41.2% and 44.4% against influenza B.

Conclusion

The I-MOVE MCCS provided brand-specific pVE for the vaccines with highest coverage. Brand-specific pVE against influenza $A(H_1N_1)pdm09$ and $A(H_3N_2)$ may differ, but season-specific sample size differences may affect VE. Furthermore, information on previous vaccination, natural immunity, duration of protection, vaccine content is needed to interpret these observed results.

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

ABSTRACT ID: 918

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

O17.2 Low influenza 2016-17 vaccine effectiveness against A(H3N2) hospitalised influenza among elderly in Europe: results from the I-MOVE+ multicentre study

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Background

The predominant circulating influenza virus in the 2016-17 was A(H3N2). ECDC early reports suggested that the incidence and mortality was high especially among elderly. With the I-MOVE+ network, we conducted a multicentre test-negative design case control study in 30 hospitals in 10 European countries to measure influenza vaccine effectiveness (IVE) against A(H3N2).

Methods

Hospital teams included patients aged ≥65 years swabbed ≤7 days after onset of symptoms compatible with severe acute respiratory infection (SARI). They collected information on demographics, influenza vaccination (2015-16 and 2016-17 seasons) and underlying conditions. Cases were patients RT-PCR positive for influenza A(H3N2) and controls those negative for any influenza virus. Using logistic regression we measured IVE against influenza A(H3N2) adjusted for potential confounders by age group and 2015-16 vaccination status.

Results

We included 1073 A(H3N2) cases and 1531 negative controls. The 2016-17 influenza vaccine coverage was 52% among cases and 58% among controls; 90% (1289/1434) of vaccinated patients were also vaccinated in 2015-16. Adjusted IVE against A(H3N2) was 17% (95%CI:1;31) overall; 25% (95%CI:2;43) among the 65-79 years old and 10% (95%IC:-15;30) among the ≥80 years. The 2016-17 IVE was 39% (95%CI:-3;59) among unvaccinated patients in 2015-16 and -2% (95%CI:-44;28) among those vaccinated in 2015-16.

Conclusion

In Europe, the 2016-17 season IVE against hospitalisation with A(H3N2) influenza among elderly was low, particularly among those aged 80 years and above. Although imprecise, our results suggest a negative effect of 2015-16 vaccination on the 2016-17 IVE. To further understand the role of repeated seasonal vaccination, long term studies should integrate epidemiologic, virological and immunological aspects.

Keywords: Influenza vaccine, Effectiveness, Case control studies, Hospitalisation

ABSTRACT ID: 885

PRESENTED BY: Marc Rondy (m.rondy@epiconcept.fr)

O17.3 Effectiveness of the 2016/17 tetravalent live and inactivated influenza vaccines against A(H3N2) 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 have performed a similar influenza virologic surveillance. During the influenza season 2016/17 we estimated the effectiveness (VE) of the tetravalent live attenuated influenza vaccine (LAIV4) and of inactivated influenza vaccines (IIV) in preventing laboratory-confirmed influenza A(H3N2) cases among children in a pooled analysis.

Methods

From week 48/2016 to 14/2017, sentinel paediatricians systematically swabbed ARI (acute respiratory illness) patients for testing of influenza viruses by PCR. We compared A(H3N2) cases and influenza-negative controls. We estimated vaccine type specific VE against laboratory-confirmed A(H3N2) 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 1,395 included patients (mean age 7.7 years, 53% males), 506 (36%) tested positive for A(H3N2). Among children aged 2-17 years the adjusted VE for LAIV4 was 56% (95%CI: 18-76%) and for IIV 56% (95%CI: 21-75%). LAIV4-VE in 2-6-year-old children was 68% (95% CI: 34-85) and IIV-VE 52% (95%CI: -141-91). In children aged 7-17 years VE estimates for LAIV4 and IIV were 41% (95%CI: -119-84) and 57% (95% CI: 18-77) respectively.

Conclusion

Our study indicates similar moderate preventive effect of LAIV4 and of IIV against influenza A(H3N2) 2016/17 among 2-17-year-old children and adolescents. Our IIV-VE-estimates were similar to or slightly higher than early estimates reported for the US (CDC) or for Europe (I-MOVE), whereas no comparable estimates for LAIV4 were publicly available yet. We inform stakeholders and health professionals to discuss influenza vaccine recommendations for the coming season.

Keywords: Influenza, Human, Influenza Vaccine, Respiratory Diseases, Case-Control Studies, Prevention & Control, Surveillance

ABSTRACT ID: 975

PRESENTED BY: Johannes Dreesman (johannes.dreesman@nlga.niedersachsen.de)

O17.4 Late breaker: Effectiveness of the live adapted influenza vaccine (Fluenz) in Scottish children aged 4-11 years with severe illness presenting to hospital during the 2014/15, 2015/16 & 2016/17 seasons

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Background

A preferential offer of live adapted influenza vaccine (LAIV) (Fluenz) has been made annually to 276,00-290,000 Scottish primary school age children age 4-11 years since October 2014 onwards. All vaccines administered are recorded in a national electronic data base. In excess of 99% of the vaccine received is LAIV - uptake increased from 71.2% to 71.8% then 73% in each of the last three seasons.

Methods

The Community Health Index (CHI), a unique identifier used in all National Health Service Scotland encounters, was used to perform record linkage of this childhood vaccination with national hospitalisation and influenza laboratory PCR results. Logistic regression generated adjusted vaccine effectiveness (VE) (Age, Sex, Previous Year Vaccine Time).

Results

Significant preliminary LAIV seasonal influenza VE was identified in Scottish primary school children aged 4-11 years presenting to hospital in each of the last three seasons against laboratory confirmed influenza (VE 59%;95%CI(40-72), 66%;95%CI(54-75) and 56%;95%CI(32-72)) in 2014/15, 2015/16 & 2016/17 seasons respectively). VE for inactivated injectable vaccine was not significant for any season though limited by a small number of observations. Stratification by strain shows that VE was significantly greater against B strains than A strains in 2014/15 & 2015/16 (Flu B VE 94%;95%CI(74-99) & 84%;95%CI(73-90) versus Flu A VE 44%;95%CI(19-64) & 47%;95%CI(24-64) respectively) but not in the 2016/17 season (Flu B VE 61%;95%CI(22-80) versus 55%;95%CI(19-75)). Further stratification of A strains into subtype showed significant VE against the dominant circulating A strain in each of the seasons (H3N2 in 14/15 and 16/17, and H1N1 in 15/16).

Conclusion

These findings support the UK JCVI position on the preferential use of LAIV in the UK programme and its continued roll out across the UK Devolved Administrations.

Keywords: Influenza, vaccine, effectiveness, children, hospital, LAIV

ABSTRACT ID: 1394

PRESENTED BY: Jim McMenamin (Jim.McMenamin@nhs.net)

O17.5 Late breaker: Prices of paediatric vaccines study for 2016 National Immunisation Programs in EU/EEA

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Background

Prices paid for the vaccines in the National Immunisation Programmes (NIPs) vary significantly around Europe, but a direct comparison is difficult due to confidentiality issues. This study compares the vaccine prices in the NIPs per child under 18 in the EU/EEA countries and Switzerland by using different combinations of pricing data.

Methods

We categorised the most commonly used vaccination schedules into standard (DTaP/IPV/Hib/HepB/MMR) and recent (HPV/PCV/RV/MenC) vaccines subgroups. Information on the price per child for all vaccines and each subgroup separately was collected (on-line survey) from NIP experts in each participating country.

Results

Twenty out of 32 countries answered the survey. The price per child for all vaccines ranged from 111€ to 1018€. The differences are poorly explained by the GDP per capita or the size of the birth cohort. In the tax-funded systems (18 countries) the price per child for the standard vaccines ranged from 59€ to 117€ in countries using pentavalent and 98€ to 220€ in countries using hexavalent vaccine. Also the number of doses influenced the prices. In the social insurance systems (2 countries) the price was 1.8–4.4-fold higher than in the other hexavalent countries. In the recent vaccines subgroup, the average price per child was 130€ for the countries that included PCV and HPV, and 142€ for the countries that in addition included RV vaccine in the schedule.

Conclusion

The price per child for all vaccines and for vaccine subgroups differ notably in the EU/EEA countries. Prices in the NIP are lower in countries where vaccines are tax-funded and nationally procured. Improved procurement systems could lead to substantial savings or possibilities to add more life-saving vaccines to the NIPs.

Keywords: Immunisation programme, childhood vaccinations, costs

ABSTRACT ID: 1428

PRESENTED BY: Milda Sakalauskaite (milda.sakalauskaite@thl.fi)

Parallel Session 18: Vaccine- preventable diseases (4)

O18.1 Suboptimal measles vaccination coverage among children during a measles outbreak in centers for foreigners, Poland, 2016-2017

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Background
During weeks 24/2016–5/2017, a measles outbreak in nine centres for foreigners in Poland resulted in 127 notified cases. In week 39/2017, we investigated in the most affected centre – one with a mobile population, offering short-term first shelter to arriving asylum seekers, to identify risk groups and estimate child vaccination coverage.

Methods
Cases were those meeting the probable/confirmed EU case definition and notified from the centre to the National Institute of Public Health during weeks 27-42/2016. We compared cases with all those registered in the centre during weeks 27-39/2016 who did not become cases (non-cases). Age, sex and nationality were recorded at registration. In week 39/2016, we obtained measles vaccination status of all children, present in the centre, from their parents. We calculated proportions, odds ratios (OR) and 95% confidence intervals (95%CI) allowing for clustering in families.

Results
We identified 42 cases from four nationalities (83% Russian, 57% male, 90% <10 years old, 93% without documented pre-exposure vaccination) and 1,481 non-cases. Compared with ≥10 year olds, <1 year olds (before routine vaccination eligibility: OR=27 (95%CI 7.7-96)) and 1-9 year olds (OR=14, 95%CI 5.2-38) had higher odds of measles. Based on parental recall, measles vaccination coverage among 1-17 year-olds (n=100) was 75% (95%CI 60-90%) for one dose and 42% (95%CI 25-58%) for two doses. Based on records only, coverage was 32% (95%CI 16-48%) and 30% (95%CI 15-45%), respectively.

Conclusion
Our findings indicate low measles vaccination coverage among asylum-seeker children, arriving in Poland, which could lead to future measles outbreaks in this vulnerable group. Measles vaccination among children <10 years of age should be prioritized in this setting.

Keywords: measles, refugees, disease outbreaks, vaccination

ABSTRACT ID: 1014

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

O18.2 Small-scale analysis of measles vaccination coverage among children starting school in 2015 in North Rhine-Westphalia, Germany

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Background
Two-dose measles vaccination coverage (VC) among children at school entry has increased from 88.1% in 2007 to 94.3% in 2015 in North Rhine-Westphalia (NRW). However, measles VC varies between NRW's 53 districts, with the risk of local pockets of susceptibility where measles outbreaks could occur. Identification of these pockets is crucial for targeting preventive and control measures.

Methods
We analysed data from the 2015 school entry examinations (SEE) in Münster district, where measles VC has been below the NRW average for several years. The vaccination status of 2,356 children starting school was recorded in 45 schools by the local health authorities (LHA). Completeness and timeliness of the two-dose measles vaccination were estimated. The number of incompletely vaccinated children was analysed by school and local physician. Children who had not received two doses of a measles vaccine were defined as susceptible.

Results
Nine percent (221/2,356) of children had not received two measles vaccinations; 539 (25.3%) of those completely vaccinated received the second dose late. Measles susceptibility among school starters ranged from 3.2% to 60.0% (median 8.8%) per school. High proportions (20.8-60.0%) of susceptible children were identified in five schools. Of 30 local physicians providing vaccination, one was identified as healthcare provider for 32% of measles-susceptible children in Münster.

Conclusion
We recommend that LHAs perform small-scale analysis of SEE data in NRW to identify pockets of susceptibility, and based on these findings, implement tailored interventions like information programs or catch-up campaigns for schools, families and physicians. In outbreak situations, LHAs can target control measures for schools with higher measles susceptibility.

Keywords: vaccination, measles, disease susceptibility, child preschool

ABSTRACT ID: 880

PRESENTED BY: Sebastian Thole (sebastian.thole@lzg.nrw.de)

O18.3 Population immunity to measles in Ontario, Canada

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Background

Measles has been eliminated in the Americas and has not circulated in Canada since 1998; vaccine uptake in Ontario is >95% for some birth cohorts. Sero-epidemiology combines cross-sectional antibody prevalence studies with epidemiological analysis to assess population immunity. We conducted a sero-epidemiology study to determine whether Ontario, Canada meets the herd immunity threshold required to sustain measles elimination and to identify groups at higher risk of outbreaks, in light of Ontario's changing immunisation programs.

Methods

We used a modified BioPlex 2200 MMRV IgG assay developed by our group to test 1,199 residual sera from patients aged 1-39 years obtained from a private laboratory. We reference-tested negative and equivocal sera using a plaque reduction neutralization test. We interpreted our results in the context of Ontario's historic and current immunisation program and vaccine uptake data.

Results

Of 1,199 sera, 1035 (86.3%) were positive for measles immunity, 70 (5.8%) were equivocal and 94 (7.8%) were negative. The proportion of positive sera was highest for those 1-5 years, with 180/199 (90.5%) above the protective threshold, and lowest for those age 12-19 years, with 158/199 (79.4%) above the protective threshold. Most of the study cohort were eligible for two measles vaccine doses.

Conclusion

Measles population immunity is reflective of an elimination setting. Higher than expected non-immune individuals, despite very high vaccine uptake, may be indicative of waning immunity. Results from this study will help to assess population susceptibility and current immunisation strategies.

Keywords: measles, seroepidemiologic studies, herd immunity, immunity

ABSTRACT ID: 858

PRESENTED BY: Shelly Bolotin (shelly.bolotin@oahpp.ca)

O18.4 Who is at risk of measles in England? An age-specific estimation of measles susceptibility in individuals born 1985-2014

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Background

In England, estimating measles susceptibility helps anticipate outbreaks and identify under-immunised groups for vaccination. We estimated measles susceptibility in 2015-16 for cohorts born 1985-2014 and validated it against disease incidence.

Methods

We adjusted cohort-specific MMR1 and MMR2 vaccine coverage, estimated at age two and five years and extracted from child health records (CHRs), for known under-ascertainment and added coverage from catch-up campaigns. We assumed no natural immunity and 95% and 99.75% vaccine effectiveness for one and two doses respectively. For each birth cohort, we extracted vaccine coverage in 2015-16 from primary care records to identify vaccination outside the routine schedule and to estimate vaccination status among those who entered England post immunisation age. We calculated susceptibility by cohort as the proportion of individuals likely non-immune despite any routine or supplementary vaccination activities. We compared susceptibility with measles incidence by year of birth in order to validate our findings.

Results

Median susceptibility was 7% (range 1.5-11.1). Among cohorts eligible for two doses, those born in 2000-2003 were most susceptible (9.2-10.5%) and had the highest measles incidence. Among those born from 2000, MMR coverage estimates in primary care data and CHRs were comparable. Prior to 2000, primary care data quality precludes coverage estimation.

Conclusion

Measles susceptibility in England is sufficient to sustain transmission in specific age cohorts. Similar coverage estimates in primary care and CHR data among those born from 2000 suggest no large groups of unvaccinated foreign-born children and minimal vaccination after age five. Poor primary care data quality in older cohorts preclude estimating coverage or susceptibility in foreign-born adults. Estimating coverage in this group and improving MMR coverage in susceptible cohorts will aid measles elimination in England.

Keywords: measles, vaccination, epidemiological monitoring, England

ABSTRACT ID: 996

PRESENTED BY: Michael Edelstein (michael.edelstein@phe.gov.uk)

O18.5 Late breaker: Sero-survey to assess the measles susceptibility among the Tyrolean population using retrospective data (1997-2016), Austria

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Background
Measles elimination in Europe has been a goal for many years but not yet been achieved. Besides reliable vaccine coverage estimates, seroepidemiologic studies are considered useful tools to identfy susceptible sub-populations and subsequently tailor immunisation strategies.

Methods
We conducted a retrospective survey of blood samples which were examined for measle antibodies during a period of 20 years, 1997 until 2016 resident in Tyrol.Samples from persons admitted to an oncologic ward, transplant ward or who were considered to be immunosuppressed during the examination were excluded as well as health care workers which were screened during concerted actions.

Results
Among 17753 study participants, the susceptibility levels necessary to achieve elimination as suggested by WHO exceeded the WHO recommendations of less than 15% of susceptibles in children aged less than 5 years (30%), less than 10% in children aged five to nine years (16%), less than 5% in persons 10 years and older (17% for children aged 10 to 14 years). Only among persons born prior to 1970 the observed susceptibility levels were below the requested 5%.

Conclusion
Sero-epidemiological Studies are useful tools despite ethical and financial constraints. Our method provides a cheap and useful tool to better identify measles susceptible subgroups and may contribute to reach the goal of elimination.

Keywords: Measles, vaccination, seroepidemiologic studies, disease eradication

ABSTRACT ID: 1368

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PARALLEL SESSION PROGRAMME
DAY 3, WEDNESDAY, 8 NOVEMBER
14:30-15:30

Parallel Session 19: HIV, sexually transmitted infections and viral hepatitis (3)

O19.1 Outbreak of hepatitis A among men who have sex with men (MSM), Normandy, France, and December 2-16 to April 2017: implications for targeted vaccination.

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Background
Since October 2016, several European countries have reported the circulation of specific genotype-IA strains of hepatitis A virus mainly affecting MSM. We describe an ongoing concomitant outbreak in Normandy. Investigation aimed to plane public health action.

Methods
An epidemic case was defined as a case of hepatitis A infected with one of the genotype-IA strains, a probable case as a case of hepatitis A with unknown strain. Sexual exposure was documented for every male case. An enhanced surveillance of MSM cases was implemented. It collected data on sexual exposure to hepatitis A, unsafe sexual practices, means and places of encounter in the 2 months preceding the onset of symptoms and the knowledge and perceptions of hepatitis A and its mean of prevention (vaccination).

Results
Between 1 December 2016 and 30 April 2017, 30 hepatitis A cases living in Normandy were notified: 24 were men (M/F=4, median age=26) of which 17 cases declared themselves MSM. There were 19 confirmed epidemic cases (18 VRD5212016 strains and 1 RIVM HAV16-090 strain), 3 probable cases (all MSM) and 2 sporadic cases. Among 13 MSM cases who answered the questionnaire, 4 did not report sexual intercourse. Sexual practices reported (n=9) included group sex (n=4) and anonymous sexual intercourses (n=6). Cases also declared using apps and dating websites (n=8). None of them were immunized against hepatitis A virus, but vaccination had been proposed to 4 of them.

Conclusion
The described hepatitis A outbreak in MSM was detected while several European countries reported similar clusters. Enhanced surveillance data were used to implement a target immunization campaign in MSM in specific venue and using apps to promote it. Better awareness of MSM vaccination recommendations is necessary.

Keywords: Hepatitis A, Men having sex with men, enhanced surveillance, public helaht action

ABSTRACT ID: 1059

PRESENTED BY: Nathalie Nicolay (nathalie.nicolay@ars.sante.fr)

O19.2 Communicating prevention messages in the digital age: Using dating applications and mobile websites to reach men who have sex with men during an outbreak of hepatitis A in Berlin, 2017

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Background

Preventing onward tranmission of hepatitis A virus (HAV) through vaccination of close contacts is challenging when sexual contacts remain anonymous. In an ongoing HAV outbreak among men who have sex with men (MSM) in Berlin, cases used different dating applications to meet sexual partners, often anonymously. To prevent further cases, we launched a campaign on three applications and eight mobile websites used for anonymous dating among MSM. We evaluated the effectiveness of different mobile media platforms in reaching MSM in Berlin.

Methods

Outbreak notices were placed between 10 March and 1 April 2017, targeted at users located within Berlin. Users were invited to click a link to a public health website for information about the outbreak, HAV transmission routes and vaccination recommendations. We computed frequencies of notices shown and click-through-rates (CTR), and investigated the independent effect of advertisement size (full-screen vs. partial-screen) and mobile media placement (app vs. website) on click numbers using a multivariable Poisson regression model.

Results

Notices appeared 1,920,180 times and were clicked 8,831 times (CTR 0.46%), for a daily average of 101,906 notices and 365 clicks. Most notices (85%) were placed on dating apps. CTR was higher on apps than mobile websites (0.50% vs. 0.24%) and for full-screen than partial-screen notices (5.9% vs. 0.24%). In the multivariable model, we found a significant increase of expected number of clicks using apps (incidence rate ratio (IRR) 3.13; 95%-CI 1.79-5.46) and full-screen notices (IRR 3.14; 95%-CI 1.94-5.08).

Conclusion

Mobile media provided a rapid means to target a substantial number of MSM in Berlin who used dating applications to seek anonymous sex. The use of full-screen notices and dating apps is an important complement to case-based contact tracing.

Keywords: Hepatitis A, Contact tracing, social media, disease outbreaks

ABSTRACT ID: 992

PRESENTED BY: Claudia Ruscher (claudia.ruscher@lageso.berlin.de)

O19.3 Late breaker: The use of PrEP among men who have sex with men in Europe: Results from a 2017 Hornet/ECDC survey

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3. Hornet Gay Social Network, California, USA

Background

Pre-exposure prophylaxis (PrEP) is the use of antiretroviral medication to prevent the acquisition of HIV. Currently seven European countries provide PrEP through publicly funded health services, although there are numerous reports of off-licence use. The objectives of this study were to examine current use of PrEP, likelihood of future use, and indicators of potential PrEP candidacy in an opportunistic sample of European men who have sex with men.

Methods

The European Centre for Disease Prevention and Control and Hornet Gay Social Network sent out a survey in eight languages using inbox messages for users of the Hornet application between 17 June and 16 August 2017.

Results

Of the 12053 responses received from all 55 countries in Europe and Central Asia, 10.7% reported being HIV-positive. Among the 10764 non-HIV positive respondents, 1071 (9.9%) reported currently taking PrEP, most frequently obtained from a physician (28.1%), the internet (24.8%), friends (10.1%), and/or research studies (10.1%). More men on PrEP reported being screened for a sexually transmitted infection (STI) in the previous year than those not on PrEP (87.0% vs. 69.2%; $p<0.001$). Approximately 22.0% of those not on PrEP and 84.9% of those on PrEP agreed that they were likely to use PrEP in the next six months. Among men not on PrEP, 16.7% had been diagnosed with an STI and 4.9% had used post-exposure prophylaxis during the previous year.

Conclusion

These findings provide a snapshot of PrEP use in Europe and illustrate a high level of non-licenced current use, high likelihood of use in the next six months, and unmet need for PrEP use based on reported risk behaviour.

Keywords: Pre-Exposure Prophylaxis, men who have sex with men, mobile applications, HIV prevention

ABSTRACT ID: 1377

PRESENTED BY: Anastasia Pharris (teymur.noori@ecdc.europa.eu)

Parallel Session 20: Food- and waterborne diseases and zoonoses (5)

O20.1 Use of gp60 subtyping in the investigation of cryptosporidiosis cases linked to two swimming pools, and the identification of a rare subtype of Cryptosporidium hominis, England, October 2016

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Background

In October 2016, the North East Health Protection Team (HPT) was notified of four cases of cryptosporidiosis among users of two swimming pools (pools A and B). Available case information did not elicit other common exposures. We investigated to identify the outbreak source, and ensure implementation of appropriate control measures.

Methods

We identified cases through laboratory notification and self-report to the HPT. The national Cryptosporidium Reference Unit performed speciation and gp60 subtyping on faecal specimen Cryptosporidium isolates. Probable primary cases had diarrhoea and reported swimming in one or both pools 1-12 days prior to illness; confirmed cases had reference laboratory confirmation. Secondary cases had contact with primary cases 1-12 days prior to illness. We conducted descriptive analysis of the cases' exposure histories, obtained by interview.

Results

We identified eleven primary (eight confirmed, three probable) and 11 secondary (five confirmed, six probable) cases in nine households. The median age was seven years (range 1-65); 57% were male. The pools were the only common exposure. Eleven isolates were subtyped: four C. parvum (four different subtypes) and seven C. hominis IdA16. The IdA16 cases were primary and secondary all associated with using pool B. All C. parvum cases were primary; two used pool A only. Pools closed voluntarily for environmental investigations, and provided swim hygiene advice.

Conclusion

Our investigation identified a complex outbreak, with secondary transmission, involving exposures to two swimming pools. IdA16 is rare, isolated from only three previous UK cases. We hypothesise that C. hominis cases arose from a common exposure (pool B) and the C. parvum cases were likely sporadic. This outbreak highlights the value of speciation and subtyping in investigations, and in informing Cryptosporidium microbiological epidemiology.

Keywords: Cryptosporidium, molecular typing, disease outbreaks, swimming pools

ABSTRACT ID: 941

PRESENTED BY: Helen Bagnall (helen.bagnall@phe.gov.uk)

O20.2 From patient to farm – using whole genome sequencing as a tool to identify the source of a two-stage outbreak of Shiga toxin producing Escherichia coli (STEC) O157:H7 in Sweden

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Background

During the early autumn of 2016, Swedish authorities investigated an outbreak of STEC O157:H7. The first signal was that five cases had consumed ground beef meat skewers from the same supermarket chain. The outbreak strain reoccurred in February 2017.

Methods

An Outbreak Group was formed, consisting of members from relevant authorities. The Outbreak Group commissioned interviews with standardized questionnaires, trace-back of food items, collection of receipts, environmental sampling on farms and analysis of suspected food items. Epidemiological typing using whole genome sequencing (WGS) was performed on human, food and environmental STEC isolates.

Results

20 cases from seven counties during the autumn of 2016 formed a tight cluster in the WGS analysis. Not all cases had consumed skewers but all had eaten ground beef meat. The ground beef meat skewers were traced back to a slaughterhouse and further back to three potential farms. One farm was found positive with the outbreak strain. Hygiene measures were put in place both at the farm and at the slaughterhouse. However, several months later, in February 2017, six additional cases were identified with the outbreak strain. The trace-back investigation indicated the source to be frozen ground beef meat from the same slaughterhouse as in 2016. Six out of the 26 cases developed HUS (haemolytic uremic symdrome) which clearly shows the higher pathogenic potential of this specific outbreak strain of O157:H7.

Conclusion

Ground beef meat produced at one slaughterhouse, caused a two-stage outbreak with meat distributed to several counties in Sweden, connected by epidemiological typing. In addition, the outbreak addresses the need for thorough follow up on the source of infection and the need to assess all evidence in an outbreak investigation.

Keywords: STEC, Disease Outbreaks, One Health, Molecular Typing, Surveillance

ABSTRACT ID: 1089

PRESENTED BY: Emma Löf (emma.lof@folkhalsomyndigheten.se)

O20.3 Enhancing laboratory surveillance and follow-up of hepatitis A cases in Norway, 2016

L. Veneti (1,2), B. Guzmán (1), H. Elshaug (3), K. Franer (1), H. Lange (1), J. Ocampo (1), T. Scharffenberg (1), K. Stene-Johansen (3), L. Sunde (1), L. Vold (1)

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Background

In Norway, Municipal Medical Officers (MMOs) implement public health measures for reported hepatitis A (HAV) cases, including administering post-exposure prophylaxis (PEP) to close contacts. Specimens from confirmed HAV cases are further genotyped at the reference laboratory only during outbreaks. In 2016, the Norwegian Institute of Public Health (NIPH) initiated enhanced surveillance of HAV to increase ability to identify clusters and conducted a survey among MMOs to identify gaps in reporting and follow-up procedures.

Methods

We requested laboratories to send HAV specimens from all reported cases to the reference laboratory for genotyping. We interviewed MMOs using semi-structured questionnaires to obtain information on control measures and PEP for HAV cases reported in 2016.

Results

We interviewed MMOs who followed-up 37 (88%) of the 42 reported cases. 29 (69%) specimens were genotyped and four clusters were identified (10 cases; 2-3 cases per cluster). Of those 10 cases in clusters, 8 were identified through genotyping and 2 were only epidemiologically linked with previous cases. The enhanced system identified six HAV cases from four local laboratories that were not reported to NIPH. In 24/37(65%) reported cases, MMOs followed the current guidelines on control measures/PEP. For 9/37 (24%) cases, close contacts did not receive the required PEP and for 4/37 (11%) received either immunoglobulin or vaccine as PEP, but not according to the guidelines.

Conclusion

Enhanced laboratory surveillance using genotyping identified HAV clusters that would have gone undetected and additional cases not reported from laboratories. Adherence to guidelines by MMOs was suboptimal. We recommend continuing enhanced laboratory surveillance to increase the sensitivity of the system and improve information provided to MMOs to reinforce correct implementation of guidelines at the local level.

Keywords: hepatitis A, Norway, enhanced surveillance, follow-up, ahderence, control measures

ABSTRACT ID: 1056

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

Parallel Session 21: Late breakers (2)

O21.1 MRSA in people who inject drugs: prevalence, risk factors and molecular epidemiology

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8. School of Social and Community Medicine, University of Bristol, Bristol.
9. NIHR Health Protection Research Unit in Evaluation of Interventions at University of Bristol, Bristol.

Background

In 2015 Bristol in the South West of England experienced a substantial increase in the number of community acquired cases of methicillin resistant Staphylococcus aureus (MRSA) infection in people who inject drugs (PWID). We aimed to conduct a base line study to characterise and estimate the prevalence of MRSA colonisation in PWID and use whole genome sequencing (WGS) to test evidence of a clonal outbreak of MRSA in PWID.

Methods

In late 2016, 153 PWID in Bristol were recruited through a community survey. Participants completed a behavioural questionnaire and were swabbed for MRSA. Univariate logistic regression was used to identify factors associated with MRSA colonisation. Phylogenetic analysis was performed on lineage-matched MRSA from: Bristol PWID (screening and retrospective bacteraemia) and non-PWID (screening) and reference lab database isolates.

Results

The MRSA colonisation prevalence was 9%. Colonisation was associated with frequently injecting outside (OR:5.5, 95% CI:1.34-22.7), hospital contact in past month (4.3, 95% CI:1.34-13.80) and injecting in groups of three or more (15.8, 95% CI:2.51-99.28). Persons reporting one of: injecting outside, injection site skin and soft tissue infection or hospital contact accounted for 12/13 MRSA positive cases (sensitivity 92.3%; specificity 51.5%). The majority of carriage isolates belonged to a single lineage (CC5). Phylogenetic analysis identified three distinct genetic clusters with evidence of a dominant clade associated with infection and colonisation among PWID, and two more genetically distant clades.

Conclusion

MRSA colonisation in PWID in Bristol is substantially elevated compared to population estimates (<0.1%-1.5%). The data provide evidence of community-based transmission and increased infection risk depending on colonising strain and injecting practice. Targeted interventions are needed to reduce MRSA infections in PWID, further development work and novel ideas are required.

Keywords: Methicillin-Resistant Staphylococcus aureus, Drug Users, Substance Abuse, Intravenous, Sequence Analysis, DNA,

ABSTRACT ID: 1379

PRESENTED BY: Simon Packer (simonpacker@nhs.net)

O21.2 Spread of methicillin-resistant Staphylococcus aureus (MRSA) through portable medical devices: lessons to be learned from Portugal

João Graveto (1), P. Costa (1), H. Albano (2)., C. Santos (1), E. Fernandes (1), N. Osório (3), S. Alarico (4), V. Oliveira (3)

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Background

Currently, Portugal faces one of the highest levels of Staphylococcus aureus resistance in Europe, leading to burdensome outcomes for public health. A substantial contamination rate of portable medical devices used by nurses was identified in a large tertiary hospital. We described the extent of contamination and investigate risk factors for colonization.

Methods

Descriptive-correlational and cross-sectional study. Target population corresponds to all nurses who provide direct patient care in the referred setting. Medical devices were swabbed and cultured in Mannitol salt agar (MSA). For the isolates obtained the latex agglutination test was performed to investigate S. aureus. Additional information regarding medical devices management was collected by individual questionnaire. Data were analyzed with IBM SPSS 20.

Results

Between April and June 2017, 100 portable medical devices from 50 nurses in medical wards were tested. The most representative devices were tourniquets (68%), adhesive rolls (56%), scissors (26%) and thermometers (20%). Colonies of Staphylococcus coagulase positive (32%) and negative (27%) were identified, ranging from 1.0x101 CFU/mL to above 1.5x103 CFU/mL. The highest CFU/mL values were observed in reusable tourniquets and thermometers. Overall, and regarding Staphylococcus isolates, 66.6% were MRSA. Data retrieved from questionnaires evidences lack of device cleaning (32.7%), lack of staff training (42%), unfamiliarity with guidelines (82%), lend of medical devices to other health professionals (92%) and reuse of these devices between patients (100%).

Conclusion

Underlying lack of training, access to specific institutional guidelines and inefficient management of these devices, including lack of cleaning/disinfection, reuse between procedures/patients and sharing them with other professionals were associated with MRSA. Prospectively develop pathways for medical device management, ensure staff training and potentiate the use of single-use medical devices are recommended to prevent/control future outbreaks.

Keywords: Methicillin-Resistant Staphylococcus aureus, hospital, medical devices

ABSTRACT ID: 1386

PRESENTED BY: Paulo Costa (paulocosta.15@gmail.com)

O21.3 Prevalence of Candida auris in patients admitted to intensive care units in England, 2017: preliminary results

Ashley Sharp (1), Andre Charlett (3), Berit Muller-Pebody (3), Bharat Patel (2), Rebecca Gorton (4), Jonathan Lambourne (5), Martina Cummins (5), Robin Smith (6), Damien Mack (6), Susan Hopkins (6), Andrew Dodgson (7), Nelun Perera (8), Gopal Rao (9), Elizabeth Johnson (10), Andrew Borman (10), Silke Schelenz (11), Rebecca Guy (3), Joanna Conneely (3), Rohini Manuel (2), Colin S Brown (3)

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11. Royal Brompton Hospital

Background

Candida auris is an emerging fungal pathogen first identified in Japan in 2009. It is associated with bloodstream, wound, and other infections, especially in critically ill patients. Most C. auris is resistant to fluconazole and multidrug-resistant isolates have been identified. Hospital outbreaks have been reported worldwide. The UK has detected 210 cases since 2013 (155 colonisations and 55 clinical infections including 28 candidaemias) across 20 hospitals including three large outbreaks. C. auris is highly transmissible and once established in a hospital it is difficult to eradicate. We piloted admission screening across seven intensive care units (ICU) in order to estimate the prevalence of C. auris in this population and inform public health guidance.

Methods

We selected geographically dispersed ICUs with diverse populations reflecting the global distribution of C. auris. We implemented screening for all adult admissions. We screened multiple body sites and used MALDI-TOF to ID any Candida growth. Data will be linked to routine data sources to obtain health and demographic indicators.

Results

Preliminary results from 416 adults across four sites were negative for C. auris. The estimated prevalence of C. auris is between 0.0% and 0.8% (upper 95%CI). The screening target of 1000 patients is due to be reached by October 2017.

Conclusion

These findings suggest that C. auris colonisation is rare in the UK. The sensitivity of this screening protocol is not known and it is possible that low level colonisation was missed. This is the first attempt in Europe to systematically characterise C. auris colonisation. The results of this pilot will inform national risk assessment and public health recommendations with respect to hospital screening, empirical antifungal treatment and infection control.

Keywords: Candida auris, surveillance, infection control, hospital

ABSTRACT ID: 1427

PRESENTED BY: Ashley Sharp (ashley.sharp@phe.gov.uk)

Poster Abstracts

MODERATED POSTER SESSION A
DAY 1, MONDAY, 6 NOVEMBER
15:40-16:40

Track 1: Antimicrobial resistance (1)

A 1.1 Community antibiotic prescribing for respiratory tract infections in Malta: one-year trend and associated influencing factors

Erika Anne-Marie Saliba Gustafsson (1), A. Dunberger (1), P. Zarb (2), M.A. Borg(2, 3), S. Rosales-Klintz (1), N. Orsini (1), C. Stålsby Lundborg (1)

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Background

Effective surveillance is essential to contain antibiotic resistance. In Malta, community antibiotic consumption data at prescription-level are unavailable. Without ongoing surveillance it is challenging to devise strategies tailored towards specific local needs and measure the impact of an antibiotic prescribing intervention in such a community.

Methods

In order to understand general practitioners' (GPs) antibiotic prescribing patterns in Malta, we set up a surveillance system to analyse the one-year trend in diagnosis-specific antibiotic prescribing for respiratory tract infections (RTIs) and identify factors which influence their prescribing. All active GPs (n=378) and trainees (n=34) were invited. Data were collected monthly between May '15 and Apr '16 over a 1-week period, resulting in 12 surveillance weeks. GPs received SMS reminders and three-monthly feedback reports. Univariate and logistic regression analyses were used to identify significant predictors for prescribing.

Results

In total, 33 GPs consulted 4636 RTI patients. The majority (53%) were female and the median age was 32 years. Most patients (65.4%) visited a GP after 1-3 symptomatic days. The top three complaints were sore throat (47%), rhinorrhoea (37%) and productive cough (32%) and the top three diagnoses were common cold (33.4%), pharyngitis (16.2%) and bronchitis (12.5%). Almost half (46%; n=2118) received antibiotic treatment. The two most frequently prescribed antibiotic classes were beta-lactam, penicillins (36%) and macrolides (35%). Factors associated with prescribing included years of GP practice, daily number of patients examined, pharmacy practice, location of consultation, fever, sore throat, previous antibiotic use, suspected viral aetiology, common cold and regular client.

Conclusion

Antibiotic prescription rates are high in Malta. Efforts are needed to develop tailored interventions which target GPs specific needs and patient behaviour in order to successfully reduce their prescription rates.

Keywords: Antibiotics, Prescribing patterns, Surveillance, General practitioners, Respiratory tract infections

ABSTRACT ID: 766

PRESENTED BY: Erika Anne-Marie Saliba Gustafsson (erika.saliba@ki.se)

A 1.2 Evaluation of the English Enhanced Surveillance System for carbapenemase-producing Gram-negative bacteria

Daiga Jermacane(1,2), Dean Ironmonger(2), Rachel Freeman(3), Paul Cleary(2), Berit Muller Pebody(2,3), Russell Hope(2,3), Isabel Oliver(2)

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2. Field Epidemiology Service, National Infection Service, Public Health England, UK
3. Healthcare Associated Infection & Antimicrobial Resistance Dept. Public Health England, UK

Background

Due to the growing number of cases and outbreaks of carbapenemase-producing Gram-negative organisms (CPO), an electronic reporting system (ERS) for the enhanced surveillance of CPO was implemented by Public Health England (PHE) in May 2015. We evaluated ERS, to determine if it is meeting its objectives to improve surveillance of CPOs.

Methods

We evaluated uptake, coverage, and completeness by comparing extracts from ERS with reference molecular data from the Antimicrobial Resistance and Healthcare-Associated Infections laboratory (AMRHAI) system. We estimated the proportions of isolates of Gram-negative bacteria, where expression of an acquired carbapenemase was suspected, reported through ERS with full characterisation, out of total number of referrals for suspected CPO at AMRHAI.

Results

A total of 7,632 suspected CPO cases were referred to AMRHAI between 5 May 2015 and 31 December 2016; 4,031 (53%) were reported through ERS. The proportion of organisms reported through ERS rose over time, reaching 73% by the end of 2016. The number of laboratories in England participating in ERS reached 116/133 (87%) by the end of 2016. There were large variations in adoption of the ERS by region; laboratories in West-Midlands, Yorkshire and the Humber and the North-West had highest uptake (›53%). The completion rate for enhanced data fields on risk factors was low (range: 0-32%).

Conclusion

Although ERS has increased in coverage and improved the identification of CPOs, completeness of enhanced risk factor data has been poor. We are using qualitative methods to explore barriers and identify opportunities to improve the system.

Keywords: antimicrobial resistance, electronic reporting system (ERS), carbapenemase-producing Gram-negative bacteria, carbapenemase-producing Gram-negative organisms (CPO), carbapenemase producers, Antimicrobial Resistance and Healthcare Associated Infections (AMRHAI)

ABSTRACT ID: 797

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

A 1.3 Prevalence of extended-spectrum beta-lactamase-producing Enterobacteriaceae in asylum-seekers in Rhineland-Palatinate, Germany, 2016-2017

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Background

Colonization with extended-spectrum β-lactamase-producing Enterobacteriaceae (ESBL-PE), particularly those also producing carbapenemase (C-PE), is a risk factor for infections with limited antimicrobial treatment options. Prevalence in Germany is low (ESBL-PE: 5.6-7.2%, C-PE: 0.0-0.2%), but remarkably higher in persons returning from long-distance travel (ESBL-PE 43.8-57.6%, C-PE 0.0-1.7%). As prevalence data in the countries of origin are sparse, the influx of asylum-seekers raised concerns about an import of ESBL-PE/C-PE into European populations and hospitals. We describe the prevalence of ESBL-PE/C-PE in a large sample of asylum seekers arriving in Rhineland-Palatinate to assess the need of enhanced control measures upon hospital admission.

Methods

From April 2016 to March 2017, we expanded mandatory stool testing for enteropathogens in asylum seekers by including antibiotic resistance screening of Enterobacteriaceae. We classified countries of origin into three main regions. We analysed data by region, age, and sex, using multivariable logistic regression.

Results

In total, 296 of 1,544 samples (19.2%; 95% CI: 17.2-21.2%) contained 319 ESBL-PE (317 E. coli, 2 K. pneumoniae). ESBL-PE prevalence in asylum seekers from Afghanistan/Pakistan was 27.5% (109/397), Syria 20.4% (66/324), Ethiopia/Eritrea/Somalia 11.9% (43/362), and 16.9% (78/461) from other regions. Women were more likely to be colonized with ESBL-PE (aOR: 1.30, 95% CI: 1.00-1.68). No C-PE were detected, resulting in a prevalence estimation of 0.0-0.2% (97.5% CI).

Conclusion

Prevalence of ESBL-PE in asylum seekers exceeds that in the German population, but is lower than in Germans returning from long-distance travel. As prevalence of C-PE in asylum seekers and the German population is similar, we do not recommend pre-emptive screening and isolation of asylum seekers upon admission to regular hospital wards, if based solely on demographic and geographic factors covered in this study.

Keywords: Antimicrobial Drug Resistance, Refugees, Mass Screening

ABSTRACT ID: 805

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

A 1.4 Antimicrobial resistance of toxigenic and non-toxigenic Corynebacterium diphtheriae and Corynebacterium ulcerans in Germany 2011-2016

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Background

High vaccination rates led to decreasing incidence of toxigenic (DT) corynebacteria and the disease diphtheria, while non-toxigenic (NT) strains increased as infectious agents of endocarditis, septic arthritis or wound infections. Recommended first line antibiotic is penicillin or erythromycin but reliable susceptibility data are not available for potentially toxigenic species and limited information are prepared by EUCAST and CLSI for the genus. This study aims to examine antibiotic susceptibility (AS) profiles of DT and NT C. diphtheriae and C. ulcerans strains and provide data needed for the update of international guidelines.

Methods

The AS profiles of 230 NT and 118 DT strains isolated during 2011-2016 at the German consultant laboratory for Diphtheria from human and veterinary C. diphtheriae and C. ulcerans were tested using: CLSI broth microdilution with 12 and E-test with 3 different antibiotics respectively.

Results

Preliminary data of 182 NT and 37 DT Corynebacterium spp. isolates show that 23 % (n=43) and 59 % (n=22) were penicillin resistant, respectively. Erythromycin resistance was observed for 2 % (n=4) and 8 % (n=3) NT and DT isolates. 86 % of tested C. ulcerans isolates (n=30) were clindamycin resistant. No resistance against gentamicin, vancomycin or linezolid was observed.

Conclusion

23 % and 59 % of infections caused by NT or DT corynebacteria are not treatable by penicillin, the first line antibiotic. 86 % of C. ulcerans strains, often found in wound infections were resistant against clindamycin, the recommended antibiotic for these infections. Resistance against other classes of tested antibiotics was rare. These preliminary data point to developing resistance against the most commonly used antibiotics, therefore performing AS testing should be recommended for all clinical strains.

Keywords: diphtheria, corynebacterium spp., antibiotic resistance, EUCAST

ABSTRACT ID: 863

PRESENTED BY: Durdica Marosevic (djurdjica.marosevic@gmail.com)

A 1.5 Outpatient antibiotic usage in Austria – a comparison of sales and insurance reimbursement data, 2012-15

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Background

According to the most recent European report on antibiotic consumption, based on insurance reimbursement data (RD), total antibiotic consumption in Austria in 2012 was below the average of 30 European countries. The aim of this study was to characterize systemic outpatient antibiotic usage in Austria, using sales data (SD) to assess the reliability of RD in estimating outpatient antibiotic usage, needed to monitor observed antibiotic resistance.

Methods

SD and RD for 2012-2015 were provided by IMS Health and the Austrian social insurance fund, respectively. Antibiotic quantities were standardised using defined daily dose per 1000 inhabitants per day (DID), in accordance with the anatomical therapeutic classification (ATC). We analysed antibiotic usage by substance level (ATC level 5) and year, and compared DID estimates from the two data sources.

Results

Outpatient antibiotics usage estimates based on SD and RD were 19 and 14 DID in 2012 (SD-RD difference: 25%), 20 and 17 DID in 2013 (17%), 18 and 14 DID in 2014 (23%), and 19 and 14 DID in 2015 (24%). The greatest deviations between SD and RD were observed for sulfametriaxol+trimethoprim (25-fold higher), sulfametrole+trimethoprim (6-fold), amoxicillin (3-fold) and ciprofloxacin (3-fold). Based on SD, the annual median DID of the most-used antibiotics from 2012 to 2015 were amoxicillin/enzyme inhibitor (4.5, IQR 4.4-4.6), amoxicillin (2.3, 2.3-2.4), ciprofloxacin (1.73, 1.72-1.73), clarithromycin (1.6, 1.5-1.7) and doxycycline (1.2, 1.1-1.2).

Conclusion

From 2012 to 2015, antibiotic usage estimates from sales data were consistently higher than RD. As RD do not include antibiotics priced below the eligibility threshold for reimbursement, the use of RD alone will underestimate true outpatient antibiotic consumption in Austria. We recommend using both sources of information for prospective surveillance of antibiotic consumption.

Keywords: Antibiotics consumption, health insurance, antibiotic sales, international medical statistics health, antibiotics price

ABSTRACT ID: 843

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A 1.6 Late breaker: First outbreak in France of multi-drug-resistant Shigella sonnei infections in primary school, Southwestern France, March–May 2017

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Background

Shigella spp. are frequently associated with outbreaks. Emergence of multi-drug resistance (MDR) can hinder oral treatment options. In March 2017, a primary school in Southwestern France notified health authorities of 50 absent students with gastroenteritis including 4 with Shigella sonnei-positive stool culture. We investigated to identify the outbreak source and to stop transmission.

Methods

We conducted a retrospective cohort study among all 317 students and search for illnesses among staff and students' household members. Confirmed case was defined as laboratory-confirmed Shigella sonnei infection in a student, staff or household member with onset between March 10–April 7, and probable case as gastrointestinal illness in a person with an epi-link to a confirmed case. Parents completed a self-administered questionnaire to collect symptoms and exposures. All students, symptomatic staff and household members were requested to provide a stool sample to local laboratories. Shigella isolates were whole-genome sequenced at the National Reference Center (NRC).

Results

As of May 2017, questionnaires and stool specimens were obtained for 289 and 288/317 (91%) students, respectively. We identified 83 cases (29 confirmed, 54 probable). Ten confirmed cases occurred among household members, 2 among staff. Index cases were 3 siblings returning from Vietnam. School attack rate was 29%. Forty-six students received oral antibiotherapy, 5 were hospitalized, all recovered. Twenty-four isolates were analysed at the NRC: all were resistant to third-generation cephalosporins, azithromycin, cotrimoxazole, ciprofloxacin, tetracyclins and presented a unique sequence-type.

Conclusion

This is the first outbreak identified in France associated with this imported MDR Shigella sonnei isolate. Reinforcement of hand hygiene and a one-week school closing period allowed circumscribing the outbreak. A study is ongoing to assess the impact of dispensed antibiotherapy on duration of shedding.

Keywords: Outbreak, Shigella sonnei, drug-resistance, School students

ABSTRACT ID: 1435

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Track 2: Healthcare-associated infections (1)

A 2.1 Increased rates of Clostridium difficile infection (CDI) in Finnish hospitals with high CDI prevalence at admission, 2008-2015

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Background

Hospital-based surveillance of Clostridium difficile infections (CDI) has been conducted in Finland since 2008; hospital-specific rates are ranked to provide feedback to participating acute care hospitals. We aimed to determine whether hospital-specific CDI rates are associated with testing frequency or PCR use.

Methods

Cases were hospitalized patients meeting the CDI EU case definition (origin: nosocomial, other healthcare facility, community) notified during 2008-2015. We obtained data on CDI testing frequency in 2014-2015 from two hospital surveys and data on PCR availability from the reference laboratory. We used as denominators patient-days and number of admissions to calculate rates and prevalence at admission, respectively. To examine the relationship between annual CDI rate and testing frequency we calculated Spearman correlation coefficients (rho) and incidence rate ratios (IRRs) using mixed effect negative binominal regression.

Results

We identified 6,664 CDI cases in 19 hospitals; 4,928 (74%) were nosocomial. PCR was introduced in 2008 in two hospitals and was available in all by 2014. During 2014-2015, annual hospital-specific CDI rates varied from 0.14 to 1.33 and testing frequency from 0.92 to 41.53 /1,000 patient-days (rho=0.22). Overall annual nosocomial rates decreased significantly ($p<0.001$) from 0.59/1,000 patient-days in 2008 to 0.36 in 2015; overall annual CDI prevalence at admission varied from 0.33 in 2014 to 0.99/1,000 admissions in 2008. CDI rates increased (IRR=1.21; 95%CI=1.04-1.42) with increasing prevalence at admission, but not with testing frequency (IRR=1.02; 95%Cl=1.00-1.04) or PCR use (IRR=0.94; 95%Cl=0.77-1.15).

Conclusion

More sensitive CDI diagnostics and increased testing frequency were not associated with increased CDI rates. The association between prevalence at admission and nosocomial rate suggests that prevalence should be part of surveillance feedback to inform strengthened control measures in hospital with high prevalence at admission.

Keywords: Clostridium difficile infections, Hospital-based surveillance, Nosocomial infections

ABSTRACT ID: 824

PRESENTED BY: Jana Prattingerová (jana.prattingerova@gmail.com)

A 2.2 Transmission of Clostridium difficile from symptomatic cases in Belgian hospitals, 2015-2016

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Background

Clostridium difficile is an important cause of hospital-associated (HA) infections. However, the extent of transmission within hospitals is unclear. We aimed to estimate what proportion of HA C. difficile infections (CDI) in Belgian hospitals resulted from case-to-case transmission within the same hospital, in order to guide prevention measures.

Methods

Between 1/1/2015 and 31/1/2016, 30 hospitals voluntarily recorded all CDI cases and sent isolates for typing to National Reference Laboratory. We defined (1) HA-CDI as CDI episode with clinical symptoms' onset ≥ 2 days after admission, (2) possible secondary case as a HA-CDI sharing the same ribotype as a previous (HA or non-HA) CDI in the same hospital and isolated within ≤ 31 days (3) recurrent as an episode in the same person with onset of symptoms >15 days and <8 weeks after the first. We excluded from analysis (1) hospitals with $>30\%$ missing typing data, (2) episodes occurring during the first month of the study and (3) recurrent episodes.

Results

Thirty hospitals registered 1,398 CDI episodes (median number per hospital: 43; range 2-144); 54% (753/1,398) were HA-CDI. After excluding 6 hospitals with $>30\%$ missing typing data, we identified 147 different ribotypes from 995 isolates corresponding to 1,137 episodes; 70/147 (48%) ribotypes were identified once. We found 137/477 (29%) possible secondary cases (range 0%-55% across hospitals; median: 21%).

Conclusion

The different circulating C. difficile strains in Belgium suggest a variety of transmission routes. The majority of HA-CDIs could not be attributed to case-to-case hospital transmission, although variation between hospitals was high. More discriminatory typing methods are needed to assess whether secondary cases are really linked. We recommend further studies to identify main transmission routes within hospitals to better control HA-CDIs.

Keywords: Clostridium difficile, epidemiology, transmission

ABSTRACT ID: 844

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A 2.3 Conversion of the ECDC point prevalence survey 2011-2012 data on surgical site infections into incidence estimates using Rhame and Sudderth's method

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Background

Compared to incidence surveillance of surgical site infections (SSIs), point prevalence surveys (PPSs) are less resource intensive, but they only represent cross-sectional data. We aimed to investigate how accurately SSI incidence can be estimated from the ECDC PPS data using Rhame and Sudderth's method (RSM).

Methods

We included 159 hospitals from 12 EU/EEA countries that participated in both the ECDC PPS and ECDC SSI incidence surveillance in 2011-2012. Only SSIs diagnosed during hospital stay were included. We used the median length of hospital stay of all surgical patients (LA) and surgical patients with an SSI (LN), and the median interval between hospital admission and SSI onset (INT), to estimate SSI incidence from PPS data with RSM (Incidence = Prevalence*LA/(LN-INT)). The estimated and observed incidence in each specialty were compared using Spearman's correlation coefficients.

Results

We included 3 327 operations from five specialties from the PPS and 115 218 from incidence surveillance. The estimated incidence for all countries combined fell within the 95% confidence interval of the observed incidence only for orthopaedics and neurosurgery. It was underestimated for digestive tract and cardiovascular surgery, and overestimated for obstetrics. The correlation coefficient between the estimated and observed incidence in countries varied by specialty: cardiovascular, 1; orthopaedics, 0.8; digestive tract, 0.4; not calculated for obstetrics and neurosurgery because of limited number of operations.

Conclusion

RSM provided accurate estimates of SSI incidence only for some specialties. This is possibly due to the limited number of included hospitals and operations, especially from the PPS. Further studies and new methods are needed to better understand the relationship between SSI prevalence and incidence. In the meantime, incidence surveillance remains the preferred method of SSI surveillance.

Keywords: Surgical Wound Infection, Public Health Surveillance, Incidence, Prevalence

ABSTRACT ID: 984

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A 2.4 Sex/gender analysis in Cochrane reviews of mechanical ventilation associated infections is uncommon

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Background

Infections caused by mechanical-ventilation are common in intensive care units (ICUs) and increase morbidity, mortality, and healthcare costs. Their control continues to be an unresolved issue worldwide with evidence suggesting that mechanical-ventilation epidemiology shows sex/gender differences. These differences are often not considered in studies, which limits the applicability of research findings to decision making. We aim to describe the extent to which sex and gender based analysis (SGBA) is considered in Cochrane reviews of interventions for preventing infections related to mechanical ventilation in the healthcare setting.

Methods

Study design: 'methodology study'. We searched the Cochrane Database of Systematic Reviews for active reviews published before January 1, 2017. We screened 6694 records and included those reviews evaluating any intervention attempting to prevent infection caused by mechanical ventilation. To extract key information about sex and gender we considered the domains of the 'Sex and Gender in Systematic Reviews Planning Tool' (SGSR-PT).

Results

The preliminary analysis of the 7 included reviews showed that SGBA was absent. The reviews met none of the SGSR-PT criteria. The background never described the relevance of sex/gender to the review question. The inclusion/exclusion criteria for studies in the reviews never considered sex/gender differences. Data were never disaggregated by sex. There were no subgroup analyses by sex, and no review highlighted any sex/gender differences as research gaps.

Conclusion

SGBA is absent in Cochrane reviews on mechanical ventilation infections. This raises concerns about the quality and applicability of these reviews and highlights that there is much room for improvement to support informed decision making in this field.

Keywords: Sex, Gender, Ventilation, Epidemiology

ABSTRACT ID: 927

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A 2.5 Late breaker: Management of Pocket Clinical Devices by Nurses: determinant factors and microbiological assessment

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Background

Clinical devices (CDs) are often kept and carried in nurse's uniform pockets, frequently used in patient care, becoming contaminated with organic fluids and infectious agents. Thus, it is intended to understand how nurses in medical units from a hospital in the central region of Portugal manage these specific CDs.

Methods

Descriptive-correlational and cross-sectional study. Target population corresponds to all nurses who provide direct patient care in the referred setting. Data was analyzed with IBM SPSS Statistics version 20.

Results

Fifty nurses were included, with 383 observations of CDs kept in their uniform pockets. One hundred microbiological samples were taken. Nurses often share these devices with other nurses (90%), physicians (52%) and assistants (40%). They reuse CDs between patients and during complex procedures/techniques, such as peripheral vein catheterization/optimization, wound treatment or nasogastric intubation. Regarding decontamination practices, 77.6% disinfect these devices, although only 14% clean it before this process. Lack of training (42%) and access/knowledge to/of institutional guidelines regarding CDs management (82%) emerged as gaps.

Concerning microbiological results, 53% of the CDs were contaminated. Coagulase-positive (32%) and negative (27%) Staphylococcus colonies were identified, varying between 0.1x102 and ›1.5x103 CFU/mL (respectively), as well as Enterococcus spp. (8%) varying between 0.1x102 and 3.0x102 CFU/mL. In relation to Staphylococcus isolates, 66.6% were Methicillin-Resistant Staphylococcus aureus. Significant statistical association between the microbiological incidence in nurses' pocket CDs, nurses' uniforms and hands was verified ($p = 0.048$; $p = 0.009$).

Conclusion

Results evidence the competence, ethical responsibility and technical role of nurses in the management of CDs. However, it highlights the need for further research in other clinical contexts, in order to compare results and produce guidelines that fill some of the witnessed information gaps.

Keywords: Device, Medical, Infection Control, Nurses, Nursing Care

ABSTRACT ID: 1372

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Track 3: Food- and waterborne diseases and zoonoses- Salmonella

A 3.1 An outbreak of Salmonella Enteritidis phage type 8, MLVA type 2-9-7-3-2, following a christening reception in Central Greece, June 2016

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Background

In June 2016, a Salmonella Enteritidis outbreak phage type PT8, multiple locus variable-number tandem repeat analysis (MLVA) type 2-9-7-3-2 occurred among the 133 attendees of a christening reception in Central Greece, following five consecutive years with no documented S. Enteritidis outbreaks in the country. The outbreak involved previously healthy adults, with one related death causing media attention. We investigated the outbreak to identify the source(s) of infection in order the appropriate public health measures to be implemented. An additional reason for further investigating this outbreak was its possible association with the concurrent 2016/17 Europe-wide outbreak of S. Enteritidis outbreak of the same MLVA type.

Methods

We conducted a retrospective cohort study. We defined a case as an attendee having diarrhoea (≥3 loose stools in 24 hours) within 72 hours of the christening. Environmental investigation/inspection of the restaurant's premises was conducted. Whole-genome-sequencing (WGS) was performed and data were compared to the European outbreak.

Results

Of the 122/133 (91.7%) respondents, 56 met the case definition. The cheesy penne pasta was the most likely vehicle of infection (RR 7.80; 95% CI 3.62–16.8). The most plausible cause of the outbreak was food safety violations (inadequate heat treatment and storage). The restaurant license was suspended for four months. S. Enteritidis isolates, typed as PT8, MLVA-type 2-9-7-3-2 with single-nucleotide-polymorphism (SNP) address 1.2.3.323.323.2409.5628.%, were different from those of the European outbreak (with SNP address 1.2.3.175.175.175.% or 1.2.3.18.359.360.%).

Conclusion

S. Enteritidis outbreaks remain a public health threat in Greece and training of food handlers on food safety should be intensified. Advanced molecular data can help us distinguish unrelated outbreak strains.

Keywords: Salmonell enteritidis, Disease outbreaks, Salmonella Food Poisoning, Greece

ABSTRACT ID: 974

PRESENTED BY: Constantine Vassalos (constas.vassalos@gmail.com)

A 3.2 Whole genome sequencing of Salmonella Chester from 2000-2016 in Norway enables comparison of geographically distinct outbreak clusters

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Background

Salmonella Chester was among the 20 most common serovars causing human infections in Europe in 2014. During summer 2016, Norway observed an increase in S. Chester cases among travellers to Greece. In this study, our aim was to develop a whole genome sequence (WGS) based core genome multi-locus sequence typing (cgMLST) methodology in order to investigate genetic relatedness of S. Chester for early outbreak detection and surveillance.

Methods

We included isolates from 46 (46/86, 53% of total) S. Chester cases (male 50%; age range 7-86 years; median age 41.5 years) from the years 2000 to 2016. 78% had confirmed travel-history to either Europe (n=13), Asia (n=12), or Africa (n=11). We performed paired-end sequencing on Illumina MiSeq (250x2, coverage ≥ 50), and developed an ad-hoc cgMLST scheme for Salmonella enterica subsp. enterica using Ridom SeqSphere+ (v.4.0). Genetic relatedness defined by cgMLST was compared to a genome mapping approach using CSI Phylogeny 1.4.

Results

3226 target core genes (3106491 bp) were identified based on LT2 (NC_003197.1) as reference and 27 query genomes. Four phylogenetic clusters corresponding to the geographical regions, the genome mapping approach, and sequence types (ST) were identified with a distance of >700 alleles: ST411 and a single locus variant (n=17) primarily acquired in Southern Europe; ST1954 (n=10) acquired in Africa; ST343 (n=11) and ST2063 (n=8) primarily acquired in Asia. The Southern European cluster was further divided into Greek (n=10) and Cypriote (n=4) clones with ≤ 10 allele differences within the clones.

Conclusion

WGS of S. Chester from Norway shows geographically distinct clusters, indicating a possible outbreak during summer 2016 travel-related to Greece. We recommend implementing WGS based S. Chester surveillance for accurate and timely detection of future outbreaks.

Keywords: Salmonella, sequence analysis, multilocus sequence typing, bacterial genomes, genotyping

ABSTRACT ID: 849

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A 3.3 No decrease of human Salmonella Enteritidis despite Salmonella control programmes in poultry in the European Union, 2013-2015

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Background

The implementation of EU-wide Salmonella control programmes in poultry 10 years ago, together with ECDC surveillance of human infections has contributed to a reduction in the number of human salmonellosis cases by 30% in the EU. However, S. Enteritidis human cases increased during 2013-2015 and several recent multistate outbreaks of S. Enteritidis have occurred.

Methods

Trends and notification rates 2008-2015 were analysed by ECDC for human salmonellosis cases reported annually by EU Member States to TESSy. Trends on food, animals and food-borne outbreaks were analysed by EFSA for data reported by EU Member States.

Results

There was a statistically significant ($p < 0.01$) decreasing EU trend of confirmed human salmonellosis cases 2008-2015. However, the EU notification rate in 2015 was 5.0 % higher than in 2013. The most common serovar, S. Enteritidis represented 45.7% of all reported serovars, with 31,829 confirmed cases in 2015, an increase of 9.4% compared with 2013.

There was a statistically significant decreasing trend in EU prevalence of flocks positive to Salmonella target serovars in fowl and fattening turkeys 2007-2015. However, in 2015, as compared with 2013, prevalence of S. Enteritidis increased (range; 13%-150%) in fowl and turkeys, except breeding fowl. S. Enteritidis, the second most common serovar in fowl in the EU in 2015, increased by 39% compared with 2013.

Conclusion

The positive public health impact of the Salmonella control programmes in poultry has been a success story in the EU. Recent S. Enteritidis outbreaks and trends in monitoring data raise questions as they indicate a reversal of the declining trend in EU in humans and poultry. Further cross-sectorial investigations are needed to better understand underlying reasons for the increase

Keywords: Salmonella, Salmonella Enteritidis, zoonoses, human and integrated food-chain surveillance, food-borne outbreaks, trend monitoring

ABSTRACT ID: 1080

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A 3.4 An outbreak of Salmonella Enteritidis PT 6c in Austria, related to a traditional Austrian cheese, 2015-2016

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Background

In October 2016, the National Reference centre (NRC) identified a cluster of cases from four of the nine Austrian provinces, of Salmonella (S.) Enteritidis PT 6c indistinguishable by Multiple Locus Variable-Number Tandem Repeat Analysis (MLVA) and core genome Multi Locus Sequence Typing (cgMLST). We aimed to describe the outbreak and identify the source(s).

Methods

Cases were defined as Austrian residents infected with S. Enteritidis PT 6c of MLVA pattern 2-10-13-7-1, 2-9-13-7-1 or cgMLSType complex 2, identified since week 50/2015. The NRC analysed all veterinarian and food isolates of S. Enteritidis PT 6c, detected during routine examinations or from suspected food since week 50/2015 by using MLVA and cgMLST. We interviewed cases using a structured questionnaire on food exposures.

Results

Between weeks 51/2015 and 44/2016, 33 cases were reported in Styria (n=28; 85%) and three other Austrian provinces (n=5; 15%). Of those, 22 (67%) resided in one of the 13 Styrian districts (district X); 29 (88%) occurred during weeks 27-44. The median age of cases was 54 years (range 0-79); 58% were male; 14 (42%) reported consumption of artisanal cheese ("Steirerkas"), produced in district X. S. Enteritidis isolated from this "Steirerkas" and from the asymptomatic excreting cheese producer were indistinguishable from the outbreak strain. After the ban of this cheese production in week 44, no further cases occurred.

Conclusion

Our findings suggest that the artisanal "Steirerkas" was the likely source of the outbreak. The outbreak strain could have entered the cheese production chain through the excreting producer. We recommend reinforcement of adherence to the Austrian standard operating procedures on food safety practices for artisanal food producers.

Keywords: Salmonella Enteritidis, cheese, Austria, outbreak

ABSTRACT ID: 842

PRESENTED BY: Karin Taus (karin.taus@ages.at)

A 3.5 A Food Poisoning Investigation: Salmonella Attack Because Of The Unsafe Food Handling in Purbalingga, Indonesia-2016

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Background

On 22nd May 2016, there was a report of 20 civilians from Binangun's village who were admitted to the hospital through because of gastroenteritis following a recitation event. This investigation was done to confirm the outbreak, determine the risk factors, and develop control measures.

Methods

We did an unmatched case control study. Cases were people who developed at least one gastrointestinal sign (diarrhea, abdominal pain, vomiting, headache) after attending the recitation event. Controls were people who not developed gastrointestinal sign after attending the recitation event.We collected cases from health centers and community, were interviewed using structured questionnaire. Samples from leftover foods, feces, and vomit sent to laboratory for biological culture examination. Ocular inspection was done in the cooking area and food handlers were interviewed.

Results

There were 103 cases and 103 controls. About 53% were female, age between 26-35 years (17%) housewife (29%), and felt diarrhea and abdominal paint (90%). Laboratory test had identify salmonella sp. The analytic study shown that consumption of telur balado was significant (OR = 31.2; 95% CI=11.61-83.84). Telur balado was the first food cooked and stored in the room's temperature for about 12 hours. Telur balado was a local food for spicy egg. Pelling process was the most vulnerable step for cross contamination.

Conclusion

The outbreak was caused by consumption of telur balado that was contaminated by salmonella sp. Peeling process by food handler was possible contamination's route of salmonella. Salmonella's multiplication was triggered by time's storage of food. We recommended to socialize hand washing with soap for food handler, and to keep short period between cooking time and meal time.

Keywords: Foodborne Diseases, Salmonella, Egg, Food Handling, Temperature

ABSTRACT ID: 777

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Track 4: Hepatitis B & C

A 4.1 Healthcare-associated hepatitis B and C transmission to patients in EU/EEA: A systematic review highlights higher-risk settings and variability among countries

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Background

Healthcare-associated transmission was the second most commonly reported hepatitis B (HBV) and hepatitis C (HCV) transmission route according to 2006-2012 European surveillance data, but data quality/completeness issues hinder comprehensive characterisation of healthcare-associated transmission of HBV/HCV. We carried out a systematic review of published literature on healthcare-associated transmission of HBV/HCV in Europe to complement surveillance data and identify higher-risk settings.

Methods

We searched the PubMed database (01/2006-12/2016) for publications, reporting transmission events after 2000, related to a healthcare setting/procedure. An event was defined as transmission to patients from a single source. We collected data on number of patients, country and setting type.

Results

28 HBV and 33 HCV events were identified in 44 publications from 16 countries, resulting in 339 newly infected patients. Most were reported from the United Kingdom (7 HBV, 3 HCV events), Italy (5 HBV, 4 HCV), Spain (1 HBV, 7 HCV) and France (3 HBV, 3 HCV). Haemodialysis units accounted for 13 (21%) events (1 HBV, 12 HCV), nursing homes for 8 (13%, only HBV) oncology wards for 5 (8%, 2 HBV, 3 HCV) and CT/MRI scanning units for 5 (8%, only HCV). Active case finding among recipients of blood products from occult hepatitis B donations resulted in the identification of 6 (10%) events.

Conclusion

Events were reported from settings known to pose higher risk (haemodialysis units), but also from settings perceived to be at lower risk (CT/MRI scanning units, oncology wards), which underlines the importance of following universal precautions in all settings, and possibly the need to carefully review procedures to enhance the implementation of universal precautions in settings like CT/MRI scanning units.

Keywords: hepatitis B, hepatitis C, cross-infection, disease outbreaks

ABSTRACT ID: 1010

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A 4.2 How can we improve hepatitis B testing and management in primary care? A cross-sectional survey of GPs in England, 2015-17

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Background

Chronic hepatitis B (HBV) infection can lead to life-threatening liver disease. In the UK, an estimated 180,000 people are carriers and the disease is known to be underdiagnosed and undertreated. As part of EMPACT-B, a nurse-led intervention study aimed at improving HBV contact-tracing and management, we ascertained GPs' understanding of HBV infection and their perceived barriers and enablers to HBV diagnosis.

Methods

In November 2015, we asked 1,324 GPs across 2 England regions about HBV-related knowledge and practice, using a questionnaire. We reported the proportion of GPs answering each question along with 95% confidence intervals (95%CI).

Results

254 GPs (18%) returned the questionnaire. Of those, 189(74%, 95%CI 68-79%) correctly identified hepatitis B surface antigen (HBsAg) as a marker of current HBV infection, but only 154(61%, 95% CI 54-66%) recognised IgM anti-HBc as a marker for differentiating acute from chronic cases. 219 GPs (86%, 95%CI 81-90%) believed HBV knowledge among patients to be one of the main enablers to improved testing uptake and 208(82%, 95%CI 77-86%) selected a lack of HBV knowledge among patients as a barrier to testing. Of all GP responders, 227(89%, 95%CI 85-93%) reported HBV training and education would be beneficial, and 185(73%, 95%CI 67-78%) reported knowledge of treatment options as a knowledge gap.

Conclusion

GPs perceive gaps in knowledge among patients and healthcare professionals as a factor potentially contributing to the under-ascertainment of chronic hepatitis B in England. Improving HBV awareness and knowledge among patients, their contacts, and increasing HBV-focused training for GPs, particularly in the interpretation of laboratory results and the treatment options, can improve case ascertainment and chronic HBV management in primary care.

Keywords: Hepatitis B, survey, questionnaire, testing, barriers, enablers

ABSTRACT ID: 1035

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A 4.3 High seroprevalence and low number needed to screen to link cases to care from hospital emergency department testing for HIV, hepatitis B and C in London, UK, November 2015 to August 2016

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Background

Rates of blood borne viruses (BBV) HIV, hepatitis B and C (HBV, HCV) in London exceed the English average, requiring new settings for testing and linkage to care (LTC). We aimed to quantify seroprevalence, demographic risk factors and describe provisional LTC outcomes from BBV testing in a hospital emergency department (ED) between 20/11/2015 and 7/8/2016.

Methods

We offered HIV antigen/antibody, HBV surface antigen and HCV antibody/RNA testing to our study population of adult ED attendees having routine bloods taken. Cases were contacted and records searched to assess diagnostic status (new/known) and eligibility for LTC. We estimated seroprevalence and risk factors among the study population using survey weights and logistic regression, adjusting for age, sex, ethnicity and homelessness. Number needed to screen (NNS) to link a BBV case to care was calculated as the inverse of weighted prevalence among fully-linked (attending two follow-up clinics) cases.

Results

6,211 of 24,981 patients were tested (uptake 25%) with 257 positive (4.1%) for at least one BBV. Weighted seroprevalence estimates (95% CI) for HIV, HBV and HCV-RNA were 0.8% (0.6-1.1), 0.6% (0.5-0.9) and 1.4% (1.2-1.8), respectively. Being male (HIV/HBV/HCV), aged 40-49 years (HBV/HCV), homeless (HCV), of black (HIV/HBV) or white (HCV) ethnicity were associated with infection. 85 BBV cases (33%), including 31 new diagnoses (12%), required LTC: 35 were fully-linked (NNS=256); 27 remained unlinked, including 11/21 homeless cases. 146 (57%) were known diagnoses already engaged in care (KEC).

Conclusion

Seroprevalence that exceeded London estimates and a low NNS support BBV testing in this setting. Not testing patients identifying as KEC and referring homeless cases to outreach services would improve detection and management of cases requiring LTC, thereby boosting the programme's public health impact.

Keywords: Seroepidemiologic Studies, Emergency Service Hospital, Hepatitis C, Hepatitis B, HIV,

ABSTRACT ID: 833

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A 4.4 Opt-out testing in a non-routine setting identified high seroprevalence of previously undiagnosed hepatitis B and C, London Emergency Department, October 2016 – February 2017

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Background

In the UK, London has the highest rate of hepatitis B (HBV) and C (HCV) infections but many remain undiagnosed, highlighting the need for innovative case detection strategies. We describe seroprevalence and risk factors for HBV and HCV infections amongst Emergency Department (ED) attendees at one London hospital to assess the effectiveness of opt-out testing in a non-routine setting.

Methods

We calculated uptake of a hepatitis test (HBV surface antigen [HBsAg] or HCV antibody [Ab] /antigen [Ag]) offered to ED patients (aged ≥16 years) having venepuncture between 12/10/2016-15/02/2017 using an ordering system preselected for hepatitis testing. We estimated weighted seroprevalence and identified risk factors for seropositivity using logistic regression, 95% CIs and p values, adjusted for demographics and ED arrival time.

Results

Testing uptake was 74% (11,485/15,624). We identified 70 HBsAg, 239 HCV-Ab, and 149 HCV-Ag positive attendees. Weighted seroprevalence of HBsAg was 0.50% (95% CI 0.38-0.66%); HCV-Ab 2.38% (95% CI 2.06-2.76%); and HCV-Ag 1.55% (95% CI 1.29-1.87%). Strongest risk factors for HBsAg positivity were being; aged 50-69 years (aOR 13.42, 95% CI 3.18-56.60) or Black/Black British ethnicity (aOR 13.56, 95% CI 5.63-32.65) and for HCV-Ag; being male (aOR 4.21, 95% CI 2.74-6.47) or aged 30-49 years (aOR 3.73, 95% CI 2.14-6.51). Where diagnosis status is currently known, 23% (10/43) of HBsAg and 17% (10/58) of HCV-Ag attendees were newly diagnosed. Outcomes of engagement with care services will be summarised.

Conclusion

High testing uptake was facilitated by using a preselected hepatitis testing ordering system. Higher HBV and HCV prevalence were observed in this ED population than national estimates demonstrating the potential to identify previously undiagnosed hepatitis cases in this setting. Cost-effectiveness estimates should be further explored.

Keywords: Hepatitis B, Hepatitis C, Emergency Service, Hospital, Blood

ABSTRACT ID: 854

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A 4.5 Detection and evaluation of chronic hepatitis B and C patients who were lost to medical follow up

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Background

Treatment options for chronic hepatitis B (hepB) and C (hepC) have improved rapidly last years. Detecting patients who are lost to follow up, enables to bring them back to medical concern and evaluate their treatment indication. Long term complications as well as viral transmission can hereby be prevented. To identify the most effective detection method, we compared detection using laboratory records to detection using regional public health service (RPHS) mandatory notification records.

Methods

Two local laboratories identified patients with positive HBsAg/anti-HCV test results in the past 15 years in the region of Arnhem. The RPHS selected all notified patients for the same period. Only patients of general practitioners (GPs) who agreed to perform evaluation were included. Laboratory and RPHS selections were compared and overlap was calculated. GPs referred patients with active hepatitis to a hospital and followed up patients with inactive hepatitis.

Results

In total 282 hepB and 53 hepC patients were detected: 273/282(97%) and 49/53(92%) by a laboratory, 91/282(32%) and 12/53(23%) by the RPHS. Evaluation was not needed in 121/282(43%) hepB patients, mainly because they already were under medical supervision, and not possible in 102/282(36%) patients for several reasons. Out of 59 hepB patients with a known indication for evaluation, 22(37%) were evaluated: 7 were referred to a hospital and 15 followed up. One hepC patient had a known indication for evaluation.

Conclusion

Detection and evaluation of chronic hepatitis B/C patients in the region of Arnhem showed that these methods are effective in detecting patients with an indication for treatment. Detection by laboratory records was more effective than by RPHS notification records. We recommend RPHSs to collaborate with local laboratories to detect chronic hepatitis B/C patients

Keywords: chronic hepatitis B, chronic hepatitis C, methods, therapy, public health

ABSTRACT ID: 800

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A 4.6 Diagnostic yield of a combined public health and primary care birth cohort testing strategy to detect hidden Hepatitis B and C cases

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Background

Both chronic hepatitis C and B virus (HCV; HBV) infections are generally asymptomatic and many infections remain undetected or are diagnosed at a late stage. Studies that evaluate best-practice hepatitis testing strategies are needed to be able to better detect this hidden population. In this prospective cohort study we aim to determine the diagnostic yield (test uptake and positivity rate) of a combined public health and primary care birth cohort testing strategy in detecting hidden cases of HCV and HBV.

Methods

All patients aged between 40 and 70 (n=6,743) registered with family practices (n=11) serving two higher prevalence areas (hotspots) in the South of the Netherlands were invited (i.e. estimated HCV prevalence of 1%; national estimated prevalence: 0.1-0.4%).

Results

Test uptake was 51% (n=3,434). No active/chronic HCV infections were detected: 0.0% [95%CI 0.0 to 0.1%]. The positivity rate of anti-HCV was 0.2% (n=7) [95%CI 0.1 to 0.4%], HBsAg was 0.3% (n=9) [95%CI 0.1 to 0.5%], and anti-HBc was 4.1% (n=142) [95%CI 3.5 to 4.9%].

Conclusion

This best-practice testing strategy is effective in achieving a high test uptake. However, it completely fails to detect hidden chronic HCV infections and is not recommended for lower prevalence countries.

Keywords: Hepatitis B Virus, Hepatitis C Virus, Public Health, Primary Health Care

ABSTRACT ID: 869

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Track 5: Influenza and other respiratory viruses (1)

A 5.1 Re-aligning WHO Influenza Transmission Zones

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Background

Since the 2009 H1N1 pandemic, The World Health Organization (WHO) developed influenza transmission and vaccination zones to facilitate monitoring of epidemics and use of influenza vaccines. The availability of more accurate influenza data has enabled the re-alignment of country groupings based on similar epidemiological trends

Methods

EPIPOI software was used to perform a time-series hierarchical clustering analysis of 131 countries' influenza A and B detections. Geographic clusters were generated based on similar transmission patterns within the same and in adjacent transmission zones between 2011 and 2016.

Results

Several countries demonstrated similar trends to those in adjacent zones. Guatemala, Martinique, Guadeloupe, Mexico, and Jamaica clustered with countries in the North America zone rather than with the Central American and Caribbean zone. Patterns in the Islamic Republic of Iran aligned with the Western Asia zone rather than the Southern Asia zone. Similarly, Georgia's transmission trends were more contiguous with Eastern Europe compared to Western Asia. Finally, Cameroon's and Uganda's patterns justify their shift to the Western Africa zone. This corresponds to their assigned Western Africa vaccination zone.

For some regions, the data was inconsistent. A year-by-year analysis for South-East Asia and Eastern Asia was conducted to assess the consistency of groupings. Indonesia aligned more closely with Japan, Mongolia, China, and the Republic of Korea every year between 2011 and 2016. Pakistan's 2011 to 2016 grouping was inconsistent; however a year-by-year analysis justified its shift to Western Asia.

Conclusion

Some of the existing WHO transmission zones would change, allowing for a better alignment of transmission with vaccination zones. There remains uncertainty with the groupings for a few countries. As more data becomes available, more robust seasonality analyses can be conducted.

Keywords: Influenza, World Health Organization, epidemiology, Cluster Analysis

ABSTRACT ID: 1050

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A 5.2 Phylogenetic analysis of the hemagglutinin (HA) gene of A(H3N2) influenza viruses circulating in Northern Italy during the 2016-2017 influenza season

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Background

A(H3N2) influenza virus predominated in Europe during the 2016-2017 season, characterised by an excess mortality in people >65 years concurrent with A(H3N2) circulation.

A molecular and evolutionary characterisation of A(H3N2) detected in Lombardy (Northern Italy) within the Italian Influenza Surveillance Network (InfluNet) during 2016-2017 season was performed.

Methods

549 respiratory samples from ILI outpatients (525/549=95.6%) and SARI/ARDS inpatients (24/549=4.4%) were collected in Lombardy from week 46-2016 to week 17-2017. Influenza viruses were typed (A/B) and subtyped (H1pdm09/H3N2) by real-time RT-PCR. A(H3N2) HA complete gene (nt. 1-1778) was phylogenetically analysed.

Results

Influenza viruses were detected in 52.3% (287/549) specimens; 93.4% (268/287) were A(H3N2). 34% (91/268) was sequenced. All HA sequences clustered in the genetic group 3C, sub-group 3C.2a, which included the vaccine strain A/HongKong/4801/2014 (similarity: 98.3-99.4%). Most (78/91=85.7%) sequences were A/Bolzano/7/2016-like (similarity: 98.7-99.9%) and belonged to sub-clade 3C.2a1, characterised by amino acid (aa) substitutions N171K (in epitope D), I406V and G484E. 41% of these sequences had mutation T135 (loss of a glycosylation site). Two additional sub-clades were identified: 3C.2a2 (7/91=7.7%) and 3C.2a3 (4/91=4.4%), characterised by aa changes N121K/S144K (epitope A/D) and T131K/R142K (epitope A), respectively.

57 mutations in 54 aa positions were identified, many at single sequence level. Most (>80%) aa changes were detected in HA1 subunit and >50% occurred in epitope A or D. No signature substitutions were observed in HA sequences of A(H3N2) strains detected in SARI/ARDS cases or vaccinated individuals.

Conclusion

The majority of A(H3N2) viruses circulating in 2016-2017 season clustered in sub-clade 3C.2a1, molecularly and antigenically similar to A/HongKong/4801/2014 vaccine strain. Several HA variants were identified. Full-length sequencing will be useful to define the molecular and evolutionary characteristics of these A(H3N2) viruses.

Keywords: Influenza A virus, H3N2 subtype, hemagglutinin, phylogenetic analysis, molecular characterisation

ABSTRACT ID: 916

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A 5.3 Whole-genome deep sequencing of A(H3) influenza virus detected among vaccinated and unvaccinated individuals during 2016/2017 season, Portugal

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Background

Vaccination is the best way to prevent influenza. This study aims to analyze the whole genome of influenza viruses from vaccinated and unvaccinated cases and reveal possible viral genetic causes assigned to the vaccine failure.

Methods

In the scope of the EuroEVA/I-MOVE project, nasopharyngeal swabs were collected from patients with influenza-like illness selected in primary care settings. Viral RNA was extracted directly from biological samples and after multiplex PCR amplification, the whole genome was sequenced for 84 influenza A(H3) viruses by deep sequencing on a MiSeq platform. The influenza gene sequences were assembled using an in-house multi-software pipeline with a mean depth of coverage of 1144x. Multiple gene alignments and mutational analysis were performed on MEGA software 6.0.

Results

All A (H3) virus clustered in the 2 genetic groups 3C.2a and 3C.2a1 (predominant). Sixteen viruses (19%) were from vaccinated individuals (10% in 3C.2a and 25% in 3C.2a1 groups). Only 7 cases of vaccine failure presented amino acid substitutions, not found among unvaccinated cases. No difference was found between vaccinated and unvaccinated groups in the p-distance, number of synonymous and nonsynonymous substitutions of viral genes. Only 5 cases of vaccine failure harbored nucleotide variants on their genome (from 7 detected sequence variants, only one has changed the amino acid).

Conclusion

The proportion of vaccinated cases was higher in the new 3C.2a1 group than in 3C.2a. Few amino acid substitutions found only in vaccinated cases occurred sporadically, as well as the nucleotide variants, most of them are synonymous substitutions. We found no differences in the type of selection, driving the viruses detected in vaccinated and unvaccinated cases.

Keywords: Influenza, whole-genome, deep sequencing, genetic variants

ABSTRACT ID: 1083

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A 5.4 Changes in Influenza B virus lineages circulating in Denmark, 2011-2016

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Background

The contribution of Influenza B Victoria and Yamagata lineages to all influenza cases is highly variable each year. Denmark recommends influenza vaccination with a trivalent vaccine, which includes only one influenza B lineage. During the 2015-16 influenza season, vaccine effectiveness against influenza B among individual age 65 and over was estimated at 4.1% (95% CI: -22.0-24.7). This study aimed to characterize influenza B viruses in order to inform on circulating strains and provide molecular data supporting the observed lack of protection induced by the trivalent vaccination in Denmark in 2015-16.

Methods

The study included over 1800 influenza B samples from the national influenza surveillance system for seasons 2011-12 to 2015-16. Lineages Yamagata and Victoria were identified by qRT-PCR. Ten samples from each lineage and each season were subsequently randomly selected for whole genome sequencing. Phylogenetic analyses of the neuraminidase and hemagglutinin sequences were performed.

Results

Lineage Yamagata represented 96% of influenza viruses characterized from 2011 to 2015, when the Victoria lineage became dominant. Phylogenetic analyses suggested multiple strains introduction during each influenza season. Focusing on the 2015-16 season, mismatches were observed between vaccine strains and the strains circulating in Denmark, and three amino acid changes, located in antibodies recognition sites were observed among Victoria strains.

Conclusion

The change to the dominance of the Victoria lineage during the 2015-16 season, not included in the trivalent vaccine that year, was unforeseen. This unpredictability as well as the occurrence of mutations in virus strains represent an important challenge for public health authorities. It highlights the need for molecular surveillance of circulating strains and for the evaluation of the public health benefits of the quadrivalent vaccine.

Keywords: Influenza, Denmark, Phylogeny, Genotype, Respiratory infections

ABSTRACT ID: 960

PRESENTED BY: Celine Barnadas (celine.barnadas@gmail.com)

A 5.5 Surveillance and characterisation of influenza viruses among patients with influenza-like illness in Bali, Indonesia, July 2010-June 2014

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Background

Influenza surveillance is particularly important in Indonesia, given continued circulation of Highly Pathogenic Avian Influenza A/H5N1 in poultry, and the high fatality rate of human A/H5N1 cases. However, epidemiological and clinical data on influenza virus circulation among humans in this country has been limited. This study aimed to characterize and compare the epidemiological and clinical characteristics of influenza viruses in humans through surveillance among patients with influenza-like illness (ILI).

Methods

ILI patients were recruited through systematic interval sampling at 21 sentinel health facilities across all nine regencies in Bali from July 2010 to June 2014. PCR-based assays were used for detection and subtyping of influenza viruses from nasopharyngeal swabs. Demographic, behavioural and clinical data were collected through questionnaires and tested for associations with influenza using chi-squared tests and logistic regression.

Results

Of 2077 ILI patients, 291 (14.0%) tested positive for influenza A, 152 (7.2%) for influenza B, and sixteen (0.77%) for both influenza A and B. Of the influenza A isolates, the majority (198; 61.2%) were A/H3N2, followed by A/H1N1-pdm09 (80; 26.1%), while 36 (12.4%) were of indeterminate subtype. Clinical predictors for infection varied by virus type, with onset of symptoms during the wet season the strongest predictor for influenza A (adjusted odds ratio [AOR] A/H3N2: 4.97; 95%CI: 3.24-7.61), and measured fever (≥38oC) more strongly associated with influenza B (AOR: 1.62; 95%CI: 1.10, 2.39).

Conclusion

Influenza circulates year-round among humans in Bali with higher activity during the wet season. High rates of contact with poultry and pigs among ILI cases and influenza detection viruses that could not be subtyped through conventional assays, highlight the need for molecular studies characterizing epidemiological and evolutionary dynamics of influenza in this setting.

Keywords: Influenza, surveillance, virus, Indonesia, ILI

ABSTRACT ID: 779

PRESENTED BY: Dewi Aisyah (dewi.aisyah.14@ucl.ac.uk)

A 5.6 Biennial pattern in enterovirus D68 infections from 2010 to 2016, Lyon, France

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Background

Enterovirus D68 was identified in 1962. Rarely reported before 2008, its epidemiology changed with the emergence of different clades. In 2014, a US-wide outbreak comprised 1,153 patients. An upsurge of acute flaccid myelitis (AFM) of unknown etiology occurred simultaneously with patients having a 10-fold increased chance being EV-D68 positive. In 2016, European countries experienced an upsurge of infections, including AFM. We aimed at identifying patterns in the epidemiology of EV-D68 to support establishment of an active surveillance in Europe.

Methods

We conducted retrospective screenings of respiratory specimens from 11,257 hospitalized patients in Lyon (2010 to 2016). Clinical presentations were reviewed. Phylogenetic relationships were reconstructed based on VP1 gene sequences using Maximum-Likelihood. Evolution rates of EV-D68 were estimated by GenBank-retrieved sequences with known sampling dates using Bayesian-MCMC. Bayesian skyline plots were used to explore the relative genetic diversity over time.

Results

156 infected patients were found, mainly diagnosed with asthma and bronchiolitis, 70.5% being under five years of age (28.2% under one). We observed a biennial pattern: 2010 (n=7), 2011 (n=1), 2012 (n=55), 2013 (n=0), 2014 (n=41), 2015 (n=1), 2016 (n=51). Strong seasonality was not observed suggesting a circulation throughout the year. New subclades were emerging for each epidemic reflecting selection for new variants. Skyline plots show an elevation of genetic diversity matching with epidemics suggesting greater variation in years of high activity.

Conclusion

A possible explanation for this cyclic pattern is EV-D68 being circulating between epidemics with positive selection for virulent strains resulting in a waning immunity of the population. Enhanced by newborns, this accumulation of susceptible individuals favours the epidemics. The recent dynamics of EV-D68 and its association to AFM emphasise the need for a systematic surveillance.

Keywords: enterovirus D68, enterovirus infection, phylogeny, longitudinal studies, emerging communicable diseases

ABSTRACT ID: 1005

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A 5.7 Infectious diseases among refugees in Berlin, September 2015 – February 2016

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Background

From 09/2015 to 02/2016 low-threshold medical care for refugees was provided in two mass accommodations and at one registration facility in Berlin. We analysed attendees' demographic characteristics and infectious disease (ID) to improve the planning of such services.

Methods

We analysed anonymised data collected by attending physicians (handwritten individual documentation) and coded diagnoses using the International Classification of Diseases (ICD10). We excluded consultations with unreadable documentation. Chi2-test was used to compare groups.

Results

We included data from 11,908 consultations (199 excluded). The median age of attendees was 24 years (range: 0-88 years) and 32% (3,777/11,247) were <18 years. Forty percent (4,333/10,903) were women. Syria (43%, 4,269/9,957) and Afghanistan (23%, 2,261/9,957) were the most frequent countries of origin.

Of a total of 13,925 diagnoses, 6,913 (52%) were infectious diseases: 4,960/6,913 (72%) were acute respiratory infections (ARI), 612/6,913 (9%) gastroenteritis and 269/6,913 (4%) lice or scabies. ARI were diagnosed in 2,389/4,327 (55%) children versus 2,571/9,598 (27%) adults (p=0.000), gastroenteritis in 440/4,327 (10%) children versus 172/9,598 (2%) adults (p=0.000) and lice or scabies in 113/4212 (10%) children versus 156/4,327 (2%) adults (p=0.000). For 122 (1%) consultations hospitalisation was subsequently initiated.

Conclusion

Many refugees in mass accommodation in Berlin suffered from ID, especially children. Almost all diagnosed ID could be handled by the provided general medical services and subsequently referrals to hospital were rare. High numbers of ARI can probably be explained by the co-occurring winter season. Crowded living conditions may contribute to increased ID transmission. If mass accommodation cannot be avoided, operators need to ensure adequate food and kitchen hygiene, sanitation, and isolation of infectious patients, as well as provision of low-threshold medical care.

Keywords: Refugees, Asylum seekers, Communicable Diseases, Healthcare, Ambulatory Care Facilities, Crowding

ABSTRACT ID: 1013

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Track 6: Emerging and vector-borne diseases (1)

A 6.1 Dengue, chikungunya and zika seroprevalence worldwide: a systematic literature review

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Background

With the global emergence and re-emergency of arboviruses like dengue, chikungunya and more recently zika, significant public health problems have arisen. The determination of seroprevalence is critical to assess the gaps in population immunity but requires extensive organization and is time and resource intensive. A review of scientific literature was undertaken to address the spatial and temporal distribution of seroprevalence studies and describe the alternative procedures of the general methodology.

Methods

Studies published between 2000 and 2017 that focused on dengue, chikungunya and/or zika seroprevalence were included. A search of Pubmed, Lilacs, SciELO, WHOLIS and Scopus online publications using key words of "arbovirus infection" or "dengue" or "chikungunya" or "zika", combined with "sero-epidemiologic studies" or "seroprevalence" or "seroepidemiology" or "serosurvey" was conducted.

Results

We identified 122 eligible studies, 98 describing serosurveys for dengue, 37 for chikungunya and 5 for zika viruses, conducted in a total of 66 countries. Most dengue studies were conducted in Asia (34%), Chikungunya in Africa (52%) and Zika in Oceania. The temporal distribution of chikungunya studies was concomitant with the virus expansion since 2004. Enzyme Linked Immunosorbent Assay and Neutralization Tests were used in 73% and 23 % of studies respectively. The average proportion of asymptomatic infections was higher for dengue (67%) than for chikungunya (27%). Common socio-demographic, economic and environmental factors associated with infection were identified.

Conclusion

Seroprevalence studies provide important and useful information on exposed population and the potential impact of past and future outbreaks. Results highlighted the heterogeneity of infection levels on a global scale as well as within countries and revealed substantial gaps in epidemiologic knowledge of entomological and behavioral factors associated with seroprevalence.

Keywords: Arbovirus, Seroprevalence, Survey, Methodology, Worldwide

ABSTRACT ID: 1071

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A 6.2 Estimating the probability of arbovirus outbreaks in large southern European city infested by Aedes albopictus

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Background

The presence of the mosquito species Aedes albopictus, competent vector of Chikungunya (CHIKV) and Dengue (DENV), and the possible arrival of infected travellers returning from endemic countries may represent a public health risk for Southern European countries. The aim of this work was to assess the weekly risk of CHIKV, DENV and ZIKA virus outbreaks in Rome tackling both the risk of infected-host introduction and patterns of local transmission.

Methods

The probability of infected-host introduction was estimated by a binomial process dependent from the number of infected cases in endemic country and the probability of travelling to Rome. A geometric process with means RoHV (reproductive number for host to mosquito transmission) and RoVH (mosquito to host) estimated the probability of successful transmission. Outbreak probability was estimated in 3 scenarios of different vector-host contact ratio and 2 scenarios of epidemic outbreaks in 5 different endemic countries. Weekly data of global cases and inbound and outbound Rome travellers were joined with field-derived estimates of A. albopictus abundance within the city.

Results

The model correctly estimated the number of DENV and CHIKV imported cases notified to the national health system. The estimated outbreak probability was ≤1% for both DENV and CHIKV under scenarios of low vector-host contacts, but the risk increased significantly (i.e. DENV outbreak risk =21%; CHIKV outbreak risk=47%; null for Zika) under a scenario of higher vector abundance, still consistent with the abundance data from infested hot spots within the urban area.

Conclusion

This work disentangles the role of seasonality of mosquito dynamics, traveller's inflow and temporal pattern of infected cases in endemic countries in building up an outbreak risk model.

Keywords: arbovirus, outbreak risk model, Aedes albopictus

ABSTRACT ID: 1054

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A 6.3 Seroprevalence of hantaviruses and Leptospira in muskrat and coypu trappers in the Netherlands

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Background

Leptospira spp. and Seoul hantavirus (SEOV) are zoonotic pathogens with rats as their main reservoir. Brown rats are a frequent bycatch in traps placed to catch muskrats or coypus. Recently, brown rats originating from one region tested positive for SEOV in the Netherlands. Brown rats have also been shown to carry leptospires in the Netherlands, which consequently can infect humans via direct contact or surface water contact. The aim of the study was to determine the potential health risk by assessing the exposure of Dutch muskrat and coypu trappers to hantaviruses, specifically SEOV, and Leptospira spp.

Methods

Participating trappers provided serum samples and completed an online questionnaire. The serum was tested for the presence of antibodies against six hantaviruses and eight Leptospira serovars.

Results

A total of 402 muskrat and coypu trappers were contacted of whom 260 persons completed the online questionnaire (65%), and 246 (61%) and 162 (40%) blood samples were tested for antibodies against hantaviruses and Leptospira spp., respectively. Contact with muskrats (95%) was most commonly reported, followed by contact with brown rats (89%), and coypus (18%). Two participants tested positive for leptospires, leading to a seroprevalence of 1.2% (95% CI: 0.3-4.4%). The seroprevalence of hantavirus in Dutch muskrat and coypu trappers was 0.4% (95% CI: 0.1-2.3%), with one participant testing positive. None of the participants tested positive for SEOV.

Conclusion

The results indicate that the risk of exposure to hantaviruses, in particular SEOV, and leptospires is low for muskrat and coypu trappers. The use of personal protective equipment most likely plays an important role in preventing exposure, especially to Leptospira.

Keywords: Leptospira, hantavirus, Seoul virus, seroepidemiologic study, occupational exposure, rats

ABSTRACT ID: 856

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A 6.4 Inequities in access to maternal and child healthcare and poor child outcomes in rural Sierra Leone: findings of a mixed methods study.

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Background

Sierra Leone has the world's highest estimated maternal and child mortality. Following the Ebola outbreak 2014-2016, we aimed to describe health and health-seeking behaviour amongst pregnant women and children<5 years (under5s), to inform health service planning.

Methods

In October 2016-January 2017, we conducted a sequential mixed-methods study in urban and rural areas of Tonkolili District comprising household survey targeting women and carers of under5s, followed by in-depth interviews also including community leaders and health workers. We selected 30 clusters in each area: by random GPS points (urban) and by random village selection stratified by population size (rural). We collected data on health-seeking behaviours, barriers to healthcare, childbirth, outcomes and mortality using structured questionnaires. Qualitative interviews exploring topics identified through the survey were conducted with a purposive sample and analysed thematically.

Results

We surveyed 608 women and 643 carers of 1092 under5s, and conducted 72 in-depth interviews. Under5s mortality was substantially higher rurally (1.55/10,000/day vs urban 0.26/10,000/day). 48% (rural) and 31% (urban) women gave birth outside of a health facility; of those, 96% and 66% did so without skilled assistance. Barriers, including costs of healthcare and physical inaccessibility of healthcare facilities, delayed or prevented 90% (95%CI:80-95) (rural) vs 59% (95%CI:48-68) (urban) of women from receiving healthcare during pregnancy/labour. Participants expressed mistrust of the health system due to poor previous experiences, lack of medications, and payment demanded for "free" healthcare. Barriers and mistrust led participants to use alternative healthcare providers, such as traditional healers.

Conclusion

Findings indicate inequity in access to maternal and child healthcare, and poor child outcomes in rural Tonkolili. Healthcare services should be urgently orientated to meet substantial needs of women and children in rural Sierra Leone.

Keywords: Maternal Health, Maternal Mortality, Child Health, Child Mortality, Delivery of Health Care, Sierra Leone

ABSTRACT ID: 817

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A 6.5 Reporting notifiable communicable diseases by using hospital electronic medical record systems: an effectiveness assessment

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Background

Taiwan Centers for Disease Control (TCDC) has established the web-based National Notifiable Disease Surveillance System (NNDSS) that allows healthcare personnel to report notifiable communicable disease cases to the central and local public health authorities (PHA) since 2003. With the increasing popularity of cloud computing technology and the adoption of information exchange standards on automatic data transfer, TCDC has initiated a project of "Reporting Notifiable Communicable Diseases by Using Hospital Electronic Medical Record (EMR) Systems" in collaboration with selected hospitals since 2013. Within the project, an information exchange platform serves to provide participating hospitals with updated case definitions and comprehensive test results for the reported cases automatically.

Methods

In this effectiveness study, we used a structured questionnaire to conduct satisfaction surveys among the staffs from the 20 participating hospitals in 2013 by the pretest-posttest design. We collected the questionnaire data using Microsoft Excel and analyzed with SAS software.

Results

The result showed that 74% of hospital staffs considered reporting diseases using the hospital EMR system was easier than that of using the original web-based reporting system. The average time required to complete reporting a case was reduced by 2 minutes and 50 seconds. 78% of the hospital staffs were satisfied with disease reporting using hospital EMR.

Conclusion

This study suggests that the efficiency of communicable disease reporting can be markedly improved by integrating the disease reporting module within the hospital EMR systems. This is to achieve a two-way information exchange between hospitals and PHAs, increasing the efficiency of disease control actions.

Keywords: electronic health records, cloud computing, disease notification, communicable diseases, Taiwan, hospitals

ABSTRACT ID: 791

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A 6.6 Strengthening local and regional infectious disease control in South-Netherlands by using a secure web-based dashboard for real-time data exchange

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Background

The ongoing occurrence of outbreaks demonstrates the importance of real-time surveillance and rapid detection for adequate infectious disease control on both national and local levels. Therefore, software systems should be able to exchange high quality data and information in a secure and timely manner between public health services (PHS).

Methods

All six PHS in South-Netherlands (almost 4 million inhabitants) joined forces during a one-year pilot on strengthening regional infectious disease control and implemented a secure real-time custom-developed infectious disease data dashboard. The PHS already used the same real-time web-based software suite for registration and management of disease notifications.

Results

The HPZoneDashboard South-Netherlands provides an aggregate view on real-time data from all 6 PHS using various filters: what (case, contact, exposed person, outbreak, enquiry), which location (PHS), which infection (disease), when (time period), and where (context, e.g. daycare center, care home). Data are based on an agreed common (anonymised) minimal data set and are connectedly presented in tabular, graphical and geographical (GIS) views. Automated disease trigger alerts derived from weekly historical data analysis are shown in traffic light colours with warning and action lines.

Conclusion

This dashboard provides the PHS with useful real-time local and regional data analysis reports. Regional infectious disease control and epidemiological research have been enhanced using the embedded features and query facility of the dashboard for early detection of possible outbreaks, monitoring diseases trends and exploring associations. The dashboard has improved best practice and cooperation among the PHS and underpinned data quality, consistent data registration and legal agreements. During the next three-year follow-up project PHS will also explore possibilities for antimicrobial resistance surveillance, cross-border cooperation with Flanders and fusion with national surveillance and control.

Keywords: communicable disease control, computer systems, real-time, surveillance, epidemiology

ABSTRACT ID: 1047

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Track 7: Food- and waterborne diseases and zoonoses (1)

A 7.1 Challenges in controlling norovirus transmission in semi-closed populations: Lessons learnt from an outbreak at a hotel in Norway

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Background

On 17 February 2017, local health and food authorities were notified about over 20 people reporting gastroenteritis during or after their stay at one hotel. We investigated the outbreak to describe its extent and identify its source to implement control measures and stop transmission.

Methods

We conducted a cohort study among persons staying or working at the hotel 15-24 February. Using an online questionnaire we collected information on symptoms, meals and exposures to common areas in the hotel. We defined cases as persons who vomited or had diarrhoea during or within 3 days after their stay at the hotel from 15-24 February. We performed univariable and multivariable data analysis. Stool samples were analysed and genotyped. We inspected the premises including kitchen facilities.

Results

Of 436 respondents, 161 were cases (attack rate 37%). Epidemiological analysis did not give any conclusive results regarding source and mode of transmission, but data suggested a point source outbreak peaking two days after a guest vomited in the hotel reception. Norovirus with identical genotype GII.P7 was identified in all eight tested stool samples. No irregularities in kitchen hygiene were identified. Use of chlorine-based disinfectant-solutions at critical control-points, enhanced hand hygiene, and cleaning/disinfection measures during a four day closure did not prevent further cases. After a ten days closure with extensive cleaning/disinfection measures and replacement of reception and corridor carpets, no more gastroenteritis was reported.

Conclusion

This prolonged norovirus outbreak was only controlled through exhaustive control measures including partly refurbishment of the hotel. Norovirus has a potential for continued environmental spread, especially when vomiting occurs in highly-frequented areas. Hotels should have procedures in place for guiding measures when events with potential infectious spreading takes place.

Keywords: Norovirus, Gastroenteritis, Disease outbreaks, prevention & control

ABSTRACT ID: 850

PRESENTED BY: Astrid Lovlie (astrid.louise.lovlie@fhi.no)

A 7.2 A norovirus outbreak following a dinner party among healthcare workers (HCWs) in a hospital in Eastern Norway, 2016

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Background

On 11 April 2016, the NFSA reported an outbreak of gastroenteritis following a dinner party on 7 April among HCWs from an Eastern Norway hospital department. Leftovers were served to night shift colleagues and at the department lunch the following day. We investigated the outbreak in order to describe its extent and determine its source.

Methods

We conducted a retrospective cohort study among attendees of the dinner, lunch or night shift. Through an online questionnaire we collected information on food exposures and gastrointestinal (GI) illness. We defined cases as individuals who reported vomiting and/or diarrhea between 7-11 April. Relative risks (RR) were calculated with 95% confidence intervals (CI) using multivariable logistic regression. People with GI-symptoms were asked to deliver a stool sample for enteropathogenic testing. A site investigation was performed at the catering company.

Results

The response rate was 65% (36/55). 15 respondents met the case definition (AR 56%). The most frequently reported symptoms were malaise (100 %), nausea (93 %), diarrhea (87 %) and vomiting (73 %). Consumers of pasta salad (RR 7.7, CI 1.1-52) and spinach pie (RR 2.1, CI 1.1-3.9) were more likely to experience illness. No patients at the hospital department became ill. One stool sample tested positive for norovirus. Site investigations showed that catering personnel and building visitors shared bathrooms.

Conclusion

We conclude that the pasta salad produced by a local catering company and served during the dinner party, night shift and lunch was the most likely source, and norovirus the most likely agent based on Kaplan Criteria and one fecal sample. We emphasize that catering companies and food handlers should always practice good hygiene, including having designated toilets for personnel.

Keywords: Disease Outbreaks, Norovirus, Health Personnel, Gastroenteritis

ABSTRACT ID: 1084

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A 7.3 Food-borne norovirus in a national chain of Mexican-themed restaurants in the UK, October 2016: customer studies

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Background

Over a fortnight in October 2016, gastroenteritis was reported from staff and customers in 22 branches of a national restaurant chain. Identical norovirus genotype II.6 was identified from 31 cases across the UK. We conducted a case-control study in Cardiff branch customers to identify the vehicle of infection, complemented by customer cohort studies in other branches and a national staff cohort study.

Methods

Cases and controls were identified via restaurant booking lists and customers self-reporting illness to environmental health departments (EHD). We asked participants to complete online questionnaires and distribute the link to co-diners. Cases were defined as participants who developed diarrhoea or vomiting or two other gastrointestinal symptoms, within 72 hours of eating at the restaurant; controls were other diners. We calculated odds ratios (OR) with 95% confidence intervals (CI) for each menu item and component ingredients of specific dishes.

Results

We identified 7 cases and 22 controls from the booking lists and 6 cases and 3 controls from EHD. Cases were more likely to have eaten chicken tostadas (OR= 28.0, CI: 2.51-1310; 7/13 cases exposed) and any dish including defrosted, pre-cooked chicken (used un-reheated in the tostadas) (OR=9.78, CI: 1.51-103.28; 11/13 cases exposed), than controls. The same product, introduced just prior to the outbreak in all branches, was implicated in 92 participants in a cohort study using booking lists in the Edinburgh branch (RR=3, CI: 1.6-5.5; 32/41 cases exposed).

Conclusion

Coincident illness in multiple branches suggested a contaminated nationally distributed food item. Customer studies implicated the newly-introduced pre-cooked chicken product. Contaminated nationally distributed food items provide the opportunity for large outbreaks and restaurants should take care with new products, particularly those not subject to further cooking.

Keywords: Norovirus, gastroenteritis, foodborne diseases, surveys and questionnaires

ABSTRACT ID: 937

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A 7.4

Incidence and risk factors of Blastocystis infection in a rural community, Thailand

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Background

Blastocystis sp. is one of the most common intestinal protozoa in humans. Blastocystis infected patients may present with a wild range of gastrointestinal symptoms such as abdominal pain and diarrhea. A few report showed the association between Blastocystis infection and irritable bowel syndrome. However, most Blastocystis infected patients in Thailand presented with no symptoms. A few modes of transmission including waterborne, foodborne, zoonotic and person-to-person have been documented. Our research aimed to identify the incidence and the risk factors of Blastocystis infection in a rural community, Central Thailand. Our study also provided additional information including persistent/reinfection rate and clearance rate of Blastocystis infection.

Methods

The prospective cohort study was performed in 4 villages in PhraPloeng community, Khao Cha Kan district, Sakaeo province, Thailand from February to December 2016.

Results

The incidence of Blastocystis infection in this community was 8.97 per 100 person-years. The persistent/reinfection rate was 46.41 per 100 person-years. The clearance rate was 75.73 per 100 person-years. Multivariate analysis using Poisson regression, drinking unboiled water was significantly related with Blastocystis infection (IRR = 8.07, 95% CI = 1.12 – 8.47).

Conclusion

Our information indicates waterborne transmission of Blastocystis sp. in this community which should draws attention to public health policy to improve the quality of water in rural communities.

Keywords: Blastocystis infection, Water-bourne transmission, Abdominal pain

ABSTRACT ID: 855

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A 7.5

It's not Irritant Contact Dermatitis, It's Bacillus anthracis! an Outbreak Investigation of Cutaneous anthrax in Kulon Progo, Indonesia, 2017

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Background

On December 21st 2016, Kulon Progo district health office received a report from a primary health center about 12 cases of unusual skin lesions (blister) in one village. Investigation was conducted to verify the diagnosis, determine the presence of outbreak and to do control measure.

Methods

This was cross sectional descriptive study. Interview with structure questionnaire through house to house in Ngaglik,Penggung,Ngroto and Wonosari sub-village from December 21st 2016-February 2nd 2017 was done to ascertain additional person with skin lesion and to find out the history of exposure. Person with skin lesion (papule/vesicle/blister/eschar) during August 2016–February 2017 was categorized into suspect, probable and confirm case of cutaneous anthrax (CA) based on CDC guideline 2010. One health team consisted of human and animal health was established. Specimens of case were collected for laboratory test of pathogen. Environment assessment, examination of livestock and its products were also done.

Results

There were 5 suspect, 16 probable and 1 confirm case among 169 persons. Out of 17 cases, 82.4% was male, age range 28-75 years, 88.2% farmer and 70.6% had lesion in hand. Laboratory test of case's specimen, soil in slaughtering place and remaining goat meat were positive for Bacillus anthracis. The highest probability to get CA was people in Ngaglik (AR= 4.65%). During August-December 2016, 11 sick or sudden death of livestock were slaughtered and consumed in Ngaglik.

Conclusion

Outbreak of CA in Kulon Progo was declared since January 16th 2017. One health team had done risk assessment to monitor and prevent further spread of anthrax in the neighboring area. Enhancement of disease surveillance and vaccination of anthrax for livestock around epidemic area was given gradually.

Keywords: Cutaneous Anthrax, One Health, Outbreak, Risk Assessment

ABSTRACT ID: 804

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A 7.6 Estimation of the size of a norovirus outbreak in restaurant customers using capture-recapture methodology – Edinburgh, 2016

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Background

A large-scale UK-wide norovirus outbreak associated with a chain of Mexican restaurants occurred in October 2016. An Edinburgh restaurant customer cohort study (CS) based on table booking records found 41 cases among 92 respondents (attack rate (AR) 45%). Although additional cases were reported through customer complaints, we suspected that not all had been identified. We aimed to estimate the size of this outbreak in Edinburgh using a capture-recapture approach.

Methods

Cases were customers who ate at the Edinburgh restaurant between 26/10-28/10 and developed gastrointestinal symptoms within 12-72 hours. As part of the CS, customers completed and forwarded an online survey to co-diners. Customers could also separately self-report illness to Environmental Health Officers (EHO). The total number of customers over these dates was calculated using the number of dishes prepared by the restaurant. We estimated the number of cases using the Lincoln-Petersen method and calculated the AR among customers.

Results

Of approximately 1,472 customers, 66 reported illness (CS=36; EHO=25; both=5). The estimated number of cases was 246 (95%-CI 127-366) and the estimated AR was 17% (95%-CI 9-25%). The sensitivities of case-finding through CS and EHO reports were 17% (95%-CI 11-32%) and 12% (95%-CI 8-24%), respectively.

Conclusion

The estimated number of cases was considerably higher than that reported to public health authorities and the CS overestimated overall AR. Though the individual probabilities of self-reporting to EHO and participating on CS may be different, the outbreak size was likely underestimated. In the context of wide-spread outbreaks, we recommend the identification of additional information sources and the application of capture-recapture methodology to estimate AR and outbreak size. Caution should be taken when extrapolating a small cohort study AR to all customers.

Keywords: underreporting, capture-recapture, norovirus, outbreak investigation

ABSTRACT ID: 778

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Track 8: Vaccine- preventable diseases (1)

A 8.1 Evaluation of the Italian integrated measles and rubella surveillance system in Apulia region, three years after its introduction

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Background

As recommended by WHO Plan for measles and rubella elimination, an integrated measles and rubella surveillance system (IMRSS) was established in 2013, in Italy. We assessed a set of performance indicators of IMRSS, three years after its implementation in Apulia.

Methods

We extracted data on suspected measles and rubella cases reported to IMRSS between 01/01/2013 and 30/06/2016. We estimated system sensitivity in detecting suspected cases using the capture-recapture method for three data-sources (IMRSS, routine notification system and hospitalisations); the log-linear model with the lowest Akaike Information Criterion was selected. Data quality was described as the completeness of variables and timeliness as median time interval between the local alert to regional reporting. We calculated the rate of suspected cases with laboratory investigation, the origin of infection and the positive predicted value (PPV).

Results

Four rubella and 127 measles suspected cases were reported to IMRSS. Due to the low number of rubella cases, we focused our analysis on measles. Of 127 suspected cases, 82 were laboratory confirmed. IMRSS sensitivity was 82% (95%CI:75-87%). Completeness was >98% for mandatory variables and 57% for “genotyping”. The median time interval between the local alert to regional reporting was three days; 35% of cases were reported ≤24h. The rate of laboratory investigation was 77%. Origin of infection was identified for 85% of cases and PPV was 64%.

Conclusion

The Apulian IMRSS provides good quality data and meets the WHO sensitivity target according to WHO plan for eliminating measles and rubella. Sustained efforts should be made to improve timeliness, completeness of laboratory related variables and PPV of IMRSS by raising awareness amongst the Local Public Health Authorities of its importance in achieving the elimination goals.

Keywords: Keywords: Measles, Rubella, Surveillance system, Evaluation, Apulia, Italy

ABSTRACT ID: 923

PRESENTED BY: Iulia Adelina Turiac (adelinaiulia@yahoo.co.uk)

A 8.2 Underestimation of measles vaccine uptake in 10-16 year olds after the 2013 national measles, mumps and rubella vaccination catch-up campaign in England

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Background

In response to a national increase in measles incidence, a measles, mumps and rubella (MMR) vaccination catch-up campaign was launched in England in April 2013. The campaign targeted children aged 10-16 years as Child Health Information Statistics (CHIS) data indicated sub-optimal MMR coverage in this cohort. In August 2013 the vaccination status of a multistage sample of 6,644 children recorded as unvaccinated on CHIS was validated against primary care records, and identified 2,414 children without a record of measles vaccination. We estimated the proportion of unvaccinated children in this cohort after the catch-up campaign to inform future vaccination programmes.

Methods

Parents of the 2,414 reportedly unvaccinated children were invited to report the measles vaccination status of their children as a binary response by text message, and complete a survey exploring timing of vaccination and reasons for non-recorded vaccination. These data were then used to adjust national vaccine uptake estimates for children aged 10-16 years.

Results

Responses were received for 577 (23.8%) children, 382 (66.2%) of whom reported receiving a measles-containing vaccination. We estimated the proportion of unvaccinated 10-16 year old children in England as 4.0% (95% confidence interval, (CI): 3.4–4.7%). The reason reported most often by survey respondents for non-recorded MMR vaccination was receiving vaccination overseas (61.2%, 30/49).

Conclusion

Measles vaccine coverage in this cohort is higher than previously reported and has exceeded the national target of 95% coverage. Estimates of measles vaccine uptake based on national statistics and GP records do not accurately reflect historic vaccination in older children, particularly in children vaccinated abroad. Future vaccine catch-up campaigns should consider validating vaccination status in areas of reportedly low vaccine uptake prior to implementing supplementary immunisation activities.

Keywords: Measles, Measles Vaccine, Measles-Mumps-Rubella Vaccine, Immunization Programs, Electronic Health Records

ABSTRACT ID: 1007

PRESENTED BY: Lara Utsi (lara.utsi@phe.gov.uk)

A 8.3 Laboratory-based Evaluation of the Acute Flaccid Paralysis Surveillance System in Oyo State, southern Nigeria, 2008-2014

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Background

In September, 2015, Nigeria was delisted from the list of polio endemic countries globally. In Oyo State, no case of Wild Polio Virus (WPV) has been reported since February, 2009. We evaluated the AFP surveillance system to assess its laboratory- based attributes with focus on stool collection, arrival and testing of specimens in the laboratory.

Methods

We reviewed AFP surveillance data obtained from the Oyo State Ministry of Health. We used the Centre for Disease Control and Prevention updated guidelines for evaluating public health surveillance system to assess the laboratory surveillance quality indicators. Variables abstracted were AFP cases, proportion of Wild Polio Virus (WPV) confirmed cases, Annualized Non-polio AFP (NPAFP) rate, proportion of stools collected within 14 days of onset of paralysis, at least 24 hours apart, and the proportion of stool arriving at the laboratory in good condition. The sensitivity of the system was measured by the NPAFP rate. Data was cleaned and analyzed using Microsoft Excel 2010

Results

Of the 897 AFP cases detected, 20 (2.2%) were laboratory confirmed WPV. The sensitivity of the system was consistently above the target of ≥ 2/100,000 population. The proportion of stools collected within 14 days of onset of paralysis, at least 24 hours apart was 893/897(99.5%) and the proportion of stool arriving at the laboratory in good condition was 891/897 (99.3%). Positive Predictive Value was 2% (2008 -2009), and 0% (2010-2014).

Conclusion

Specimen collection and arrival to the laboratory was optimal. This may be due to the presence of a national reference laboratory in the State. The specimens were received in the laboratory in good condition. The laboratory-based attributes of the AFP surveillance system of Oyo State is good.

Keywords: AFP, Surveillance, Evaluation, Wild Polio Virus, Nigeria

ABSTRACT ID: 1099

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

A 8.4 Laboratory-based Surveillance System evaluation for Measles, Oyo State, southern Nigeria, 2008-2014

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Background

Measles is associated with high mortality and morbidity in Africa and other developing countries. Measles remains a leading cause of less than 5 years mortality in Nigeria. Case-based surveillance is one of the strategies adopted by the WHO African region to reduce mortality and morbidity caused by the illness. We analysed the measles case-based surveillance data in Oyo State, to assess the collection, timeliness of arrival and testing of specimens in the laboratory

Methods

We conducted a secondary data analysis of measles case-based surveillance records from the Oyo State Ministry of Health, between 2008 and 2014. The WHO recommendations for Measles case-based surveillance was used to assess the laboratory-based surveillance quality indicators. Variables abstracted were proportion of cases from which blood specimen was collected, proportion of serum specimen arriving the laboratory within the recommended 3 days of collection, proportion of cases that were positive for measles IgM, and proportion of serum specimen arriving the laboratory in good condition. Data was cleaned and analyzed using Microsoft Excel 2010.

Results

2,592 suspected cases were investigated and 568(21.9%) were positive for measles IgM. Proportion of cases from which blood specimen was collected was 100% (Target is ≥ 80%). Timeliness of serum specimen arriving at the laboratory within the recommended 3 days of collection was consistently 100% (Target is ≥ 80%) and the proportion of serum specimen arriving at the laboratory in good condition was 100% during the review period (Target is at least 90%).

Conclusion

Blood specimen was collected from all the cases. Timeliness of specimen arrival at the laboratory was good and all specimens arrived at the laboratory in good condition. The Oyo State laboratory-based surveillance quality indicators are reliable.

Keywords: Case-based surveillance, Measles, Oyo State, Nigeria

ABSTRACT ID: 1097

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

A 8.5 International external quality assurance for laboratory identification and capsular typing of Streptococcus pneumoniae

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Background

An international External Quality Assessment (EQA) scheme for pneumococcal serotyping has been performed for 11 years, by a network of pneumococcal reference laboratories. Since 2005, EQA panels of seven isolates have been distributed biannually. We report the performance, acceptability and usefulness of pneumococcal EQA scheme, in order to maintain high quality of pneumococcal serotyping for public health surveillance purposes.

Methods

Concordance of serotyping results from 22 EQA panels distributed in 2005–2016 was assessed, and discrepant results evaluated. A questionnaire regarding acceptability and usefulness of the EQA scheme was distributed to all participants.

Results

The number of participating laboratories increased from two in 2005 to eight in 2016. Serotyping was performed by both phenotypic and molecular methods. Altogether 154 pneumococcal isolates were tested. Of the more than 92 known serotypes, 49 were included in the 22 EQA panels, comprising all serotypes included in the 13-valent pneumococcal conjugate vaccines, and all but one serotype (serotype 2) in the 23-valent polysaccharide vaccine. Discrepant results were observed in eight EQA panels, involving 11 isolates (7.1%, 95% CI: 0.04 to 0.12). Of these, four results (2.6%, 95% CI: 0.01-0.07) remained inconsistent after repeated testing. All participating laboratories reported that the EQA scheme was useful for quality assurance purposes.

Conclusion

The EQA participation helps ensure typing procedures are kept at a high standard and provides data for displaying compliance with accreditation. Results show that comparable serotyping data can be obtained in different laboratories. The EQA allows independent assessment of traditional and new technologies, by providing validation data revealing limitations of both genotypic and phenotypic methods. The EQA scheme will be continued.

Keywords: External quality assessment (EQA), Streptococcus pneumoniae, serotype, capsular phenotyping, capsular gene based typing

ABSTRACT ID: 813

PRESENTED BY: Hans-Christian Slotved (hcs@ssi.dk)

A 8.6 Integration of molecular parameters in the study of the epidemiology of measles genotype B3 in Spain from 2006 to 2016

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Background

Measles virus (MeV) is a morbillivirus which causes a highly contagious but vaccine preventable disease. This virus is targeted for elimination in Spain through a National Plan set in 2001. The objective of this work was to integrate molecular and epidemiological data of MeV B3 genotype, responsible for outbreaks in Spain between 2006 and 2016 in order to clarify their origin and the transmission pathways involved.

Methods

We did the phylogenetic analysis based on the N-450 sequence recommended by WHO for MeV genotyping and analysed a total of 310 Spanish sequences, together with 2066 sequences from GenBank. We used the MeaNS database (Public Health England, UK), to identify specific MeV variants. Phylogenetic trees were constructed by maximum likelihood (PhyML) using the best evolutionary model selected by JModeltest and αLRT-SHlike for statistical value.

Results

We found 27 haplotypes among the Spanish sequences, grouped in fifteen phylogenetic clusters. The most important outbreaks were caused by the MVi/Harare.ZWE/38.09-variant in 2011, MVs/WesternAustralia.AUS/2.14-variant in 2014, the haplotypes MVs/RioGrandedoSul.BRA/33.10 in 2010 and 2011 and MVs/Granada.ESP/43.10/ in 2010 and 2011. We identified 19 sporadic cases, 14 of them belonged to variants previously described. We detected six cases with unique sequences probably derived from imported haplotypes which produced outbreaks in Spain.

Conclusion

We identified the predominant haplotypes, the variants and the origin of the genotype B3 causing outbreaks in Spain in the last decade. The variant analysis allowed us to discriminate different transmission chains in the context of what was previously thought to be a single outbreak, based only on epidemiological data. The integration of molecular parameters in the study of the epidemiology of measles is recommended to verify the elimination status regionally.

Keywords: Measles virus, Genotype B3, Molecular epidemiology, Outbreak

ABSTRACT ID: 821

PRESENTED BY: Fátima Amaro (fatima.f.amaro@gmail.com)

Moderated Poster Session B
Day 2, Tuesday 7 November
15:40-16:40

Track 9: Antimicrobial resistance (2)

B 9.1 Acinetobacter baumannii isolates from invasive samples at tertiary care center in Kosovo

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Background

Infections caused by bacteria of genus Acinetobacter are significant health care challenge worldwide. Nowadays Acinetobacter baumanii has emerged as an important healthcare-associated and multidrug-resistant microorganism.

Methods

The aim of the study was to assess the occurrence of Acinetobacter baumannii from blood and cerebrospinal fluid at the University Clinical Center of Kosovo and to evaluate the antimicrobial susceptibility patterns. The specimens were collected during three year period (2014-2017) at the only tertiary care center with 2100 beds. The study was carried out within the Department of Microbiology at the National Institute of Public Health of Kosovo. Identification and susceptibility testing of bacteria were detected by VITEK 2 Compact and disc diffusion methods. Results for susceptibility were interpreted based on EUCAST standards.

Results

A total of 173 samples grew isolates of Acinetobacter baumannii; 136 blood cultures and 37 cerebrospinal fluid cultures. Out of 173 strains of Acinetobacter baumannii, 168 (97.1 %) samples were multidrug-resistant Acinetobacter baumannii . Majority of samples were identified from the neonatology wards – 147 strains (85%), followed by adult intensive care unit – 16 (9.2%) . Resistance rates for imipenem and meropenem, were 91.3 % and 92.5%, accordingly. Isolates were 90.7% resistant to quinolones and 95.4% to amikacin and gentamicin. There were no isolates of Acinetobacter baumanii with resistance to colistin.

Conclusion

This study confirmed a high incidence of nosocomial infection and revealed high rates of resistance among Acinetobacter baumanii in Neonatology and Intensive Care Units. These results confirm the necessity of implementation of effective infection control measures, proper usage of antimicrobial agents and further molecular investigation.

Keywords: Acinetobacter baumanii, multidrug-resistant, nosocomial infection, invasive samples

ABSTRACT ID: 912

PRESENTED BY: Arsim Kurti (arsimpz@hotmail.com)

B 9.2 Influence of antibiotic consumption on the antibiotic sensitivity of pneumococcus

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Background

The antibiotic susceptibility (AS) of pneumococcus (SP) varies throughout EU countries, probably due to differences in antibiotic consumption and infection prevention measures. The relationship between the AS of SP and previous antibiotic therapy in adult patients with invasive pneumococcal disease (IPD) was studied.

Methods

The cases of IPD reported to the Obligatory Declaration Disease System by the Ramón y Cajal Hospital (period 2013-2015). The relationship between the previous consumption of antibiotics and the reduced AS (ASR) against beta-lactams or macrolides was studied by logistic regression, adjusting for age, history of risk, serotypes and administration of the 7-valent vaccine (VCN7). The vaccination status was completed by consulting the Vaccination Information System. The AS study was carried out in the Regional Public Health Laboratory, using the cut-off points of the EUCAST classification. Serotypes were classified as included in the VCN7 (sVCN7), additional from the VCN13 (sVCN13n7) and not included (sNI). The confidence level was 95%.

Results

In the study period, 81 cases were reported. The median age was 71 years. 6.2% had received the VCN7. 14.8% had received prior antibiotic therapy. 19.8% of SP showed ASRs to beta-lactams and 20.9% to macrolides. 37.5% of the cases produced by sVCN7 and 9.0% of those produced by sVCN13n7 presented ASRs to beta-lactams. In relation to ASR to macrolides these figures were 37.5% and 18.0%, respectively. In the multivariate analysis the OR between the ASR for at least one of the antibiotics and the previous consumption of antibiotics was 2.80 (IC95: 0.66-11.92).

Conclusion

Data indicate that the incidence of IPD by SP with SAR to beta-lactams or macrolides is higher in cases that have previously received antibiotic therapy.

Keywords: invasive pneumococcal disease, antibiotic sensivity, Streptococcus pneumoniae¸7 valent pncompc vaccine.

ABSTRACT ID: 917

PRESENTED BY: Abelardo Fernandez Chávez (abefernandez@hotmail.com)

B 9.3 Identification and Distribution of Pathogens in a Major Tertiary Hospital of Indonesia

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Background

Healthcare-setting acquired infections are subject to substantial selection pressure and are frequently associated with drug resistance. This is the first such detailed study benchmarking the type and sensitivity of bacterial pathogens in a major tertiary referral hospital within Indonesia.

Methods

Data on the type of bacteria and their sensitivity to antibiotics were retrospectively identified from clinical samples taken from patients between January 1st 2015 and June 30th in Sanglah Hospital. Data were collected from culture-data records and bacteria were isolated from clinical specimens including blood, urine, sputum, cerebrospinal fluid (CSF) and other specimens. Identification and antibiotic sensitivity tests were conducted based on the micro-dilution method using Vitek-2 Compact machine.

Results

Of the 4681 specimens assessed, 2185 (47%) showed bacteria growth. Coagulase-negative staphylococci (18%) were the most commonly isolated bacteria, followed by Escherichia coli (17%), Klebsiella pneumoniae (10%), Acinetobacter baumanii (9%) and Staphylococcus aureus (6%). All isolated Gram-positive bacteria were susceptible to linezolid and vancomycin. A total of 38% of S. aureus were classified as MRSA. We identified that most Gram-Negative organisms implicated in nosocomial infections were resistant to quinolones and cephalosporins, but remained susceptible to carbapenems and aminoglycosides (amikacin).

Conclusion

Our study provides a detailed evidence-base for an under-reported yet very densely populated area of Southeast Asia in the context of global literature and provides a frame of reference for developing local guidelines to promote antimicrobial stewardship.

Keywords: antimicrobial resistance, resistance, Indonesia, hospital

ABSTRACT ID: 781

PRESENTED BY: Dewi Aisyah (dewi.aisyah.14@ucl.ac.uk)

B 9.4 The German statutory surveillance system for invasive Methicillin-resistant Staphylococcus aureus infections should be simplified – results of an evaluation, 2016/2017

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Background

In Germany, mandatory notification of invasive Methicillin-resistant Staphylococcus aureus (MRSA) infections to local health authorities (LHAs) was introduced for laboratories in 2009 to improve nation-wide monitoring of MRSA and support prevention and control of nosocomial infections (NIs). In 2016/2017, we evaluated the system to examine whether its objectives were met.

Methods

We conducted semi-structured interviews with voluntarily participating stakeholders to assess simplicity and usefulness and estimated completeness of 2009-2016 surveillance data.

Results

We interviewed 38/378 (10%) LHAs, 10/16 (63%) state health authorities (SHAs) and 5 laboratories. All LHAs reported that data collection requires contacting the hospitals with 10/13 (77%) stating that part of the clinical information collected is not contributing to prevention of NIs. Data collection was considered too extensive by 12/36 (33%) LHAs with 19/36 (53%) needing >3 days to complete and 17/36 (47%) reporting a workload of >30 minutes/case. To improve the system, several LHAs suggested reducing the amount of information collected. The system was considered useful by 21/37 (57%) LHAs (≥7 points on a 1 to 10 scale), while 9/37 (24%) did not find it useful (≤4 points). LHAs stated that more frequent contacts to hospitals are a reason for usefulness; 34/38 (89%) LHAs and 9/10 (90%) SHAs made use of surveillance data for reports. Between 2009-2016, data completeness for 27,706 cases reported reached ≥90% for core epidemiological variables (demographic information, symptoms).

Conclusion

The objectives of the statutory surveillance system were met partially. While it improved MRSA monitoring, prevention of NIs benefitted only indirectly by strengthening collaboration between LHAs and hospitals. As investigations are resource intensive, reducing the quantity of clinical information only to those needed for prevention of NIs could simplify the system.

Keywords: Disease Notification, Program Evaluation, Methicillin-Resistant Staphylococcus aureus, Telephone Interviews

ABSTRACT ID: 950

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

B 9.5 Late breaker: Species characterization and anti-microbial sensitivity profile of coagulase negative staphylococcus

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Background

This study was undertaken to obtain data about different species of significant Coagulase negative Staphylococcus (CoNS), study the antimicrobial sensitivity patterns especially the methicillin resistance through the assessment of minimum inhibitory concentration (MIC).

Methods

75 CoNS isolates were characterized using a modified simple scheme and antimicrobial sensitivity pattern of these isolates were studied thru disk diffusion method as per CLSI. MIC for both Cefoxitin and Oxacillin were estimated for all the isolates using microbroth dilution technique and e-test strip method.

Results

The isolates were characterised into 7 different species. Staphylococcus epidermidis (32%) was the most common species followed by Staphylococcus hemolyticus (27%).

65.3% isolates were showing resistance to Cefoxitin. 29.3% of isolates was found to be resistant to Tetracycline. For Cotrimoxazole, ciprofloxacin and erythromycin, the resistance was seen to be 57.3%, 62.6%and 81.3% respectively.

Oxacillin MIC testing revealed 19 and 20 isolates to be within sensitive range as per e-test and microbroth dilution respectively with 0.125mcg/ml as the most common sensitive MIC value by both methods. Cefoxitin MIC testing revealed 18 isolates to be the sensitive range of MIC by both the techniques and most common MIC value in the sensitive range was 1mcg/ml.

Conclusion

The simplified scheme of identification was able to characterize more than 95% of the isolates and after testing on a larger sample size can be considered as a fast and cost effective option in similar resource limited setting. S.epidermidis (32%) was found to be the most common species. The high level of methicillin resistance (65.3%) among the isolates highlights the general level of increasing drug resistance in bacteria and also the possibility of these organisms to harbor and spread resistance in this setting.

Keywords: antimicrobial resistance, coagulase negative staphylococcus

ABSTRACT ID: 1436

PRESENTED BY: Arun Wilson (arunwilly@gmail.com)

Track 10: Emerging and vector-borne diseases (2)

B 10.1 Validation of a two-tier diagnostic testing for Francisella tularensis ssp. in the Netherlands.

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Background

After six decades of absence, tularemia re-emerged in the Netherlands since 2011, thus far with 16 isolated human cases and few infected hares in different parts of the country. As of November 1st 2016, the disease is reportable. Therefore, we wanted to validate tularemia serological diagnostics for future implementation in order to increase the diagnostic capacity at RIVM.

Methods

A commercial enzyme-linked immunosorbent assay (ELISA) with an in-house confirmatory western blot (WB) were selected based on specificity, sensitivity, and throughput. Both assays, based on different antigens, were validated to investigate the utility of the two-tier testing and possible cross-reactivity. Specimens included positive controls, previously positive tested tularemia sera from Sweden and the Netherlands (n=27); negative controls, sera from blood donors from before 2011 (n=10); specimens from Dutch patients infected with diseases with symptoms similar to tularemia (EBV, CMV, Bartonella (n=10 each) and Toxocara, Ascaris (n=5 each)) and two cross-reactivity controls, positive Brucella sera. All samples were tested by ELISA and WB. Samples were considered borderline if the results were within 20% of the pre-determined cut-off.

Results

All positive controls were detected by both ELISA and WB and all negative controls were negative by ELISA and WB. All but one specimen from diseases similar to tularemia were found to be ELISA and WB negative.

Conclusion

In conclusion, the combination of the ELISA with WB enables specific (98.44%) and sensitive (100%) detection of tularemia and is suitable for routine diagnostic and larger seroprevalence studies. In daily practice, only ELISA positive samples will have to be confirmed by WB. Following implementation we recommend active information dissemination to healthcare facilities on the availability of a test which improves laboratory diagnosis of tularemia.

Keywords: enzyme-linked immunosorbent assay (ELISA), western blot (WB), serology, Francisella tularensis

ABSTRACT ID: 852

PRESENTED BY: **Zsofia Igloi (zsofia.igloi@rivm.nl)**

B 10.2 Enterovirus D68 and A71 recognized by the Acute Flaccid Paralyses (AFP) Surveillance in Northern Italy in 2016

Laura Pellegrinelli, C. Galli, E. Pariani, V. Primache, S. Binda

Background

Acute Flaccid Paralyses Surveillance (AFPS) is the strategic system to monitor the emergence of polioviruses (wild and vaccine-derived) in polio-free countries and it is a sensitive case-based scheme to recognize non-polio enteroviruses (NPEVs). We report the findings of AFPS activities in Lombardy (Northern Italy) during 2016 in the framework of the Italian nationwide AFPS.

Methods

Physicians enrolled children <15 years who met the WHO definition of AFP case. Clinical samples were collected for virological investigations and analysed by virus isolation in RD and L20B cell cultures, and by RT-PCR assay specific for the 5′ noncoding region (nt. 179-575) of EVs. EV-positive specimens were further analysed by sequencing a fragment of the EV-VP1 (nt. 2602-2977) gene.

Results

In 2016, 15 AFP cases were reported in Lombardy with an incidence of 1.07/100'000 children <15 years. The median age of AFP cases was 3.6 years [inter-quartile range (IQR): 4.8 years]; 93% of cases were males. No polioviruses were identified and NPEVs were detected in 20% (3/15) of AFP cases. Molecular characterization and phylogenetic analysis of NPEVs showed the presence of one Echovirus-25, one EV-D68 (similarity >98.6% with sequences of B3 lineage identified in the 2016 Dutch outbreak) and EV-A71 (similarity >98.4% with sequences of subgenogroup C1 detected in the 2015 German epidemic).

Conclusion

The results of 2016 AFPS confirmed the absence of poliovirus in the surveyed area, and provided valuable and up-to-date information on the occurrence of NPEVs of public health concern in Northern Italy. The unpredicted detection of EV-D68 and EV-A71, sharing high nucleotide similarity with viruses involved in the latest European outbreaks, emphasises the importance of monitoring NPEVs through AFPS to help public health response.

Keywords: surveillance, acute flaccid paralyses, non-polio enterovirus infection, EV-D68, EV-A71

ABSTRACT ID: 915

PRESENTED BY: **Laura Pellegrinelli (laura.pellegrinelli@unimi.it)**

B 10.3 Should acute Q fever patients be screened for valvulopathy to prevent chronic Q fever?

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Background

Screening of acute Q fever patients for cardiac valvulopathy, and ensuing antibiotic prophylaxis, is considered an important measure to prevent chronic Q fever related endocarditis. During the Q fever epidemic in the Netherlands, routine screening echocardiography was discontinued, which has raised controversy in the international literature. The aim of this study is to compare the long-term outcome between acute Q fever patients that had a newly detected valvulopathy and those who had not.

Methods

Patients diagnosed with acute Q fever in 2007 and 2008, and who participated in a previous cohort study were included. At that time, echocardiographic screening was still recommended. We retrospectively reviewed all screening echocardiographs, and checked for development of chronic Q fever eight years after the acute episode. Risks of developing chronic Q fever (probable and proven infection taken together) in relation to presence or absence of valvulopathy was analysed with logistic regression.

Results

512 Participants were included in this cohort, of whom 306 people received a screening echocardiography. There was no significant difference in occurrence of chronic Q fever between patients who had a newly detected valvulopathy (2/82, 2.4%, one probable and one proven) and those who had no valvulopathy (2/192, 1.0%). The two patients with a newly detected valvulopathy who developed chronic Q fever at a later stage did not receive antibiotic prophylaxis. In the entire cohort, four patients developed proven chronic Q fever, one with endocarditis, and three with an infected aneurysm.

Conclusion

There was no difference in outcome between patients with a newly detected valvulopathy and those who had not. The two patients with a newly detected valvulopathy who developed chronic Q fever, could have benefitted from antibiotic prophylaxis.

Keywords: Chronic Q fever, Coxiella burnetii, echocardiography, heart valve disease, endocarditis

ABSTRACT ID: 811

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B 10.4 Long term cognitive functioning of patients with chronic Q-fever and Q-fever fatigue syndrome: a pilot study

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Background

Two long term sequelae have been described after an acute Q-fever infection; 1-5% develop chronic Q-fever (CQ) and approximately 20% develop Q fever fatigue syndrome (QFS). Narratives illustrate that these patients can suffer from concentration and memory problems long after the acute infection. A pilot study was performed to gain understanding in long term cognitive functioning of CQ and QFS patients in the Netherlands.

Methods

A cross-sectional study with neuropsychological testing was performed by a trained psychologist. Cognitive performance of CQ (N=30) and QFS (N=32) patients on four domains, information processing speed, memory, working memory and executive functioning, are compared to age and education matched control groups (N=23; N=21) and to normative data to classify a participant as having cognitive impairment, no dementia (CIND). Underperformance was measured to detect a suboptimal performance or effort during neuropsychological testing.

Results

The percentage of underperformance in CQ patients was high (38%) compared to controls (14%). Results show differences on all domains (except information processing speed) between CQ patients and controls, with memory being significantly lower after correction for age and level of intelligence (p=0.035). More CQ patients were classified as CIND (23%) compared to controls (4%) (p=0.056). QFS patients score slightly worse on all domains (except memory) compared to controls, however, differences are less apparent and not significant.

Conclusion

Results show lower cognitive performance in CQ patients compared to controls, but also a high percentage of underperformers which might explain this difference. Differences between QFS patients and controls was even less clear. This pilot study suggests no major cognitive impairment in QFS patients, however, highlights a need for further research in CQ patients.

Keywords: Q fever, Sequelae, Long Term Effects, Cognitive Dysfunction, Neuropsychological Tests, Pilot Study

ABSTRACT ID: 1029

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B 10.5 Knowledge, attitudes, and practices regarding ticks and tick-borne diseases, Finland, 2016

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Background

Tick-borne encephalitis (TBE) and Lyme borreliosis (LB) are endemic in Finland with tens and thousands of cases, respectively, reported annually. We performed a field survey to investigate people's knowledge, attitudes and practices (KAP) regarding ticks, tick-borne diseases, and prevention strategies.

Methods

The KAP were assessed using a pre-validated anonymous questionnaire consisting of 39 questions and statements in the cities of Parainen and Kotka, located in high-risk areas of tick-borne diseases, particularly of TBE. On two consecutive days in July 2016, individuals were approached and invited to participate in the survey. In attitudes and practices sections, each question was scored and analysed with ordered logistic regression model.

Results

In total, 101 individuals responded for a response rate of approximately 80%. The TBE vaccination rate among respondents was 40%. The best known preventive measures were having vaccination against TBE (88%), and wearing long sleeves and pants against ticks (81%). Two-thirds incorrectly identified the ring-like rash as a TBE symptom. Of all respondents, 78% incorrectly thought that TBE can be treated with antibiotics; 55% that vaccine protects against LB; and 46% that it protects against ticks. The minority (14%) believed tick repellents to be effective. Quick removal of an attached tick was most frequently applied (97%) preventive behaviour. Repellents were used by 21% when visiting tick-infested areas. Significant associations were found between the vaccinated status and having a correct belief that the vaccine protects against TBE ($P<0.001$) but not against ticks ($P<0.05$), or LB ($P<0.001$).

Conclusion

In areas at high-risk of LB and TBE, we identified a number of gaps in knowledge and misbeliefs. Our results improve public health communication tools on tick-borne diseases, especially those on intervention strategies.

Keywords: tick-borne diseases, tick-borne encephalitis, knowledge, attitudes, practices

ABSTRACT ID: 763

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B 10.6 Lyme borreliosis in Germany: description of surveillance data 2013-2016

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Background

Lyme borreliosis (LB) is a tick-borne disease with high public interest presenting with different clinical manifestations. In 9/16 German federal states, notification of the three most common forms (erythema migrans (EM), neuroborreliosis (NB) and lyme arthritis (LA)) is mandatory. We describe surveillance data in order to allow an estimation of disease burden, detect trends and to identify risk groups and high-incidence regions.

Methods

We used cases of clinical EM, symptomatic laboratory-confirmed NB and LA and LB without specified manifestation notified in the 9 federal states, 2013-2016, to calculate incidence and incidence rate ratios (IRR) by time, place and person.

Results

Altogether, we observed 45,181 cases. Disease onset peaked yearly in July/August. Incidence decreased from 41/100,000 in 2013 to 26/100,000 in 2015, then increased again to 38/100,000 in 2016.

Mean annual incidence was slightly higher in eastern than western Germany (IRR=1.06, 95% confidence interval 1.04-1.07) with marked regional variations on district level (range 0.5-138/100,000).

Median age of cases was 54 years with peaks in boys (5-9 years, mean incidence 36/100,000) and women (50-69 years, mean incidence 56/100,000). 42,312/44,564 with known manifestation (95%) experienced EM only, 2,275/44,564 (5%) had severe forms (1,256/44,564 (2.8%) NB and 1,019/44,564 (2.2%) LA). Overall 54% were female, but more men had extra-cutaneous manifestations (NB (56%) and LA (52%), $p<0{,}001$). Hospitalization was recorded for 1,589/38,097 (4.3%; 778/1,158 (68%) of NB and 78/877 (8.9%) of LA).

Conclusion

LB is frequent in Germany, with a high proportion of NB-cases requiring hospitalization. Health authorities should promote prevention strategies among the general population (tick-bite-protection, prompt tick removal and early medical consultation) with communication strategies tailored to identified risk groups and raise awareness among physicians to facilitate early diagnosis and treatment.

Keywords: Lyme borreliosis, surveillance, Germany

ABSTRACT ID: 989

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Track 11: Food- and waterborne diseases and zoonoses (2)

B 11.1 Shigatoxin producing Escherichia coli O103:H2 outbreak after school trip to Austria due to raw cow milk at a hotel buffet, 2017

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Background

Following a school ski-trip to Austria from 11-18/02/2017, 10/25 participants developed gastroenteritis. The group from Lower Saxony (Germany) shared meals in a hotel.

Methods

We conducted a retrospective cohort study using a self-administered questionnaire on clinical symptoms and food consumption, calculating attack rates (AR) and relative risks (RR). We defined cases as trip participants presenting with diarrhoea or vomiting 10/02/17-25/02/17 and/or laboratory-confirmed shiga-toxin-producing Escherichia coli (STEC). Stool samples of all participants, samples of milk served in the hotel and from the milk delivering dairy farm were examined by polymerase-chain-reaction and typed using pulsed-field-gel-electrophoresis (PFGE) and Next-Generation-Sequencing (NGS). Environmental investigations at the hotel were carried out by the Austrian authorities. Active case finding was recommended to public health institutes in other German federal states with visitors to the same hotel in February.

Results

All 25 participants completed the questionnaire; 14 were cases (AR=56%) with disease onset 17-19/02/2017 (13/22 students, 1/3 teachers). Eight of 14 (57%) were female; 13/20 participants who had consumed cold milk fell ill (RR=3.25; 95%-confidence-interval=0.55-19.32). Twelve of 25 stool samples were STEC-positive. Shigatoxin1a-gene and eaeA-gene positive STEC:O103:H2 were detected in 8/12 patient's stool samples (6/8 identical PFGE- and NGS-patterns) and 2/18 dairy farmcattle (2/2 same PFGE-pattern). Unlabelled raw milk had been offered at the hotel during February 2017. Two other federal states reported gastroenteritis in at least 45/266 visitors to the same hotel, one of them with the outbreak strain.

Conclusion

Microbiological evidence identified raw milk as the vehicle, supported by food history. Cases may have been misclassified due to the short period of pathogen-excretion. Austrian authorities obligated the hotel to provide exclusively pasteurised milk. We recommend re-emphasizing the risk of raw milk consumption to providers.

Keywords: STEC, retrospective cohort study, raw milk, PFGE, NGS

ABSTRACT ID: 1002

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B 11.2 Mapping of control measures for STEC infections in Europe, 2016. How can we reduce the burden of unnecessary public health measures following-up STEC cases?

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Background

In Norway, strict control measures have been implemented for STEC cases belonging to risk groups for transmitting the disease, requesting clearance after 3-5 negative specimens. In 2013, the introduction of culture independent diagnostics increased the number of laboratory-confirmed cases, including less virulent strains. In 2016, we reviewed control measures for STEC cases implemented by public health institutes in EU/EEA countries to revise the recommended control measures for cases in Norway.

Methods

We interviewed public health experts from these institutes, responsible for STEC guidelines, using a semi-structured questionnaire and revised the respective guidelines in Norway. Respondents (31 EU/EEA countries) were invited through the Food- and Waterborne Diseases and Zoonoses network organized by ECDC.

Results

All 14 participating countries (response 45%) reported using isolation and PCR for routine testing of STEC. All tested for shiga toxin-1(stx1), stx2 and eae. Five (36%) countries differentiated control measures for cases belonging to risk groups based on clinical and microbiological disease characteristics. Only Denmark differentiated control measures based on routinely conducted subtyping. In all countries, but Norway, clearance was obtained with <=3 negative specimens. After this review, the revised guidelines in Norway recommended control measures and follow-up only for cases infected with virulent STEC strains associated with haemolytic uremic syndrome (HUS) and obtaining clearance with 3 negative specimens.

Conclusion

The study assisted the revision of the guidelines which will lead to a decrease of the number of STEC cases needing clearance, reducing the socioeconomic impact on cases and their families (including paid sick leave for parents/workers, children excluded from kindergarten). We recommend continuing follow-up only of cases caused by virulent strains able to cause HUS to reduce the burden of unnecessary public health measures.

Keywords: STEC,virulent strains, control measures, guidelines, European

ABSTRACT ID: 1012

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B 11.3 Review of infectiousness and infectious period of shiga toxin producing E. coli

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Background

Shiga toxin producing Escherichia coli (STEC) cause gastroenteritis. The O157 and 'big six' serotypes are associated with outbreaks and haemolytic uremic syndrome (HUS). Secondary infections of STEC can occur by person-to-person transmission. To prevent secondary transmission the Dutch Public Health Services have constituted guidelines for the exclusion of people infected with STEC from school or work. Current guidelines are based on literature published before February 2008. Meanwhile new diagnostic methods have come to a rise which may lead to new insights regarding infectiousness and infectious period of STEC in general or of certain serotypes.

Methods

A review of literature published between 1 January 2006 and 31 December 2016 was performed in PubMed. Infectiousness and infectious period of STEC were assessed using secondary attack rate and shedding time as proxies.

Results

Of 1107 non-duplicate articles 54 full text articles were included. The most common STEC serotypes described were O157 (n=35) and O26 (n=14). 22 studies provided data on shedding period. Shedding time ranged between 1 and 237 days. The median overall shedding time was 30 days. Two studies found an increased shedding time in children compared to adults. Two studies concerning serotype O104 describe a shorter shedding time after antibiotic treatment. Four studies described intermittent shedding. Secondary transmissions were discussed in 35 studies. Of 21 studies detailed data was available. The secondary attack rate ranged from 2% to 62% with a median of 12%. In outbreaks in which the majority of primary cases were children more secondary cases occurred.

Conclusion

These findings supply evidence to exclude children, infected with O157 and other known STEC pathotypes, from school or daycare. Intermittent shedding underscores the need for consecutive negative stool samples.

Keywords: "shiga toxin", "escherichia coli", "shiga-toxigenic escherichia coli", "Disease Transmission, Infectious", "Disease Outbreaks"

ABSTRACT ID: 847

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B 11.4 Exposure to Campylobacter and associated risk factors: a comparison of three approaches for analyzing serological data from population-based studies

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Background

Although campylobacteriosis is the most-reported zoonosis in Europe, it is generally accepted that reported cases represent a fraction of the true burden of infection, and may not fully capture risk factors. Serosurveys can characterise population exposure, but we lack optimal cut-offs for Campylobacter serological assays. We aimed to estimate population-level exposure to Campylobacter and associated risk factors in the Netherlands, using three innovative approaches.

Methods

We conducted a population-based cross-sectional serosurvey in the Netherlands from February 2006-June 2007, including an epidemiological questionnaire. Anti-Campylobacter spp. IgG, IgM and IgA were measured using ELISA, and analysed using three different modelling approaches: a) seroincidence estimation, using reference values of antibody peak levels and decay over-time after Campylobacter exposure; b) two normal distributions of true positives/negatives fitted to the log-transformed IgG distribution to derive seroprevalence and the individual probability of being positive/negative; and c) log-transformed IgG levels. Multiple linear regressions were used to analyse risk factors using the three alternative methods.

Results

From 1559 respondents, seroincidence was estimated at 1.61 infections/person-year (95%CI: 1.58-1.64) and seroprevalence at 68.1% (65.4-70.9). The three approaches identified similar risk factors, although seroincidence had narrower confidence intervals and results could be interpreted in terms of risk: risk was higher in females [exp(b)=1.07(1.04-1.11)], older ages [vs. 15-34 years; for <5, 5-14, 35-54 and 55-70 years: 0.60(0.58-0.63), 0.74(0.71-0.78), 1.08(1.03-1.13) and 1.08(1.01-1.16), respectively], non-Dutch background [Moroccan/Turkish: 1.25(1.14-1.37); Caribbean: 1.14(1.03-1.25)], low socioeconomic status [1.05(1.01-1.10)], ever travelling outside Europe [1.05(1.01-1.09)], and eating undercooked meat [1.04(1.01-1.08)].

Conclusion

Campylobacter exposure estimated here is much higher than infection rates shown by clinical studies, but risk factors are similar to those previously described. The three methods yielded comparable results, although the seroincidence approach provided more precise estimates.

Keywords: Campylobacter, Serology, Incidence, Prevalence, Risk Factors

ABSTRACT ID: 839

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B 11.5 Cholera suspected cases analysis occurring in the Commune of Baradères, February 2017.

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1. Publick Health Ministry and Population

Background

Cholera is an acute global diarrheal disease, two serogroups responsible for Vibrio cholerae “O1” and “O139”. The contamination is by fecal-oral route and most of the time the infected persons are asymptomatic, treatment can be done by oral rehydration salt. According to a WHO estimation, each year the world faces to 1.3 by 4 million cholera cases and 21 000 by 143 000 deaths. A case-fatality rate of 0.76% has been observed for 172,454 cases reported by 42 countries in 2015. Since October 2010, Haiti has had an overall case-fatality rate of about 1.18% and a prevalence of 7.2%. This study aims to analyze the link between the consumption of Binard source’s water and cholera suspected cases admitted to Baraderes’ center in February 2017.

Methods

This is a case-control analytical study of cholera suspected cases admitted to the Baraderes UTC. The demographic and clinical variables, as well as the evolution of the suspected cases and the source of the Vibrio Cholerae are collected and analyzed using Excel 2010, Epi Info 7.2.

Results

The investigation focused on 70 people, including 47.14% Men and 52.86% Women, the average age is 27 years. 35 of the investigated were suspected of having cholera, the under 10 years with 34.3% were the most affected. The P-value “p = 0.046 ‹0.05”, the risk of contracting the disease was 4 times higher in cases than Witnesses.

Conclusion

People who have consumed Binard source’s water were 4 times more exposed than those who do not, it would be kind that access of drinking safe water and sanitation facilities to be available for the residents.

Keywords: Cholera, Suspected,Cases, Analysis

ABSTRACT ID: 752

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B 11.6 Investigation of long-term sequelae among sporadic cryptosporidiosis cases in the Netherlands, 2013-2016.

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Background

Cryptosporidium is a food and waterborne parasite that causes moderate to severe diarrhoea and has been linked with the development of reactive arthropathies. During a three-year case-control study in the Netherlands to identify risk factors for sporadic cryptosporidiosis, we also carried out a follow-up study among cases in order to identify long-term sequelae of Cryptosporidium infection.

Methods

In the case-control study we included cases who were laboratory confirmed. They were invited to complete a follow-up questionnaire four months after diagnosis. We compared the frequencies of reported symptoms four months after diagnosis to those reported four months before and during illness and calculated odds ratios (OR) using logistic regression adjusting for age, sex, study year and Cryptosporidium species.

Results

Of 906 cases available for inclusion, 443 (49%) responded. After exclusion for recent travel and key missing data, 237 (26%) were included in the analysis. Median age was 20 years (range 1-80); 59% were female and 41% male; 28% determined as C. hominis and 72% as C. parvum. Commonly reported symptoms four months after diagnosis included fatigue (52%), diarrhoea (43%) and abdominal pain (40%), while 18% reported joint pain, mostly in the knee (11%), fingers (6%) or shoulders (6%). Compared to before illness, cases were more likely to have dizziness (OR=2.61; 95%CI:1.60-4.25), headache (OR=2.23; 95%CI:1.54-3.24), eye-pain (OR=2.12; 95%CI:0.93-4.85), joint pain (OR=1.84; 95%CI1.21-2.81), fatigue (OR=1.8; 95%CI:1.37-2.37), weight loss (OR=1.73; 95%CI:1.10-2.72) or diarrhoea (OR=1.47; 95%CI:1.07-2.03).

Conclusion

Our results demonstrate that the disease burden following cryptosporidiosis extends beyond the acute disease period with cases reporting intestinal and extra-intestinal symptoms up to 4 months following infection. Cryptosporidiosis should be considered as a possible diagnosis for people with protracted symptoms following an acute diarrheal illness.

Keywords: Cryptosporidium, case-control studies , long term sequela, the Netherlands;

ABSTRACT ID: 867

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Track 12: Hepatitis A in MSM

B 12.1 Cluster of hepatitis A cases among men who have sex with men in Malta, 2017

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Background

Since February 2016, the number of cases of hepatitis A virus (HAV) infection among men who have sex with men (MSM) has been increasing in Europe. In February 2017, the Infectious Disease Prevention and Control Unit (IDCU) in Malta detected the first case of HAV among MSM. We investigated to identify the likely route of transmission and implement control measures.

Methods

Confirmed HAV cases are routinely reported to the IDCU. We defined cases as MSM with positive anti-HAV IgM since 01/01/2017 with reported sexual activity 50 days prior to disease onset. We traced close sexual contacts of cases and actively followed them up by offering HAV vaccination and advice on prevention and control measures.

Results

Between January and March 2017, three cases of HAV infection were identified in MSM, all of whom were epidemiologically linked. Their ages ranged from 35–38 years; all required hospitalisation. The index case travelled to Italy one month before symptom onset and had sex with multiple partners at a swimming pool party. The second case was a sexual contact of the index case and the third was a sexual contact of the second case. The third case had another sexual contact who did not get infected as he was vaccinated against HAV. None of the cases had practiced safe sex or were vaccinated against HAV.

Conclusion

Sexual transmission among MSM was the most likely route of infection. This outbreak highlights the need for raising awareness about the risk of sexual transmission of HAV among MSM. We recommend conducting cross-sectional studies to identify knowledge and risk behaviours contributing to HAV infection and estimate HAV vaccination coverage among MSM in Malta.

Keywords: Hepatitis A virus, Malta, Disease Outbreaks

ABSTRACT ID: 762

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B 12.2 Adapting national guidance to control a community outbreak of hepatitis A in an area of low endemicity, Wales, 2016

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6 On behalf of the Outbreak Control Team

Background

Incidence of hepatitis A in Wales is low (annual incidence 0.48/100,000 2004-15). Around 70% of infected children are asymptomatic. We describe a community outbreak of hepatitis A involving 3 schools (primary and secondary) in South Wales between March and June 2016 and reflect on the adequacy of the control measures used.

Methods

We defined a case as anyone in South Wales epidemiologically linked to a serological and/or RNA positive confirmed case of hepatitis A during the 15-50 days before onset of symptoms (diarrhoea, vomiting, fever, nausea, AND jaundice, or jaundice-associated symptom). Cases were reported by laboratories and GPs (notification on suspicion). We offered household and primary school contacts immunisation as per national guidance; later on we offered vaccination to street-friends and secondary school contacts. We calculated mass vaccination uptake.

Results

Seventeen cases were identified, 71% in children under 16. All cases had an epidemiological link to either a school or a household case (excepting the earliest case) and no travel history. Street-friends were the only epidemiological link between 2 cases in different schools. 139 household contacts were identified. All schools had a transmission event preceding whole-school vaccination (overall uptake 85%, reaching 1,574 individuals. The last case occurred 13 days after school vaccination intervention in school attended, indicating interruption of transmission.

Conclusion

We recommend extending guidance to include actions taken that helped curb this outbreak: 1) vaccinating in secondary school and 2) broadening the household contact definition to include street-friends. Based on our learning we further suggest 3) vaccinating upon identification of a single case who attended school whilst infectious regardless of source, so that transmission is promptly interrupted.

Keywords: Hepatitis A, outbreak, schools, immunisation

ABSTRACT ID: 1052

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B 12.3 Investigation of a Hepatitis A Outbreak amongst MSM in Berlin

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8. Institut für Mikrobiologie und Hygiene Regensburg, Germany

Background

Hepatitis A (HAV) vaccination is recommended and free for individuals at increased sexual risk in Germany. An ongoing outbreak of HAV in Berlin is predominantly affecting men who have sex with men (MSM): 107 confirmed cases were reported among individuals 18 years or older, from week 46/2016 to 18/2017, and 92% were male. We investigated this outbreak to describe the population affected and identify potential strategies for intervention.

Methods

Cases were defined as individuals aged ≥18years, with laboratory confirmed HAV notified in Berlin since week 46/2016. We conducted telephone interviews on exposures, vaccination history and barriers to care. Diagnostic specimens were submitted for genotyping. A survey on vaccination practices was mailed to specialist healthcare providers.

Results

Of 44 cases interviewed, median age was 32 (interquartile range 29-40.5), 61.4% foreign-born, 97.7% male, and 95.5% MSM, 39.0% of MSM were HIV-positive. Most had health insurance (93.2%) and a regular healthcare provider (90.9%). Cases were unvaccinated (79.5%), incompletely vaccinated (9.1%), had unknown vaccination history (9.1%) or vaccinated following exposure (2.3%). Of unvaccinated cases, 61.7% were unaware of recommendation. Amongst MSM, 88.1% reported multiple sexual partners and 76.2% had anonymous partners in the 8 weeks before symptom onset.

Genetic analysis of all outbreak cases with samples submitted found 3 distinct clusters of known MSM-related hepatitis A strains (RIVM-HAV16-090 28.4%, V16-25801 38.6%, VRD-521-2016 33.0%).

Physician respondents (n=43 of 60) reported 93% provided HAV vaccine for MSM, and 93% were aware of MSM vaccination recommendation.

Conclusion

Cases were unvaccinated despite good access to healthcare, free vaccination and physicians providing vaccination for this target population. Strategies to address this include providing targeted information to both MSM and physicians, to ensure vaccination completeness.

Keywords: Hepatitis A, Disease Outbreaks, Homosexuality male, Vaccination, Epidemiologic methods, Germany

ABSTRACT ID: 994

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B 12.4 Outbreak of hepatitis A associated with men who have sex with men (MSM), July 2016 to April 2017

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Background

In July 2016, Public Health England detected three new genotype IA HAV strains primarily infecting men who have sex with men (MSM). We describe the outbreak and the public health actions implemented to prevent further transmission.

Methods

A confirmed case was an England resident with HAV infection with one of the specific outbreak sequence and symptom onset after 31 June 2016. A probable case a laboratory-confirmed HAV infection with contact with a confirmed case and/or who identifies as MSM. Demographics, travel and sexual history were collected using questionnaires.

Results

Up to April 2017, 215 confirmed cases and 48 probable cases were reported across England, of which 64% in London and 74% among MSM; 31% reported travel, 57% were hospitalised and no deaths were reported. Median age was 32 years (range 10-78). MSM cases had a median of 2 sexual contacts (range 1-41) and 85% of contacts were anonymous or casual. Of all MSM cases, 33% used dating apps to meet partners and 43% used a public venue for sexual contact.

Conclusion

The outbreak, occurring in the context of related hepatitis A outbreaks among MSM in Europe, has extended beyond MSM and led to a near doubling of hepatitis A incidence in England compared with the same period in the previous year. Investigations suggest initial multiple importations were followed by endemic transmission in the England MSM population. A high proportion of anonymous sexual partners and dating apps have likely amplified the outbreak. A communications campaign via web and sexual health services has raised awareness and promoted safe sexual practice. MSM vaccination has been prioritised but is hampered by global shortages of hepatitis A vaccine.

Keywords: hepatitis A, outbreak, sexually transmitted infections

ABSTRACT ID: 1053

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Track 13: Sexually transmitted infections (STI)

B 13.1 Increase of positivity rates of Neisseria gonorrhoeae and Chlamydia trachomatis infections among men and women in France, 2001-2015

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Background

In France, surveillance of Neisseria gonorrhoeae (NG) and Chlamydia trachomatis (CT) infections is based on voluntary networks of laboratories, which were estimated, in 2012, to cover 23% of NG and 18% of CT infections. The aim of this study is to describe positivity rates of NG and CT infections between 2001 and 2015.

Methods

Biologically confirmed cases and the total number of diagnostic tests are reported each year at the French national public health agency. We calculated positivity rates by sex as the proportion of individuals diagnosed positive. Chi-squared test was used to analyse trends over time.

Results

Between 2001 and 2015, the NG positivity rate among men was 4.29% (95% confident interval [CI]:3.95-4.63%). It rose from to 1.92% to 7.29% between 2001 and 2011 and felt to 3.90% in 2015 (p-value=0.02). Among women, this rate was 0.15% (95%CI: 0.04-0.27%). It increased from 0.02% in 2001 to 0.6% in 2015 (p-value<0.0001). Over the same time period, the CT positivity rate was 6.22% for men (95%CI: 5.95-6.49%). It doubled from 3.18% in 2001 to 6.50% in 2015 (p-value=0.001). Among women, the CT positivity rate was 5.87% (95%CI: 5.69-6.05%) and increased constantly from 2.83 in 2011 to 6.60% in 2015 (p-value<0.0001).

Conclusion

Despite CT screening recommendations targeting young women and men visiting STI clinics since 2004, CT and NG infections positivity rates rose significantly between 2001 and 2015 for men and women. This could be explained by the increase screening for CT in high risk population combined with the use of nucleic acid amplification tests and by a real augmentation of incidence. Systematic screening should be expanded to main sexually transmitted infections in any health care facilities or general practitioners.

Keywords: Chlamydia trachomatis, bacterial infections, Sexually Transmitted Diseases, Neisseria gonorrhoea

ABSTRACT ID: 1037

PRESENTED BY: Nelly Fournet (nelly.fournet@santepubliquefrance.fr)

B 13.2 Changing epidemiology of penicillinase producing Neisseria gonorrhoeae in England and Wales, 2007-2015

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Background

A previous study of the Gonococcal Resistance to Antimicrobials Surveillance Programme (GRASP) found that 27% of penicillinase-producing Neisseria gonorrhoeae (PPNG) harboured the TEM-135 enzyme. TEM-135 is one amino-acid substitution from an extended-spectrum β-lactamase (ESBL); ESBLs are active against cephalosporins which are the last line treatment for gonorrhoea. This analysis examined trends and risk factors associated with PPNG.

Methods

GRASP is a sentinel surveillance programme which collects consecutive N. gonorrhoeae isolates from patients attending 27 specialist sexual health clinics in England and Wales. PPNG was defined as any β-lactamase positive isolate. A test for trend was carried out for the proportion of all isolates with PPNG between 2007 and 2015. Multivariable logistic regression was used to identify risk factors for PPNG stratified by year.

Results

Between 2007 and 2015, the proportion of all isolates that were PPNG increased two-fold (7.6% vs. 15.6%; p<0.001). In 2007-2013, the odds of isolating PPNG were higher in heterosexual men (aOR 2.76; 95% CI: 2.08-3.67 vs. men who have sex with men-MSM), with increasing age (aOR 1.03 per year increase; 95% CI: 1.02-1.04), and in those reporting recent sex abroad (aOR 3.67 95% CI: 2.85-4.71). In 2014-2015, the odds of isolating PPNG were higher in MSM (aOR 1.69; 95% CI: 1.10-2.61 vs. heterosexual men), those of black African ethnicity (aOR 2.23; 95% CI: 1.24-4.02, vs. white ethnicity), and those with HIV positive status (aOR 1.49; 95% CI: 1.13-1.97).

Conclusion

PPNG has increased since 2007 and after 2014 PPNG isolates were no longer associated with recent sex abroad suggesting more local transmission. There is a need to improve health promotion among HIV-positive MSM to reduce spread of PPNG and the potential of ESBL emergence.

Keywords: Neisseria gonorrhoeae, Penicillinase, Cephalosporins, HIV Seropositivity, Homosexuality Male, Health Promotion

ABSTRACT ID: 857

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

B 13.3 Evaluating of the impact of non-participation to infectious disease prevalence estimation in a population based study among migrants in Finland

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Background

Migration influences the epidemiology of infectious diseases in many European countries, including Finland. Since 1995, all cases of hepatitis B and C, syphilis, HIV and tuberculosis (TB) have been recorded to the National Infectious Diseases Register (NIDR). We aimed to assess the feasibility of communicable diseases prevalence estimation in a migrant population based study.

Methods

The prevalence and risk factors for hepatitis B and C, syphilis, HIV and TB were evaluated in the migrant population based health interview and examination survey in Finland in 2010-2012. Screening for hepatitis B and C, syphilis and HIV was offered during the health check-up. A random sample of 3000 migrants of Kurdish, Russian or Somali origin was invited to participate. Those 2173 who had immigrated 1995 or after were included in the analyses. Linkage of the sample to the NIDR enabled the evaluation of the impact of non-participation.

Results

Altogether 1420 migrants (65.3%) participated to the study. The notification rate for TB was significantly higher among the non-participants (2.0%) than the participants (1.6%) (p=0.03). No differences in the notification rates of neither hepatitis B nor C, HIV nor syphilis were observed. Among those who accepted testing, the prevalence of hepatitis B was 2.3%, hepatitis C 1.6%, syphilis 1.2% and HIV 0%. The proportion of new diagnoses was 53% of the hepatitis B, 62.9% of the hepatitis C and 88.2% of the syphilis cases.

Conclusion

Migrant population based surveys are feasible to estimate infectious diseases prevalence and risk factors. Non-participation did not influence the prevalence estimation with the exception of TB. More research is needed to understand how TB related stigma influences the decision to participate to a health surveys.

Keywords: communicable diseases, prevalence, transients and migrants

ABSTRACT ID: 810

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B 13.4 External quality assessment (EQA) of serologic tests for syphilis (STS) among 23 Norwegian laboratories, 2015

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Background

Norway has neither a syphilis reference laboratory nor a national periodical STS EQA programme. However, in May 2015 STS were included in the first round of the biannual general virology/serology EQA programme from the NIPH. Performance and inter-laboratory comparability were assessed, in order to improve diagnostics and surveillance.

Methods

The EQA scheme was distributed to 23 laboratories, most of which only perform STS screening themselves. Four serum samples were distributed blindly on dry ice, including two samples from patients with recent syphilis infection, one sample from a patient with remote infection and one negative sample. The laboratories were asked to analyse the panel with their standard STS methodology and return results with interpretation and comments.

Results

22/23 laboratories returned results. The laboratories used three different syphilis total antibody chemiluminescence immunoassays for screening, and the qualitative results were fully concordant. Qualitative results from testing with TPPA (Treponema pallidum particle agglutination assay) or TPHA (Treponema pallidum haemagglutination test) (n=5) were concordant, except for the remote infection sample, where only two laboratories reported concordant results. Quantitative results for Rapid Plasma Reagin (RPR) testing (n=6) were discordant for both RPR reactive samples, with a reported titre range of 4-32 and 2-16, respectively.

Conclusion

Results from confirmatory testing of remote infection with TPPA/TPHA varied between laboratories. RPR testing results were up to eightfold different. We highly recommend that initial and follow-up RPR testing after syphilis treatment are performed at the same laboratory. Preliminary results from this first round of syphilis EQA indicate the need for a reference laboratory, a regular syphilis EQA programme and training of laboratory personnel in TPPA/TPHA/RPR testing, in order to improve consistency for diagnostics and surveillance.

Keywords: Syphilis,Syphilis Serodiagnosis,Laboratory Proficiency Testing,Clinical Laboratory Techniques,

ABSTRACT ID: 1075

PRESENTED BY: Rikard Rykkvin (rikryk@gmail.com)

Track 14: Vaccine- preventable diseases (2)

B 14.1 Vaccine confidence among mothers of young children in Slovenia

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Background

High public and parental confidence is important to maintain vaccination coverage needed for community-level protection against vaccine preventable diseases. Declining trends in vaccination coverage and the rise of anti-vaccine movements are a call for better monitoring of vaccine confidence to inform the development of communication strategies and address confidence gaps.

Methods

We conducted the first nationwide cross-sectional survey to measure and characterize vaccine confidence among mothers of children <2 years old in Slovenia and its relation to confidence in different sources of information about paediatric vaccinations. The sampling frame included women registered in national Perinatal Information System giving birth in 2014-2015 (N= 39,497).

Results

We sent out 3,854 questionnaires, the response rate was 44.4%. While 46.8% (95% confidence interval (CI): 44.4-49.2%) mothers were vaccine confident, 34.2% (95% CI: 32.0-36.6%) were undecided. We found a correlation (Spearman's rho= 0.457) between vaccine confidence and confidence in the child's paediatrician. Mothers that were confident in paediatrician were more likely to be vaccine confident (odds ratio: 7.7; 95% CI: 5.3-11.3). Physicians were most frequently reported trusted information source among vaccine confident and undecided (97.6%; 95% CI: 96.2-98.5% and 87.5%; 95% CI: 84.5-90.1% respectively). Among mothers who were completely vaccine not confident less than one-third expressed trust in any information source examined other than their friends (51.9%; 95% CI: 43.1-60.6%).

Conclusion

Low vaccine confidence observed and marked proportion of undecided could in the future influence vaccination coverage and require public health intervention. Communication strategies and activities should first address this group and be focused on paediatricians as the most trusted source with positive association to vaccine confidence. Not confident mothers require alternative strategies to be considered.

Keywords: vaccines, vaccine confidence, Slovenia

ABSTRACT ID: 991

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B 14.2 Timing of receipt of primary immunisations in London and factors influencing late receipt

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Background

In order to maximise population protection vaccines should be administered on time to a high proportion of the population. The UK primary course that protects against diphtheria, tetanus, pertussis, polio and Haemophilus influenzae type b (DTaP/IPV/Hib) is scheduled at 2, 3 and 4 months of age. We measured timeliness of receipt, and whether this was influenced by ethnicity or deprivation.

Methods

We extracted vaccination history for 315,381 children born March 2001 to April 2010 from Child Health Information Systems in nine London health service areas. We determined and compared mean age of completion amongst ethnic groups and deprivation quintiles.

Results

Overall, 257,596/311,002 children (82.8%) had completed the primary series by one year and clear peaks were observed at 2, 3, and 4 months for receipt of each dose. Among children completing by one year, average completion age was 146 days (4.8 months) and varied by 28 days between earliest (Vietnamese/Chinese) and latest (Somali) ethnic groups and 6 days between earliest (least deprived) and latest (most deprived) deprivation quintiles. Of the 53,406 children 'not completely vaccinated' by one year, 35,163 (65.8%) had not started the primary course. Ethnic groups previously identified as having lowest vaccination coverage (Polish, Nigerian, Somali) had greatest proportions (>67%) of completely unvaccinated children (relative to those who had received one or two doses).

Conclusion

In London, the majority of primary vaccinations received within one year of age were given according to schedule regardless of ethnicity or deprivation. While those who initiate vaccination receive their doses on time, identifying and vaccinating children who have not started their primary course is necessary to improve coverage in ethnic groups with lowest vaccination coverage.

Keywords: vaccination, immunisation, ethnicity, deprivation, timing, late

ABSTRACT ID: 865

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B 14.3 Is it possible to reach midwifes through educational trainings about vaccination offered by scientific and medical experts?

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2 Bavarian State Ministry of Health and Care (StMGP)

Background

As previous studies showed, the midwifes' attitude towards vaccination can affect the attitude of the expectant mother. It is therefore important that midwifes are well informed about the vaccination recommendations. The Bavarian Midwifes Association is an important member in the independent Bavarian Immunisation Network (LAGI), which includes furthermore public health service, medical practitioners, medical associations, scientists, health insurances and pharmacists.

Methods

LAGI established a gratuitous regular educational training for midwifes to provide information about current vaccination recommendations. Main topics are vaccinations for children, women and medical staff including possible and discussed side-effects and myths. All referees are members of LAGI: a paediatrician, a gynecologist and a professor of microbiology. Participants get educational credits and evaluate the course.

Results

The training courses are offered twice a year in different parts of Bavaria since 2014, with about 30 to 40 participants per class. Evaluations indicate a brought acceptance of the course. In the last class 100% of midwifes were satisfied with the performance of all referees, 74% even rated it as good to very good. Furthermore, 100% agreed, that the course was well prepared and organised, but 11% indicated, that learning success could be increased by stronger involving participants, e.g. with exercises and group work. In the free text feedback, a few midwifes encouraged to take information provided by vaccine deniers more into account or to invite referees which are against vaccination.

Conclusion

The offered training courses are well attended. It seems important, that all organizing partners collaborate on the basis of mutual respect. Furthermore, based on the results of evaluations the future concept is augmented with further opportunities for active participation and additional focus on vaccine deniers' arguments.

Keywords: vaccination training midwifes

ABSTRACT ID: 1086

PRESENTED BY: Maria-Sabine Ludwig (maria-sabine.ludwig@lgl.bayern.de)

B 14.4 Association of vaccination coverage against diptheria in Latvian adults with primary health care factors

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2. EPIET Programme

Background

Diphtheria is a highly contagious communicable disease. More than 20 years Latvia has reported the highest average incidence in Europe. In 2014 the total number of confirmed diphtheria cases in Latvia among adults was 11, of which only two adults were vaccinated against diphtheria.

Methods

The aggregated data from the Center for Disease Prevention and Control cross-sectional research on Health Behavior among Latvian Adult Population 2014 were analysed. We used unadjusted (OR) and adjusted odds ratio (aOR) to identify factors associated with adult vaccination against diphtheria.

Results

According to the research in 2014 the vaccination coverage against diphtheria in adult population reached to 70.5%. Vaccination levels were higher in females 72.7% (95%CI 70.4-75.0) than males 68.0% (95%CI 65.5-70.3). Adults from rural areas are more than two times likely to have been vaccinated compared to the adults who are resident in capital city (OR 2.3, 95%CI 1.9-2.9). Visiting GP at least once during last 12 months increased the likelihood of being vaccinated (aOR 1.7, 95%CI 1.4-2.0) compared to adults who did not attend at all. Patients who expressed that GP practice working hours are convenient, are more likely (aOR 1.6, 95%CI 1.2-1.2.1) to be vaccinated. Individuals who found that it was easy to contact GP were more likely to be vaccinated (aOR 1.5, 95%CI 1.1-2.0). If the GP provided information about the importance of vaccination the likelihood of being vaccinated increased (aOR 3.9, 95%CI 3.1-5.1).

Conclusion

The vaccination against diphtheria in Latvian adult population is significantly associated to the primary health care management. The recommendations on vaccination communication needs to be improved in primary health care centers in Latvia, in accordance with international recommendations.

Keywords: Diphtheria, vaccination, adults, health behaviour, general practitioners

ABSTRACT ID: 946

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B 14.5 Interactive vaccination coverage maps – a multipurpose tool for programme monitoring and health system development

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Background

Finland is in the process of introducing a major administrative reform of health and social services. Measles-mumps-rubella (MMR) vaccination coverage in children was chosen as one of the indicators for comparing the performance of the newly formed counties' health systems. MMR is given twice within the National Vaccination Programme, i.e. at 12 to 18 months and 6 years of age.

Methods

Vaccination coverage, the percentage of vaccinated in a population, is monitored in real-time through the National Vaccination Register and can be calculated also on sub-national levels. The target population depends on the vaccine of interest. So far, MMR coverage has been estimated in two-year-olds. In future, MMR coverage will be also monitored for seven-year-olds.

Results

Vaccination coverage varies over time and differs markedly between regions. While on average 95% of the two-year-olds were vaccinated with MMR, sub-national figures range from <85% to 100%. To present the estimates in a clear and user-friendly way, interactive maps have been created: https://www.thl.fi/roko/rokotusrekisteri/atlas/atlas.html?show=infantbc. These maps show the vaccination coverage colour-coded on a county level, the national average, time trends, and tables with the underlying population count. Regional outliers can be easily identified and the performance of the counties' health systems can be directly compared using MMR coverage as one proxy to it.

Conclusion

The maps revealed that the national average is not useful for measuring a vaccination programme's success on a sub-national level. In contrast, county-specific figures arising from automated data collection and analysis processes are vital for the real-time monitoring of a vaccination programme's performance. They can be used for identifying pockets of low coverage, for targeting interventions, and for rewarding counties which manage to improve or maintain high coverage.

Keywords: measles-mumps-rubella vaccine, vaccination coverage, vaccination register, vaccination schedule

ABSTRACT ID: 1020

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B 14.6 Diseases and prenatal care of undocumented migrants 2016-2017 in Lower Saxony, Germany

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Background

In 2015, more than 1.2 million people applied for asylum in the European Union. An unknown number of undocumented migrants (UDM) is without residence permit for the country they currently live in. They are usually excluded from healthcare and surveillance systems. In 2016, a project to facilitate healthcare access for UDM for acute diseases, preventive services and prenatal care was implemented in Lower Saxony, Germany.

Methods

We analysed the first year of the project (February 2016-February 2017) by describing number of visits, socio-demographics and scope of diseases to identify special medical needs for consultations. Information about diagnoses and medical treatment was obtained from treating physicians using WHO International Statistical Classification of Diseases (ICD-10, German Modification).

Results

Visits increased over time from 3 to 11/month. Altogether, 108 UDM received 317 medical treatments. Median age was 30 years (range: 0-86), 16 (15%) were younger than 18 years and 50% were female. Most UDM were from Balkan countries (33%), Central Africa (22%) and the Middle East (18%). Acute symptoms resulted in 152/317 treatments (48%), predominantly toothache (n=29/317, 8%), medical check-up caused 21/317 (7%). Sexually transmitted infections (HIV, hepatitis and chlamydia) were diagnosed in 12/108 UDM (11%). Four of 108 UDM (4%) required hospitalisation. Twenty-one UDM (20%) asked for prenatal care (gestation week at first visit: 10-36, median=27).

Conclusion

Over time, UDM increasingly used the services of the project. Over 1/3 UDM belonged to particularly vulnerable groups (pregnant women, children<18y) that would otherwise miss out on medical care and prevention (e.g. prenatal care, immunisation). We recommend extending the project in time and place to build trust with hard-to-reach people and strengthen prevention, detection and treatment of communicable diseases.

Keywords: undocumented migrants, cross-sectional study, prenatal care, medical check-up

ABSTRACT ID: 979

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Track 15: Influenza and other respiratory viruses (2)

B 15.1 Predominance of influenza A(H3N2) virus genetic subclade 3C.2a1 during 2016/17 influenza season in Europe

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2. World Health Organization (WHO) Regional Office for Europe
3. Influenza Surveillance Network of the WHO European Region

Background

The influenza season 2016/17 in Europe was dominated by A(H3N2) viruses. Recent reports have indicated genetic heterogeneity of circulating A(H3N2) viruses and diversification of the haemagglutinin (HA) gene from the current vaccine virus A/Hong Kong/4801/2014 (clade 3C.2a). Estimated mid-season A(H3N2) vaccine effectiveness (VE) was 38% for all age groups in Europe. We analysed circulating A(H3N2) viruses to compare them with the current vaccine virus and to explore reasons for suboptimal VE.

Methods

Virological surveillance data reported to ECDC from week 40/2016 to week 5/2017 by the national influenza centres (NICs) from 24 countries of the WHO European Region were used to analyse the genetic and antigenic characteristics of the circulating influenza viruses. Antigenic data were obtained by haemagglutination inhibition assays. Available haemagglutinin (HA) sequences were analysed phylogenetically to compare them with the vaccine virus.

Results

1,878 A(H3N2) viruses were analysed genetically and/or antigenically (n=1531 and n=601, respectively). All of the 918 sequenced A(H3N2) viruses carried amino-acid substitutions on antigenic and/or glycosylation sites of HA; 905 clustered in genetic clade 3C.2a, 667 of which fell in a newly emerged subclade 3C.2a1, and 13 in 3C.3a. However, limited available antigenic data showed no evidence of antigenic change.

Conclusion

We have detected wide circulation of a newly emerged 3C.2a1 subclade of A(H3N2) viruses in Europe. The HAs of circulating viruses are genetically diverse from the current vaccine virus and specific subclusters within 3C.2a1 accumulate amino-acid substitutions on antigenic sites. Simultaneous circulation of genetically diverse strains of A(H3N2) viruses may partly explain suboptimal VE estimates reported this season in Europe. More detailed antigenic data are needed to fully understand the effect of the virus evolution.

Keywords: influenza virus, amino acid substitution, Europe, vaccination

ABSTRACT ID: 812

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B 15.2 Estimating the disease burden and economic impact of seasonal influenza – Pilot of an online training tool for communities of practice.

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2. Global Influenza Programme, World Health Organization
3. Mirna Robert Epidemiology, Gorinchem, The Netherlands
4. Netherlands School of Public and Occupational Health, Utrecht, The Netherlands
5. VetPot Video & Graphics, Utrecht, The Netherlands
6. EconEpi, Hamburg, Germany
7. Transmissible, Houten, The Netherlands.

Background

Reliable estimates for disease burden and economic impact of seasonal influenza are needed for better understanding the impact of influenza in vulnerable populations, as a guide for evidence based policy.

The World Health Organization (WHO) has published two manuals for estimating disease and economic burden associated with influenza. Training of public health officers to appropriately use these manuals is vital. We designed, developed and implemented an online training tool, aimed to build an international community of practice for influenza burden estimates.

Methods

We developed a curriculum consisting of 10 epidemiological and 10 economical tutorials, based on the WHO manuals. The tutorials are embedded in the OpenWHO platform and are integrated with pre- and post-test elements, participant discussion forums, and online collaborative training assignments. The pilot training is planned in September 2017.

Results

Twenty participants from five countries are selected through a convenience sample, to participate in the pilot courses. At ESCAIDE we will present the average training workload, the ease of navigation, clarity of the video lectures, and the usefulness of the online discussion forums and tests. Key stakeholder opinions towards 'Community of Practice' will be described as well as the success rate of the online collaborative project for the training participants of the pilot.

Conclusion

Online learning platforms offer an increasing amount of training opportunities for public health. The pilot results will show to what extend our instructional design succeeded in stimulating active communities of practice, that train together to improve use and implementation of the WHO influenza burden of disease and economic burden manuals.

Keywords: Influenza, burden of disease, economic burden, online training, communities of practice

ABSTRACT ID: 942

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B 15.3 Impact of Influenza: Epidemiology of Seasonal Influenza in 0-14 Year Olds in the South East of Ireland 2010-2016

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Background

Influenza activity varies from year to year and can cause a significant burden of disease annually in Ireland. Outcomes in children with influenza are more severe than in adults. The aim of this paper is to provide an overview of the epidemiology of influenza in children in the South East of Ireland over a six year period and examine the impact on hospital admissions.

Methods

A retrospective descriptive review of seasonal laboratory confirmed cases of influenza over a six year period in the South East in 0-14 year olds was conducted. Hospitalisation rates, risk group and vaccination details were collated on the selected cohort. Data was extracted from the National Computerised Infectious Disease Reporting system, the South East Child Health System and the South East Hospital Patient Administration System .Descriptive analysis was performed using SPSS v22.

Results

There was a total of 624 seasonal laboratory confirmed influenza cases in 0-14 year olds in the South East between 2010-2016, which accounted for 35% of all South East confirmed cases over that time period. Three Hundred and twenty four (54%) cases in the 0-14 age group were admitted to hospital and 12 (4%) of these were admitted to ICU.

Conclusion

The availability of hospitalisation rates, risk group and vaccination details among children during the influenza season reflects disease burden and may be used to inform Irish Health Service winter planning.

Keywords: Influenza, Pediatrics, Epidemiology, Public Health Surveillance

ABSTRACT ID: 892

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B 15.4 The suitability of case definition for severe acute respiratory infection in recognising influenza and respiratory syncytial virus (RSV) infection in hospitalised Finnish elderly

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Background

The burden of influenza is high in elderly. The burden of respiratory syncytial virus (RSV) among different age groups is less clear. We evaluated the sensitivity and specificity of symptoms/signs belonging to case definition for severe acute respiratory infection (SARI) in recognising patients with influenza and RSV infection.

Methods

A test-negative case-control study to measure influenza vaccine effectiveness against SARI caused by influenza among elderly (I-MOVE+) was conducted during seasons 2015/2016-2016/2017. Patients hospitalised with pre-defined reasons were systematically screened. SARI case definition included at least one systemic symptom/sign (fever, feverishness, malaise, headache, myalgia, deterioration of general condition) and at least one respiratory symptom/sign (cough, sore throat, shortness of breath). Respiratory specimens were obtained <7 days after symptom onset and analysed by multiplex real-time RT-PCR including influenza and RSV.

Results

Of 304 patients sampled, 25 (8%) didn't fulfill SARI criteria; none of them had influenza or RSV infection. Of the remaining 279, 54 (19%) had influenza alone, 22 (8%) had RSV infection alone and two had both infections concurrently. Of both influenza and RSV infection patients, 92% were hospitalised with (suspicion of) acute respiratory or unspecified infection. The most sensitive symptoms/signs were fever, deteriorating of general condition and cough (94%-92%) in recognising influenza, and fever, cough and shortness of breath (87%-83%) in recognising RSV infection. The highest specificity had sore throat, myalgia and headache in recognising both influenza (81%-75%) and RSV infection (80%-73%). Of influenza and RSV infection patients, 64% and 25%, respectively, were identified at the hospital by samples obtained for clinical purposes.

Conclusion

According to our descriptive analysis, it seems possible to develop common case definition for recognising influenza and RSV infections among elderly needing acute hospitalisation.

Keywords: Respiratory Syncytial Viruses, RSV, influenza, elderly

ABSTRACT ID: 931

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B 15.5 Adapting RSV surveillance in France in the light of a future vaccine introduction

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Background

While respiratory syncytial virus (RSV) infections are a known major cause of hospitalization for bronchiolitis among young children (<2 years), its incidence and severity in elderly (>65 years) is poorly documented. Anticipating the introduction of RSV vaccines, we evaluated whether RSV infections among young children and elderly could be estimated from routine surveillance data in France, to identify improvements needed in the surveillance.

Methods

RSV laboratory data (2015-2017) were obtained from the sentinel influenza surveillance (2.1% of GPs and 4.1% of pediatricians) and the hospital-based laboratories network. Bronchiolitis cases (2009-2015) were recorded in national emergency ambulatory and hospital consultations, and hospital discharge databases.

Results

The seasonal RSV increase in young children can be monitored using bronchiolitis data from emergency consultations. RSV hospitalization rates for them can be approximated from hospital discharges following bronchiolitis. Within sentinel influenza surveillance, before the influenza season only 5.0% (1442/28,957) of acute respiratory infections in young children and 1.1% (53/4,945) among elderly were eligible for RSV testing (influenza-like illnesses). Bronchiolitis hospitalization rates due to RSV are difficult to estimate in elderly as 92.8% (2,646/2,851) are without causal agent specified. Hospital-based laboratory reports do not record age, and testing criteria may vary between hospitals.

Conclusion

Available emergency bronchiolitis consultation and hospital discharge data provide reasonable proxy estimates for RSV among young children. The few detected RSV cases through sentinel influenza surveillance are likely not representative of RSV incidence throughout the year since testing is limited to influenza-like illnesses. Testing elderly who present with acute respiratory illness in GP offices and nursing homes for RSV would help assessing their RSV incidence and hospitalization rate, and thus support policy decisions regarding the RSV vaccine introduction in France.

Keywords: Respiratory Syncytial Virus Infections/epidemiology, Hospitalization, Incidence, Bronchiolitis, Viral, Public Health Surveillance

ABSTRACT ID: 934

PRESENTED BY: Brecht Ingelbeen (brechtingelbeen@gmail.com)

B 15.6 First insight into the distribution of A and B subtypes and G genotypes of respiratory syncytial virus (RSV) in Denmark 2006-2016.

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Background

In Denmark the annual number of RNA-positive RSV samples is approximately 1,700-2,500. The number of cases is underestimated and currently no RSV-surveillance is in place. The objective of the study was to get an overview of the RSV genotypes circulating in Denmark, to obtain baseline data for future surveillance and immunization programs.

Methods

A retrospective analysis of 498 samples positive for RSV during a 10-year study period (2006-2016). Samples were initially categorized according to RSV-A and RSV-B subtypes by a real-time reverse transcriptase (RT) PCR targeting the nucleoprotein. A convenient subset of samples (N=67) were further characterized with regards to the G-protein using in-house RT-PCRs. Samples genotyped were from the beginning (2005/2006), middle (2009/2010, 2010/2011) and end (2014/2015, 2015/2016) of the study period. These PCR products were sequenced and a maximum likelihood phylogeny of aligned sequences and reference strains were made to determine G genotypes.

Results

A total of 260 samples (52%) were RSV-A and 170 (34%) RSV-B, whereas 68 samples (14%) were non-typeable. RSV-A genotypes NA1 (middle of study period), NA2 (beginning and middle), SAA1 (beginning) and ON1 (end) and RSV-B genotypes BA9 (end), BA10 (middle), GB3 (middle) and GB13 (throughout) were all demonstrated. In addition an unknown RSV-B genotype was found (middle). Genotyping was not straight-forward as there are no standard for assigning genotypes.

Conclusion

This study demonstrates for the first time the distribution of sub- and genotypes of RSV in Denmark. Subtypes RSV-A and RSV-B co-circulated in all years and genotyping revealed the presence of several genotypes of each subtype. These data provide important and timely baseline information for future implementation of RSV-surveillance in Denmark. It is recommended that genotyping of RSV should be standardized.

Keywords: respiratory syncytial virus, genotyping, surveillance

ABSTRACT ID: 830

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Track 16: Late breakers

B 16.1 Epidemiological links between tuberculosis cases identified twice as efficiently by whole genome sequencing than conventional molecular typing

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Background

Patients with Mycobacterium tuberculosis isolates sharing identical DNA fingerprint patterns can be epidemiologically linked. However, municipal health services in the Netherlands are able to confirm an epidemiological link in only around 20% of the patients with isolates clustered by the conventional variable number of tandem repeat (VNTR) genotyping. This research aims to investigate whether whole genome sequencing (WGS) is a more reliable predictor of epidemiological links between tuberculosis patients than VNTR genotyping.

Methods

Both VNTR genotyping and WGS were performed on all Mycobacterium tuberculosis isolates received at the National Institute for Public Health and the Environment in the Netherlands in 2016. Epidemiological links were investigated for all patients that shared a VNTR profile with at least one other patient in 2016. The proportion of epidemiological links identified among patients clustered by either method was calculated.

Results

In total, 542 isolates were sequenced, of which 25% (134/542) were clustered on the basis of VNTR and 13% (68/542) by WGS. Confirmed epidemiological links among WGS clustered cases (57%) were almost twice as common than among cases clustered on the basis of VNTR (31%).

Conclusion

WGS is a more efficient tool to identify epidemiological links between tuberculosis cases than VNTR genotyping, and will allow more efficient transmission tracing, as epidemiological investigations based on false clustering can be avoided.

Keywords: Mycobacterium tuberculosis, molecular epidemiology, whole genome sequencing, Netherlands

ABSTRACT ID: 1392

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B 16.2 Increasing the awareness of public health risks related to do-it-yourself biology (DIYbio) among EU Member States and the DIYbio community

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Background

Do it yourself (DIY) bio is a movement of enthusiastic amateur scientists whose objective is to achieve science democratization. Since its birth in 2008, the DIYbio community has grown considerably and now counts more than 5000 members worldwide. The activities of DIYbio groups pose possible new risks for public health in Europe. The capability to perform advanced gene editing on microorganisms, together with lack of recurrent proper training, represents a concern.

Methods

The European Centre for Disease Prevention and Control (ECDC) is developing a project to provide information to the European Union (EU) Member States (MS) and to the DIYbio community to increase their awareness of the risks to public health associated with DIYbio activities, such as the spread of antibiotic resistance and the release into the environment of invasive GMOs; and suggestions to facilitate the prevention and the mitigation of such risks.

Results

As a first step, ECDC has developed a document to provide information about DIYbio activities and to increase the awareness about the main potential risks associated with those activities. The next step in this project will be the creation of a thematic web page to support health authorities of EU MS, and DIYbio members, providing information about synthetic biology and DIYbio, analysing the related risks for biosecurity and biosafety, and providing suggestions for mitigation.

Conclusion

Risk mitigation will be the main goal of the ECDC approach on DIYbio: open meetings, interactive training, good laboratory practice (GLP), and biosafety support are some examples of measures that could be considered to be put in place to mitigate the risks.

Keywords: DIYbio, biological risk, synthetic biology, risk mitigation, gene editing

ABSTRACT ID: 1393

PRESENTED BY: Orlando Cenciarelli (orlando.cenciarelli@ecdc.europa.eu)

B 16.3 Group A Streptococcus outbreak in a Canadian military training facility: A field investigation

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Background

Between December 2016 and May 2017, four cases of invasive group A Streptococcus (GAS) infections were reported in a Canadian Armed Forces training facility in Quebec, while only one case was reported in the previous six years. A field investigation was launched to characterize the outbreak, and identify associated risk factors to limit transmission.

Methods

Throat culture data and associated demographic data from historical cases were analysed. Throat cultures of contacts of an invasive GAS case were examined. Investigators tracked invasive and severe GAS cases, and conducted site visits and case interviews. Molecular typing and phylogenetic relationships were analyzed using whole genome sequencing.

Results

Since 2014, an increase in the percentage of positive GAS throat cultures occurred at the training facility despite a stable population size (average 2,400 trainees per year). Between September 2016 and July 2017, 406 cases (four invasive, 402 non-invasive) were identified and GAS-positivity rates peaked in November and March. Six non-invasive cases were hospitalized. Cases were typically trainees in their first four weeks of training. Among contacts (n = 63) of one invasive case, 32 had Streptococcus-compatible symptoms and were screened; 18 were GAS-positive. Reluctance to seek medical care, challenges in following cough etiquette, and low compliance with antibiotics were identified. The outbreak sequence type (emm6) was infrequently identified elsewhere in Canada and outbreak isolates were highly related phylogenetically.

Conclusion

This is the first report of a GAS outbreak among Canadian military trainees. Increased surveillance of GAS infections and increased control measures were implemented in-garrison. No further invasive GAS cases were identified. Ongoing surveillance and interventions to improve antibiotic compliance and medical consultation may help to more rapidly detect and prevent future outbreaks.

Keywords: Infectious disease outbreaks, military personnel, Canada, Streptococcus pyogenes, DNA sequence analysis

ABSTRACT ID: 1405

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B 16.4 Novel food vehicle for Campylobacter infections: results of a case-case study in Quebec, Canada

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Background:

Campylobacteriosis is widespread globally and known risk factors include contaminated foods and water. In 2015, clusters of campylobacteriosis in Quebec led to the hypothesis of veal liver consumption as a risk factor. A prospective nested matched case-case study investigated the association between veal liver and campylobacteriosis. Concurrently, animal livers were tested for different pathogens.

Methods:

Campylobacteriosis cases aged 45 and older were recruited via the Quebec notifiable diseases registry between September 2016 and May 2017. Cases were matched for age, gender and date of laboratory confirmation to salmonellosis cases. Subjects were interviewed using a standardized questionnaire. Matched univariate and multivariate regression analyses determined odds ratios (OR) for exposure variables. Livers at slaughterhouses and retailers were tested for Salmonella, Campylobacter and Escherichia coli O157:H7.

Results:

Cases were more likely to eat veal liver than controls on univariate analysis (McNemar OR = 9.5; 95% CI 3.4 to 26.2; p = 0.000001). Unmatched univariate analysis among veal liver consumers indicated that adequate cooking was protective (OR = 0.1; 95% CI 0.002 to 0.7; p = 0.02). The association with veal liver remained statistically significant when adjusting for multiple comparisons. Campylobacter was detected in 37% of chicken livers and 3228% of veal livers sampled at slaughterhouses and retailers. Salmonella was detected in 22% of chicken livers and 3% of veal livers. E. coli O157:H7 was not detected in veal or chicken livers sampled.

Conclusion:

This study identified a statistically significant association between veal liver consumption and campylobacteriosis whereas no previous research has described this relationship. Campylobacter was detected in veal livers at slaughterhouses and at retailers. Recommendations on safer cooking of veal liver and preventing cross-contamination of livers during processing are warranted.

Keywords: Epidemiologic studies, Campylobacter infections, foodborne illnesses, risk factors, food microbiology

ABSTRACT ID: 1406

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B 16.5

Investigating one outbreak of Salmonella Kottbus and finding two, Germany 2017

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Background

In July 2017, German national surveillance data indicated an increase of the rare serotype Salmonella (S.) Kottbus, mostly in Northern Germany. We investigated the outbreak to identify the source and control it.

Methods

Cases were defined as notified S. Kottbus infections in persons with symptom onset after 20th June 2017 without recent travel abroad. Human and food isolates were analysed using whole-genome sequencing (WGS). We conducted a case-control study (CCS) including adult cases with 'outbreak' strain or un-sequenced isolates from three Northern states. We interviewed cases. Age-group, sex and district-matched controls were interviewed by a research service institute. We performed unconditional logistic regression adjusted for age-group and sex.

Results

As of 11th September, 66 cases were notified (56% female, median age 55 years (range 0-91)). WGS identified two clusters: 24 cases (83%) with 'outbreak'-strain and five with a different strain ('cluster 2').

For CCS, data from controls were available within 4 days. Seventeen cases and 96 controls were included. Cases were more likely to have consumed raw smoked ham (OR 17; 95%-CI 2-148), bought at store X (OR 28; 95%-CI 5-173); 9/10 recalled one specific ham product.

A pork isolate with the 'outbreak'-strain originated from the state where the ham was produced.

Four cases (two 'cluster 2', two un-sequenced isolates) reported quail egg consumption as common exposure.

Conclusion

Epidemiological and microbiological analyses indicate raw smoked ham as source of one outbreak. WGS combined with interviews found a second outbreak potentially associated with quail egg consumption, an unusual food item in Germany. Our investigation highlights the importance of WGS to distinguish between strains even of rare Salmonella serotypes and the time effectiveness of using research service institutes.

Keywords: Salmonella, Disease Outbreaks, Foodborne diseases, Germany

ABSTRACT ID: 1426

PRESENTED BY: Anja von Laer (WielandA@rki.de)

B 16.6

Unusual increase of travel-associated Legionnaires' disease cases in May-June 2017, true or fake?

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Background

Legionnaires' disease, an atypical form of pneumonia, is caused by inhaling aerosols containing Legionella bacteria. The European Legionnaires' Disease Surveillance Network (ELDSNet) performs real-time surveillance of travel-associated Legionnaires' disease (TALD) cases. The scheme observed in May-July 2017 an unusual increase in reported TALD case-reports.

Methods

Cyclical linear regression models were used to estimate the expected number fitted on weekly data for 2012-2016 to analyse the increase.

Results

Seven hundred and three cases of TALD were reported in the first seven months, compared to an average of 427 cases in the preceding five years (P-value < 0.000001). Time series analyses showed an increase above previous years for cases with onset from week 18-26 in 2017. Compared with the model predicted number on previous years for this time period, the excess increase was 45%. Persons aged ≥70 years were particularly affected. The increase was observed from ten EU/EEA countries, and to several EU and non-EU travel destinations. Among the EU countries, Italy and Spain as travel destinations experienced a doubling of TALD cases compared to the same period in 2016. Greece and France as destinations also had significant increases.

Conclusion

To our knowledge no changes in the surveillance system or diagnostic methods has been introduced this year that could explain this increase. Travel volumes had increased but not to the extent that may completely explain this sudden increase in this period. Unusually warm weather in southern Europe was observed in March-June which could have influenced the man-made water systems in which Legionella bacteria could be found.

It is yet to be seen whether this unusual observation is due to an earlier season or an overall amplification of cases in 2017.

Keywords: Legionnaires' disease, surveillance, seasonality

ABSTRACT ID: 1429

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MODERATED POSTER SESSION C
DAY 3, WEDNESDAY 8 NOVEMBER
15:40-16:40

Track 17: Food- and waterborne diseases and zoonoses (3)

C 17.1 Ten years of foodborne outbreaks in France, results of the mandatory notification surveillance system, 2007-2016

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Background

In France, surveillance of Foodborne outbreaks (FBO) relies on mandatory reporting. Objectives of this system are to identify food vehicles and causative agents in order to stop the outbreak and take prevention and control measures. We present the results of FBO surveillance from 2007 to 2016.

Methods

A reportable FBO is defined as the occurrence of at least two human cases experiencing similar symptoms, usually gastrointestinal, and resulting from the ingestion of a common food. FBO are either reported to the public health or to the food safety authorities. Data are analyzed at the French national public health agency. Chi-squared test was used to analyse trends over time.

Results

The number of notified FBO increased from 1,093 in 2007 to 1,456 in 2016 (p-value=0.001). In total, 12,316 FBO were notified affecting 116,075 persons of which 6,901 (6%) were hospitalised and 48 (0.04%) died. A causative agent was isolated from human or food samples in 2,399 FBO (20%) with no significant trend over the period (p-value=0.09). For 6,795 FBO (55%), a causative agent was suspected (from 36% in 2007 to 64% in 2016, p-value=0.006). The main isolated agent was Salmonella (1,030 FBO). The most reported food vehicles were complex foods (27%) and meat products (15%). FBO occurred in collective catering (33%), commercial restaurant (36%) or household settings (31%). Non-compliances with regulation were identified in 32% of the outbreaks (p-value=0.08). Preventive or control measures were taken for 31% of FBO (p-value=0.06).

Conclusion

The French FBO surveillance system allows epidemiological, microbiological and environmental investigations. However, efforts should be encouraged to confirm more frequently agents responsible for FBO, in order to adjust control measures and to monitor plans in food production.

Keywords: Foodborne Diseases, surveillance, foodborne outbreak, mandatory reporting

ABSTRACT ID: 1028

PRESENTED BY: Nelly Fournet (nelly.fournet@santepubliquefrance.fr)

C 17.2 Shigella outbreak among students from a student society

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Background

On the 30th of March 2017 a cluster of shigella flexneri infections was identified among students from a student society, starting with three microbiologically confirmed cases. Initial investigation suggested that more students were affected, and an association with food consumed at the society was suspected. An outbreak investigation was initiated to determine the extent of the outbreak, and look for possible sources.

Methods

An electronic questionnaire-based cohort study was conducted among the 1791 members of the student society. Cases were defined as members of the student society who had suffered diarrhea, whether or not in combination with other (gastrointestinal) complaints, starting within a week after visiting the student society between the 10th and 17th of March 2017.

Results

The response rate was 26%. 30% (n=162) of the respondents had suffered diarrhea or other gastrointestinal complaints between the 10th of March and the 26th of April, showing a peak around the 17th and 18 of March (including seven microbiologically confirmed cases) and a smaller peak around the 4th and 5th of April. Of the students who consumed food or drinks on the student society on the 15th of March, a large percentage (65%) developed diarrhea. Consumption of lasagne and salad on 15th March was significantly associated with diarrhea (LR 33,05; p=0,000) Though, cases had occurred beforehand.

Conclusion

This was an unusually large outbreak. The outcome of the questionnaire indicates attending the society, and consumption of food on 15th of March were risk factors. However, several cases had already occurred beforehand. Most likely, multiple transmission routes have been involved, through use of toilets, food handling, and bar tendering. Exposure may have been increased through food handling, explaining the first peak.

Keywords: shigella, infection, disease outbreaks, shigella flexneri, infection control

ABSTRACT ID: 985

PRESENTED BY: Mare de Boer (mariska.petrignani@denhaag.nl)

C 17.3 A Clostridium perfringens outbreak in Wales associated with a root vegetable, January 2017

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5. Public Health England, London, UK

Background

Cases of gastroenteritis were reported following social functions held at a sports club on the 28th and 29th January 2017. We investigated the outbreak to identify the source(s) of infection, interrupt transmission and provide appropriate guidance.

Methods

Environmental health officers administered food exposure questionnaires to attendees of both functions. Cases were persons who ate at either function and developed diarrhoea or abdominal pain within 60 hours, or were laboratory confirmed. We calculated attack rates (AR) and, using logistic regression, adjusted odds ratios (OR) with 95% confidence intervals (CI) for food items served. We obtained stool samples and food from function 2 for microbiological analysis. Staff were interviewed regarding food preparation and storage.

Results

Questionnaires were completed for 87% (122/141) of attendees. ARs were 33% (19/58) and 61% (39/64) for functions 1 and 2, respectively. Swede served in function 1 was strongly associated with illness (OR=11; CI: 1.08-108.84). There were no significant associations in function 2.

Three stool samples were positive for C. perfringens enterotoxin G. Symptoms were consistent with toxin-mediated gastroenteritis at both functions. Microbiological tests on food were within normal ranges. Swede was the only item prepared in advance and served at both functions. Food items were cooled and stored at inappropriate temperatures within the premises' cellar.

Conclusion

Whilst meat is most commonly implicated in C. perfringens outbreaks, our investigation implicated swede as the vehicle of infection for function 1. This demonstrates that C. perfringens can germinate in non-meat food items, if the pathogen is introduced during storage or from equipment. This emphasizes the importance of appropriate temperature control and avoidance of cross-contamination for all food items. Guidance regarding the cellar temperature was provided to the premises.

Keywords: Clostridium perfringens, vegetables, Foodborne diseases, gastroenteritis

ABSTRACT ID: 935

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C 17.4 Finding the source of a prolonged Listeria monocytogenes outbreak from 2012 to 2016 in Germany

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Background

Since November 2012 a new pattern (PFGE 13a/54 /cgMLST Type CT1248) in human isolates of Listeria monocytogenes (Lm) serotype 1/2a has been observed in Southern Germany. An investigation of outbreak cases (pattern 13a/54) conducted in 2013 did not identify a possible source. In June 2015 three new cases in Baden-Wuerttemberg raised the number of cases to 50. We investigated the ongoing outbreak using new genetic methods to detect and eliminate the source of infection.

Methods

We interviewed new outbreak cases from 2015 to 2016 employing standardized questionnaires on food consumption and purchase. We also included pre-existing questionnaires from cases 2012-2014. We calculated the frequency of consumption for food items and location of purchase. Food authorities tested food items for Lm; we compared results of PFGE-typing and Next Generation Sequencing from human and food isolates.

Results

15 questionnaires analyzed up to July 2015 showed high consumption of pork products (pork meat 100%) and 80% purchase in Supermarket A. We suspected pork products as the source of infection and recommended prioritizing Lm isolates from pork products for further genotyping. From February 2016 Bavarian food authorities increased screening of pork products and detected Lm in a batch of juniper-flavored pork belly of a Bavarian producer in March 2016. Molecular analysis confirmed genetic identity with the outbreak strain. The patient with onset in April 2016 reported purchase of pork belly in Supermarket A and consumption within the incubation period. The outbreak totaled 78 cases and ended in 2016.

Conclusion

Epidemiological and microbiological evidence resulted in an official warning and withdrawal of all products from this producer. The source of the longest and most extensive listeria outbreak in Germany seems to be identified.

Keywords: Listeria monocytogenes, outbreak, genotyping, questionnaire, pork products

ABSTRACT ID: 848

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C 17.5 An outbreak of febrile gastroenteritis in two long-term care facilities, associated with Listeria monocytogenes-contaminated raw milk cheese — France, 2016.

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Background

Non-invasive Listeria monocytogenes (Lm)-associated febrile gastroenteritis is underdiagnosed and underreported in France where approximately 400 invasive listeriosis cases are reported annually since 2009. In July 2016, two Lm-meningitis cases were reported among residents of two distinct assisted-living facilities (ALF) in central France, who attended a festive meal followed by reports of febrile gastroenteritis. We investigated to identify the source of the outbreak and recommend control measures.

Methods

We defined a presumptive case as fever, headache or asthenia and gastrointestinal symptoms in a resident or staff meal attendee, within 2 weeks after the meal, and a confirmed case as laboratory-confirmed Lm infection in a meal attendee. We conducted a retrospective cohort-study at both ALF and calculated adjusted risk ratios (aRR). Participants' stool samples were collected and tested for Lm. Suspected food items were tested for enteric pathogens and traced back. Lm isolates were typed by pulsed-field gel electrophoresis (PFGE) and core-genome multilocus sequence typing (cgMLST).

Results

We identified 19 cases (four confirmed, 15 presumptive); four were hospitalized, one died. Twelve cases including 2 (17%) meningitis occurred among residents (median age 88 years, range 52–101) and seven among staff (median age 37 years, range 15–76). Two stool samples cultured positive for Lm. Raw-milk cheese consumption was associated with illness (aRR =33.7; 95% CI, 3.8–297). Traceback investigation implicated a local cheese producer; hygiene violations were identified and implicated cheeses were recalled. All human and food isolates were indistinguishable by both PFGE and cgMLST.

Conclusion

Raw-milk cheese was the vehicle of this outbreak. Lm-gastroenteritis developed in both residents and staff whereas invasive listeriosis solely developed among residents. Serving at-risk food to at-risk population in ALF should be avoided.

Keywords: Listeriosis, disease outbreak, assisted living facilities, foodborne diseases, cohort study

ABSTRACT ID: 757

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C 17.6 Watch out the Presence of Bacillus cereus in Birthday Party! A Food Poisoning Outbreak Investigation in Kulon Progo,Indonesia, 2016

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Background

On August 13th 2016, students of an elementary school in Pengasih sub district were admitted to public health center for acute vomit. Investigation was done to describe the outbreak, to identify source and risk factors, and to prevent future outbreak

Methods

A retrospective cohort study was conducted. Active case finding was done by defining a case as person who had at least one symptom (nausea, stomachache, dizzy, diarrhea, and vomit) after attending birthday party in school on August 13th. Laboratory test of consumed cake, the similar cake with consumed cake from same store, and vomit of students, observation in cake store, and interview with students and teachers using structured questionnaire were done. Data were analyzed with log-binomial regression.

Results

Among 90 attendees, we identified 38 cases (AR= 42%); 86.84% had nausea and 26.32% vomited. The most case was male (52.63%) and in 4th grade (52.63%). The median incubation time was 80 minutes. People who ate birthday cake were likely to develop foodborne illness at statistically significant levels (RR=50.63;95%CI=7.26-352.94). Microbiology test identified mold in both of cake sample and Bacillus cereus in consumed cake sample. Cake was bought on the afternoon of August 12th and stored at ambient (room) temperature. Cake was served and consumed by students on the morning of August 13th with unhygienic condition, without hand washing (RR=2.27;95%CI=1.18-4.38).

Conclusion

This outbreak was associated with consumption of birthday cake contaminated with Bacillus cereus (emetic toxin). Contamination was most probably during storage at home and preparation at school. We recommend to all people at school to active hand washing and store bread product in temperature under 10°C, in refrigerator, to prevent growth of mold and pathogenic bacteria.

Keywords: Bacillus cereus, emetic toxin, hand washing, storage

ABSTRACT ID: 803

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Track 18: Emerging and vector-borne diseases (3)

C 18.1 Potential use of Zika virus IgG avidity and IgA ELISA tests to discriminate past and recent infections

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Background

Zika (ZIKV) and Dengue (DENV) viruses share clinical, epidemiological and antigenic features making difficult the serological diagnosis. Avidity tests are based on the fact that IgG antibodies synthesized after a primary infection have lower affinity for the antigen than those produced later. Furthermore, IgA has been successfully used as an indicator of recent DENV infections. In order to improve the serological diagnosis of ZIKV, we have evaluated ZIKV-IgA and ZIKV-IgG avidity assays.

Methods

We studied forty patients returning from ZIKV endemic areas with confirmed ZIKV infection by Real Time PCR and/or serology (IgM and/or seroconversion). Time elapsed after illness onset (dao) was available for 37 patients; samples were classified according to their stage as initial (≤5 dao), active (6-20 dao) and late (>20 dao). As controls, sixteen patients with known recent or past DENV infection were included. ZIKV-IgG avidity and ZIKV-IgA were determined with commercial ELISA.

Results

For Low Avidity IgG (LA-IgG), the sensitivity was 42.5%, and the specificity 56.3%. Regarding ZIKV-IgA, sensitivity was 65% and specificity was 93.8%. For both approaches simultaneously, the corresponding figures were 27.5% and 100%. LA-IgG was more frequently detected at active and late stages (94.1%) and IgA at the initial and active ones (88.9%).

Conclusion

This work suggests that relying in one of the techniques alone to determine a recent ZIKV infection may not be useful due to false results, derived from complicated kinetics of antibodies in flaviviruses infections. However, the date of collection provides useful information and can help to choose the best technique to use at a certain moment and to interpret LA-IgG and IgA results, improving the serological diagnosis of ZIKV in the absence of molecular diagnosis.

Keywords: Zika virus, Dengue virus, IgG avidity tests, IgA

ABSTRACT ID: 932

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C 18.2 Knowledge, attitude and practices regarding malaria among local and migrant populations, Sofades, Central Greece, 2014

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Background

In 2012-2013, a cluster of 12 malaria cases were reported in Sofades municipality, Central Greece, an agricultural area with migrants from malaria endemic countries. In June-July 2014, we conducted communication campaigns targeting locals and migrants and periodic house-to-house fever screening of migrants. We conducted two knowledge, attitude and practice (KAP) surveys before (June 2014) and after (September 2014) the interventions to evaluate their effectiveness.

Methods

In both surveys, we randomly selected households using spatial sampling and included one randomly selected individual in each household. In the second survey, we also selected a simple random sample of migrants, only present after June. We interviewed participants using a structured questionnaire. We defined knowledgeable about malaria if >1 correct answer regarding transmission, symptoms and/or prevention were provided and sufficiently protected if >1 mosquito protection practices (MPPs) (repellents, insecticides, window-nets) were used. We calculated prevalence differences adjusted for socioeconomic factors (aPD) using binomial regression.

Results

101 locals participated in the first survey, and 153 locals and 137 migrants in the second. Among locals, 45% (45/101) knew about malaria before the intervention and 77% (118/153) after (aPD=34%; 95%CI=22%-45%); 87% (88/101) were sufficiently protected before and 79% (121/153) after (aPD=-10%; 95%CI=-19% to-0.5%); 60% (56/93) would seek healthcare within 48 hours before versus 55% (83/151) after (aPD=-6%; 95%CI=-19% to-6.8%). After the intervention, 72% (98/137) of migrants knew about malaria; 99%(130/131) of migrants would seek healthcare within 48 hours versus 55% (83/151) of locals (aPD=35%; 95%CI=22%-47%). None of migrants used >1 MPPs.

Conclusion

Despite the interventions and an increase in malaria knowledge among locals, use of MPPs did not increase. Systematic education is needed to ensure better compliance with malaria preventive practices.

Keywords: Malaria, mosquito control, Greece, migrants

ABSTRACT ID: 1046

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C 18.3 Outbreak investigation of Malaria- Pratapgarh District, Rajasthan, India, 2016.

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Background

Although India aims for malaria elimination by 2024, there were 1.1 million malaria cases with 561 deaths in 2014. Thorough outbreak investigations can identify gaps and target local interventions to help achieve elimination goals. On 22 September 2016, a malaria outbreak was reported from Pal, District Pratapgarh in Rajasthan. We investigated to describe the epidemiology and provide recommendations.

Methods

We defined a suspect case of malaria as acute febrile illness in a resident of Pal sub-centre area between 1 September-31 October 2016 and a confirmed case as smear-positive suspect case. We searched for cases by reviewing outpatient registers of health facilities. We evaluated all suspect cases by peripheral blood smear. We also conducted an entomological survey and environmental assessment.

Results

We identified 639 cases (441 suspect, 198 confirmed). Among confirmed cases, 45% were female; median age was 12 years (3 month – 75 years). Attack rate was 3% in Pal sub-centre but highest in Balaliya village (9%). Among 198 confirmed cases, 177 (89%) were positive for Plasmodium falciparum. There was 615 mm rainfall in August 2016 (53% above average from 2008-2015). Water accumulation was found around Jakham river bank and hand-pumps. Among 12 sites surveyed, three were positive for adult Anopheles culicifacies. There was no residual spray in last three years, and Pal sub-centre health facility was vacant for six months before the outbreak.

Conclusion

This was a malaria outbreak of mostly P.falciparum with limited health resources, lack of spraying and heavy rainfall likely contributing. We recommend providing a permanent staff at the sub-centre health facility, indoor residual spray and co-ordination with village leaders to prevent water accumulation around hand-pumps while using larvicides at other water accumulation sites.

Keywords: Malaria, Pal, Anopheles, Plasmodium falciparum

ABSTRACT ID: 945

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C 18.4 Immunological response to live attenuated plague EV-strain vaccine in humans, Almaty region, Kazakhstan, 2014-2015

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Background

To protect humans against plague, an annually administered and locally produced live-attenuated Yersinia pestis EV-strain vaccine has been in use in Kazakhstan since the 1950s. Current evidence suggests that IgG antibodies against the EV-strain's F1 antigen (IgG-F1) correlates with a protective immunological response (IR) against disease. This investigation aims to estimate the level and duration of IR in the vaccinated

Methods

We enrolled in a prospective cohort study 493 individuals scheduled for vaccination in 2014. Blood samples were collected from them just before vaccination and at 4, 8, and 12 months afterwards. Passive hem-agglutination assay was used to measure IgG-F1 in samples. Based on prior evidence, we considered an IgG-F1 titer of at least 1/160 as indicative of a protective IR. We collected information on factors that could affect the individuals' IR. McNemar's matched-pair test was used to compare IR before and after vaccination. Unmatched analysis was used to assess associations of protective IR with the study factors among those available for testing at month-4

Results

5% (24/493) had protective IR just before vaccination. Among the available for testing at the 4, 8, and 12 months, the protective IR rate was 26% (120/454), 15% (65/441), and 11% (48/453) respectively (p-value for all matched comparisons was <0.001). In the unmatched analysis the odds of developing a protective IR was higher among those with 5+ previous vaccinations compared to the newly vaccinated in 2014 (OR 12.1, 95% CI 2.3-63.6)

Conclusion

The observed immune resposne is modest and wanes quickly within a year. Repeated vaccinations seem to improve the IR. Annual vaccination need to be continued and further research is needed to develop a more potent and enduring plague vaccine

Keywords: plague, attenuated vaccine, immunological response, kazkahstan

ABSTRACT ID: 921

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C 18.5 Late breaker: Autochthonous chikungunya outbreak in France, July-September 2017

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Background

The 2006 epidemic of chikungunya in the South West Indian Ocean islands and subsequently in India and South-East Asia has revealed that Aedes albopictus could act as an efficient vector of chikungunya virus (CHIKV). This led to the implementation of enhanced surveillance of CHIKV and other Ae. albopictus-transmitted arboviruses in area colonized by the vector mosquito in France. In early August, an autochthonous chikungunya case was confirmed in Var department, south-eastern France. We investigated to determine the source of infection and the extent of a possible dissemination of the chikungunya virus.

Methods

We conducted door-to-door visits in the index case neighbourhood, asked local health professionals, and reviewed the surveillance database for person with symptoms compatible with CHIKV infection. Cases were confirmed by real-time RT-PCR or classified as probable based on serological evidence. Genetic analyses were performed on the index case sera. Entomological prospections and vector control measures were implemented in the area of the investigation.

Results

To date, we have detected nine cases (seven confirmed and two probable). All lived in the same neighbourhood. Genomic characterisation identified a strain belonging to the "East Central South African" lineage and carrying an adaptive mutation facilitating transmission by Ae. Albopictus. Despite unfavourable weather conditions, entomological prospections detected the presence of adult mosquitoes and breeding sites attributable to a high number of rainwater storage tank in the neighbourhood.

Conclusion

This outbreak is the third occurrence in France of local transmission of CHIKV. The two largest involved a strain harbouring a mutation facilitating transmission by Ae. albopictus. Chikungunya posing an increasing threat in Europe, regular awareness and training campaigns should be conducted among health professionals to improve the effectiveness of this surveillance.

Keywords: Chikungunya virus, Disease Outbreaks, France, Arboviruses, Mosquito Vectors

ABSTRACT ID: 1403

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C 18.6 Late breaker: A large outbreak of haemorrhagic fever with renal syndrome in Zagreb, 2017

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Background

In March 2017, an outbreak of haemorrhagic fever with renal syndrome (HFRS) was identified in Zagreb. We investigated to describe the extent of the outbreak and identify risk factors for infection.

Methods

We compared laboratory confirmed cases of Hantavirus infection in Zagreb residents with onset of illness after January 1 2017, with individually matched controls from the same household or neighbourhood. We calculated adjusted matched odds ratios (amOR) using conditional logistic regression.

Results

Between January 1st and August 1st 2017, 78 cases were reported: 96%(n=75) Puumala and 4%(n=3) Dobrava virus. Age ranged from 19-71 years (median 36), and 73% (58) were male. Case numbers peaked in May 2017 (week-19). Overall, 83% (66/78) were hospitalized and 1 case required haemodialysis. Compared with 78 controls, cases were more likely to report visiting a forest (maOR=37; 95%CI 3.8-349), visiting Mount Medvednica (maOR=41; 95%CI 4.3-380) and observing wild rodents (maOR=17, 95% CI 2.1-144). Among participants who had visited Mount Medvednica, cases were more likely to have observed wild rodents (maOR=22; 95%CI 2.1-217), drunk water from a spring (maOR=15; 95% CI 1.2-186), cycled (maOR=13; 95%CI 1.1-149) or had a picnic on the ground (maOR=12; 95%CI 1.1-133). Over three-quarters of cases (76%, 60/78) had visited Mount Medvednica prior to becoming ill.

Conclusion

Our study indicated that recreational activity around Mount Medvednica was associated with HFRS. We recommend enhanced control of rodent populations near human recreational areas when an outbreak is identified. Tourism board should advise visitors on prevention measures to reduce the risk of HFRS infection, including hand hygiene during outdoor activities and avoiding contact with rodents and their excreta.

Keywords: Hemorrhagic Fever with Renal Syndrome, Case-Control Studies, Disease Outbreaks, Rodentia

ABSTRACT ID: 1431

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Track 19: Healthcare-associated infections (2)

C 19.1 Trends and outcome of healthcare-associated and community-onset bloodstream infections due to Staphylococcus aureus in Finland 2004-2015

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Background

All laboratories in Finland notify blood culture positive findings to the National Infectious Disease Register (NIDR). Staphylococcus aureus (SA) is one of the most common pathogens isolated from blood; number of SA findings has continuously been increasing. In order to explore targets for prevention, we analyzed the trends and outcome of healthcare-associated (HA) and community-acquired SA bloodstream infections (BSI) in Finland during 2004-2015.

Methods

Hospitalizations for all persons with SA-BSIs notified to NIDR during 2004-2015 were obtained from the national hospital discharge registry, and deaths within 30 days after SA-BSI from population registry. BSIs were defined as HA, if a positive blood culture was obtained ≥48 h after hospital admission, or if the patient had preceding hospital discharge within 48 h of the positive culture. Incidence rate ratios (IRRs) with 95% confidence intervals (CI) for trends were calculated using negative binomial regression.

Results

The overall annual SA-BSI rate increased from 19.4/100,000 population in 2004 to 37.6 in 2015 (IRR=1.05; 95%CI, 1.002-1.104); the trend strengthened as the age increased. The annual HA rate varied between 8.1-13.5/100,000; no overall trend was seen, but in persons aged >70 years an increasing trend was present (IRR=1.04; 95%CI, 1.004-1.07). HA accounted for 34.6-42.2% of all SA-BSI. BSI rate for methicillin-resistant SA remained stable (range, 0.51-0.87/100,000; 1.8-3.1% of all SA findings). Annual mortality was 2.0-6.7/100,000 with no overall trend, but in persons aged >70 years an increasing trend (IRR=1.06; 95%CI, 1.01-1.13) was observed. Case-fatality did not increase.

Conclusion

Burden of SA-BSI among elderly hospitalized patients seemed to increase, even if only HA BSIs associated with acute-care hospitalization were considered. National and local infection control efforts should focus to HA BSIs, which are potentially preventable.

Keywords: Staphylococcus aureus, Bloodstream infection, Surveillance, Healthcare Associated Infections

ABSTRACT ID: 1070

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C 19.2 Sex/gender analysis in Cochrane reviews of Catheter-related bloodstream infections

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Background

Catheter-related bloodstream infections (CR-BSIs) are an important cause of morbidity and mortality worldwide although may be decreasing in incidence in some areas, possibly as a result of widespread prevention efforts. The evidence suggests that CR-BSIs shows sex/gender differences (SGBA), but these differences are not considered in studies. Moreover, the lack of SGBA in Cochrane reviews may represent a barrier to support informed decision making. We aim to describe the extent to which SGBA is considered in Cochrane reviews of interventions for preventing CR-BSIs.

Methods

We searched the Cochrane Database of Systematic Reviews for active reviews published before January 1, 2017. We screened 6694 records and included those reviews evaluating any intervention attempting to prevent CR-BSIs. To extract key information about sex and gender we considered the domains of the 'Sex and Gender in Systematic Reviews Planning Tool' (SGSR-PT).

Results

The preliminary analysis of the 14 included reviews showed that SGBA was absent. The reviews met no SGSR-PT criteria. Sex and gender terms were used interchangeably in the included reviews. The background never described the relevance of sex/gender to the review question. The inclusion/exclusion criteria for studies in the reviews never considered sex/gender differences. Data were never disaggregated by sex. There were no subgroup analyses by sex, and no review highlighted any sex/gender differences as research gaps.

Conclusion

SGBA is absent in Cochrane reviews on prevent CR-BSIs. This raises concerns about the quality and applicability of these reviews and highlights that there is much room for improvement to support informed decision making in this field.

Keywords: Catheter, Blodstream infections, sex, gender

ABSTRACT ID: 995

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C 19.3

Large numbers of occupational blood exposure accidents outside the hospital (2006-2014, Netherlands) requires turning to profile-based preventive actions

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Background

This study assess the profiles of victims of occupational blood exposure accidents outside the hospital and its management by Public Health Service (PHS) South Limburg, 2006-2014.

Methods

We conducted a retrospective cohort study including all non-hospital employees with such accident in our region, using univariate and multinomial regression analysis. A standardized case report form collected data on sex, age, occupation, location, time of reporting and occurrence, vaccination status, type of injury, source information and serostatus (hepatitis B (HBV), hepatitis C (HCV), HIV), risk assessment, action taken and outcome of victim testing.

Results

A total of 975 accidents were reported, mostly occurring in nursing homes (49%) and during home care (17%). HBV vaccination coverage ranged from 18% (household workers) to 91% (policemen, nurses and nursing-assistants). Among nurses, assistants, students and household-workers injuries were mostly caused by subcutaneous needles (51-67%) and lancets (25%) where as for policemen biting (26%), scratching or spitting (70%) were the causal acts. Elderly workers (>50 years) reported later and were less often vaccinated (76%) ($p < 0.05$). Late reporting was also noted in police, home care and ambulance settings. For 419 accidents (43%) there was a risk on both HBV and HCV/HIV; mostly (>50%) in ambulance, medical sterilization, police and dental practice settings. For 52% of all accidents actions were necessary (mostly HBV immunisation). Source serostatus testing was done for 356 cases (37%): 5 HbsAg-positive (prevalence 1.4%), 7-HCV positive (2%), 10 HIV-positive (2.8%). No employees seroconverted.

Conclusion

Custom-made prevention guidance and measures are necessary, based on hepatitis B coverage and blood exposure accidents' profile and targeting each occupational risk group and setting, e.g. household-workers (vaccination), police, homecare, ambulance reporting time), elderly workers or sources (less testing).

Keywords: blood-borne pathogens, occupation, risk, occupational accident

ABSTRACT ID: 1044

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C 19.4

Burden of Staphylococcus aureus infection following elective surgery in England

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Background

Universal pre-admission methicillin-resistant Staphylococcus aureus (MRSA) screening in England was introduced in 2009. We assessed residual burden of S. aureus surgical site infection (SSI) and bacteraemia in patients undergoing orthopaedic, cardiothoracic, gastroenterology, neurosurgery, gynaecological and general surgery.

Methods

Public Health England national mandatory S. aureus bacteraemia and SSI surveillance records for surgery between April 2010 and March 2014 were linked by unique patient identifier to hospital admissions data (NHS Digital Hospital Episode Statistics) to identify elective surgery. SSIs were prospectively identified during 30d after surgery (1y if implant used) and bacteraemia up to 18 months post-surgery (2013/14 surgery only). SSI risk was assessed from a subset of hospitals achieving >70% response from 30d post-discharge SSI patient questionnaires. The study was supported by a grant from Pfizer Inc.

Results

A total of 126 episodes of S. aureus bacteraemia (9 MRSA) were identified for patients undergoing elective surgery in 2013/14 (n=86,364), a risk of 0.15% bacteraemia (0.01% MRSA). No difference was observed in the proportion of S. aureus or MRSA bacteraemia cases that had a prior S. aureus or MRSA SSI (11% for both). Of the operations analysed (n=100,508) to assess SSI risk (surgery between 2010-2014), the overall SSI risk was 2.83% (2,841). S. aureus accounted for 14.15% of SSIs with an overall risk of 0.40% (402), ranging from 0.32% for hip replacement surgery to 1.15% for large bowel surgery. MRSA was an infrequent cause of SSI across all categories with an overall risk of 0.04% (43).

Conclusion

A small residual burden of MRSA infection remained during an era of universal MRSA screening. The continual significant overall burden of S. aureus infection indicates the need for additional interventions.

Keywords: Staphylococcus aureus, surgical wound infection, England

ABSTRACT ID: 1042

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C 19.5 Assessment of Possible Healthcare Associated Infection Pathogens at a Military Hospital, Lagos State, Nigeria, November, 2015

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Background

Healthcare associated infection (HCAI) are infections among patients in hospital setting that become manifest only after 48hrs of hospital stay, which are caused by pathogens acquired in healthcare settings. They are a major cause of death and increased morbidity in hospitalized patients. In November, 2015, we assessed the prevalence of possible nosocomial pathogens at a military hospital in Lagos State, Nigeria.

Methods

Hospital areas such as theatre, treatment room, nurses' station, male surgical ward, vital signs room, accident and emergency room, labour room, and post-natal ward were randomly sampled for the survey. We collected swabs specimens from specific sites such as table tops, faucets, door handles, beddings and equipment using sterile swab sticks. The swabs were inoculated on nutrient, chocolate and McConkey agar plates and incubated at 37ºC for 24hrs. We characterized isolates by Gram reaction and biochemical methods.

Results

Out of the 83 sites cultured, 31(37.3%) yielded significant growth. Organisms isolated include Staphylococcus epidermidis (32.2%), Staphylococcus aureus (22.6%), Escherichia coli (12.9%), Klebsiella pneumoniae (9.7%), Streptococcus pyrogenes (9.7%), Aspergillus spp. (9.7%) and Proteus mirabilis (3.2%) were isolated. These isolates were from sterile and non-sterile sites, fomites and hospital equipment. Non-sterile sites were less likely to have microbial growth when compared with sterile sites; (Odds ratio: 0.78, CI: 0.20 – 3.03). However, this association was not statistically significant.

Conclusion

Organisms isolated pose risk to sterile procedures and patients care with attendant burden on their recovery. We educated the hospital community on the importance of hand washing with soap and recommended adherence to regular sterilization and disinfection procedures of relevant sites where patient care is administered towards reduction of healthcare associated pathogens.

Keywords: Healthcare associated infection, Nosocomial pathogens, sterile, fomites

ABSTRACT ID: 750

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Track 20: HIV and viral hepatitis

C 20.1 Impact and Challenge After 2 Years Implementation of PITC- A Program To Prevent HIV/AIDS Transmission in Purbalingga, Indonesia-2016.

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Background

Provider-Initiated HIV Testing & Counseling (PITC) refers to HIV testing and counseling which is routinely recommended by health care providers to persons attending health care facilities as a standard component of medical care. In Purbalingga, PITC has been implemented since 2014, but the case reports in Purbalingga are still below the estimated number. This study aims to describe output of PITC and identify the barriers that occur during implementation.

Methods

This is a descriptive study. We interviewed 22 HIV/AIDS programmers at the public health center (PHC) using a structured questionnaire, and in-depth interviews with two midwife coordinators (representative for urban and rural areas). Analyze HIV / AIDS surveillance data from 2012.

Results

The number of patien testing HIV/AIDS has increased over the past two years in several PHC (27%), but its still quite low after compared with trend of HIV/AIDS prevalence. Approximately 91% PHC does not counsel in private rooms, and 55% PHC does not have workflow management for patient test results. Midwives often get rejection from pregnant women patients especially those from rural areas because of the stigma. The involvement and coordination of stakeholders (doctors, midwives, tuberculosis programmers, laboratory technician, health promotion, nurses) at PHC are below 50%, unavailability of health policy regulations is suspected to be a possible cause.

Conclusion

The trend number of HIV/AIDS testing at the PHC is still low. Implementation of PITC has not appropriate with the principle of confidentiality, gets low acceptable, and poor coordination among the stakeholders. We recommended to distribute leaflet about PITC HIV/AIDS in antenatal care, and published a legal local regulations and a letter of assignment to officers who will be involved in PITC HIV/AIDS.

Keywords: HIV, Counseling, Confidentiality, Health Policy, Health Care Provider, Rural

ABSTRACT ID: 776

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C 20.2 Virologic response among HIV-infected adults on antiretroviral therapy in a tertiary facility in Enugu state Nigeria, 2009-2014.

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Background

Early and sustained viral suppression with effective Antiretroviral Therapy (ART) has been linked to good clinical outcome in HIV-infected patients. Resource constraints limits pre-ART resistance testing to ensure potent customized ART in our environment. We therefore assessed the virologic response to the first line ART regimen recommended by the national guideline.

Methods

We reviewed the records of 478 HIV infected adult patients initiated on ART in our facility between 2009 and 2014, who did not miss any drug pick-up or laboratory appointments during the first year on ART. Extracted data was analyzed with Epi Info 7. We determined the proportion of patients who achieved undetectable viraemia [viral load (VL) ‹ 400copies/ml] at 12weeks and 24weeks, compared this across different ART regimen and determined factors influencing early viral load suppression.

Results

Of the 478 patients studied, 310(64.8%) were females, 346(72.4%) were between 30-49yrs old. While 332(69.5%) patients achieved undetectable viraemia at 12 weeks of ART, 356(74.5%) achieved it at 24 weeks. After 12 weeks on ART, 112(74.7%) of 150 patients on Tenofovir/Emtricitabin/Efavirenz, 184(67.1%) of the 274 on Zidovudin/Lamivudin/Nevirapin and 32 (66.3%) of the 49 patients on Tenofovir/Lamivudin+Nevirapin achieved undetectable viraemia. This difference was not statistically significant (p-value=0.13). Patient age, sex, marital status, baseline CD4 count, TB co-infection status, WHO clinical stage of disease and plasma viral load at ART initiation were not significantly associated with early viral load suppression.

Conclusion

Some patients started on the recommended first-line ART in our setting still had detectable viraemia at 24weeks on ART. This could have implications for early virologic failure. The three ART regimen compared were equally effective. Resistance testing prior to ART initiation is recommended.

Keywords: HIV, Viral Load, Antiretroviral Therapy, Nigeria.

ABSTRACT ID: 1076

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C 20.3 Non-adherence to anti-retroviral therapy among HIV-infected individuals in Kyrgyzstan: prevalence and risk factors, 2014-2016

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Background

Currently in Kyrgyzstan, antiretroviral therapy (ART) is freely provided to HIV-infected individuals if medically indicated. Strict adherence to ART is required: it improves patients' survival and quality of life; it also prevents HIV transmission and drug resistance. This study objectives are to identify the prevalence of and factors associated with non-adherence to ART so that strategies can be designed to help maintain adherence

Methods

We randomly selected 432 HIV-infected individuals, aged ≥18 years, from among all those who started ART during Jan 2014-Sep 2016 in Kyrgyzstan. Non-adherents were individuals either lost to follow-up or who missed ≥4.5 days of treatment per 30 days during the study period. None-adherence was established by counting tablets prescribed, dates of visits for treatment, and the number of tablets reported taken. We used individual case investigation forms and medical records to collect information on known risk factors for non-adherent and details of treatment regimens. We used logistic regression to assess the risk factors and non-adherent associations

Results

The overall non-adherence rate was 50% (214/432). The highest non-adherent rates were among the following: alcohol abusers 61% (50/82), those who received multi-tablet regimens (≥2 tablets/dosage) 60% (65/109), drug users 57% (89/155), and individuals aged ‹40 years 53% (144/271). In multivariate analysis, treatment regimens of ≥2 tablets/dosage (OR=2.1, 95% CI 1.0-4.1), age ‹40 years (OR=1.7, 95% CI 1.1-2.6), and alcohol abuse (OR=1.6, 95% CI 1-2.8) were associated with non-adherence

Conclusion

The observed non-adherence rate is unacceptably high. Adherence can be improved by introducing the one tablet/day treatment regimens, establishing regular contact with those under ART, and providing them with appropriate counselling, especially those ‹40 years of age or with substance abuse

Keywords: HIV, anti-retroviral treatment, adherence, Kyrgyzstan

ABSTRACT ID: 922

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C 20.4 Development of HIV and hepatitis C behavioural and biological surveillance indicators among key populations in Canada

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Background

The Public Health Agency of Canada is renewing the Tracks Enhanced Surveillance Systems which monitor trends in the prevalence of HIV and hepatitis C and other sexually transmitted blood-borne infections and in behaviours associated with the acquisition and transmission of these pathogens. Given recent changes in hepatitis C treatment, HIV biomedical prevention and endorsement of 90-90-90 targets, an updated list of indicators was developed to ensure the information generated from the Tracks is relevant, actionable and feasible.

Methods

A literature review and environmental scan of key indicators and risk factors was conducted. Screening criteria were applied to further refine the list to determine whether the indicator was: 1) relevant (i.e., met surveillance objectives and/or international reporting requirements on HIV/AIDS); 2) useful for public health action (i.e., informed prevention and treatment programs and policy); and 3) feasible (can be collected through an interviewer- or a self-administered survey method). Surveillance experts and other government and stakeholder partners were consulted to assess and refine the list of indicators using the same criteria.

Results

75 indicators were identified and classified into four themes: socio-demographic factors and social determinants of health (n=15); risk behaviours: drug use (n=12), sexual (n=10); health care and prevention services: use (n=9), testing (n=8), treatment (n=10); and health outcomes (n=11). 6 previous indicators on risk behaviours were removed and 9 new indicators were added to measure the HIV and the hepatitis C care cascades.

Conclusion

A new streamlined list of relevant, feasible and actionable indicators was developed for enhanced HIV and hepatitis C surveillance. Use of refined indicators is expected to positively impact data quality: improve acceptability in using the system and improve validity and reliability of data collected.

Keywords: Canada, HIV infections, Hepatitis C, Prevalence, Public health

ABSTRACT ID: 1043

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C 20.5 Hepatitis C among Vulnerable Populations: A Seroprevalence Study of Homeless, IDU and Prisoners in London

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Background

Although Injecting Drug Users (IDUs), homeless and prisoners are considered have a great risk of HCV infection and play as a key role of disease transmission, capturing the accurate data in these group is challenging. Knowing the burden of the disease among these groups would inform the development of targeted strategies to reduce HCV transmission. The aim of this study was to estimate the prevalence of HCV in these vulnerable populations.

Methods

We conducted a cross-sectional study between May 2011 and June 2013 in London. Participants were recruited from homeless hostels, drug treatment services and a prison. A questionnaire was administered and blood samples were collected to be tested for hepatitis C.

Results

We recruited 1207 participants including 491 individuals who were homeless (40.68%), 205 drug users (16.98%), and 511 prisoners (42.34%). Eight percent of patients had active HCV infection and 3% had past infection. Overall, 51 (24.88%) of people recruited in drug treatment services, 65 (13.24%) of people recruited at homeless residential sites and 20 (3.91%) prisoners recruited in this study were infected with HCV. This study found that 56.62% (95%CI:47.9%-65%) of HCV infected participants had a history of homelessness, imprisonment and drug use. Multivariate logistic regression identified two factors that were associated with increased risk of HCV: injecting drugs (OR=45.39, 95%CI: 22.37-92.12) and age ›50 yo OR=5.89 (95%CI: 2.47-14.05).

Conclusion

This study confirmed the high prevalence of HCV among these three groups linked to drug use and age. More than half of HCV infected individuals had the intersecting risk factors of homelessness, prison and drug use, highlighting the vulnerability of these patients. Reducing the burden of HCV among vulnerable patients is fundamental to lessen HCV transmission.

Keywords: hepatitis C, drug users, prisoner, homeless, prevalence

ABSTRACT ID: 780

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C 20.6 Differences in HIV molecular surveillance capacity among European Union countries, 2016

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Background

While the prevalence of human immunodeficiency virus (HIV) drug resistance (DR) in Europe was estimated at 8.3% in 2010, there is currently no European Union (EU) -wide surveillance of HIV subtypes and DR. Molecular surveillance of HIV (subtypes and DR) is required to monitor trends over time among risk groups, to support effective use of antiretroviral drugs and prevent further spread of drug resistant HIV. We aimed to assess capacity for HIV molecular surveillance in EU/European economic area (EEA) countries, to inform comprehensive HIV DR surveillance implementation.

Methods

In July 2016, national experts on sexually transmitted and blood borne infections and microbiology from EU/EEA countries were invited to participate in an online survey on HIV molecular surveillance capacity, using the EUsurvey tool. We calculated proportions using the number of non-missing values as denominators.

Results

Responses were received from 21 (n=21/30;70%) EU countries. All respondent countries perform sequence-based characterisation of HIV strains for resistance testing. Thirteen (n=13/21; 62%) countries reported using HIV sequence data (subtype and/or drug resistance) for surveillance purposes at national level. Similar sampling strategies, indicators and laboratory methods were reported by those countries. In addition, nine (n=9/13;69%) of them stated that clinical, epidemiological and sequence data were routinely linked for analysis. Human resources (n=13/21;62%), data ownership (n=13/21;62%) and ethics concerns (n=9/21;43%) were among the main obstacles identified by responding countries to sharing national sequence data at an international level.

Conclusion

This study identified differences in capacity for HIV molecular surveillance among participating EU countries, and challenges in participating in an EU wide system. Issues of insufficient personnel, ethical and data protection concerns need to be addressed in order to introduce comprehensive HIV DR surveillance in Europe.

Keywords: surveillance, HIV, drug resistance, European Union

ABSTRACT ID: 976

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Track 21: Vaccine- preventable diseases (3)

C 21.1 PERTINENT, an active sentinel hospital-based surveillance system of Bordetella pertussis in infants younger than one year in EU/EEA: results after one year of implementation.

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Background

In October 2015, the European Centre for Disease Prevention and Control funded PERTINENT, Pertussis in Infants European Network, to increase homogeneity, sensitivity and data completeness of pertussis surveillance. Active surveillance includes 41 hospitals from six countries of the EU/EEA. The objectives are to measure pertussis incidence, vaccine effectiveness (VE), describe severity in hospitalised infants and identify risk factors for pertussis.

Methods

We developed a generic protocol (https://sites.google.com/a/epiconcept.fr/pertinent/home) and laboratory guidelines recommending culture and a series of two PCRs to identify Bordetella pertussis. We visited study-sites to standardise protocol implementation. Cases are hospitalised infants aged ‹1year testing positive for B.pertussis. Study-sites collect demographic, epidemiological, clinical and laboratory information, pertussis vaccination status and likely source of infection.

Results

During December 2015-March 2017, of 1,014 infants with clinically whooping cough 173 (17%) were laboratory-confirmed, median age was 2 months. All 173 cases were B.pertussis PCR positive, 39 of 96 (38%) were culture positive. Sixty-three cases (36%) had at least one severity criterion as defined by the protocol. One case died after six days at the hospital. Siblings were the most likely source of infection for 44 (34%) of the 129 cases with available information. Vaccination status was documented for 80 of 84 infants eligible for vaccination: 42 (53%) received at least one dose and five (6%) were fully vaccinated. The other 89 infants (51%) were too young to be vaccinated.

Conclusion

During the first pilot year, a common surveillance protocol was successfully implemented and the data completeness achieved is encouraging. The low pertussis incidence precluded precise estimation of VE. A larger sample size and improved data quality will permit measurement of VE by number of doses and identification of risk factors.

Keywords: Whooping Cough, Public Health Surveillance, Burden of Disease, Pertussis Vaccine

ABSTRACT ID: 983

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C 21.2 A case investigation of neonatal pertussis; role of care taker as a source of infection, Petchaburi, Thailand 2016

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Background

On June 5th, 2016, We received the notification of a suspected severe neonatal pertussis from a hospital. We immediately started outbreak investigation in the family and hospital. The objectives aimed to confirm diagnosis and outbreak, identify the source of infection and to implement control measures.

Methods

We conducted a descriptive study. We reviewed medical records and did active case finding in the family, community and the hospital. A case defined as a person who had chronic cough for more than 2 weeks with laboratory confirmed Bordetella pertussis by real-time PCR. We did contact tracing among family members and health care worker and then collected nasopharyngeal sample for PCR testing.

Results

A 29 days-old, female infant was lab-confirmed pertussis by PCR. She had symptom at 7 days of age with upper respiratory tract infection (URI). Then 2 weeks later, she developed persisting cough and pneumonia developed at 29 days with suspected pertussis, Total 15 closed contacts in the household was identified and 4 of them was positive B. pertussis by PCR (26%). The positive people were parents, grandmother and relative. Only father was URI. His onset was after the index case. Thirty four close contact among health care workers both out patient department and obstetric wards were identified and none of them was positive B. pertussis by PCR. Six high risk people in the community were identified and lab returned negative.

Conclusion

The infant was delayed diagnosis and treatment due to the clinicians were not familiar with the disease. The source of infection should be in the family because of the lab confirmation. We give health education to the clinicians and nurses for early detection and treatment for infants.

Keywords: Pertussis, Newborn, Parent, Outbreak, Thailand

ABSTRACT ID: 1082

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C 21.3 An Outbreak Investigation of Chickenpox in a Buddhist School, Bangna District, Bangkok Province, April 29 – August 1, 2016

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Background

A chicken pox outbreak was detected among Buddhist novice in a school, Bangna District, Bangkok. We conducted outbreak investigation in the school with aims to verify diagnosis, confirm outbreak, describe epidemiological characteristics, determine risk factors, and give a specific recommendation for prevention and control measures.

Methods

A descriptive study was conducted. We did active case finding in the school. The suspected case definition of chickenpox was any Buddhist novice in the school who developed a multiple stage of rash included maculupapular, vesicle, pustule or scales in multiple body area in the same time during April 29 – August 1, 2016. Laboratory investigation was confirmed by VZV-IgM by ELISA for 6 cases and Tzank smear for 6 cases. Analytic epidemiological study was performed by case-control study and performed multiple logistic regression for get rid of confounder. Environmental survey in the school was also carried out.

Results

Total 78 cases were met case definition with attack rate was 26.53%. Median age was 13 years old (range 12-17 years old). Six cases (50%) were laboratory confirmed by ELISA-IgM (5) and Tzank smear (1). The most common clinical presentation was vesicle (98.70%) and form scales (53.80%) . Propagated source outbreak pattern was described. The independent risk factor in the multiple logistic regression models was having close contact with the case (adjusted OR = 8.29 95% CI; 1.03 – 66.57).

Conclusion

Varicella vaccine campaign may benefit in emergency situation of outbreak and prevents the future outbreak. But the vaccine is expensive. Prevention measures and recommendation included health education, early detection and prompted case isolation was a powerful non-pharmaceutical intervention and control. There was no additional case after followed up for 42 days.

Keywords: Chickenpox, Outbreak, Buddhist novice, Bangkok

ABSTRACT ID: 1090

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C 21.4 Invasive pneumococcal disease in elderly people in 7 Italian regions, 2011-2016

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Background

Elderly people represent a high-risk group for invasive pneumococcal diseases (IPD). PCV13, used for children vaccination in Italy since 2010, was introduced in 2017 for vaccination also in the elderly. Data regarding IPD are available through the Italian nationwide surveillance system of invasive bacterial diseases (MIB) (http://www.iss.it/mabi).

Methods

We analyzed all IPD cases reported in the MIB surveillance in subjects ≥65 years in the period 2011-2016 from 7 Italian Regions (Emilia-Romagna, Friuli-Venezia Giulia, Lombardia, P. A. Bolzano, P. A. Trento, Piemonte, Veneto) representing one third of the Italian population. We estimated total incidence of IPD and incidence of IPD due to vaccine serotypes (VS) or non-vaccine serotypes (NVS) in this age group.

Results

Overall, 3138 IPD cases were reported in the MIB surveillance in the study period. IPD incidence increased from 6.5 in 2011 to 12.7 cases/100,000 inhabitants in 2016. VS incidence remained stable during the years, from 3.5 in 2011 to 3.8 cases/100,000 inhabitants in 2016. NVS incidence increased consistently, from 3 in 2011 to 9 cases/100,000 inhabitants. In 2016 the most frequent serotypes were 8 (15.4%), 3 (14.1%), 22F (9.5%), and 12F (8.7%).

Conclusion

The increase in IPD incidence in the elderly is difficult to evaluate. The progressive adherence of the Regions to the MIB surveillance likely affected this increasing trend. NVS accounted for the majority of IPD cases in the last years of the study, indicating the occurrence of a serotype replacement phenomenon due to PCV13 use in children. Among vaccine serotypes, serotype 3 remained a leading cause of IPD. Continuous implementation of the IPD surveillance is warranted in order to better evaluate the future impact of PCV13 in the elderly.

Keywords: Streptococcus pneumoniae, 13 valent pneumococcal vaccine, surveillance, invasive pneumococcal disease, aged

ABSTRACT ID: 1072

PRESENTED BY: Romina Camilli

C 21.5 Syndromic surveillance for contact tracing following a meningococcal meningitis case during a mass gathering event

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Background

On 01/08/2016 a nineteen-year-old Italian girl residing in Rome, was hospitalized for meningitis caused by Neisseria meningitides in Vienna on the way back from the World Youth Day (WYD) in Kracow. Given the high number of attendees coming back from the WYD, we used the syndromic surveillance system as additional tool for contact tracing.

Methods

The Emergency Departments (EDs) in Lazio Region have an electronic registration platform where demographic, signs, symproms and diagnosis are registered for each access using the ICD-IX-CM codes. The syndromic surveillance system, implemented during the extraordinary Jubilee 2015-16, monitors the accesses to 43 EDs through the monitoring of 14 syndromes defined as the presence of 1 or more ICD-IX-CM codes. During the health surveillance period we monitored the registration of a subset of codes linked to clinical presentation of meningitis or keywords (usually registered in the fields "History" or "Notes" of the platform) related to the mass gathering events, i.e. "Krakow", "meningitis", "meningococcus", "World Youth Day".

Results

During the surveillance period, 91 accesses to EDs of region potentially correlated with the case were highlighted: 24 with ICD-IX-CM related to meningitis diagnosis (66.7% "Other alterations of consciousness") and 67 with keywords in "History" or "Notes" fields (11.9% with diagnosis "Fever" and 10.4% with "Headache"). These cases were immediately subject to control actions. No Meningococcal Meningitis was diagnosed.

Conclusion

Syndrome surveillance has allowed early detection of further possible contacts in addition to those reported by classical surveillance systems. This method could be a useful tool for contact tracing if epidemic events occur during mass gathering. Studies aimed at improving sensitivity and specificity of the system are needed.

Keywords: neisseria meningitidis, contact tracing, population surveillance, public health

ABSTRACT ID: 926

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C 21.6 Ongoing measles outbreak in Greece: 2017

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Background

This is a report of an ongoing measles outbreak in Greece, which started in Northern Greece at the end of May 2017. Up to the beginning of September the outbreak had expanded in various parts of Greece. The aim of this study is to present the laboratory and epidemiological data.

Methods

Samples of serum and/or pharyngeal swab were collected from the patients. Sera were tested for the presence of IgM antibodies and pharyngeal swabs were tested for the presence of measles virus RNA with Real-time RT-PCR. For measles typing, sequencing of the nucleoprotein gene of measles virus was applied in the samples that tested positive in first place.

Results

One hundred cases had been reported in Greece: 82 laboratory-confirmed, 15 epidemiologically- linked and three suspected.

Sixty-five (79%) of confirmed cases belonged to Greek-Roma population, four cases (5%) involved Romanian-Roma people, eight cases (10%) were people of Greek nationality and five cases (6%) were immigrants. The cases that involved Roma population belonged to children aged from 8 months to 15 years of age. Of the eight people of Greek nationality, five were older than 25 years of age and two of them were healthcare workers.

To date, 32 measles virus strains were studied in terms of nucleotide variation and phylogeny. Measles virus genotype B3 was identified in all cases.

Conclusion

The measles outbreak in Greece was originally observed in Roma children, and later spread to Greek non-minority adults. As in other EU countries with confirmed cases of measles and/or measles outbreaks, the genotype observed is B3. This outbreak highlights the need to vaccinate hard-to-reach populations, as well as to maximize the vaccination coverage of the general population.

Keywords: measles, outbreak, sequencing, Greece

ABSTRACT ID: 1397

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Track 22: Vaccine effectiveness and impact studies

C 22.1 Estimating age-specific vaccine effectiveness using data from a large measles outbreak in Berlin (2014/2015), Germany – Evidence for waning immunity?

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Background

Elimination of measles by 2020 is a WHO goal in 5/6 regions including Europe. It is based on high coverage (>95%) with two doses of a measles-containing vaccine (MCV2), very high vaccine effectiveness (VE) and life-long vaccine-induced immunity. Analysis of measles antibody titres and avidity over time suggest the existence of waning immunity, but the extent at the population-level is unknown. If present, VE estimates should decrease with age.

Methods

We used data from a large measles outbreak in Berlin (2014/2015) to estimate age-specific VE for MCV2 using the screening method. In absence of a vaccination register in Germany, we performed a literature review on vaccination coverage (VC) in Berlin. Uncertainty in the two input variables (i.e., VC and proportion of MCV2 cases), was evaluated by using Monte-Carlo-Simulation.

Results

741 measles cases (median age: 18 years) were analysed in four different age groups (2-5, 6-17, 18-28 and 29-38 years). Of those 39 (5%) had received MCV2. This proportion was highest in adults 29-38 years (10%). Average VC estimates per age-group varied from 45% (29-38 years) to 86% (6-17 years). No Berlin-specific VC estimates were found for adults. We estimated VE of >99.7% (95%-Credible Interval (CrI): 99.5-100%) in each of the three younger age groups, but a significantly lower VE of 97.3% (95%-CrI: 94.0-99.0%) in the oldest age group.

Conclusion

The very high VE in persons aged 2-28 years is sufficient for measles elimination, in contrast to VC. Lower VE in adults aged 29-38 years hints towards waning immunity provided that natural immunity is negligible. More accurate information about the immune status of Berlin's adults is needed to assess the extent of waning immunity.

Keywords: measles, waning immunity, vaccine effectiveness, elimination, Monte-Carlo-Simulation

ABSTRACT ID: 1032

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C 22.2 Possible positive non-specific effect of live tuberculosis vaccine (BCG) observed on infections among less than 3 months old infants – a register-based study

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Background

Live vaccines potentially have non-specific effects that protect against other infections than those the vaccines are targeted against. The national vaccination program (NVP) in Finland was changed on September 1st, 2006: before BCG was given to all newborn babies and afterwards to babies in risk groups (foreign-born parents from high-incidence countries). Thus, vaccination coverage in newborns diminished from almost 100% to a fraction overnight. We studied the non-specific effects of BCG in the frame of NVP using before-after design.

Methods

We compared the incidence of infections between children born 1.7.2004-30.6.2006 (BCG-eligible) and an age- and season-adjusted reference cohort born 1.7.2007-30.6.2009 (BCG-non-eligible) using Poisson regression. These cohorts were restricted to children with Finland-born parents. Infection was defined as at least overnight hospitalization notified to the national hospital discharge register with an ICD10 diagnosis compatible with infection as the primary diagnosis. Follow-up began at birth and lasted 3 months (the scheduled age for DTaP-IPV-Hib vaccination), and from 4 months until first birthday.

Results

The incidence rate ratio (IRR) of the BCG-eligible cohort (N=100479) compared to BCG-non-eligible cohort (N=101664) for infection was 0.92 (95%Cl 0.88-0.97) for the 3-month follow-up. After 3 months of age, the BCG-eligible had more infections than BCG-non-eligible children (IRR 1.17 (1.13-1.22)).

Conclusion

BCG vaccination was associated with a lower incidence of infections during the first three months of life. The difference cannot be attributed to lung tuberculosis, since only few paediatric cases occurred in Finland during 2000's. The disappearance of non-specific effect after administration of an inactive vaccine has been described earlier and our observation is in line with this. However, careful analysis of background factors possibly biasing the result is warranted.

Keywords: Vaccine, Non-specific effects, BCG, infants

ABSTRACT ID: 971

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C 22.3 Congenital rubella syndrome in Spain, 1997–2016 – the success of a vaccination program

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Background

As a country with a highly immunized population, Spain achieved elimination of endemic rubella and congenital rubella syndrome (CRS) at the end of the year 2015. The objective of the study was to describe the cases of CRS notified in Spain during the years 1997-2016 to evaluate actions and recommend the interventions required for maintaining the status of elimination of CRS.

Methods

We obtained individualized data on all cases of CRS notified along the study period from the Spanish Surveillance System. We described clinical, microbiological and demographic data, including maternal background information. We calculated the incidence of CRS utilizing the annual number of births obtained from the Spanish National Institute of Statistics.

Results

Of the 21 cases of CRS 90% were confirmed by laboratory. The most common clinical signs among the laboratory confirmed cases were congenital heart disease (63%), cataracts (37%) and hearing loss (37%). 82% of the cases of CRS were born to unvaccinated, foreign-born mothers residing in Spain (cumulative incidence for the study period 1.10/100.000 births). 21%, 36%, 29% and 14% of these mothers were born in Eastern Europe, Africa, South America and Asia, respectively. The last case of CRS born to a Spanish mother was notified in 2005 (cumulative incidence 0.04/100.000 births).

Conclusion

Most cases of CRS were born to foreign-born mothers residing in Spain. To prevent CRS, particular attention must be paid to the identification and immunization of foreign-born females of fertile age. In the future, the sensitivity of CRS surveillance should be improved due to the extremely low circulation of the rubella virus in Spain.

Keywords: Congenital rubella syndrome, rubella, surveillance, rubella vaccine, Spain

ABSTRACT ID: 878

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C 22.4 Vaccine effectiveness against Haemophilus Influenzae serotype b following introduction of Hepatitis B containing vaccine in the Netherlands.

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Background

Haemophilus influenzae serotype b (Hib) vaccine has been used in the Netherlands since 1993. Hexavalent DTaP-IPV-Hib-HBV vaccine was introduced for high-risk infants in 2006, and universally in 2011. In 2016, an increase in invasive Hib disease was reported. We estimated Hib vaccine effectiveness (VE) to assess whether the increase in Hib disease is explained by decreased VE, and related to the addition of the Hepatitis B (HBV) component.

Methods

Culture-confirmed invasive Hib cases are reported through nation-wide laboratory-based surveillance. Vaccination status is ascertained through the population-based vaccination register. We selected cases aged <5 years reported between 2003-2016. We estimated VE using the screening method comparing the proportion of cases vaccinated to population vaccine coverage estimates at 2 years of age. VE was calculated using logistic regression by age, reporting year and cohort (no HBV, HBV for risk groups, and universal HBV).

Results

Hib vaccination status was known for 165 of 170 cases; 59% were vaccinated. Vaccine coverage was around 95% during the study period. VE was estimated at 95% for children 0-2 years and 68% for 3-4 years ($p<0.01$), with no time-trend from 2003-2016 ($p= 0.16$). Adjusting for age and compared to no-HBV cohort, VE was similar for cohorts with HBV for risk groups ($p=0.39$), or universal HBV ($p=0.13$). VE for each cohort was, respectively, for children 0-2 years: 95%, 92% and 97%; and for children 3-4 years: 65%, 48% and 81%.

Conclusion

Our results support the current vaccination program, as Hib VE has not changed over time or by the addition of the HBV component. VE was high for 0-2 year-olds but waned thereafter. Further studies using a control group are under way to confirm this result.

Keywords: Haemophilus influenzae type b, Immunization Programs, diphtheria-tetanus-acellular pertussis-inactivated poliovirus-Haemophilus influenzae b conjugate-hepatitis B vaccine, Population Surveillance

ABSTRACT ID: 911

PRESENTED BY: Susana Monge (susana.monge@rivm.nl)

C 22.5 Clinical features of invasive disease caused by Haemophilus influenzae serotype b in a high vaccination coverage setting

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Background

Vaccine coverage of around 95% in the Netherlands has drastically decreased the incidence of invasive Haemophilus influenzae serotype b (Hib). However, this serotype still causes 19% of invasive H.influenzae infections. A national study characterized invasive Hib infections, overall and by vaccination status, to better understand the influence of immunization on clinical presentation.

Methods

We included all culture-confirmed invasive Hib cases reported through laboratory-based surveillance in the Netherlands (2005-2013) in cohorts eligible for vaccination (born ≥1993). We retrospectively reviewed patient records from participating hospitals, including information on clinical presentation, predisposing factors, disease course and outcome. Individuals were considered sufficiently vaccinated if they received ≥2 doses under 1 year of age or ≥1dose when ≥1 year. We compared Hib vaccinated and non-vaccinated cases.

Results

Thirty-one of 56 hospitals participated, providing information for 51/119 cases. The majority (n=41; 80.4%) was vaccinated. Male:female ratio was 1:1. 31.4% were <1year, 51.0% 1-<5 years and 17.7% ≥5 years old. Clinical presentation included meningitis (64.7%), pneumonia (9.8%), epiglottitis (5.9%) and invasive infection without focus (3.9%). The vaccinated presented less frequently with meningitis (58.5% vs. 90.0%, $p=0.08$), but no significant difference was observed regarding predisposing factors (29.3% vs. 20.0%, $p=0.71$), development of complications (31.7% vs. 30.0%; $p=1.00$) or sequelae (21.6% vs. 10.0%, $p=0.66$). Eight of nine cases requiring ICU admission and all four deceased patients were vaccinated; in both groups, 50% had non-immunocompromising predisposing factors.

Conclusion

In a context of high vaccination coverage, invasive Hib disease still occurs in vaccinated children in the absence of predisposing factors. Although the number of cases in this analysis was small, the severity of disease was comparable suggesting that vaccinated cases did not experience a milder progression following hospital admission.

Keywords: Haemophilus influenzae type b, Disease Progression, Mortality, Hospitalization

ABSTRACT ID: 909

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C 22.6 Late breaker: Direct and overall effect of 13-valent pneumococcal conjugate vaccine against invasive pneumococcal disease caused by serotype 3 pneumococcus in European children: results of SpIDnet multicentre study

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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 direct and overall effects of 13-valent pneumococcal conjugate vaccine (PCV13) against serotype 3 IPD in children under five years-old.

Methods

To measure the direct effect, we compared the vaccination status of serotype 3 IPD (cases) to that of nonPCV13 IPD (controls) reported from January 2012 to December 2016. Exposure was defined as at least one dose or full vaccination PCV13. We calculated the pooled direct effect as (1-vaccination odds ratio)*100, adjusted for age, underlying conditions, notification year and site. To measure the overall effect, we calculated incidence rate ratios (IRR) comparing serotype 3 IPD incidence in each PCV13 years 2011-2016 to the average incidence during PCV7 period, by site. We used random effects meta-analysis to estimate the pooled overall effect as (1-IRR)*100.

Results

For the direct effect analysis, we included 91 cases and 942 controls. The effect of at least one dose PCV13 against serotype 3 IPD was 63% (95% confidence interval (CI): 36-79) in 2-59-month-olds and of full vaccination 54% (95%CI: 6-77) among 12-59-month-olds (n=491). After PCV13 introduction, the total number of serotype 3 IPD cases was 51, 23, 42,27, 28, 54 in each year 2011-2016, respectively. Pooled overall effect against serotype 3 IPD fluctuated between a decrease of 55% (95%CI: 11-78) in 2012 and +1% (95%CI: -44 to 32) increase in 2016.

Conclusion

Our results suggest a moderate direct effect and no clear overall effect against serotype 3 IPD after six years of PCV13 vaccination programmes. Surveillance data are crucial for developing new generations of pneumococcal vaccines.

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

ABSTRACT ID: 1407

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Track 23: Influenza and other respiratory viruses (3)

C 23.1 Previous influenza vaccinations did not modify the seasonal influenza vaccine effectiveness in 2016/17 – results from a Finnish register-based cohort study

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Background

Several studies suggest that previous influenza vaccinations (IVs) could attenuate vaccine effectiveness (VE). This study targets the effectiveness of IV in 2016/17, an early peaking A(H3N2) dominant season, and three previous seasons in Finnish elderly entitled to free IV from 65 years on.

Methods

We conducted a register-based cohort study using Cox regression to assess VE in the elderly aged 70-100 years in Finland. Laboratory-confirmed influenza A was the outcome. IV in 2016/17 was the time-varying exposure. All analyses were adjusted for age, sex, presence of chronic diseases, and number of hospitalisations in 2015. We additionally stratified and adjusted for previous IVs, a categorical variable with three levels, and tested for interaction between IV and previous IVs.

Results

The cohort comprised 751534 individuals of which 49.4% were vaccinated in 2016/17 and 46.8%/ 24.0%/ 29.2% were never/ sporadically/ always vaccinated in the previous three seasons. We counted 7119 cases. Stratum-specific VE estimates were similar: 38.9% (95%CI: 31.8%;45.3%, never), 34.4% (28.1%;40.3%, sporadic), and 39.2% (33.0%;44.8%, always). Accordingly, the interaction between IV and previous IVs was statistically non-significant (p-value: 0.466). The fully adjusted model estimated the pooled VE at 36.7% (33.0%;40.1%) and revealed that the previously vaccinated had a statistically significant higher risk of influenza than the not previously vaccinated. The hazard ratio of the both always previously and currently vaccinated to the neither previously nor currently vaccinated was 0.839 (0.788;0.893).

Conclusion

We observed moderate VE in 2016/17 in Finland and identified previous IVs as a confounder, not effect modifier, of the association between influenza and IV. With the beneficial effect of IV in 2016/17 outweighing the negative effect of previous IVs, our results support the recommendation of repeated, annual IV.

Keywords: flu, influenza, vaccination coverage, vaccine effectiveness, register-based cohort study, repeated influenza vaccinations

ABSTRACT ID: 1021

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C 23.2 The role of previous season vaccination and mutations in circulating strains over the 2016-17 influenza vaccine effectiveness in Spain

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Background

The Spanish 2016-17 influenza season was dominated by influenza A(H3N2). We estimated the influenza vaccine effectiveness (IVE) against confirmed A(H3N2) influenza within the cycEVA study, considering the previous season vaccine effect and the genetic mutations characterizing the circulating virus.

Methods

Six primary care sentinel networks participated in the cycEVA study. We used a test-negative case-control study, where cases were PCR/culture positive for influenza A(H3N2) and controls negative for any influenza virus. We estimated the adjusted IVE (aIVE) using a logistic regression model and adjusting for potential confounders. We estimated the aIVE for patients vaccinated in the season 2016-17 only, in the season 2015-16 only and in both seasons, using non-vaccinated as reference. We randomly sampled influenza A(H3N2) strains to be genetically characterized.

Results

We selected 589 A(H3N2) cases and 799 controls. The overall aIVE was 23% (95%CI: -15-48) and 65% (95%CI: 34-82), 14% (95%CI: -97-63) and -21% (95%CI: -95-26) for those vaccinated in 2016-17 only, 2015-16 only, and in both seasons, respectively. Overall, 142/336 (42%) characterized A(H3N2) strains harbored mutations in potential relevant amino acid positions (antigenic sites A or B), rendering a group-specific aIVE of 38% (95%CI: -27-69) compared to 59% (95%CI: 14-80) for rest of the strains.

Conclusion

Our results suggest an overall suboptimal aIVE of the 2016-17 influenza vaccine that could partially be explained by the high percentage of A(H3N2) circulating strains with mutations in potential relevant amino acid positions. We found a negative interference of the previous season vaccination, possibly compatible with the genetic differences between 2016-17 circulating and vaccine strains and the similarities between 2015-16 and 2016-17 A(H3N2) vaccine strains. Further research is needed to disentangle the prior season vaccination effect.

Keywords: Influenza vaccine, Influenza A(H3N2), Influenza vaccine effectiveness, test-negative design

ABSTRACT ID: 1027

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

C 23.3 Influenza vaccine: a protective factor against the severity of influenza, Spain, 2010-2016

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Background

Surveillance of severe hospitalized confirmed influenza cases (SHCIC) in Spain provides information about influenza severity, complications and seasonal influenza vaccination status. Recent findings suggest a preventive effect of influenza vaccination on complications, Intensive Care Unit (ICU) admissions and death. We investigated the effect of influenza vaccinations on theses outcomes among the SHCIC.

Methods

We conducted a retrospective cohort study using data of SHCIC covering the influenza seasons 2010-11 to 2015-16. We fitted Poisson log-linear models to analyse the vaccine effects on complications (pneumonia, acute respiratory distress syndrome and multiple organ failure), ICU admissions and death. The models were adjusted for conditional probability of being influenza vaccinated given the individual's sociodemographic and clinical characteristics (propensity scores quantiles), virus type/subtype, antiviral treatment, season and region.

Results

Among the 8,248 SHCIC, 2,201 (27%) were vaccinated and 6,047 (73%) unvaccinated. Their vaccination coverage ranged from 15% to 42% for seasons 2010-11 and 2014-15, respectively. Vaccinated SHCIC compared to unvaccinated were more frequently men (58% vs. 55%, p = 0.03), were older (median age 76 years vs. 51 years, p <0.001) and had chronic diseases more often (93% vs. 66%, p <0.001). Vaccinated SHCIC were less likely to develop pneumonia (IRR: 0.90; 95%CI 0.85-0.96), acute respiratory distress syndrome (IRR: 0.82; 95%CI 0.68-0.99) or be admitted to ICU (IRR: 0.80; 95%CI 0.68-0.95). Vaccinated SHCIC aged 15-64 years and vaccinated SHCIC positive for A(H1N1)pdm09 were less likely to be admitted to ICU and/or die (IRR: 0.83; 95%CI 0.70-1.0 and IRR: 0.81; 0.69-0.93, respectively).

Conclusion

Our study showed that seasonal influenza vaccinations could not always prevent hospitalization due to influenza, but that it was protective against complications, ICU admissions and death amongst SHCIC in Spain.

Keywords: Influenza virus, seasonal influenza vaccine, vaccine effectiveness, severe influenza, mortality

ABSTRACT ID: 925

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C 23.4 Low vaccine effectiveness against influenza A(H3N2) in Europe: Estimates from the I-MOVE multicentre case control study

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Background

We undertook a multicentre test-negative case-control study using the I-MOVE (Influenza Monitoring Vaccine Effectiveness in Europe) sentinel practitioner surveillance networks in twelve European Union (EU) countries to measure 2016/17 influenza vaccine effectiveness against medically-attended influenza-like illness (ILI) laboratory-confirmed as influenza A(H_3N_2).

Methods

Practitioners were instructed to systematically select ILI patients to swab within seven days of symptom onset.

We compared odds of vaccination between influenza A(H_3N_2) positive and negative patients. We calculated vaccine effectiveness (aVE) against A(H_3N_2), adjusted for study site and potential confounders (age, onset time and presence of chronic conditions). We stratified aVE by age group, 2015/16 vaccination status and tested for interaction between 2016/17 and 2015/16 season influenza vaccination.

A random selection of A(H_3N_2) virus swabs was genetically characterised.

Results

We included 10,764 ILI patients among whom 4,726 were influenza A(H_3N_2) positive. aVE against A(H_3N_2) was 27.2% (95%CI: 15.4-37.3) overall, 29.1% (95%CI: -8.3-53.5), 32.4% (95%CI: 16.2-45.5) and 13.5% (95%CI:

-11.6-32.9) among those aged 0-14, 15-64 and 65+ years, respectively.

aVE was -14.5% (95%CI: -51.6-22.6) among those vaccinated in 2015/16 and 49.0% (95%CI: 30.0-62.9)(p<0.001) among those vaccinated in 2016/17 only.

Among the 821 viruses sequenced, 812 belonged to the vaccine virus A/Hong/Kong/4801/2014 3C.2a clade; of which 625 belonged to subclade A/Bolzano/7/2016 3C.2a1 and 184 to three other subclades. Among subclade 3C.2a1 viruses, 438 belonged to four further clusters.

Conclusion

The 2016/17 aVE against influenza A(H_3N_2) was low overall and by age group. Circulating A(H_3N_2) viruses had a diverse composition of antigenic determinants, possibly explaining the low aVE. While 2015/16 vaccination may modify the effect of 2016/17 vaccination, long-term studies integrating epidemiological, virological and immunological aspects are needed to better understand the role of repeated vaccination.

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

ABSTRACT ID: 964

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C 23.5 Effectiveness of trivalent inactivated influenza vaccine for northern hemisphere during the 2010-2016 post-pandemic seasons: a meta-analysis of test-negative studies

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Background

The main public health strategy for containing influenza is annual vaccination. Every year, WHO recommends a trivalent inactivated Influenza vaccine (TIV) for the northern hemisphere (NH) that differs from that for the southern hemisphere. We did a meta-analysis of test-negative-design (TND)-studies published after the 2009-2010 pandemic to assess NH-TIV effectiveness (NH-TIVE) by type/subtype and age-group in order to offer recommendations on improving NH-TIV protectiveness.

Methods

We searched Medline for TND-TIVE-studies published May 2011-December 2016. Inclusion criteria: influenza confirmed by reverse-transcription-PCR; NH-TIVE reported at type/subtype-level, by age-group, for ≥1 NH-season. We calculated pooled NH-TIVE (as 1 minus odds ratio) and confidence intervals, using random-effects model, and studied heterogeneity through I2.

Results

In 2011-2016, 2,047 studies, published on influenza vaccine effectiveness, included 51 TND-studies reported NH-TIVE; only few referred to preschools (n=5) and school-age children (n=4). Regardless of age and season, NH-TIV provided moderate protection [NH-TIVE=52%(46-58); I2=89.6] against seasonal influenza in NH, while conferring substantial protection [NH-TIVE=67%(63-71); I2=39.1] against A(H1N1)pdm09. NH-TIVE for B was moderate [NH-TIVE=56%(48-62); I2=83.5] but very varied across age-groups and seasons, being insignificant among working-age group in 2014/15 season. NH-TIV protection against A(H3N2) was minimal [NH-TIVE=31%(16-43); I2=92.3], failing for two consecutive seasons (20133/14 and 2014/15). The elderly were less protected by NH-TIV; and were offered no protection for A(H3N2) across seasons.

Conclusion

In the 6-year-post-pandemic period NH-TIV appeared to protect 1 out of 2 people but more evidence is needed to confirm TIV-protective benefit in children. Optimisation of influenza vaccination for the elderly remained a major task for public health stakeholders. Increasing availability of vaccines containing both B lineages would improve protection, while A(H3N2) needs new methods of vaccine manufacturing.

Keywords: influenza, Human, Influenza Vaccines, Seasons, Aged, Child

ABSTRACT ID: 972

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C 23.6 Patients benefit from vaccination of health care workers for seasonal influenza in the University Hospital of Lyon, France

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Background

Vaccination of healthcare workers (HCW) against seasonal influenza is a public health issue subject to controversial debates. Vaccination uptake is frequently low, providing limited protection against nosocomial influenza. In selected sensitive wards, such as short-term geriatrics or infectious diseases, we aimed to show a reduced risk of nosocomial influenza transmission and the indirect patient's benefit by HCW vaccination when a 40% vaccination threshold is obtained.

Methods

Vaccination coverage of HCW was promoted in sensitive wards and influenza cases monitored in sensitive and non-targeted wards. During the influenza epidemic, each virologically confirmed influenza case was investigated and categorised as nosocomial in patients having clinical signs beginning at least 3 days after admission. Specimens were sequenced by Illumina MiSeq to identify nosocomial transmission events in sensitive and non-targeted wards by combining phylogeny with patient data.

Results

Vaccination coverage in all targeted wards reached 39.3% (hospital: 26%). Large differences in individual wards were observed, e.g. 37.9% in short-term geriatrics but 79.3% in infectious diseases. In total, 105/271 cases of influenza were nosocomially acquired. The proportion of nosocomial infections in sensitive wards was 26.8% versus 62.1% in non-targeted wards. Phylogeny data confirms less transmission events in wards with higher vaccination coverage (preliminary results).

Conclusion

The vaccination campaign was effective by increasing vaccine uptake among HCW in the selected wards. The target of 40% was reached in almost all selected wards which resulted in a reduced risk of nosocomial influenza in comparison to non-targeted wards with lower vaccination coverage. Patients do benefit from HCW vaccination and regular campaigns are needed to achieve sufficient coverage.

Keywords: Influenza, Vaccination, Nosocomial Infections, DNA Sequence Analysis

ABSTRACT ID: 1001

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Track 24: Tuberculosis and other respiratory diseases (excluding viruses)

C 24.1 Evaluation of whole genome sequencing for drug susceptibility testing of Mycobacterium tuberculosis

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Background

Culture-based assays are currently the gold standard for drug susceptibility testing for Mycobacterium tuberculosis (MTB). They provide good sensitivity and specificity, but are time-consuming. The objective of this study was to evaluate whether whole genome sequencing (WGS) can replace routine culture based assays for drug susceptibility testing to reduce the time to advice on optimal drug treatment to the patient and prevent further transmission and development of additional drug resistance.

Methods

All MTB cultures sent to the national reference laboratory in 2014 (n=213) were phenotypically tested by mycobacteria growth indicator tube (MGIT) for first line drugs. WGS was performed on all isolates using the Illumina MiSeq system and data were analysed using PhyResSE online tool.

Results

Three samples could not be sequenced due to low DNA concentration; median coverage among remaining (n=210) specimens was 72 (range:8-119). Overall, 189 of 190 (99.5%) susceptible isolates were correctly predicted by WGS, and 16 of 20 (80.0%) resistant isolates were found to contain at least one resistance marker. The sensitivity of isoniazid (H) and rifampicin (R) was 81% (CI: 54.4-96.0%) and 100% (CI: 63.0-100%), respectively, and specificity 100% (CI: 98.1-100%) for both drugs. The sensitivity of ethambutol (E), pyrazinamide (Z), and streptomycin (S) were 0% (CI: 0-97.8%), 40.0% (CI: 5.3-85.3%), and 91.7% (CI: 61.5-99.8%), respectively. The specificity of E, Z, and S ranged from 97.6-100% (maxCI: 94.5-100%).

Conclusion

WGS has a high specificity for all five assessed drugs, but lacks sensitivity to predict drug resistance for some drugs, especially E and Z. WGS could be used as a pre-screening assay to identify resistant strains with confirmation by MGIT and reduces the diagnostic time to approximately one week for the majority of specimens.

Keywords: Mycobacterium tuberculosis, whole genome sequencing, drug susceptibility, microbiology

ABSTRACT ID: 759

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C 24.2 Enhanced surveillance for tuberculosis among foreign-born persons, Finland, 2014-2016

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Background

In Finland, TB cases in foreign-born residents are increasing (46% of new TB cases in 2016). We conducted enhanced TB surveillance to collect supplementary information on TB cases among recent immigrants.

Methods

TB cases were identified from the National Infectious Diseases Register. A web-based questionnaire sent to infectious disease physicians of each health care district requested data from foreign-born (if not available, most recent nationality other than Finland) TB cases notified during 2014-2016 on country of birth, date of arrival to Finland, participation in TB screening, date of first symptoms, and possible contact tracing.

Results

Questionnaires were returned for 203 (65%) of 313 foreign-born TB cases. TB was detected in arrival screening in 42 (21%) and during contact tracing of another TB patient in 18 (9%); 143 (70%) cases sought care for symptoms or were found by chance (e.g. chest x-ray because of an accident). Forty-eight (24%) cases were diagnosed within 3 months of arrival to Finland, 55 (27%) cases between 3 months and 2 years from arrival, and 84 (42%) cases after 2 years from arrival. In 8% the time of onset was not reported. Of all the cases, 17% had been in a reception centre in Finland and 15% had been in a refugee camp.

Conclusion

Screening should be considered for all immigrants from high TB incidence countries, not only for asylum seekers and refugees, since most TB cases immigrated to Finland due to other reasons, e.g. work or study. Further evaluation of screening efficacy is warranted.

Keywords: tuberculosis, screening, immigrants, asylum seekers, refugees

ABSTRACT ID: 782

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C 24.3 High burden of tuberculosis amongst unaccompanied minor asylum seekers in southwestern Germany.

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Background

Annually reported tuberculosis (TB) cases amongst foreign-born minors in southwest Germany have increased from 5 in 2012 to 69 in 2016, a trend driven by unaccompanied minor asylum seekers (UMAS). We describe the epidemiological and clinical features of TB in this population.

Methods

We performed a retrospective analysis of TB notification data in Baden-Württemberg, Germany, November 2015 to March 2017. Numerators consisted of notified TB cases aged 7 to 17, born outside Germany. Incidence rates were calculated using state-level migration data and were reported per 1000 UMAS arrived in this 17-month period.

Results

Ninety-eight TB cases were notified (18.6/1000). Median age was 16; 84% were male. 61 (62%) of diagnoses were made during asylum seeker screening procedures, 27.5% after symptomatic presentation, 6% during contact investigations. Pulmonary TB was identified in 81.6%, among which secondary infection sites were reported in 10.1%. 54 (55%) of cases were hospitalised. Treatment was completed in 34.7% of cases. Mycobacterium tuberculosis was identified by culture or PCR in 36.7% of cases. Laboratory diagnosis and drug resistance status were available for 89.8% and 55.1% of cases. Five cases were resistant for at least one first-line antibiotic (3 from Eritrea, 2 from Somalia), of which 1 was multi-resistant and 3 were poly-resistant. Highest TB notification incidences were recorded amongst those born in Ethiopia (62.5/1000), Somalia (55.8/1000) and Eritrea (29.2/1000). Incidence rates were higher among females (57.3/1000) than males (16.6/1000).

Conclusion

Intensive case follow-up and close coordination between health authorities, physicians and the youth welfare service are essential for TB diagnosis and treatment in this vulnerable population. The results underline the importance of a timely, comprehensive health assessment for UMAS, especially in migrants from highly endemic countries.

Keywords: Tuberculosis, Mycobacterium tuberculosis, Refugees, Transients and Migrants, Vulnerable Populations, Retrospective Studies.

ABSTRACT ID: 827

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C 24.4 Tuberculosis: A cross-sectional survey on knowledge, attitudes and practices among the Somali population in Finland

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Background

The annual incidence of tuberculosis (TB) in Finland has been decreasing since 1995. However, the proportion of immigrant cases has had the opposite trend. The proportion of immigrant TB cases has increased from 5.8% in 1995 to 50.6% in 2016, with the most common home country being Somalia. No study has analysed what Somalis living in Finland know about TB, hence this study aimed to map out TB-related knowledge, attitudes and practices (KAP) of this population.

Methods

We conducted a cross-sectional survey, gathering data in Helsinki Metropolitan area. The KAP were assessed by a pre-validated anonymous questionnaire, administered in either Finnish or Somali, containing 45 questions. Convenience sampling was performed, and the questionnaire was administered in mosques, shops and Islamic events. Knowledge and attitudes were dichotomised by scoring the correct answers and creating composite scores. We investigated associations between sociodemographic characteristics and both knowledge and attitudes by using logistic regression to compute odds ratios (OR) and 95% confidence intervals (CI).

Results

In total, 407 participants took part, of which 49% were male. Low level of knowledge was held by 53% of participants, and a positive attitude regarding TB by 63%. Knowledge was not associated with sex, country of birth or previous TB history. However, women were twice more likely to have a positive attitude than men (adjusted OR, 2.37; 95%CI, 1.40-4.01). Those with high knowledge are twice more likely to have a positive attitude towards TB (adjusted OR, 2.21; 95%CI, 1.32-3.69).

Conclusion

We found knowledge gaps and misconceptions regarding TB. To raise TB awareness, communication such as a seminar will be organised among Somalis in Finland.

Keywords: tuberculosis, KAP, Somali, Finland

ABSTRACT ID: 963

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C 24.5 Assessment of the performance of the tuberculosis surveillance system in Germany, 2017

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Background

Notified incidence of tuberculosis has been increasing in Germany since 2013. We evaluated the German tuberculosis surveillance system to assess accuracy of the data.

Methods

We used the 2014 WHO criteria “Standards and benchmarks for tuberculosis surveillance and vital registration systems” and assessed data for 2015 from the German national notification system and vital registration system.

Results

Of the 10 standards, 8 were applicable for Germany. Five were entirely met; the population has good access to health care with an under-five mortality rate of 4/1000 live births and 13% of total health expenditure being out-of-pocket (2014). In the national mortality register the cause of death was documented for 902,915/925,200 (98%) total deaths recorded and 27,437/925,200 (3,0%) deaths had ill-defined causes. Tuberculosis case definitions were consistent with WHO guidelines. The defined minimum set of variables was captured. Surveillance data were externally consistent: children accounted for 3.3% of new cases (196/5,865).

The standard on reporting of cases was partially met: reporting is mandatory but under-reporting was not quantified. The standard assessing data completeness and duplicate records was not met: history of previous treatment was recorded for 402 of 540 (74%) cases with previous TB and the number of unresolved duplicates was unknown. The standard regarding consistency over time (2010-2015) was not reached: the number of reported cases increased from 2013 onwards, whereas the mortality peaked in 2013.

Conclusion

The German tuberculosis surveillance system meets most, but not all applicable standards. However, the benchmark for consistency over time appeared to be not entirely tailored to low incidence countries where migration influences the trends. Improvement efforts should focus on data completeness; an inventory study has been initiated to assess underreporting.

Keywords: tuberculosis, surveillance, Germany, WHO standards

ABSTRACT ID: 1015

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C 24.6 Possible risk factors for recent transmission of tuberculosis (TB): a cohort study in Norway, 2011-15

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Background

The majority of TB cases notified in Norway are assumed to be mainly infected abroad. To identify risk groups representing recent transmission in Norway, which may be considered for targeted interventions, we performed a study to identify factors associated with Mycobacterium tuberculosis strain clusters in Norway 2011-15.

Methods

We performed a retrospective cohort study including all 1,277 TB patients notified in Norway who had their first culture positive sample taken between 2011 and 2015 with a complete, unambiguous 24-locus MIRU-VNTR (Mycobacterial Interspersed Repetitive Units-Variable Number of Tandem Repeats) genotype available. Cases with identical MIRU-VNTR genotype were defined as clustered. We identified patient and cluster characteristics, and used multivariable logistic regression to calculate odds ratios (OR) with 95% confidence intervals (CI) for factors associated with clustering.

Results

727 (57%) cases were male, 1,154 (90%) were born abroad and the mean age was 35 years (range 2-94). 783 (61%) cases had unique genotypes, and 494 (39%) cases belonged to 135 different MIRU-VNTR clusters. Being born in Norway by Norwegian-born parents (OR 3.9, CI 2.1-7.1) or being born in Africa (OR 3.0, CI 2.2-4.1) were independent risk factors associated with clustering, compared to being born in Asia. Cases older than 70 years (OR 0.19, CI 0.09-0.42) or who had resided in Norway between one and six months (OR 0.55, CI 0.33-0.91) were less likely to cluster.

Conclusion

MIRU-VNTR based strain cluster analyses suggested that being born in Norway or Africa were risk factors for autochthonous TB transmission in Norway. However, the implementation of whole genome sequencing for strain typing is recommended for a refined identification of likely risk groups and inform targeted interventions to reduce ongoing transmission.

Keywords: Tuberculosis,”Disease Transmission, Infectious”,”Cluster Analysis”,”Risk Factors”

ABSTRACT ID: 1079

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