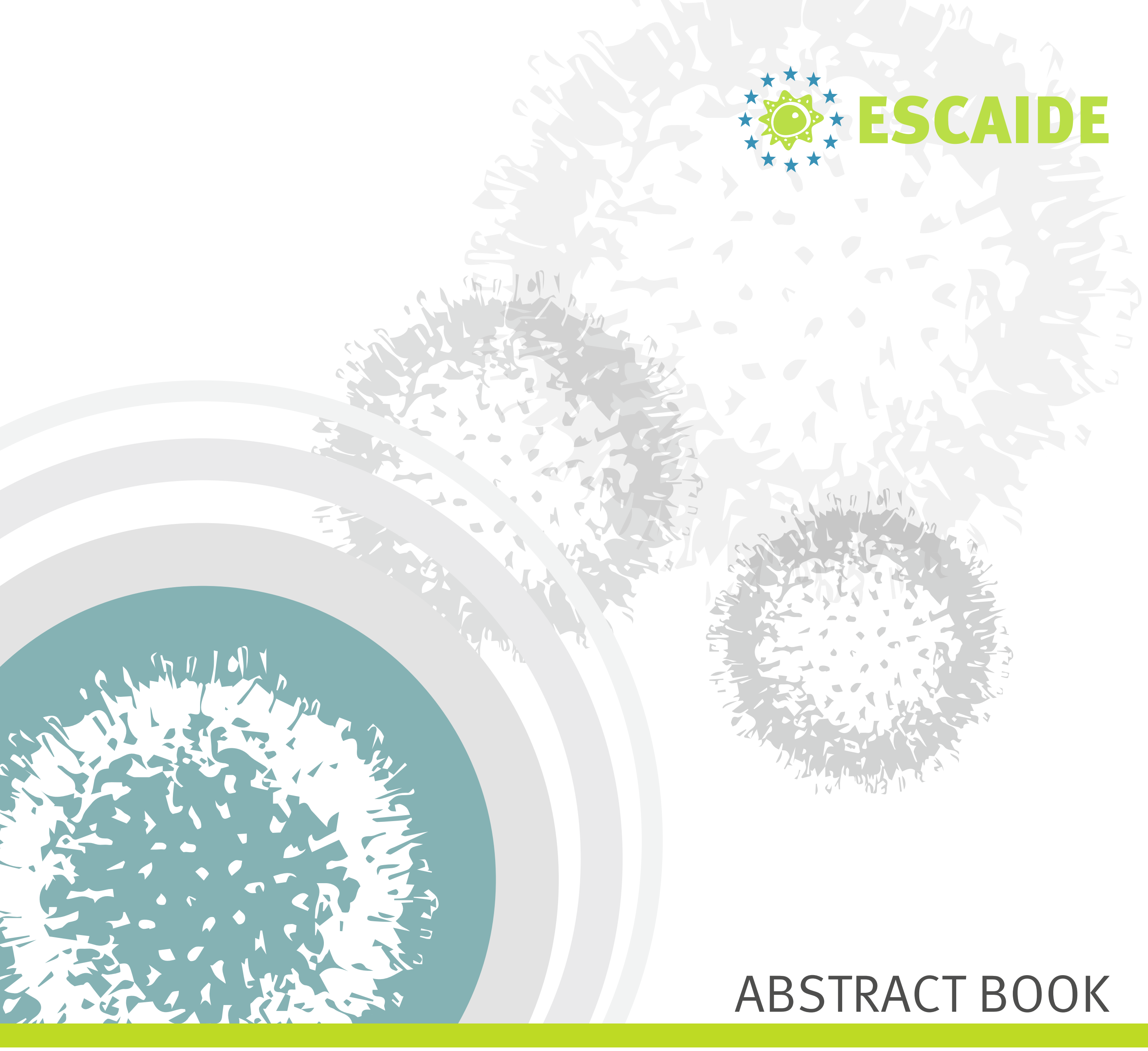
ESCAIDE



ABSTRACT BOOK

European Scientific Conference on Applied Infectious Disease Epidemiology

Saint Julian's, Malta,
21-23 November 2018

ecdc
EUROPEAN CENTRE FOR
DISEASE PREVENTION
AND CONTROL

www.ecdc.europa.eu

Welcome to ESCAIDE 2018!

It is my pleasure to welcome you to ESCAIDE 2018. After hosting the event in Stockholm for some years, it is exciting to take the conference back out ‘on the road‘, and I am thrilled that this edition is being hosted on the beautiful island of Malta. This is the furthest south that ESCAIDE has been held and I hope that you will enjoy, and feel inspired by, the unique environment of the conference and the surroundings of the Island. The Scientific Committee have developed an interesting and diverse plenary programme that addresses public health issues common to us all, such as opportunities from new technologies and methodologies, but with some deliberate focus on specific challenges facing this part of EU as a ‘neighbour’ to the wider global community. The conference begins with a keynote session reviewing pathogen emergence and capacity to respond in Africa and beyond (Plenary A). We will then debate the merits and possible challenges of the use of metagenomics and sequencing for Public Health (Plenary B), consider what has been overlooked in the epidemiology of antimicrobial resistance (AMR) in Europe (Plenary C), and consider opportunities presented by respondent driven sampling for communicable disease control (Plenary D). The programme will close with a session that draws together some of the issues identified throughout the conference by reviewing capacity and coordination of intercontinental response to emerging health threats.

As always, ESCAIDE’s core content is the presentation of submitted abstracts in parallel and poster sessions. We have over 230 abstract presentations in the programme covering a huge variety of topics addressing both disease-specific areas and more general methodological and policy related issues. This is made possible through the willingness of the many public health professionals to share their work by submitting abstracts, the large number of reviewers who guide abstract selection, the session moderators who steer the conference sessions, and finally the ESCAIDE scientific committee who oversee the scientific programme as a whole. I would like to thank everyone who has played a role in the development of the 2018 ESCAIDE programme. ESCAIDE simply would not happen without this continued support.

ESCAIDE 2018 will offer plenty of opportunities for discussion and networking, and I would encourage you to take advantage of the unparalleled collective knowledge and wisdom available. Please engage with fellow participants and speakers, ask questions and challenge both yourself and others during the formal sessions, and the many social and side-events that are taking place. Above all, this is a great opportunity to expand your professional network, share your scientific knowledge and experience with others and enhance your professional development.

I wish you an enjoyable conference, and hope the 3 days will be enriching and inspiring, and that you will leave ESCAIDE carrying new knowledge, and new contacts that will be of real benefit in your daily work.

Prof. Mike Catchpole

Chair, ESCAIDE Scientific Committee

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Scientific Committee

Mike Catchpole

Chief Scientist at ECDC, 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.

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.

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, 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, 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,

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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.

Amrish Baidjoe

Chairman of the Pathology Department, Mater Dei Hospital, Malta

Amrish is the coordinator of the R Epidemics Consortium at Imperial College in London, UK. Here they bring together different stakeholders working in the arena of public health emergencies and outbreak responses to jointly develop new tools, methodologies and training exercises for outbreak analyses using R. He currently still actively participates in international assignments in emergency situations and outbreaks. Having a background in both microbiology and field-epidemiology he undertook his EPIET training in 2015 at Institut Pasteur in Paris, France where he was part of the outbreak investigation taskforce. In 2010 he started his PhD. in close collaboration with the Radboud University, Nijmegen, the Netherlands and the London School of Hygiene and Tropical Medicine, London, UK and the Kenyan Medical Research Institute. Here he looked at patterns of heterogeneity of malaria in an area of Kenya in a large multi-partner project, strongly focussing on involvement of local communities. Before that he worked on fundamental influenza research and completed his MSc. and BSc. degree in biology of infectious diseases at Wageningen University in the Netherlands. He has been the elected president of the board of the EPIET Alumni Network (EAN) since November 2017.

Bojana Beović

Specialist in & Professor of infectious diseases, Faculty of Medicine, University Medical Centre Ljubljana & University of Ljubljana Slovenia

Bojana is a specialist in infectious diseases at the University Medical Centre Ljubljana, Slovenia and a professor of infectious diseases at the Faculty of Medicine, University of Ljubljana. She is the chair of the Slovenian Society for Antimicrobial Chemotherapy and the vice-chair of the National Intersectoral Coordinating Mechanism for Prudent Use of Antimicrobials at the Ministry of Health in Slovenia. She is the chair of ESCMID Study Group for Antimicrobial Stewardship (ESGAP). In the hospital Bojana leads the antimicrobial stewardship programme. She is involved in antimicrobial stewardship education on the national and international level. In the research area she is focused on antimicrobial stewardship and hospital-acquired infections.

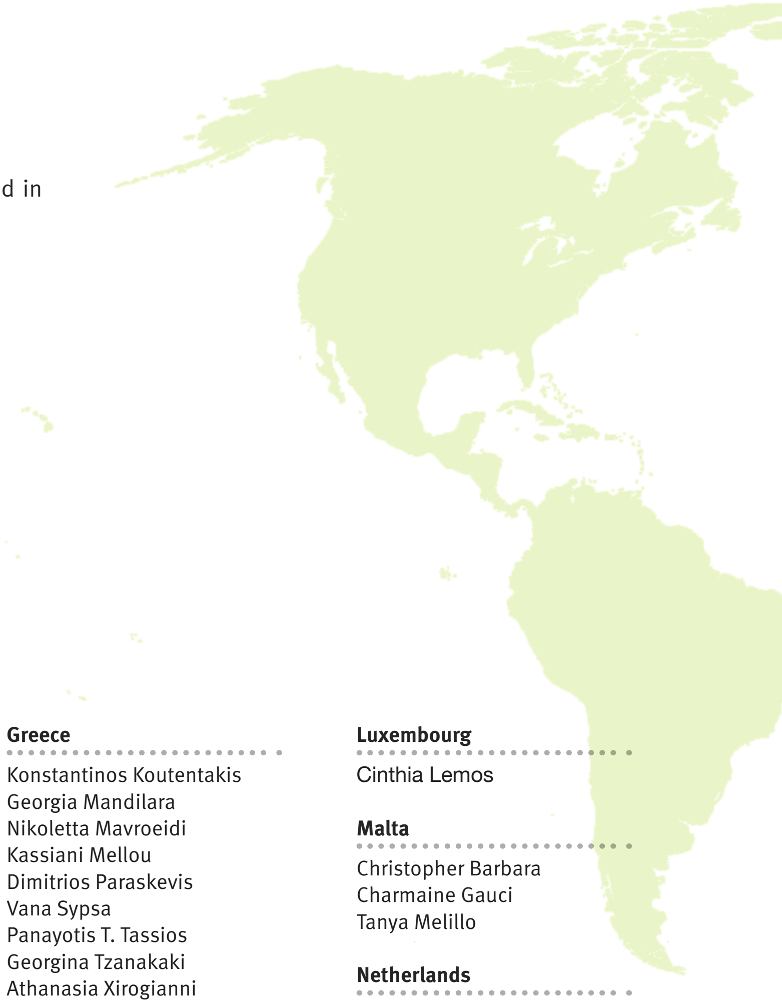
Maria Van Kerkhove

Middle East Respiratory Syndrome Coronavirus (MERS-CoV) Technical Lead, Health Emergency Program, High Threat Pathogens Unit, World Health Organization (WHO)

Maria Van Kerkhove, PhD is an infectious disease epidemiologist who specialises in outbreaks of emerging and re-emerging pathogens. Dr Van Kerkhove is from the United States and completed her undergraduate degree at Cornell University, a MS Degree at Stanford University, and a PhD in infectious disease epidemiology at the London School of Hygiene and Tropical Medicine. Dr Van Kerkhove is currently the Middle East Respiratory Syndrome Coronavirus (MERS-CoV) Technical Lead in the World Health Organization's Health Emergency Program, in the High Threat Pathogens Unit. Dr Van Kerkhove regularly participates in Missions to affected member states, including the Kingdom of Saudi Arabia, Jordan, Qatar and the Republic of Korea. Prior to WHO, she was the Head of the Outbreak Investigation Task Force at Institut Pasteur's Center for Global Health where she was responsible for establishing public health rapid response teams for infectious disease outbreaks. Dr Van Kerkhove was previously employed by Imperial College London in the MRC Center for Outbreak Analysis and Modelling where she worked closely with WHO on influenza, yellow fever, meningitis, MERS-CoV and Ebola Virus Disease.

Abstract Reviewers

The Scientific Committee warmly thanks everyone who participated in the reviewing of the abstracts submitted for ESCAIDE 2018.



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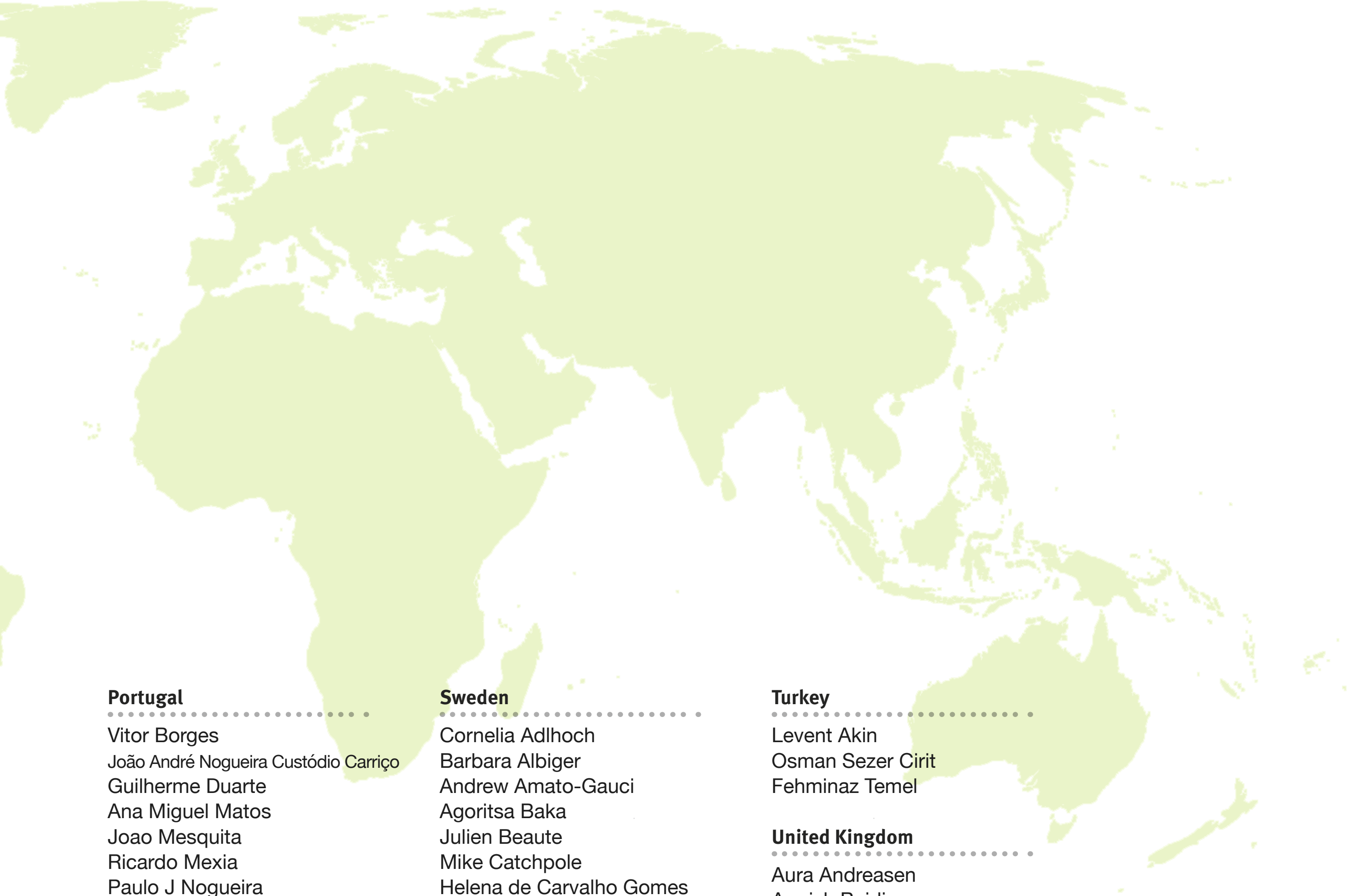

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Eurosurveillance – ECDC

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 with a limited number of copies.

The entire content is open access, free of charge for both readers and authors. All articles are indexed in the PubMed/MEDLINE, PubMed Central (PMC), Scopus, EMBASE, EBSCO and Science Central databases. Eurosurveillance is listed in the Directory of Open Access Journals (DOAJ) as green open access. Furthermore, it is listed the Sherpa/Romeo database as a journal that allows pre- and post-print archiving. It thus complies with the open access standards required by international and national funders such as the European Commission (FP7 and Horizon 2020), the World Health Organization, the World Bank and the Wellcome Trust.

The journal has been selected for coverage by Thomson Reuters and is indexed and abstracted in the Science Citation Index Expanded and in the Journal Citation Reports/Science Edition beginning with volume 14(1) 2009. The most recent impact factor, for the year 2017, is 7.1 (Journal Citation Reports, Thomson Reuters, 2018). This places Eurosurveillance at rank 5 among the 88 journals in the category Infectious Diseases. The Scopus-based SCImago Journal Rank (SJR) for 2017 ranks Eurosurveillance 58 of 2,863 journals in the category Medicine (miscellaneous). 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 2017 listed Eurosurveillance at ranks 5 and 13 among journals in the categories Epidemiology and Communicable Diseases, respectively.

www.eurosurveillance.org

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 communicabledisease 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

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The European Centre of Disease Prevention and Control (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

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.

www.tephinet.org

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EPIET Alumni Network (EAN)

TThe EPIET Alumni Network (EAN) was founded in 2000 to help develop, maintain and fortify a network of European public health epidemiologists that have participated in the European Programme for Intervention Epidemiology Training (EPIET). later this also included fellows and 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 a limited number of 'external' members who, through their work, meet similar objectives to the EAN. The EAN is an association, run by an elected voluntary advisory board ofsix elected members.

www.epietalumni.net

European Society for Clinical Virology (ESCV)

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

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

www.escv.org

European Society of Clinical Microbiology and Infectious Diseases (ESCMID)

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 over the world. For more than 35 years, ESCMID has been influential in the areas of microbiology and infectious disease, and currently reaches more than 33,000 individual and affiliated members with news, scientific opportunities and guidelines. ESCMID runs and supports many conferences and educational events, and its flagship congress, ECCMID, drew close to 13,000 delegates this year.

www.escmid.org

European Respiratory Society (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 and 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.

ERS 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

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Surveillance, Outbreak Response Management and Analysis System (SORMAS®)

SORMAS Mission

The Surveillance, Outbreak Response Management and Analysis System (SORMAS®) is a mobile and web application software that aims to improve prevention and control of communicable diseases particularly in resource-poor settings. The system is being designed by those involved in public health surveillance and disease control. SORMAS is free of charge and adheres to highest data protection standards, good scientific practice and open access policy.

Functional Features

SORMAS is a mobile eHealth System that organizes and facilitates disease control and outbreak management procedures in addition to disease surveillance and epidemiological analysis for all administrative levels of the public health system. SORMAS is characterized by the following features: Digitalized notification at health facility level, case based surveillance, bi-directional information flow, contact follow-up management, outbreak detection algorithms, interoperability with common systems, open source, mobile offline capability, inclusion of all relevant actors (e.g. laboratories), and user centered design.

Interoperability

SORMAS adheres to data standards of and enhances technical and contextual interoperability with the following systems: District Health Information System 2, Integrated Disease Surveillance and Response, Mobile Strengthening Epidemic Response System, International Health Regulations, and Epi Info.

Epidemic Prone Diseases

SORMAS includes disease specific process models for the following high priority epidemic prone diseases: Ebola, Lassa Fever, Monkeypox, Avian Influenza, Dengue Fever, Yellow Fever, Measles, Cerebrospinal Meningitis, Plague and Cholera. Furthermore, SORMAS includes a customizable process model for unforeseen emerging threats.

www.sormasorg.helmholtz-hzi.de

R Epidemics Consortium (RECON)

The R Epidemics Consortium (RECON) is international, not-for-profit, non-governmental organisation gathering experts in data science, modelling methodology, public health, and software development to create the next generation of analytics tools for informing the response to disease outbreaks, health emergencies and humanitarian crises, using the R software and other free, open-source resources. This information stand will be the occasion for you to chat with some of the core members of RECON, learn about our ongoing work, and discuss future projects.

www.repidemicsconsortium.org

Invited Speaker Biographies

ESCAIDE 2018 Keynote address: “New diseases in the ‘Old World”: Perspectives on pathogen emergence and capacity to respond in Africa and beyond”

Dr. John Nkengasong

Director, Africa Centres for Disease Control and Prevention

Prior to his current position, Dr. Nkengasong served as the acting deputy principal director (acting) of the Center for Global Health, United States Centers for Disease Control and Prevention (U.S. CDC), and Chief of the International Laboratory Branch, Division of Global HIV and TB., U.S CDC. He received a Masters in Tropical Biomedical Science at the Institute of Tropical Medicine in Antwerp, Belgium, and another Masters Degree in Medical and Pharmaceutical Sciences at the University of Brussels School of Medicine and a Doctorate in Medical Sciences (Virology) from the University of Brussels, Belgium. Between 1993-95 he was Chief of the Virology and the WHO Collaborating Center on HIV diagnostics, at the Department of Microbiology, Institute of Tropical Medicine, Antwerp, Belgium. He joined the U.S., CDC in 1995 as Chief of the Virology Laboratory, U.S., CDC Abidjan, Ivory Coast.

Dr. Nkengasong has received numerous awards for his work including, but not limited to, the U.S. Secretary of Health and Human Services Award for excellence in Public Health Protection Research, the Sheppard Award, the U.S. Director’s Recognitions Award and, most recently, the William Watson Medal of Excellence, the highest recognition awarded by CDC. Awarded for outstanding contributions and leadership in advancing global laboratory services and programs to support the President’s Emergency Plan for AIDS Relief. He is also recipient of the Knight of Honour Medal by the Government of Cote d’Ivoire, and was knighted in 2017 as the Officer of Loin by the President of Senegal, H.E. Macky Sall, for his significant contributions to public health.

He serves on several international advisory boards including the Coalition for Epidemic Preparedness Initiative – CEPI, the International AIDS Vaccine Initiative (IAVI) among others. He has authored over 200 peer-review articles in international journals and published several book chapters.

Prof. Christian Drosten

Head of the Institute of Virology, Charité – Universitätsmedizin Berlin

Prof. Christian Drosten is a physician by training. He started his career in a diagnostic virology context but expanded his research interest to viral evolution and ecology after he co-discovered the SARS-coronavirus. He has since worked on the ecology of RNA viruses in mammals and insects, while maintaining a focus on epidemiological and molecular virology of emerging coronaviruses. He has co-authored more than 280 peer-reviewed papers. He currently heads the Institute of Virology at Charité – Universitätsmedizin Berlin.

Invited Speaker Biographies

Plenary session B: "Sequencing for Public Health; the four S's (sensing, surveillance, source, attribution and sharing)"

Prof. Nick Loman

Professor of Microbial Genomics and Bioinformatics, Institute of Microbiology and Infection, University of Birmingham

Nick is Professor of Microbial Genomics and Bioinformatics in the Institute of Microbiology and Infection at the University of Birmingham and a Fellow at the Alan Turing Institute. He is supported by a Fellowship in Microbial Genomics Bioinformatics as part of the MRC CLIMB project. His research explores the use of cutting-edge genomics and metagenomics approaches to the diagnosis, treatment and surveillance of infectious disease. Nick has so far used high-throughput sequencing to investigate outbreaks of important Gram-negative multi-drug resistant pathogens, and recently helped establish real-time genomic surveillance of Ebola in Guinea and Zika in Brazil. His current work and focuses on the development and evaluation of novel molecular biology, sequencing and bioinformatics methods to aid the interpretation of genome and metagenome scale data generated in clinical and public health microbiology.

Vicky Lefevre

Acting Head of Unit, Surveillance and Response Support, European Centre for Disease Prevention and Control (ECDC)

Vicky Lefevre joined the European Centre for Disease Prevention and Control in April 2018, as Acting Head of Unit for Surveillance and Response Support. She is a veterinarian by training and started her career as policy officer with the Belgian Food Safety Agency in 2003, where she was responsible for the implementation of European and national legislation in the area of food safety. Since then, she has been professionally involved in food safety and public health from different angles. Between 2009 and 2012, she was a research programme officer with the European Commission, DG Research, responsible for the management of EU funded research projects in the area of public health, food safety and quality. In 2012, she returned to the Belgian Food Safety Agency as Director responsible for Control Policy in the area of Food Safety. She became the Director General responsible for Control Policy in the area of Plant Health, Animal Health and Food Safety in that same Agency in 2015.

Invited Speaker Biographies

Plenary session C: “What have we overlooked in the epidemiology of antimicrobial resistance (AMR) in Europe?”

Prof. Dame Sally C Davies

Chief Medical Officer, Department of Health and Social Care

Dame Sally was appointed Chief Medical Officer (CMO) for England and Chief Medical Advisor to the UK Government in March 2011, having held the post on an interim basis since June 2010. Dame Sally is an independent advisor to the UK Government on medical matters, with particular responsibilities regarding Public Health.

From 2004-2016, Dame Sally was the Chief Scientific Adviser (CSA) for the Department of Health (DH), where she was actively involved in NHS R&D from its establishment and founded the National Institute for Health Research (NIHR). In 2013, Dame Sally became a Non-Executive Director of Genomics England Ltd, wholly owned and funded by DH, to sequence 100,000 whole genomes from NHS patients by 2017.

Dame Sally was a member of the World Health Organization (WHO) Executive Board 2014-2016 and has led delegations to WHO summits and forums since 2004. She advises many governments and organisations on health and policy, holding positions on a number of Boards.

Dame Sally advocates globally on AMR. She has spoken on AMR at numerous events including, the World Health Assembly side events, the G8 Science Ministers’ meeting in 2015, the Global Health Security Initiative in 2015, and the UN General Assembly side event in 2016. She was chair of the 2013 AMR forum at the World Innovation Summit for Health (WISH) and is chair of the WHO Strategic and Technical Advisory Group on AMR. Most recently, Dame Sally has been appointed a co-convener of the UN Inter-Agency Co-ordination Group on AMR, set up in response to the AMR declaration made at UNGA 2016.

Dame Sally received her DBE in 2009. She was elected Fellow of the Royal Society in 2014 and a member of the National Academy of Medicine, USA in 2015.

Prof. Michael A. Borg

Head of Department, Department of Infection Control, Mater Dei Hospital, Malta

A clinical microbiologist by training, Prof. Michael A. Borg heads the Department of Infection Control at Mater Dei Hospital in Malta and chairs the country’s National Antibiotic Committee. He is also a past chair of the International Federation of Infection Control (IFIC) and has provided expert advice to the European Centre for Disease Control (ECDC) on the prevention & control of healthcare associated infections and the prudent use of antimicrobial agents in human medicine.

He has been involved in several EU funded projects on the epidemiology of antimicrobial resistance, prevention and control of healthcare associated infections and antibiotic use within Europe and the Mediterranean region. He has authored or collaborated in more than 80 publications on these subjects within peer reviewed journals. His latest research interests focus especially on human behaviour and change management and their role in infection prevention and control as well as antibiotic stewardship.

Invited Speaker Biographies

Plenary session D: "Respondent driven sampling for communicable disease control"

Dr. Mart Stein

Senior Researcher, Centre for Infectious Disease Control, National Institute for Public Health and the Environment (RIVM)

Dr. Mart Stein works as senior researcher at the Centre for Infectious Disease Control of National Institute for Public Health and the Environment (RIVM) in the Netherlands. He gained an MSc in Health Sciences (VU University, Amsterdam) and in Epidemiology (Utrecht University, Utrecht). His main interests are the use of respondent-driven methods combined with innovative m- and e-health for communicable disease control. He currently works on the use of respondent-driven methods to reach non-western immigrant populations and to study dynamics of health behaviour within social networks, with peer-driven interventions as ultimate goal. He also contributes to a large project, led by Prof. Dr. Anna Thorson of the Karolinska Institutet, which applies web based respondent-driven sampling to study and reduce sexual risk behaviours for HIV among men who have sex with men in Vietnam.

Mart began his professional career at the National Coordination Centre for Communicable Disease Control of the RIVM. He collaborated in the AsiaFluCap project, an international project funded by the EU and Rockefeller Foundation, aimed to assess and strengthen the health care capacity to respond to pandemics in six countries in Southeast Asia. He was awarded his PhD in communicable disease epidemiology from the Utrecht University in 2016, which focused on the use of online respondent-driven methods for studying communicable disease transmission and case finding. Mart received the Young Researcher Award (2015) and two Innovation Awards (2015 and 2016) at the National Institute for Public Health and the Environment. He also developed the game Bactemon, a serious game combined with augmented reality and hand tracking technology to improve hand hygiene among children.

Dr. Lisa G. Johnston

Epidemiologist-Independent Consultant

Dr. Lisa G. Johnston is an Epidemiologist-Independent Consultant providing technical assistance on behalf of international organizations, Universities and institutions worldwide to conduct surveys and population size estimation techniques among hard-to-reach populations, including people who inject drugs, sex workers, men who have sex with men, transgender persons, youth and migrants. She has published over 45 peer reviewed journal articles about RDS, authored several book chapters on RDS, and wrote manuals and guidance on implementing surveys and analyzing data using RDS. She is the co-founder of the Hidden Populations Methods Research Group (www.hpmrg.org) which has developed user friendly software (RDS Analyst) in R program to analyze RDS data and population size estimation techniques, and estimators to improve inference of RDS data. For more information and access to materials and publications, please see www.lisagjohnston.com.

Invited Speaker Biographies

Plenary session E:
“Intercontinental response to emerging health threats: capacity and coordination”

Dr. Nada Ghosn

Head of the Epidemiological Surveillance Program, Lebanese Ministry of Public Health

Dr. Nada Ghosn is a Medical Doctor, specialised in public health and social medicine, having graduated from Faculty of Medicine of University of Lille II. She is currently Head of the Epidemiological Surveillance Program at the Lebanese Ministry of Public Health since July 2000, whilst also teaching Epidemiology and Epidemiological Surveillance at the Faculty of Public Health of the Lebanese University, and Faculty of Health Sciences of Balamand University. Dr. Ghosn is the National Focal Person for EU projects: Episout/Episouth Plus and MediPIET I/MediPIET II.

Dr. Teresa Zakaria

Health Emergency Officer, World Health Organization (WHO)

Dr. Teresa Zakaria is a medical doctor and public health practitioner with over 10 years of experience working in response to humanitarian and public health emergencies. Dr. Zakaria is currently a Health Emergency Officer at WHO’s Headquarters, where she provides technical and operational support to WHO country operations in fragile and vulnerable settings. Prior to joining WHO, Dr. Zakaria worked with IOM, where she led the development of technical guidance and tools on mapping population movement as it relates to the potential risk of spread of diseases. Dr. Zakaria is an Indonesian national. She obtained her medical and public health degrees in Indonesia and Australia respectively.”

Plenary Session Abstracts

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Plenary Session Abstracts

PLENARY SESSION A
DAY 1, Wednesday 21. November
9:00-10:30

Plenary Session A:

Chair:
Prof. Mike Catchpole (ECDC)

Keynote address: „New diseases in the 'Old World'': Perspectives on pathogen emergence and capacity to respond in Africa and beyond"

Presented by

Dr. John Nkengasong,
The Africa Centres for Disease Control and Prevention, Ethiopia

Abstract

In the 1970s, because of the remarkable progress made in the areas of vaccines and antibiotics, public health officials felt confident that threats against infectious diseases could be eliminated. However, the emergence of infectious diseases, such as the human immunodeficiency virus, in the 1980s challenged this confidence. Recently, the world has observed the emergence and re-emergence of infectious diseases with pandemic potentials. Africa bears the highest burden of infectious disease pathogens in the world but has the weakest public health systems and infrastructure. The Ebola virus disease (EVD) outbreak in West Africa killed an estimated 11, 000 people and reversed gains made in economic growth in the affected countries. Social and environmental determinants related to urbanization, increases in population and mobility have created conducive conditions for the emergence and rapid spread of infectious diseases. In fact the population of Africa is expected to increase from 1.2 billion to 2.5 billion people by the year 2050. Additionally, the widespread use of medications has created an enormous threat of emergences of antimicrobial resistance. To address these challenges, the leadership of Africa has taken significant actions: in January 2017, the heads of state and government (HoSG) of Africa launched the Africa Centres for Disease Control and Prevention (Africa CDC), in recognition of the social, economic, and security dimensions of infectious disease threats. The Africa CDC's mission is to support Member States to strengthen its public health capacity and is establishing Regional Integrated Surveillance and Laboratory Networks (RISLNET) in order to ensure that all existing public health assets are efficiently used in the region to respond to disease needs. Because of globalization, a disease outbreak or threat anywhere in Africa is clearly a security and economic menace everywhere in the world. As such, the prevention and control of outbreaks requires public health institutions in Africa to work in a network, such as the RISLNET, in order to harness the assets that exist across the continent to better respond to disease threats.

Plenary Session Abstracts

PLENARY SESSION C
DAY 2, Thursday 21. November
9:00-10:30

Plenary Session C:

Chairs:
Prof. Bojana Beović (University of Ljubljana, Slovenia)
Dr. Chris Barbara (Mater Dei Hospital, Malta)

"What have we overlooked in the epidemiology of antimicrobial resistance (AMR) in Europe?"

Presented by

Prof. Dame Sally C Davies,
Chief Medical Officer, United Kingdom

Abstract

Antimicrobial resistance (AMR) is an escalating global threat. It places millions of lives in jeopardy through limiting our ability to treat infections as well as putting global food security and agricultural livelihoods at risk. Solving this issue demands sustained action both nationally and internationally by all sectors, and this relies on strong collaboration. There are many pieces to the puzzle when it comes to tackling AMR and this talk will discuss some of the most important steps we have to take.

In her 30 minute talk, Dame Sally will discuss the current impact of AMR, the threat it poses to future generations and interventions we are taking currently and need to take in the future to mitigate this global threat.

"What have we overlooked in the epidemiology of antimicrobial resistance (AMR) in Europe?"

Presented by

Prof. Michael A. Borg,
Mater Dei Hospital, Malta

Abstract

The epidemiology of antimicrobial resistance in the European Union shows a remarkably consistent pattern. Countries in the North consistently report low levels of resistance for practically all drug-bug combinations. As one moves down the European region, AMR prevalence increases and reaches a peak in the Southern and Eastern EU countries where levels of methicillin resistant Staphylococcus aureus, carbapenem resistant Klebsiella pneumoniae and ESBL producing E. coli have become a cause of major concern. A highly correlated similar pattern is also seen in antibiotic prescribing; countries exhibiting high levels of resistance also have higher antibiotic consumption, used for longer durations and with wider spectrum formulations. This consistent pattern is unlikely to be coincidental yet cannot be explained by conventional aetiological factors such as economy, education or healthcare infrastructure.
This presentation will review attempt to explain this epidemiological situation by focusing on potential "non-medical" factors, especially behavioural and cultural drivers that could be contributing to this state of affairs. It will also emphasise that interventions and campaigns need to take these factors into account if they are to be successful.

Plenary Session Abstracts

PLENARY SESSION D
DAY 3, Friday 23. November
9:00-10:30

Plenary Session D:

Chairs:
Prof. Dr. Aura Timen (National Institute of Public Health and the Environment and Free University of Amsterdam)
Dr. Fehminaz Temel (Public Health Institute of Turkey)

"Respondent driven sampling for communicable disease control"

Presented by

Dr. Mart Stein,
Dutch National Institute for Public Health and Environment (RIVM),
The Netherlands

Abstract

Monitoring the spread, preparing for and responding to outbreaks are key public health functions in infectious disease control. The finding of infectious cases is an essential element for taking measures aiming to prevent further spread in the population and individual health consequences. Essential as it is to public health, conventional contact tracing is a rather timely, costly and, up to a certain degree, really frustrating activity. Many public health physicians and nurses have vivid memories of their attempts to reach participants to a certain event where an outbreak occurred. In such cases, we were always too late and mostly understaffed. Studying and making use of human social networks may help to understand and control the spread of infectious diseases transmitted via direct contact. These diseases do not spread at random through a population, but follow the underlying patterns of contact networks. This entails that cases tend to cluster by time and space and their contact persons are at a higher risk for infection. With online respondent-driven detection (RDD), individuals are asked to recruit relevant contact persons from their network. These contact persons are then asked to do the same, resulting in successive waves of contact persons. The method utilizes contacts between individuals in a network to find cases. A case is reached through contact with a known case, similar to pathogens spreading through these contact relationships. RDD may therefore enhance conventional contact tracing, providing further insight in the extent of outbreaks, in a quick and less laborious manner for public health professionals.

This presentation provides participants insights in the methodology of online RDD, how this network-based approach provides epidemiological knowledge on contact networks and the spread of infectious diseases, and highlights pre-requisites for successful implementation in practice. The last section will focus on the use of RDD to study the clustering of similar health behavior (e.g. vaccination or screening behavior) within social networks and opportunities for peer-driven interventions.

"Respondent driven sampling for communicable disease control"

Presented by

Dr. Lisa G. Johnston,
Independent Consultant, Spain

Abstract

Sex workers, people who inject drugs, men who have sex with men, transgender persons, Migrants, homeless persons, youth living on the streets and other stigmatized and vulnerable populations, are at higher risk for HIV, TB, Hepatitis, and other infections. Measuring the behavioral and biological risks affecting these populations is essential to creating effective prevention programs, allocating funding and modelling future epidemic scenarios. However, these populations lack sampling frames so it is virtually impossible to collect representative quantitative data from them using common probability-based sampling methods. However, at the same time, these populations are potentially socially networked (i.e., they know each other), such that principles of social network theories can be harnessed for recruitment and to generate properties needed for probability-based sampling. Respondent driven sampling (RDS) is a highly robust and effective method to recruit samples of 'hard-to-reach' populations that are connected through social networks. RDS begins with the researcher purposefully recruiting a set number of eligible individuals, called "seeds", who themselves then recruit a set number of other eligible individuals from among their network members. This recruitment process produces "recruitment chains", with several "waves" of recruits. Participants receive compensation for both being interviewed and bringing in new participants. When all assumptions are met, the growing sample is hypothesized to eventually reach 'convergence', whereby the estimates of the characteristics of interest stabilize. An important part of RDS is a statistical analysis process based on Markov chains and biased network theories, where estimates are adjusted using each participant's social network size and information about who recruited whom. For more than a decade, RDS has been used worldwide by surveys funded by UNAIDS, WHO, UNICEF, UNODC, IOM, US CDC, National Health Programs and Ministries of Health and others.

This presentation will provide participants with an overview of the practical and relevant up-to-date information about the methodological, theoretical and analytical issues relevant to RDS when used to measure disease prevalence and risk among people who hidden and vulnerable populations.

Plenary Session Abstracts

PLENARY SESSION E
DAY 3, Friday 23. November
17:00-18:30

Plenary Session E:

Chairs:
Dr. Maria Van Kerkhove (WHO)
Dr. Marion Muehlen (ECDC)
Prof. Karl Ekdahl (ECDC)

“Intercontinental response to emerging health threats: capacity and coordination”

Presented by

Dr. Teresa Zakaria,
Health Emergency Officer, Worl Health Organisation (WHO), Switzerland

Abstract

Disease outbreaks are known to disproportionately affect the most vulnerable people – those who live in poor conditions, deprived from adequate nutrition, shelter, clean water, sanitation and access to health care. This vulnerability is further accentuated during humanitarian crises and in the context of mass population movement.

Population movement itself takes place in many forms; it may be voluntary or forced, temporary or long-term, short or long distance, internal or cross-border, it may be culturally driven, or an action of last resort, necessary for survival. The health status of those engaged in movement is influenced by multiple factors encompassing the entire movement process: before travel, while on the move, at transit and destination, and even return.

This presentation will highlight two case studies of public health emergency response in the context of humanitarian crisis and population movement: the first one will touch on the health risks faced by migrants and refugees coming into Europe, and the second one on the operational challenges of responding to the Ebola outbreak in the North Kivu and Ituri Provinces of the Democratic Republic of the Congo, in the context of a protracted humanitarian crisis.

“Intercontinental response to emerging health threats: capacity and coord nanation: Experience of Lebanon”

Presented by

N. Ghosn,
Head of the Epidemiological Surveillance Program, Lebanese Ministry of Public Health, Lebanon

Abstract

Health emergencies threats are characterized by occurrence of new critical situation related to the pathogens, the humans or the environment including the health infrastructure. An example is the armed conflict with impact on both human and environment in affected and neighboring countries.

Since 2012, Lebanon is dealing with emerging health threats with population influx from Syria exceeding 1 million. The country has benefited from international and intercontinental support with the objective of enhancing the country capacity and the coordination mechanism towards better health security.

Among various supports provided, three are listed.

The Mediterranean Programme for Intervention Epidemiology Training (MediPIET) supported capacity building in 18 countries with the objective to enhance health security related to communicable diseases in the Mediterranean and Black Sea regions. The project has built partnership with public health services, identified needed core competencies, conducted 2-years fellowship training program, and organized scientific conferences.

The MediLabSecure project supported the One Health Approach in 19 countries with the objective of consolidating laboratory network on emerging zoonotic viruses. The project conducted multi-disciplinary activities to enhance entomological surveillance and diagnostic laboratory capacity.

The International Health Regulations was voted in 2005 to enhance health security. The World Health Organization supports countries for IHR implementation with focus on fostering global partnership, strengthening national capacity, preventing and responding to international public health emergencies.

The outputs were translated in developing human resources with needed competencies, public health laboratories with new capacities and enhanced context of professional networking and coordination. The outcomes may be summarized by better disease surveillance, better outbreak detection and management and operating Emergency Operating Center.

As the Syrian displaced population is distributed within the hosting community, the national communicable disease surveillance was scaled up in particular the medical center based surveillance covering 953 units. Facing the polio outbreaks in Syria in 2013-2014 and 2017 and the increased risk of polio importation, the Acute Flaccid Paralysis and Polio surveillance was enhanced including community component and envi

Plenary Session Abstracts

continuing from page 23:

“Intercontinental response to emerging health threats: capacity and coord nanation: Experience of Lebanon”

Presented by

N. Ghosn,
Head of the Epidemiological Surveillance Program, Lebanese Ministry of Public Health, Lebanon

...ronmental sampling. The regional Mediterranean presence of West Nile Virus, lead to finally initiate WNV surveillance in 2016.

The 2014-2015 mumps outbreak affected Lebanese, Palestinian and Syrian; the investigation findings guided to enhance routine vaccination and add second MMR dose in UNRWA calendar. The 2016 Influenza A(H5N1) outbreak in poultry in the Bekaa activated the national preparedness plan, including the identification and follow up of exposed persons.

The functionalities of Emergency Operating Center includes 3 modes: watch, alert and response. Since 2018, the watch mode was initiated with daily screening and sharing information to national and regional partners.

Achievements in health security were done in the past, but still more is to be done in the future.

The public health services need to ensure needed human capacities and build their critical mass of field epidemiologists. The public health laboratories need to be supportive in the one health approach and to be ready to face emerging diseases. The emergency operating center need to proceed with the alert mode including risk assessment and link it with response mode and various response plans.

Parallel Session Abstracts

Parallel Session Abstracts

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Parallel Session Abstracts

Parallel Session 1
DAY 1, Wednesday 21. November 2018
11:00-12:40

Healthcare-associated infections

Moderator

Ágnes Hajdu

Abstracts

1.1. Validation of an electronic nationwide surveillance system for periprosthetic joint infections following primary total knee replacement in Denmark

Ingmarie Johanson [1]

M. Lindberg-Larsen [2], M. Chaine [3], M. Voldstedlund [4], S. Gubbels [5], J. Nielsen [6], B. Kristensen [7], C. Stab Jensen [8], F. Madsen [9], T. [10]

[1] Department of Data Integration and Analysis Secretariat (DIAS), Statens Serum Institut, Copenhagen, Denmark

[2] Department of Orthopaedic Surgery, Odense University Hospital, The Lundbeck Foundation Centre for Fast-track Hip and Knee Arthroplasty, Copenhagen University Hospital Rigshospitalet, Denmark

[3,4] Department of Data Integration and Analysis Secretariat (DIAS), Statens Serum Institut, Copenhagen, Denmark

[5,6,7,8] Department of Infectious Disease Epidemiology and Prevention, Statens Serum Institut, Copenhagen, Denmark

[9] Department of Orthopaedic Surgery, Aarhus University Hospital, Danish Society for Hip and Knee Arthroplasty (DSHK).

[10] Representatives from the Capital Region of Denmark, Region Zealand, Region of Southern Denmark, Central Denmark Region, North Denmark Region

Background:

Periprosthetic joint infections (PJI) following total knee replacement (TKR) are rare but severe complications. The aim of this study was to compare an algorithm for PJI from the Danish Hospital-Acquired Infections Database (HAIBA) against data from the Lundbeck Foundation Centre for Fast-track Hip and Knee Arthroplasty Database (LCDB), in order to evaluate the accuracy and applicability for automatic surveillance.

Methods:

HAIBA's algorithm combined data from the Danish National Patient Registry and the Danish Microbiology Database. PJI is defined as at least two biopsies positive for the same microorganism, taken at a reoperation between 3-90 days after TKR. The LCDB identified PJI by individual clinical assessment of patient records. The extract from the included patients who underwent TKR between January 12, 2010 and November 1, 2013 in 8 hospitals. Data from HAIBA included patients with TKR during the same period and in the same hospitals.

Results:

Among 6541 TKR performed, 43 led to a PJI in both databases, 12 PJI in the LCDB and not in HAIBA and 4 PJI in HAIBA and not in the LCDB. The sensitivity was 78.2% (43/55, 95%CI 67.3-89.1), the specificity was 99.9% (6482/6486, 95%CI 99.4-1.0). Discrepancies between HAIBA and the reference data were due to different ways of recording infections.

Conclusions: HAIBA's algorithm closely approaches surveillance based on clinical information and is applicable to monitor PJI after TKR. This is an important improvement in infection prevention and control allowing hospitals in Denmark to follow trends and supporting hospital strategy in efforts to prevent PJI and giving insight in the burden of these infections on regional and national level.

Subject: Surveillance

Keywords: joint infections, Hospital Acquired Infections, algorithm, Patient Registry

ABSTRACT ID: 828

PRESENTED BY: Ingmarie Johanson / injo@ssi.dk

1.2. Estimating inappropriate antibiotic prescribing in secondary care in England: analysis of the 2016 healthcare- associated infection and antimicrobial usage point prevalence survey

Rachel Freeman [1]

A. Doble [2], J. Islam [3], G. Hood [4], D. Ashiru-Oredope [5], S. Hopkins [6]

[1] Public Health England

[2,4,5,6] Public Health England

[3] University of Sussex

Background:

Overuse of antibiotics has been associated with the development of antibiotic resistance. The UK government has set an ambition to reduce inappropriate antibiotic prescribing by 50% by the year 2020. The aim of our study was to estimate the proportion of inappropriate antibiotic prescribing occurring in secondary care in England.

Methods:

We analysed data collected from the 2016 national healthcare-associated infection and antimicrobial usage point prevalence survey, conducted in accordance with the ECDC protocol. Analysis was restricted to the four commonest conditions: community-acquired pneumonia (CAP), bronchitis, cystitis and pyelonephritis. Prescribed antibiotic and duration of therapy were compared to national guidelines and expert elicitation to generate a level of agreement between guidance and practice.

Results:

There were 5242 patients accounting for 6848 antibiotic prescriptions. The median age of patients was 77 years, 2716 (51.8%) were female and 2516 (48.0%) were male. The most common indication for antibiotics was CAP (4078, 59.6%), followed by complicated cystitis (1010, 14.7%), bronchitis (1006, 14.7%), pyelonephritis (528, 7.7%) and uncomplicated cystitis (226, 3.3%).

Across all conditions, 5131 (65.2%) antibiotics prescribed were in agreement with national guidelines. 591 (8.6%) prescriptions exceeded the maximum duration recommended in national guidelines.

Conclusions: Our findings suggest that improvements in antibiotic prescribing can be made. A limitation of our study is that it was not possible to ascertain patient co-morbidities from the dataset; further work on estimating comorbidity through modelling McCabe score and linking to datasets that capture Charlson comorbidity index is planned. Our results provide insight into prescribing practices in secondary care and will be used to model estimates of inappropriate prescribing to inform the government's ambition.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: antibiotics, prescribing, secondary care

ABSTRACT ID: 244

PRESENTED BY: Rachel Freeman / rachel.freeman@phe.gov.uk

1.3. Occupational exposure to percutaneous injuries and prevalence of HBV, HCV and HIV among hospital staff in Poland: a multicenter study

Maria Ganczak[1]

K. Topczewska [2], M. Budnik-Szymoniuk [3], P. Kalinowski [4]

[1] Department of Epidemiology and Management, Pomeranian Medical University, Szczecin, Poland

[2] Department of Epidemiology and Management, Pomeranian Medical University, Szczecin, Poland

[3] Department of Community Nursing, Nicolaus Copernicus University, Torun, Poland

[4] Independent Epidemiology Unit, Medical University of Lublin, Lublin, Poland

Background :

Percutaneous injuries (PIs) are a major concern, since they expose susceptible health care workers (HCWs) to the risk of blood-borne infections. Objective: to estimate the overall incidence of PIs and to evaluate the prevalence of HBV, HCV, HIV among hospital staff.

Methods :

A cross-sectional study was carried out from November 2016–April 2018 in 14 randomly selected hospitals from 3 Polish provinces. Self-reported incidents, circumstances surrounding PIs and reporting of exposures were sought by use of interviewer-administered questionnaire. Anti-HBc total, anti-HCV and anti-HIV were assessed by ELISA tests.

Results :

Of the 385 participants, 80 (20.8%) had had at least one PI during the previous year, with an estimated annual number of 2.0 needlesticks/per worker, 78.7% of them did not report it; the most common reasons were the conviction that the source patient was not infected/the lack of time (both: 39.2%). The most recent PI was caused by a hollow-bore (53.5%), followed by a suture needle (22.6%). Recapping was reported by 31.7% HCWs. The highest prevalence (76.0%) of PIs was among doctors ($p<0.05$). Accidents occurred more often in the operation theatre/at the surgical wards than at the paediatric departments ($p=0.009$ and $p=0.04$ respectively). Of all the HCWs, 365 (94.8%) were fully vaccinated for hepatitis B. Anti- HBc were found in 10.0% (a half of those were not aware of an infection), anti-HCV in 0.4%, anti-HIV in 0% of 229 HCWs who agreed to be tested.

Conclusions: Hospital staff, especially those working at surgical wards, are at risk of occupationally acquired blood-borne infections due to PIs, mostly caused by needles. Such incidents are commonly underreported. Hospitals should therefore reinforce existing policies, institute better surveillance for occupational risks and enhance training of employees.

Subject: Surveillance

Keywords: occupational exposures; percutaneous injuries, blood-borne infections; HBV; HCV; HIV; medical personnel

ABSTRACT ID: 475

PRESENTED BY: Maria Ganczak / ganczak2@wp.pl

1.4. Epidemiology and impact of norovirus outbreaks in Norwegian healthcare institutions, 2006-2018

Laura Espenhain[1]

T. Berg [2], H. Bentele [3], O. Kacelnik [4]

[1] Department of Antibiotic Resistance and Infection Prevention, Norwegian Institute of Public Health

[2,3,4] Department of Antibiotic Resistance and Infection Prevention, Norwegian Institute of Public Health

Background:

Although it is mandatory to report all outbreaks in Norwegian healthcare institutions (HCIs), the burden associated with norovirus outbreaks is unknown. The aim of this study was to describe the epidemiology and impact of norovirus outbreaks in HCI in Norway.

Methods:

We carried out a descriptive analysis of all reported norovirus outbreaks in HCIs from 2006 to week 16 2018. We analysed information about onset, symptoms, number of cases among personnel and patients.

Results:

A total of 20,125 cases, including 6,947 healthcare personnel were reported in 943 outbreaks; 722 from long term care facilities (LTCFs) and 221 from hospitals with no change in number of reported outbreaks per year. Median number of cases was 15, interquartile range [9-26]. All regions reported outbreaks, with a third of the 422 municipalities having at least one outbreak in LTCFs. Vomiting and diarrhoea were main symptoms in 86% of outbreaks; "diarrhoea-only" in 8% and "vomiting-only" in 5%. In 68% of the outbreaks, symptoms lasted 1-3 days. The median number of cases was lower in outbreaks without vomiting as main symptom (9:16 persons). The peak of outbreaks happened three weeks earlier in hospitals compared to LTCFs. The estimated number of working days lost per year was at least 1738, assuming a minimum of one-day illness and two days quarantine.

Conclusions :

This is the first comprehensive description of Norwegian norovirus outbreaks in HCIs. Given that one third of all cases were healthcare professionals there is a need for further focus on infection control. Outbreaks affect all levels of healthcare and all regions. Our results suggest that hospitals, affected first, could alert LTCFs in the area in order to prevent further outbreaks.

Subject: Surveillance

Keywords: Norovirus, Public Health Surveillance, Disease Outbreaks, Health Facilities

ABSTRACT ID: 143

PRESENTED BY: Laura Espenhain / aura_espenhain@hotmail.com

1.5. Factors associated with Methicillin-Resistant Staphylococcus aureus (MRSA) acquisition rates of wards in a Singapore tertiary hospital: An electronic medical records study

Zaw Myo Tun[1]

D. Fisher [2], C. Tam [3]

[1] Saw Swee Hock School of Public Health, National University of Singapore, Singapore

[2] Division of Infectious Diseases, National University Hospital, Singapore

[3] Saw Swee Hock School of Public Health, National University of Singapore, Singapore; London School of Hygiene and Tropical Medicine, United Kingdom

Background:

The influence of patient transfers between wards in a network of hospital wards on Methicillin-resistantStaphylococcus aureus (MRSA) acquisition is unclear. We investigated ward characteristics, including ward connectivity measures, associated with MRSA acquisition rates of hospital wards.

Methods:

We used electronic records of patient transfers within a Singapore tertiary hospital during 2010-2013 to obtain measures of ward connectivity. We linked these to MRSA acquisition rates for wards with routine active MRSA screening. We used multivariable Poisson models to investigate factors associated with MRSA acquisition rates of hospital wards.

Results :

We included data from 35 wards with 92,587 eligible admissions. Overall, there were 1.8 MRSA acquisitions per 100 person-weeks (95% confidence interval (CI): 1.7-1.9). MRSA acquisition rates were higher in wards with patient in-flow volumes (rate ratio (RR) for 500-1,000 patients=5.20 (95%CI: 3.32-8.36); 2,000 or more RR=1.86 (95%CI: 1.06-3.33)) and wards receiving patients from more diverse wards (8-11 wards RR=4.16 (95%CI: 2.55-6.84); 12 or more RR=3.29 (95%CI: 2.08-5.25).

Similarly, wards with a daily average of 30 patients or more (RR=2.80, 95%CI: 1.46-5.44)) and wards with 3.5 days or longer median length of stay (RR=2.44, 95%CI: 1.49-4.04)) had higher acquisition rates. Compared to orthopaedic wards, acquisition rates were higher in other specialties: oncology RR=1.73 (95%CI: 1.22-2.45); surgery RR=4.07 (95%CI: 2.76-6.09); general medicine RR=4.21 (95%CI: 2.92-6.12); others RR=10.03 (95%CI: 5.21-19.67).

Acquisition rates were lower in critical care wards (RR=0.67, 95%CI: 0.46-0.99) and wards with beds reserved for MRSA- colonised patients (6 beds RR=0.33 (95%CI: 0.21-0.53); 14 beds RR=0.22 (95%CI: 0.11-0.43)).

Conclusions:

Our findings suggest a need to acknowledge the increased risk of MRSA acquisition in wards with higher volume and diversity of patient in-flows, and for enhancing infection control in these wards.

Subject: Modelling, bioinformatics and other biostatistical methods

Keywords: MRSA, antimicrobial resistance, social network analysis, hospital-acquired infections, epidemiology, Singapore

ABSTRACT ID: 398

PRESENTED BY: Zaw Myo Tun / zawmyotun@nus.edu.sg

Parallel Session 2
DAY 1, Wednesday 21. November 2018
11:00-12:40

Emerging and vector-borne diseases (1)

Moderator

Pawel Stefanoff

Abstracts

2.1. Lyme Borreliosis in Bavaria, Germany: Results from 5 Years of Epidemiological Surveillance

Merle M. Böhmer [1]

V. Fingerle [2]

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[2] Bavarian Health and Food Safety Authority, Oberschleissheim, Germany AND German National Reference Laboratory on Lyme-Borreliosis, Bavarian Health and Food Safety Authority, Oberschleissheim, Germany

Background:

Lyme borreliosis (LB) is the most common tick-borne disease in Europe. It is caused byBorrelia (B.) burgdorferi species pathogenic to humans. LB can affect various organ systems such as the skin (e.g. as Erythema migrans (EM)), nervous system (e.g. as acute Neuroborreliosis (NB)) or joints (e.g. as Lyme arthritis (LA)). Manifestations are categorized into early and late forms. Mandatory notification of EM, NB and LA was implemented in the German federal state of Bavaria on 1st March 2013. Study objectives were i) to describe the epidemiological situation of LB and ii) to identify risk areas/populations.

Methods:

We analysed LB cases from the first five years of mandatory notification (March 2013-February 2018) and calculated incidence (number of cases/100,000 inhabitants) by time, place and person.

Results : Overall, 20,103 cases were notified during the study period; of those 96% as EM, 2% as NB and 2% as LA. Average yearly incidence was 31/100,000. The majority of cases (55%) occurred during meteorological summer (June- August). Marked regional differences on district level (range: 1-127/100,000/year) were observed. The Bavarian Forest and parts of Franconia were identified as regions with the highest risk of LB. Increased risk for LB was also found in 5-9 year-old males as well as 50-69 year-old females. Hospitalization was recorded for 3% of cases (NB-cases: 86%).

Conclusions:

We were able to identify areas/populations in Bavaria with increased risk for LB thereby providing a basis for targeted measures to prevent LB. Since LB vaccination is currently not available, those measures should comprise i) avoiding tick bites, ii) removing ticks as soon as possible after a bite and iii) treating LB early and adequately.

Subject: Surveillance

Keywords: Lyme borreliosis, surveillance, Germany, risk areas, risk populations, preventive measures

ABSTRACT ID: 450

PRESENTED BY: Merle M. Böhmer / merle.boehmer@lgl.bayern.de

Parallel Session Abstracts

2.2. Occupational swine exposure associated with seropositivity for Ascaris suum in veterinarians in Austria, 2017/2018

Karin Taus [1]

F. Schmoll [2], H. Auer [3], S. Pekard-Amenitsch [4], F. Allerberger [5], D. Schmid [6]

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[3] Institute for Specific Prophylaxis and Tropical medicine, Centre for Pathophysiology, Infectiology and Immunology, Medical University of Vienna

Background:

Ascaris suum, a parasitic nematode, causes ascariasis in swine which represents the main reservoir. Transmission to humans occurs through exposure to swine faeces or ingestion of larvae in raw pork meat. Human A. suum infections may be asymptomatic or present as visceral larvae migrans syndrome. This study investigated the association between occupational swine exposure and A. suum-seropositivity in Austrian veterinarians.

Methods:

We recruited Austrian veterinarians during three scientific conferences in 2017. Participants completed a self-administered questionnaire on exposures associated with A. suum seropositivity and were tested for A. suum-specific IgG antibodies using an in-house Western blot. We compared participants with significant occupational swine exposure (>one swine livestock visit per week) to other participants in univariate and stratified analyses. We calculated (strata-specific) prevalence ratios (PR) with 95%CI using R version 3.4.2.

Results:

We found A. suum seropositivity of 44% (95%CI: 37.7;50.4) among 248 participating veterinarians. Participants with significant occupational swine exposure (n=62) were 1.6 (95%CI: 1.23;2.10) times more likely to be seropositive than other veterinarians. Seropositivity increased with frequency of swine exposure (across four exposure categories: 2–≥6 visits/week: p-value: <0.01). Veterinarians not using gloves during physical animal contact were 1.4 (95%CI: 1.03;1.80) times more likely to be seropositive. Among those using gloves swine exposure was no longer associated, whereas among those without glove-use the occupational swine exposure remained significantly associated with A. suum seropositive (PR: 2.13; 95%CI:1.41;3.21).

Conclusions:

Occupational swine exposure is associated with increased risk of A. suum seropositivity among Austrian veterinarians and glove-use protects against infection. Our findings indicate the importance of glove use in preventing A. suum infection in veterinarians, particularly among those with frequent swine livestock contact.

Subject: Burden of disease

Keywords: Ascaris suum, Veterinarians, Occupational Exposure, Swine, Pigs

ABSTRACT ID: 7

PRESENTED BY: Karin Taus / karin.taus@ages.at

2.3. Evaluation of the seasonal human surveillance system for neuroinvasive West Nile virus infections in France: a surveillance system that does not meet its objective

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Background:

In 2000, France implemented human surveillance for West Nile virus (WNV), to detect circulation as promptly as possible. It consists of passive surveillance of all WNV infections by the arboviruses national reference laboratory (NRL), and seasonal notification to health authorities of suspected neuroinvasive WNV infections by hospital laboratories along the French Mediterranean coast, with samples submitted to the NRL. As none of the 8 human cases identified in France from 2000 to 2016 were detected through seasonal surveillance, we evaluated the seasonal system to better inform public health surveillance priorities.

Methods:

We evaluated the usefulness, simplicity and acceptability of the seasonal surveillance system using semi-structured interviews with stakeholders. Timeliness was measured as the delay between onset and case notification, and data quality as the percentage of complete data fields in reports from 2013-2016. We compared suspect cases from surveillance data to the national hospitalization database to measure the sensitivity and representativeness of the system.

Results:

Interview respondents found the seasonal surveillance system complex and time consuming, and rated the usefulness of the notification of suspected neuroinvasive infections poor. Therefore, the acceptability of the system is low. 45% of suspected cases are notified within the target timeframe, and 46% present complete data fields. While the age distribution of suspected cases in the seasonal system is representative, the time and geographical distributions are not. The sensitivity of the system is 12% for the 2013-2016 period.

Conclusions:

The seasonal surveillance system is complex and deters ongoing participation. With appropriate screening by healthcare providers, WNV seasonal surveillance may be adequately addressed via passive submission of samples to the NRL. Seasonal notification of suspected neuroinvasive cases adds little value and could be stopped.

Subject: Surveillance

Keywords: West Nile Virus, Public health surveillance, West Nile fever, Arboviruses

ABSTRACT ID: 76

PRESENTED BY: Lauriane Ramalli / lauriane.ramalli@santepubliquefrance.fr

2.4. Circulation of non-polio enterovirus and human parechovirus types in the EU/EEA Member States, 2015-2017

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Background:

Enteroviruses (EV) and parechoviruses (HPeV) are an increasing public health concern due to recent severe EV-A71 meningoencephalitis outbreaks, acute flaccid myelitis clusters linked to EV-D68 and large outbreaks of neonatal HPeV3 infection. We analysed the circulation of EVs and HPeVs in the EU/EEA countries in order to improve recognition by frontline physicians and surveillance for these infections.

Methods:

Data request was submitted to all 31 EU/EEA countries via National Coordinating Competent Bodies in January 2018. They were asked to collect and report the aggregated number of detected and typed EV/HPeV cases by age group and month, 2015-2017. EV/HPeV typing was performed at the national public health laboratories.

Results:

25/31 EU/EEA countries participated to this study. 17,064 EV-positive samples were reported during the 3-year period and 10,886 (64%) were typed, identifying 56 types. One-third of infections were diagnosed in children <3 months of age (4,486/15,617). Most frequently typed EVs were coxsackievirus A6 (1,449 detections/ in 16 countries), echovirus 30 (E30; 1,317/19), E6 (1,248/20), coxsackievirus B5 (921/18), EV-A71 (711/19), E18 (640/17), E9 (460/14), E5 (454/9) and EV-D68 (418/15). 952 HPeV-positive samples were reported from 8 countries, and HPeV3 identified as a most common type (126/181 typed; 70%).

Conclusions :

Our study analysed the largest EV/HPeV collection from the EU/EEA countries, highlighting the wide circulation of EV/HPeVs among very young children. Coxsackievirus A6, an emerging cause of atypical hand, foot and mouth disease, was the most frequently identified type but wide circulation of EV-A71, EV-D68 and HPeV3 was also demonstrated. These data could support clinicians in recognition of EV/HPeVs linked to variable clinical presentations and promote the identification of priorities and standards for the future establishment of a European-wide surveillance network.

Subject: Surveillance

Keywords: enterovirus, parechovirus, laboratory detection, typing, Europe, outbreak

ABSTRACT ID: 246

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

2.5. Syndromic and digital surveillance of tick-borne encephalitis in Sweden, 2010-2017

Leah J Martin [1]

M. Hjertqvist [2], E. van Straten [3], P. Bjelkmar [4]

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Background:

Tick-borne encephalitis (TBE) is a vaccine-preventable, high-priority pathogen in Sweden, with increasing incidence (3.86 cases/100,000 population, 2017) and geographic spread. However, surveillance is limited to case reports. We investigated relationships between digital and syndromic surveillance data and reported TBE case data to investigate if these novel sources could provide earlier indications of disease activity.

Methods:

In Sweden, county councils provide healthcare information through a searchable website (1177.se), from which queries are extractable, and nurse-staffed telephone lines (1177 Vårdguiden). We retrospectively compared national, weekly time- series data (2010-2017) of reported TBE cases to 1177.se and Google Trends (GT) searches for “borrelia”, “tbe”, and “tick” and 1177 Vårdguiden calls for “tick bites”, including volume and peak timing, and calculated which lag times between these novel data sources and case data were most strongly correlated (Spearman rho). More in-depth analyses are planned, including investigating potential influences of media campaigns.

Results :

Searches on 1177.se for “tbe” (rho=0.85) and “tick” (rho=0.90) led case data by 8 and 7 weeks, respectively; GT searches (2012-2017) for “tbe” (rho=0.89) and “tick” (rho=0.90) led by 10 and 8 weeks, respectively; and calls for “tick bites” (rho=0.92) led by 4 weeks (all p-values <0.001). Volume discrepancies between case and supplemental data in certain years suggests areas for further evaluation, including regional analyses.

Conclusions :

Digital and syndromic surveillance data were significantly well-correlated with and preceded case data by 4-10 weeks. These novel sources may provide advanced awareness and earlier indications of disease activity. We plan to further evaluate the utility of these digital and syndromic surveillance data as supplements to reported TBE case data for national planning and preparedness in real-time.

Subject: Novel methods in epidemiology (e.g. digital disease detection, e-health)

Keywords: Public Health Surveillance, Syndromic Surveillance, Digital Epidemiology, Tick-Borne Encephalitis

ABSTRACT ID: 393

PRESENTED BY: Leah J Martin / leah.martin@folkhalsomyndigheten.se

Parallel Session 3
DAY 1, Wednesday 21. November 2018
11:00-12:40

Food- and waterborne diseases and zoonoses (1): microbiology and whole genome sequencing

Moderator

Eleanor McNamara

Abstracts

3.1. The neglected infection: Trends in Giardia cases and associated exposures after the introduction of molecular testing, 2000-2017, northeast England

Alison Waldram [1]

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[2,3] National Infection Service, Public Health England

Background:

Giardia is a common but neglected cause of infectious gastroenteritis. There is a substantial burden of undetected Giardia in the UK: for every one Giardia case notified, 14 un-reported community cases exist. Molecular testing for Giardia is becoming more popular. We aimed to assess the trend in Giardia cases and compare demographics and exposures by testing method in order to assess the impact of molecular testing for Giardia in northeast England.

Methods:

We included all Giardia cases residing in northeast England reported via the laboratory system (2000-2017) and corresponding exposure information from the northeast surveillance database. We described the trends in cases over time (2000-2017) and compared cases identified by molecular versus non-molecular methods (2012-2017) by age, sex and foreign travel using t-tests.

Results:

The trend in the number of Giardia cases in northeast England was stable (on average 43 cases per year, 2000-2012) until 2012 when a sustained increase occurred; 303 cases reported in 2017. Two of six local laboratories switched to molecular testing methods (2012-2017) producing this 600% increase in Giardia cases. There were no significant differences between molecular and non-molecular identified cases in age or sex, however foreign travel was significantly lower for molecular identified cases (34% versus 23%, $p<0.01$).

Conclusions:

Partial introduction of molecular testing has resulted in a rise of Giardia cases in northeast England: due to higher test sensitivity and opportunistic testing of all diarrhoeal samples. Cases identified by molecular methods were less likely to be travel related. We recommend that all laboratories consider the introduction of molecular testing for gastrointestinal infections in all samples, or those cases with prolonged symptoms and/or no travel history where a pathogen is not initially identified.

Subject: Burden of disease

Keywords: Giardia, Molecular testing, Exposures, England

ABSTRACT ID: 214

PRESENTED BY: Alison Waldram / alison.waldram@phe.gov.uk

3.2. Combining whole genome sequencing and epidemiological investigation to link intermittent Salmonella Agona cases to long term environmental contamination at two Yorkshire pubs

Lara A. Utsi [1]

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[4] Field Epidemiology Service, Public Health England, Leeds, United Kingdom

Background:

In October 2016, two cases of Salmonella Agona within a 5 single nucleotide polymorphism cluster (t5:13) reported eating at a pub in Yorkshire. Previous investigations into small S. Agona outbreaks in 2010 and 2012 linked to this pub chain were inconclusive. Reviewing routine sequencing results identified ongoing intermittent incidence of S. Agona t5:13 in Yorkshire. We investigated to determine the source of infection.

Methods:

We reviewed routine questionnaires from confirmed cases of S. Agona t5:13 in Yorkshire since 2010 and conducted detailed interviews with incident cases. Sequencing of environmental and historical clinical isolates from 2010 to 2013 was used to construct a phylogenetic tree.

Results:

We identified 38 cases between May 2010 and October 2017. Exposure information was obtained for 36 cases. Of these, 74% reported eating at one of two implicated premises, 16 cases at pub A and 12 at pub B. Salmonella Agona t5:13 was found in environmental samples at both pubs between 2016 and 2017 from cleaning equipment, drains, sinks, floor junctions, walls, and drainage channels inside ovens. Phylogenetic analysis demonstrated that environmental and human isolates linked to each pub shared a common ancestor, but that each site was associated with a distinct clade. Intensive deep cleaning and replacement of the ovens in November 2017 resulted in a reduction in cases, with no new cases reported between November 2017 and March 2018.

Conclusions:

This outbreak of intermittent infections over a prolonged period arose through persistent environmental contamination at two pubs with an unusual strain of Salmonella Agona. Routine sequencing can provide strong evidence, when combined with exposure information, to support the investigation and control of Salmonella outbreaks even in the absence of temporal clustering.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Infectious Disease Outbreak; Salmonella; Whole Genome Sequencing; Phylogeny

ABSTRACT ID: 226

PRESENTED BY: Lara A. Utsi / lara.utsi@phe.gov.uk

3.3. A national Salmonella Typhimurium outbreak investigation in Great Britain identifies the whole genome sequence outbreak strain in multiple animal species in different regions

Paul Crook [1]

M. Saavedra-Campos [2], L. Larkin [3], D. Curtis [4], H. Evans [5], S. Wyllie [6], R. Davies [7], J. McCormick [8], J. Lighthill [9], T. Potter [10], M. Chattaway [11], N. Elviss [12], I. Oliver [13]

[1] Public Health England

[2,3,4,5,8,11,12,13] Public Health England

[6,7] Animal and Plant Health Agency

[9,10] The Food Standards Agency

Background:

Public Health England routinely use whole genome sequencing (WGS) for Salmonella surveillance. An agreed process for sharing of animal Salmonella isolates is not established. A five single nucleotide polymorphism linkage cluster of Salmonella Typhimurium, 'the outbreak strain' (1.43.67.992.2703.3225.%), previously rarely seen, was identified in August 2017. A multi-agency national incident management team investigated.

Methods:

Cases, defined as Great Britain residents with the outbreak strain between 01 July 2017 and 03 April 2018, were interviewed. The Food Standards Agency conducted back-tracing of suspect foods. The Animal Plant Health Agency (APHA) reviewed potentially linked animal Salmonella isolates, which were sequenced. Environmental investigation was undertaken at multiple sites. A case-case study was conducted.

Results:

110 cases were reported, 60% in London, 47% in children under 10 years and 63% in Black and minority ethnic groups. One case worked on a farm where APHA had identified a high mortality Salmonella outbreak in sheep in August 2017. The outbreak strain was subsequently identified from sheep and environmental samples from this farm and linked slaughterhouses, where control measures were implemented. The outbreak strain was then identified from multiple species (cattle, chicken, lion) in different regions. Cases consumed more lamb from local butchers than expected (adjusted odds ratio 25, 95% CI 2.2-300).

Conclusions:

Only by close intelligence sharing between public, food and animal health colleagues (One health approach) was one likely source, the sheep farm, identified. WGS specificity facilitated this. However, identifying the outbreak strain in different species and locations highlights the need for work to understand the distribution of Salmonella clones in animals and the environment. An agreed process for sharing of WGS information between animal and public health agencies is recommended.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Salmonella Typhimurium outbreak sequence animal sheep

ABSTRACT ID: 339

PRESENTED BY: Paul Crook / paul.crook@phe.gov.uk

3.4. An outbreak of Listeria monocytogenes CT1234 in Austria linked by Trace-Back and Whole-genome Sequencing, 2015 – 2018

Sabine Maritschnik [1]

A. Pietzka [2], A. Falenski [3], M. Gottschald [4], L. Richter [5], F. Allerberger [6], W. Ruppitsch [7], A. Cabal Rosel [8], A. Stöger [9], S. Huhulescu [10], D. Schmid [11]

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Background:

Between November 2015 and September 2017, a total of seven invasive cases of Listeria (L.) monocytogenes serotype 1/2a occurred in Austria sharing a new pulsed-field gel electrophoresis (PFGE) pattern were identified by the National Reference Laboratory (NRL), AGES. In 2016, the NRL introduced core genome multilocus sequence typing (cgMLST). On January 26, 2018, the Ministry of Health mandated an investigation to identify the source(s) of infection and to recommend control and preventive measures.

Methods:

A confirmed outbreak case was a patient with (1) invasive listeriosis with symptoms onset on or after 1 January 2015 and (2) with L. monocytogenes having ≤2 cgMLST allelic differences from the L. monocytogenes isolate, obtained from the index case. Food/food-associated isolates of the NRL strain base, obtained between January 2016 and December 2017 and showing the same PFGE pattern were sequenced according to Ruppitsch et al.

Results:

The seven human outbreak isolates, fulfilling the outbreak case definition, and other 75 food/food-associated isolates differed from each other in less than seven alleles.Trace-back analyses of these food/food-associated isolates identified a meat processing company in Austria. Swabs from the company slicer tested positive for the outbreak strain. A detailed analysis of the company self-monitoring revealed food safety failures.

Conclusions:

CgMLST was highly discriminative in allocation of human and food/food-associated isolates to a single outbreak. It is suspected that the outbreak source was a meat processing plant slicer. We observed a reduction in the number of positive food products following installation of a new slicer. We recommend the reinforcement of the Commission Regulation

(EC) No 2073/2005 on microbiological criteria for Listeria in foodstuffs by the food safety authorities in Austria to prevent foodborne listeriosis outbreak.

Subject: Microbiology

Keywords: Listeria monocytogenes, food processing industry, outbreak, food contamination, food safety, foodborne disease, molecular typing, whole-genome sequencing

ABSTRACT ID: 335

PRESENTED BY: Sabine Maritschnik / sabine.maritschnik@ages.at

3.5. Impact of whole genome sequencing on foodborne outbreak detection and response in Canada

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[11,15] Public Health Agency of Canada, Infectious Disease Prevention and Control Branch, Centre for Foodborne, Environmental, and Zoonotic Infectious Disease, Ottawa, Canada

Background:

In 2017 the Public Health Agency of Canada implemented real-time, prospective whole genome sequencing (WGS) for Listeria monocytogenes (LM) and Salmonella, providing increased resolution compared to previous methods (pulsed field gel electrophoresis (PFGE), phage typing). The impact of this change on cluster detection and outbreak investigations in Canada will be described.

Methods:

The characteristics and trends of multi-jurisdictional clusters and outbreaks identified pre (i.e., predominantly PFGE) and post WGS implementation were examined and compared.

Results:

The number of multi-jurisdictional clusters detected decreased for LM (15 vs. 3) and increased for Salmonella (38 vs. 220). This was mirrored in the number of outbreak investigations: a decrease for LM and an increase for Salmonella, especially for Canada's most common serovars (i.e. S. Enteritidis 1 vs. 8). WGS has demonstrated that 23% of Salmonella isolates within multi-jurisdictional clusters are associated with travel. Routine sequencing of non-human isolates has improved the ability to quantify the burden of poultry, with 48% of Salmonella isolates associated with multi-jurisdictional clusters containing ≥ 1 poultry isolate. While there are currently no regulations in Canada prohibiting the presence of Salmonella in raw foods of animal origin, collaborative response to the 9 multi-jurisdictional WGS poultry-associated outbreaks has shown promise toward a framework for sustained regulatory action.

Conclusions:

Assessment and outbreak response procedures now include: evolving cluster assessment criteria, epidemiologic follow-up prioritization, exploration of new investigative approaches, enhanced collaboration among public health partners, improved integration of data collected through existing surveillance systems and changes in resource allocation. WGS has improved our detection of, and response to, foodborne outbreaks. This will ultimately help revise processes, address limitations and strengthen evidence to inform food safety policy in Canada.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Whole genome sequencing, Salmonella, Listeria monocytogenes, foodborne diseases, outbreaks

ABSTRACT ID: 469

PRESENTED BY: Courtney R. Smith / courtneyr.smith@canada.ca

Parallel Session 4
DAY 1, Wednesday 21. November 2018
14:30-15:30

Food- and waterborne diseases and zoonoses (2): epidemiology and surveillance 1

Moderator

Daniel Thomas

Abstracts

4.1. Tularemia incidence and association with rodent population dynamics, Norway, 2005-2017

Lamprini Veneti [1]

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[4] Norwegian Institute for Nature Research

Background:

Tularemia is notifiable in Norway via the Norwegian Surveillance System for Communicable Diseases (MSIS) since 1979, while the reference laboratory was established in 2005. Despite the existence of regions with higher tularemia incidence, factors explaining annual incidence variations are poorly understood. We aimed to describe the incidence of domestically acquired tularemia and examine the association with the population size of lemmings and other rodents in Norway during 2005-2017.

Methods:

We linked MSIS data with data regarding peaks of rodents collected by the Norwegian Institute for Nature Research. We conducted descriptive analysis and time series analysis allowing for trends and seasonality and calculated adjusted incidence rate ratios (aIRR) using negative binomial regression on 2005-2017 data.

Results:

During 2005-2017, 659 domestically acquired cases were reported; mean annual incidence 1.02 per 100,000 population. From 473 (72%) cases with reported potential mode of transmission, 50 % were infected from drinking water (wells, springs), 32% from contact with animals (rodents, hares), 9% from inhaling dust, and 9% from mosquitos. We observed 4-year periodicity (sine-wave p=0.294; cosine-wave p<0.001) and an increasing annual trend in tularemia cases (aIRR=1.005; p=0.003) with higher number of cases in winter (aIRR=1.97, p=0.003), summer (aIRR=1.99, p=0.002) and autumn (aIRR=4.43, p<0.001) compared with spring. Annual peak of lemmings/rodents around Norway (lemming/rodent peak year) in the current (aIRR=2.41 p<0.001) or previous year (aIRR=1.57; p=0.012) was associated with increase of tularemia cases.

Conclusions :

The seasonality and multiannual cyclic pattern of tularemia epidemics were associated with lemming/rodent density cycles, suggesting major role of lemmings/rodents in the disease spread. We recommend reinforcing infection control measures during lemming/rodent peak years and the year after, including communicating prevention guidelines on avoidance of drinking unboiled water from wells/springs.

Subject: Surveillance

Keywords: Francisella tularensis, tularemia, transmission, rodent, lemming, Norway

ABSTRACT ID: 223

PRESENTED BY: Lamprini Veneti / lambrinive@gmail.com

4.2. The prevalence and risk factors for human echinococcosis—Alaiski District, Kyrgyz republic, 2016

Aizat Arunova [1]

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Background:

In 2015, the notification rate for human echinococcosis in Alaiski District in Kyrgyzstan was 149/100,000 (122/82,000). This is almost 13 times the 2015-echinococcosis notification rate for the whole country 11/100,000 (695/6,000,000). In 2016, we conducted a study with the objectives to estimate human echinococcosis burden and identify its risk factors in the district.

Methods:

In this study, we used data from a survey conducted by the Ministry of Health in 2016. In the survey, 866 individuals were randomly selected from Alaiski district's population lists and screened for echinococcosis by ultrasound. Additionally, individuals were interviewed regarding echinococcosis-related exposures. In our analysis, cases of echinococcosis were those who had pathognomonic findings according to the WHO-2003 working group on standard ultrasound-criteria for echinococcosis. According to scientific evidence, ultrasound has 88%-98% sensitivity and 95%-100% specificity for cystic and alveolar echinococcosis. We used logistic regression to evaluate the echinococcosis- exposure associations.

Results:

Among the surveyed, echinococcosis prevalence was 24% (212/866). Of the 866 study population, 63% (542) kept dogs. Of those who kept dogs, 58% (312) fed them on unprocessed offal and 72% (388) didn't give dogs echinococcosis-anthelminthic prophylaxis. In multivariable analysis, factors associated with disease were: having a dog (OR=2.1, 95% CI 1.1-3.9) and cultivating vegetables in unprotected gardens (OR=2.0, 95% CI 1.2-3.2). Keeping dogs on leash was negatively associated with disease (OR=0.6, 95% CI 0.3-1.0).

Conclusions : The high prevalence of echinococcosis in the district is probably caused by a prevalent dog population that is not adequately kept and protected against the disease. We recommend that dogs are regularly given anthelminthic prophylaxis and that the local population are provided with health education on echinococcosis source and proper disease prophylactic measures.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: human echinococcosis, risk factors, prevalence, Alaiski district, Kyrgyzstan

ABSTRACT ID: 90

PRESENTED BY: Aizat Arunova / aizatarunova05@gmail.com

4.3. Shigellosis in Ireland: re-emergence in a new risk group

Patricia Garvey [1]

D. Igoe [2], O. Ennis [3], M. Ward [4], F. Cooney [5], A. Colgan [6], G. Cullen [7], N. DeLappe [8], M. Cormican [9], P. McKeown [10]

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Background:

Following a substantial decrease in shigellosis notifications in Ireland and internationally since the 1990s, notifications in Ireland have increased since 2015. Beacuse of this, we reviewed available data on shigellosis to describe its epidemiology in order to inform its future surveillance in Ireland.

Methods:

We described the age and sex distribution of shigellosis notifications (2004-2017). We examined foreign travel and other available risk factor data in case-based data, and transmission route data from general outbreaks notified (2004-2017). We conducted negative binomial time-series analysis to investigate incidence trends by age-group and sex.

Results:

Among 854 shigellosis notifications between 2004 and 2017, 39% of cases (n=330) were associated with foreign travel (60% where data available). Transmission by food, travel and person-to-person spread were reported in general outbreaks. Disease was commoner in males (1.3:1), particularly latterly (1.7:1 2010-2017). 74 adult males (≥15 years) were either linked with known outbreaks among men-who-have-sex-with-men (MSM) or were recorded as MSM in comments (9% of all cases, 20% of adult males). Overall, we detected an increasing trend in incidence among adult males (incidence rate ratio (IRR) =1.09 per annum (95%CI 1.05-1.14, P<0.001)) but not in children or in adult females. Among adult males in the East (which includes Dublin city), this effect was more pronounced (IRR=1.13 per annum (95%CI 1.08-1.19, P < 0.001)).

Conclusions : Foreign travel presents the strongest risk for shigellosis in Ireland and foodborne transmission has a continuing minor role. However, a rapidly increasing incidence among adult males and outbreaks among MSM reflect an emerging risk in this population. We recommend systematic collection of sexual risk factor data for shigellosis notifications to more effectively monitor shigellosis trends.

Subject: Surveillance

Keywords: Shigellosis; gastroenteric disease; sexually transmitted infection; surveillance

ABSTRACT ID: 205

PRESENTED BY: Patricia Garvey / patricia.garvey@hse.ie

Parallel Session 5
DAY 1, Wednesday 21. November 2018
14:30-15:30

International health and migration

Moderator

Ines Steffens

Abstracts

5.1. Cost-effectiveness of screening for chronic hepatitis B and C among migrant populations in the Netherlands

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Background:

Chronic infection with hepatitis B or C virus (HBV/HCV) can progress to cirrhosis, liver cancer, and even death. In a low endemic country as the Netherlands, migrants are a key risk group and could benefit from early diagnosis and antiviral treatment. Information on the cost-effectiveness of screening can promote the design and implementation of targeted interventions.

Methods :

We assessed the cost-effectiveness of screening foreign-born migrants in the Netherlands for chronic HBV and/or HCV with a Markov model using a societal perspective. Estimates on prevalence, screening programme costs, participation and treatment uptake, transition probabilities, healthcare costs, productivity losses and utilities were derived from the literature. The cost per Quality Adjusted Life Year (QALY) gained was estimated and sensitivity analyses were performed.

Results:

For most migrant groups with an expected high number of chronic infections in the Netherlands combined HBV-HCV screening is estimated to be the most cost-effective strategy, with incremental cost-effectiveness ratio's (ICERs) ranging from €4,962/QALY gained for migrants originating from the Former Soviet Union and Vietnam to €9,375/QALY gained for Polish migrants. For migrants originating from Turkey single HBV screening is the most cost-effective strategy (€6,233/QALY gained). HBV and HCV screening proved to be cost-effective for migrants from countries with chronic HBV or HCV prevalence of ≥0.41% and ≥0.22% respectively, with ICERs below the cost-effectiveness reference value of €20,000 /QALY gained. Sensitivity analysis showed that treatment costs influenced the ICER most for both infections.

Conclusions:

For most migrant populations in the Netherlands offering combined HBV and HCV screening is cost-effective. Implementation of targeted HBV and HCV screening programmes to increase early diagnosis and treatment is important to reduce the burden of chronic hepatitis B and C among migrants.

Subject: International health and migration

Keywords: Hepatitis B, Hepatitis C, screening, migrants, cost-effectiveness

ABSTRACT ID: 430

PRESENTED BY: Irene Veldhuijzen / irene.veldhuijzen@rivm.nl

5.2. A qualitative-quantitative study helped identify the most relevant issues with vaccination and improve communication in an asylum-seeker camp in Poland

Savina Stoitsova [1]

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Background:

A measles outbreak in 2016 highlighted suboptimal immunization coverage among asylum-seekers in Poland. In 2017, we used a mixed-method (qualitative/quantitative) study to understand and address issues with immunization in a camp with high vaccination refusal rates.

Methods :

Over five days we fulfilled several tasks. First, we carried out in-depth interviews with families from the main citizenships in the camp, focusing on attitudes to health, disease, and vaccination. Then, we listened to the interview records, identified major themes, and added them to a questionnaire on education, attitudes, and barriers to healthcare that also included other pre-defined questions, and was administered to all families in the camp. We calculated proportions to identify the most relevant problems and arranged a meeting that could specifically address them.

Results:

We performed in-depth interviews with six families from Russia (Chechnya), Ukraine, Tajikistan, and Azerbaijan. We identified two major themes: fear of side effects and distrust towards institutions. Out of 27 families in the camp, 23(85%) responded to the questionnaire. Parents of 10(43%) families indicated they would not vaccinate their children further, with 9 quoting fear of side effects as main reason. 17(74%) families indicated distrust towards healthcare institutions in countries of origin, and 5(22%) towards those in Poland. Finally the meeting focused on vaccine safety and engaged residents and health service representatives in positive communication, in order to increase trust.

Conclusions:

Fear of side effects and distrust towards healthcare institutions were highly prevalent in an asylum-seeker camp with high vaccination refusal rates. A mixed-method approach can be recommended in such settings, as it helped us pinpoint the relevant issues, establish trust with the residents, and carry out a tailored communication meeting within a short time-frame.

Subject: International health and migration

Keywords: vaccination, migrants, vaccination refusal, qualitative research

ABSTRACT ID: 439

PRESENTED BY: Savina Stoitsova / stoitsova@ncipd.org

5.3. High Acceptability and Satisfaction among Health Facility Informants using Mobile Digital Surveillance Outbreak Response Management and Analysis System (SORMAS) after Follow-up in Kano, Nigeria 2018

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Background : The Surveillance, Outbreak Response Management and Analysis System (SORMAS) is a mobile digital tool for surveillance and outbreak management covering 11 epidemic prone diseases (www.sormas.org) and currently being used in 15 federal states of Nigeria. We investigated usefulness and acceptability of SORMAS among users in health facilities in Nigeria.

Methods : We deployed SORMAS in all health facilities of two local government areas of Kano State, Nigeria. After completion of the user training in January 2018, we conducted repetitive user surveys through standardized questionnaires using SurveyCTO software on the users' SORMAS-tablets. Analysis included Pearson chi-square test for trends using STATA 14.

Results :

Of the 74 users of SORMAS, 35 (47%), 39(53%) and 26(35%) completed the survey at least once in February, March and April 2018 respectively. In February, March and April 2018, 20 (57%), 25 (64%), and 23 (88%) users stated that SORMAS reduced their workload, (p-value=0.329). In February, March and April 2018, 28 (80%), 33 (85%) and 24(92%) of the users indicated that they did not to have login difficulties, (p-value=0.474); 31(89%), 34 (87%), 23 (88%) stated that SORMAS would improve data quality, (p-value=0.896); and 34(97%), 38(97%) and 24(92%) would recommend the tool to their colleagues, (p-value=0.496). No statistical differences at 95% confidence interval were noted on the response patterns over time.

Conclusions :

Health facility informants in Nigeria have recurrently valued SORMAS very high on different aspects of usefulness and acceptability throughout the first three months of using it. Since we observed no significant differences over the three-month follow up, one such survey may suffice within such a period.

Subject: Novel methods in epidemiology (e.g. digital disease detection, e-health)

Keywords: MHealth, eHealth, systematic evaluation, disease surveillance, outbreak response, open source, Africa, infectious disease

ABSTRACT ID: 280

PRESENTED BY: Bernhard Silenou Chawo / daniel.tom-aba@helmholtz-hzi.de

Parallel Session Abstracts

Parallel Session 6
DAY 1, Wednesday 21. November 2018
14:30-15:30

Vaccine-preventable diseases(1): epidemiology and surveillance

Moderator

Peter Kreidl

Abstracts

6.1. Prevalence of and factors associated with pneumococcal carriage in Norwegian children, four years after introduction of the 13-valent Pneumococcal Conjugate Vaccine

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Background:

Pneumococci are often carried asymptomatically but can cause invasive pneumococcal disease (IPD). In Norway, >1,000 IPD cases occurred annually pre-vaccine introduction, mainly affecting children and elderly. Pneumococcal carriage is a prerequisite for disease, with children as main reservoir. In 2006, a seven-valent pneumococcal conjugate vaccine (PCV7) was introduced to the Childhood Vaccination Program, which was replaced with PCV13 in 2011. We aimed to estimate PC prevalence and factors associated with carriage in children attending day-care centers (DCC), 4 years after switching to PCV13.

Methods:

In 2015, we conducted a cross-sectional study in DCC using questionnaires and nasopharyngeal swabs to collect data and identify serotypes. We used chi2-test to compare carriage prevalence in 2015 with similar studies pre- PCV7 introduction, two years afterwards, and two years after switching to PCV13. We used mixed-effect multivariable logistic regression to determine associations between carriage and possible risk factors, correcting for cluster sampling.

Results:

From 40 different DCC, 896 children participated (response rate 45%; median age 44 months, range 8-80). In 2015, 48.1% [95%CI 43.7-52.5%] carried pneumococci compared to 77.7% [73.3-81.6%] (2006), 80.3% [76.5-83.6%] (2008) and 62.2% [57.9-66.4%] (2013). 2.8% [1.9-4.2%] carried vaccine serotypes in 2015 compared to 50% [44.4-55.6%] in 2006. 45.3% [40.7-50.0%] carried non-vaccine types, down from 54.9% [50.5-59.2%] in 2013, but higher than in 2006 [27.7%, 22.4-33.7%]. Combining all samples, increasing age (multiple Wald-test $p<0.001$), antimicrobial use in last three months (OR=0.42 [0.21-0.57]) and being vaccinated (OR=0.37 [0.29-0.47]) were negatively associated with carriage.

Conclusions:

Our study showed a decrease in overall carriage, mainly fuelled by the decline in vaccine serotypes after vaccine introduction. Decreased carriage will decrease transmission and reduce IPD in children, elderly and the general population.

Subject: Burden of disease

Keywords: Pneumococcal carriage, PCV13, Prevalence

ABSTRACT ID: 72

PRESENTED BY: Astrid Lovlie / astrid.louise.lovlie@fhi.no

6.2. The severity and clinical manifestation of invasive meningococcal serogroup W disease in comparison to other serogroups in the Netherlands

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Background:

In the Netherlands, invasive meningococcal disease caused by serogroup W (IMD-W) has been rare, with an average of four cases per year from 2002-2014. Since October 2015, a sudden increase in IMD-W cases was observed, which led to the decision of the Ministry of Health to implement MenACWY vaccination in 2018. In order to evaluate if IMD-W cases differ from other serogroups (non-IMD-W), we compared the severity and clinical manifestation of IMD-W with non-IMD-W for 2015-2017.

Methods:

All microbiological laboratories in the Netherlands submit Neisseria meningitidis isolates from blood, cerebrospinal fluid or other normally sterile material to the Netherlands Reference Laboratory for Bacterial Meningitis for typing. We calculated serogroup-specific (W and non-W) incidence rates (IR), incidence rate ratios (IRR), case fatality rates (CFR), and compared main clinical manifestations.

Results:

The IR of IMD-W increased significantly from 0.05/100,000 in 2015 (n=9) to 0.46/100,000 in 2017 (n=80; IRR=8.7 [95% CI: 4.6-18.6]), while the non-IMD-W IR increased slightly from 0.44/100,000 in 2015 (n=76) to 0.68/100,000 in 2017 (n=118; IRR=1.5 [95% CI: 1.2-2.1]). The mean age of IMD-W cases was significantly higher than non-IMD-W cases (41 vs 16 years, $p<0.001$). IMD-W cases more often presented with septicemia (47% vs 33%, p=0.007) or pneumonia (14% vs 6%, p=0.02) and less often with meningitis (22% vs 54%, $p<0.001$) compared to non-IMD-W cases. The CFR of IMD-W was 13% (17/133), significantly higher than for non-IMD-W (5%, 13/268, p=0.005), even after adjustment for age and clinical manifestation (p=0.03).

Conclusions:

In the Netherlands, IMD-W cases were more severe, affecting older age groups and associated with different clinical manifestations, compared to cases caused by other serogroups. Our findings support the decision to implement MenACWY vaccination in the Netherlands.

Subject: Surveillance

Keywords: Meningococcal Infections, Neisseria meningitidis, Public Health Surveillance, Disease Notification, Netherlands, Serogroup W-135

ABSTRACT ID: 69

PRESENTED BY: Anna D. Loenenbach / aloenenbach@gmail.com

6.3. Striking differences in reported pertussis incidence between Norway and Sweden not confirmed in seroepidemiology, 2012-13

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Background:

During 2009-2013 reported incidence of pertussis was 20–50 fold higher in Norway compared to Sweden, despite similar vaccination coverage and schedules (3, 5, 12 months; 4th dose at 5-6 years in Sweden with a catch-up at 9-11 for those born before 2002, and at 7-8 years in Norway), although Sweden did not vaccinate against pertussis between 1979 and 1996. To investigate the actual difference in antigen pressure, we performed a seroprevalence study.

Methods:

In 2012-2013, residual laboratory specimens (Sweden: n=3618; Norway: n=3058) from individuals 2-100 years old were collected and analyzed in each country with a harmonized in-house anti-PT IgG ELISA. The proportion of samples with IgG- anti-PT levels of 50-100 IU/ml (indicating recent exposure) and >100 IU/ml (indicating very recent exposure) were calculated by age group and country. Exact proportion tests were used to investigate if the proportions were equal between countries in each age group. Results were age-standardized to the 2012 Swedish population.

Results:

Proportion of samples indicating recent exposure differed significantly between countries only in the recently vaccinated age groups 5-6 years (10.8% Sweden, 0.8% Norway, $p<0.001$) and 7-8 years (2.0% Sweden, 8.5% Norway, $p=0.02$). Among samples indicating very recent exposure, significant differences were found for 5-6 (8.2% Sweden, 1.1% Norway, $p<0.01$), 7-8 (0.0% Sweden, 5.0% Norway, $p<0.01$), 9-11 (5.0% Sweden, 0.7% Norway, p-value<0.001) and 16-17 year olds (0.7% Sweden, 5.3% Norway, p-value=0.03).

Conclusions:

Beyond the expected differences in recently vaccinated age groups and in 16-17 year olds, we found no significant differences in pertussis seroprevalence between Sweden and Norway, suggesting similar disease burden. Our findings emphasize the need of a greater awareness of possible discrepancies in incidence reporting and the importance of laboratory method harmonization.

Subject: Surveillance

Keywords: Pertussis, Seroepidemiologic Studies, Prevalence, Incidence, Vaccination

ABSTRACT ID: 477

PRESENTED BY: Sharon Kühlmann-Berenzon / sharon.kuhlmann-b@folkhalsomyndigheten.se

Parallel Session 7
DAY 2, Thursday, 22. November 2018
11:00-12:40

Cholera

Moderator

Günter Pfaff

Abstracts

7.1. The geographical spread of the cholera epidemic in the Democratic Republic of the Congo. An analysis of national syndromic and laboratory surveillance data, 2008-17

David Hendrickx [1]

B. Ingelbeen [2], B. Miwanda [3], M. van der Sande [4], M. Mossoko [5], V. Vanlerberghe [6], O. Lunguya [7], J. Jacobs [8], M. Boelaert [9], B. Kebela [10], D. Bompangue [11], J. Muyembe [12]

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Background:

An unprecedented countrywide cholera outbreak was reported in the Democratic Republic of the Congo (DRC) in 2017. We sought to elucidate the dynamics of cholera spread in DRC that culminated in the present outbreak to inform targeted prevention and control interventions.

Methods:

We used national cholera syndromic surveillance and reference laboratory data collected from January 2008 to November 2017 to describe trends in reported cases, case fatalities and serotyping data; map annual cumulative incidences by health zone; and summarise the characteristics of major outbreaks.

Results:

In the study timeframe, 270,852 cholera cases and 5,231 deaths (1.9% case fatality) were reported. Eighty-two percent of cases were reported in cholera endemic provinces. Of 9,510 suspect case specimens submitted to the reference laboratory, 31% were laboratory confirmed. Inaba was the most commonly identified serotype (90.3%), followed by Ogawa (9.5%) and Hikojima (0.2%). We identified the occurrence of nine major outbreaks, three of which occurred in non-endemic provinces. Incidence mapping and trends in reported cases by province revealed three distinct mechanisms in the spread of cholera in DRC: (i) significant increases in the number of cases in cholera-endemic areas in eastern DRC (2011 and 2015); (ii) recurrent outbreaks progressing downstream along the Congo River (2011-2012 and 2015-2017), and (iii) spread along Congo River branches to areas that had been cholera-free for over a decade (2017).

Conclusions:

There remains an important cholera outbreak potential in DRC. Our analysis of cholera spread mechanisms over time and place provides insights in when and where to focus cholera prevention and control efforts in order to avoid more widespread outbreaks from occurring.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Cholera, epidemiology, disease outbreaks, Vibrio cholera, epidemics, Democratic Republic of the Congo, syndromic surveillance

ABSTRACT ID: 348

PRESENTED BY: David Hendrickx / david.hendrickx@rps.bwl.de

7.2. High case fatality during cholera outbreaks in non-endemic provinces, Democratic Republic of the Congo (DRC), 2008-17

Brecht Ingelbeen

D. Hendrickx [2], M. Van der Sande [3], B. Miwanda [4], H. Vochten [5], M. Mossoko [6], J. Nyakio Kakusu [7], V. Vanlerberghe 8, J. Jacobs [9], M. Boelaert [10], B. Kebela [11], D. Bompangue Nkoko [12], J. Muyembe-Tanfum [13]

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Background:

In 2017, an ongoing countrywide cholera outbreak in the DRC resulted in >53,000 reported cases and 1,145 deaths. We estimated cholera case fatalities (CF) to identify high-risk areas/groups, and guide control measures.

Methods :

We used data from 2008-17 weekly suspected cholera surveillance and 2015-17 MSF cholera treatment centre (CTC) admission registers. A cholera case was defined as acute watery diarrhoea during an outbreak, or severe dehydration or death following acute watery diarrhoea. Provinces were defined as endemic when ≥1 health zone reported cholera cases for >4 consecutive weeks every year. We calculated risk ratios (RR), comparing CF in provinces, age groups and weeks of admission throughout an outbreak.

Results:

During 2008-2017, 270,852 cases and 5,231 deaths (CF 1.9%) occurred. CF in cholera non-endemic provinces (4.3%;2,079/46,640) was three-times higher than in endemic provinces (1.4%; 3,152/224,212; RR 3.17, 95%CI 3.00-3.35). Cases aged ≥5 years had a CF of 2.1% (4,331/204,483), compared to 1.4% (911/66,008) among cases <5 years (RR 1.52, 95%CI 1.42-1.64). Among CTC patients, CF increased from 2.6% in <20 year olds (109/4,201) to 3.8% in 20-49 year olds (99/2,609; RR 1.46, 95%CI 1.12-1.91) and 4.3% in ≥50 year olds (32/752; RR 1.64, 95%CI 1.11-2.41). During the 2015-17 outbreaks, CF of CTC patients decreased throughout an outbreak from 5.1% (week 1) to 4.4% (week 5; RR 0.86, 95%CI 0.52-1.45) and 0.7% (week 10; RR 0.14 95%CI 0.04-0.45).

Conclusions:

The higher CF in non-endemic provinces and in the first weeks of an outbreak possibly reflects lower levels of natural immunity and limited disease awareness, access to treatment and water and sanitation services. Targeted use of cholera vaccine, soon after the occurrence of initial cases in non-endemic areas, may decrease CF.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Cholera/epidemiology; Disease Outbreaks; Vibrio cholera; Epidemics/history; Democratic Republic of the Congo/epidemiology

ABSTRACT ID: 277

PRESENTED BY: Brecht Ingelbeen / brechtingelbeen@gmail.com

7.3. Preparedness of primary healthcare facilities to respond to a cholera outbreak in Kinshasa, Democratic Republic of the Congo, 2018

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Background:

From November 2017 to April 2018, Kinshasa experienced a large cholera outbreak with over 1200 cases reported. For case management, five temporary cholera treatment centers (CTC) were established across the city. However, patients first reported to primary healthcare centers (HC) before being transferred to the nearest CTC. Epicurves from the past four years show a seasonal increase in case incidence every June. The current study aimed to assess the level of preparedness of HC in responding to a potential new cholera outbreak.

Methods:

Between 23 February and 9 April 2018, we conducted a descriptive cross-sectional survey in 180 out of 374 HC in Kinshasa, selected using a stratified random sampling method. Through interviews with nurses and observation, and using the mobile application Epicollect5, we collected data on availability of space for transitional isolation, prepositioning of medical supplies for cholera case management, and existing infection prevention and control (IPC) measures. We used descriptive statistics to analyze the data. GPS locations were also collected and used to map HC.

Results:

Of the 180 HC surveyed, 10% had space for transitional isolation, while 8% and 5% had pre-positioned chlorine and hydroalcoholic solutions, respectively. Cholera case definitions, hand hygiene promotion material and protection masks were available in 3%, 39% and 49% of HC, respectively. Only 25 HC (13.8%) met the minimum IPC standards (access to improved water source, improved latrines, hand washing stations, sterilization equipment and waste disposal systems).

Conclusions : The level of preparedness of HC in responding to a new cholera outbreak remains poor. The results suggest an urgent need to develop an action plan for improving IPC conditions and prepositioning of medical supplies for cholera case management in HC.

Subject: Preparedness

Keywords: cholera, preparedness, outbreak

ABSTRACT ID: 461

PRESENTED BY: Patricia Ndumbi / patricia.ndumbi@gmail.com

7.4. High cholera vaccination coverage following emergency campaign in Haiti: results from a spatial cluster survey

Ashley Sharp [1]

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Background:

Oral cholera vaccine (OCV) has increasingly been used as an outbreak control measure, but vaccine shortage limits its application. A two-dose OCV campaign targeting residents aged over 1 year was launched in three rural Communes of Southern Haiti during an outbreak following Hurricane Matthew in October 2016. Door-to-door and fixed-site strategies were employed and mobile teams delivered vaccines to hard-to-reach communities. This was the first campaign to use the recently pre-qualified OCV Euvichol. The study objective was to estimate post-campaign vaccination coverage in order to evaluate the campaign and guide future outbreak control strategies.

Methods:

We conducted a cluster survey with spatial random sampling. We identified clusters of five households and included all members eligible for vaccination. Local residents collected data through face-to-face interviews. Coverage was estimated using percentages and 95% confidence intervals accounting for the clustered sampling.

Results:

435 clusters, 2,100 households and 9,086 people were included (99% response rate). Across the three communes coverage by recall was: 80.7% (95% CI:76.8-84.1), 82.6% (78.1-86.4), and 82.3% (79.0-85.2) for two doses respectively, and 94.2% (90.8-96.4), 91.8% (87-94.9), and 93.8% (90.8-95.9) for at least one dose. Coverage varied by less than 9% across age groups and was similar among males and females. Participants obtained vaccines from both door- to-door (53%) and fixed-site (47%) vaccinators. Most participants heard about the campaign through community 'criers' (58%).

Conclusions:

Despite the hard-to-reach communities, high coverage was achieved in all areas through combining different vaccine delivery strategies and extensive community mobilisation. Emergency OCV campaigns are a viable option for outbreak control and where possible several strategies should be used in combination. Euvichol will help alleviate the OCV shortage but effectiveness studies in outbreaks should be done.

Subject: International health and migration

Keywords: Cholera, Vaccination, Haiti, Survey

ABSTRACT ID: 156

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

7.5. Late breaker: Cholera Outbreak Response in a Complex Emergency: The Importance of Oral Cholera Vaccine in Borno State, North-eastern Nigeria, January, 2018,

Kumshida Balami [1]

A. Malgwi [2], A. Njidda [3], A. Hassan [4], R. Nnaji [5], W. Eteng [6], S. Balogun [7], J. Obasanya [8], C. Owili [9], P. Nguku [10], C. Ihekwaezu [11]

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Background:

Cholera Outbreak is a global health problem amongst Internally Displaced Persons (IDPs) and areas facing complex emergencies. The insurgency in North Eastern Nigeria caused disruption in social services, and displacement of thousands into IDP camps which are overcrowded with sub-optimal Water, Sanitation and Hygiene. We confirmed, characterise the outbreak and instituted control measures with the first ever use of Oral Cholera Vaccine (OCV) in Nigeria

Methods:

We defined a Suspected Cholera Case as any person in Borno State presenting with acute watery diarrhoea and severe dehydration between 14th August to 21st December, 2017. We did a descriptive and analytic study. We conducted an OCV campaign in two phases using Polio vaccination structure targeting all people ≥ 1year of age in affected communities and IDP camps

Results:

We line-listed 6430 cases with 61 Deaths. 3512 (54.6%) Jere, 1870(29.1%) Monguno, 845 (13.3%) Dikwa, 115 (1.8%) Guzamala, 63 (1.0%) Maiduguri, 23 (0.4%) Mafa and 2 (0.03%) from Gubio Local Government Areas. 6109 (95%) cases were from IDP camps.175 stool samples were culture positive. Median age was 9years and 2780 (52%) were females. 896,919 people were vaccinated using 914,565 doses of OCV giving the coverage rate of 105%. Wastage rate was 0.4% No Adverse Events Following Immunization. Highest number of daily cases was 122 recorded on the fourth day of vaccination since then, cases declined till the end of the outbreak. Overall Case Fatality Rate, CFR (1.1%)

Conclusions:

There was a Protracted Cholera outbreak that increased in magnitude and strength affecting mostly children in IDP camps. Reactive OCV might have influenced ending of the outbreak. Despite the complex and challenging context, the outbreak was contained within four months with a Low CFR

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Outbreak Respnse, Complex Emergency, Oral Cholera Vaccine, Internally Displaced Person, Acute Watery Diarrhea, Severe Dehydration, Suspected Cholera Case

ABSTRACT ID: 558

PRESENTED BY: Kumshida Balami / abigailkumshida@gmail.com

Parallel Session 8
DAY 2, Thursday, 22. November 2018
11:00-12:40

Food- and waterborne diseases and zoonoses (3): outbreaks

Moderator

Anders Wallensten

Abstracts

8.1. Rapid investigation of hepatitis A outbreak led to recall of Iranian dates, Denmark 2018

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Background:

On 30 January 2018, we identified a patient cluster with domestic acquired hepatitis A virus (HAV) at Statens Serum Institut. HAV is not endemic in Denmark and outbreaks are rare. An outbreak investigation was initiated to identify the source and stop the outbreak.

Methods :

We tested IgM-positive samples from local laboratories for virus RNA by PCR and performed characterization by sequencing. Cases were symptomatic domestically infected HAV IgM-positive patients with sample date between 1 January and 15 March 2018. We excluded patients with a genotype IA or IB. We conducted a matched case-control study to estimate matched odds-ratios (MOR) and 95% confidence intervals (CI). Food sampling and trace-back investigations were also conducted.

Results:

We identified 30 cases; 24 were hospitalized and one died. Typing for 19 cases revealed several genotype IIIA strains. Interviews led to the suspicion of dates sold in a specific supermarket chain. Cases were more likely to consume dates than controls (MOR=14.5, 95%CI 3.23-64.6). The dates were traced back to an Iranian producer and recalled from the supermarket chain on 6 February 2018. HAV was identified in one open package of dates from a patient, and typing showed identical strains. Through international networks it was recognized that Germany and Norway had received dates from the same batches. This led to a recall in Norway; one Norwegian patient was detected with an outbreak strain.

Conclusions:

This outbreak was solved within one week from the detection of the outbreak to recall of the implicated dates by epidemiological proof. The rapid investigation is likely to have prevented further cases. International trade of ready-to-eat food from HAV endemic to non-endemic countries poses a particular risk of HAV infections.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Hepatitis A, Disease Outbreak, Case-control study

ABSTRACT ID: 303

PRESENTED BY: Luise Müller / lum@ssi.dk

8.2. Outbreak of Clostridium perfringens associated with consumption of roasted meat and gravy at a buffet on Mothering Sunday 2018

Simon Packer [1]

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Parallel Session Abstracts

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[7] South West Health Protection Team, Public Health England.

[8] Field Services, Public Health England

Background:

In March 2018 Public Health England were alerted to an outbreak of gastrointestinal illness in persons who had eaten at a restaurant in the South West of England on Mothering Sunday. We aimed to determine the source of infection and control the outbreak.

Methods:

A retrospective cohort study was undertaken among all persons who ate at the restaurant on 11th of March. Cases were defined as any person who consumed food from the restaurant and had diarrhoea or vomiting between 12:00hrs 11/03/2018 and 15/03/2018. Data were collected using a secure electronic questionnaire. Descriptive, univariable and multivariable analyses were undertaken with odds ratios (OR) and 95% confidence intervals (CI) for exposures calculated. Clinical and food samples were collected and underwent microbiological testing and molecular typing (fAFLP).

Results:

The restaurant reported 398 covers, 177 (44.4%) persons completed the survey and 146 (82.5%) provided sufficient information for inclusion in the analysis. Eighty-one (attack rate 55.5%) persons met the case definition; eating from the roasted meat buffet was associated with illness (OR: 7.8, 95% CI: 2.03-43.56). No single food item explained 100% of the cases. Independent associations between consumption of gravy (aOR: 5.35, 95% CI:2.21-12.93), lamb (aOR: 2.51, 95% CI:1.06-5.96), and eating during the later 16:00 sitting (aOR: 5.23, 95% CI:1.76-15.54) were identified. Clinical, roasted lamb, beef and turkey samples were all positive for enterotoxigenic Clostridium perfringens indistinguishable by molecular typing.

Conclusions:

We found strong evidence for a C.perfringens outbreak associated with gravy and/or lamb consumption. The data suggests cross-contamination between items, which increased with time. Roast meat buffets should ensure that meats and gravy are served immediately after appropriate cooking and that separate serving equipment are used to prevent cross contamination.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Outbreak investigation; gastrointestinal disease; Clostridium perfringens; roast meat buffet; molecular typing; infection

ABSTRACT ID: 240

PRESENTED BY: Simon Packer / simon.packer@phe.gov.uk

8.3. An outbreak of campylobacteriosis at a rural hotel in England: the ongoing risk of outbreaks due to consumption of chicken liver dishes

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Background:

A sizable body of literature supports the risk of campylobacteriosis associated with eating chicken liver pate. Despite this, outbreaks continue to occur. In January 2017, six cases of campylobacteriosis were reported, all having eaten at the same rural hotel in December 2016. Three Christmas parties were held at this venue on the same day and included 73 attendees. All three parties ate from the same set menu. The outbreak was investigated to identify the source and to implement control measures.

Methods:

A retrospective cohort study was undertaken to test the hypothesis that consumption of individual food items was associated with an increased risk of illness. Attendees were asked to complete an online questionnaire on consumption of food items and known risk factors for sporadic campylobacteriosis. We performed univariable, multivariable, dose response and sensitivity analyses.

Results:

In total, there were 19 cases of campylobacteriosis linked to the outbreak; 7 confirmed and 12 probable. Incubation period ranged between 4 hours and 4 days. Chicken liver pate was the food item most strongly associated with illness ($p < 0.001$) with a corresponding high crude relative risk (12.95). This relationship was supported by multivariable analyses, sensitivity analyses and a clear dose-response relationship.

Conclusions:

The results were suggestive of a single point source exposure with a strong association between the consumption of chicken liver pate and campylobacteriosis. This outbreak highlights that despite Food Standards Agency guidance demonstrating that simple techniques can ensure all campylobacter are killed during cooking, outbreaks in the UK and other countries continue to occur. Public and professional awareness needs to be raised further to reduce the risk of campylobacteriosis linked to incorrectly cooked chicken liver dishes.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Campylobacter, Gastroenteritis, Disease outbreak

ABSTRACT ID: 242

PRESENTED BY: Adrian Wensley / adrian.wensley@phe.gov.uk

8.4. Human brucellosis outbreak, March to September 2017, South Morocco

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Background:

Brucellosis is a zoonotic disease with a worldwide distribution especially in the Mediterranean Region. Human and animal brucellosis is a mandatory notified disease in Morocco, . On 13 July 2017, the central level has notified an increase of the human brucellosis exceeding 100 cases in Laâyoune Sakia El Hamra Region. The aim of the study is to investigate the outbreak and to propose control and prevention measures.

Methods:

We carried a retrospective descriptive survey from 06/03/2017 to 13/09/2017, we defined a case on the basis of clinical symptoms and laboratory criteria's including CDC case definition. Demographic, clinical, serological, and behavioral characteristics of patient were explored. Data analysis was performed using Epi-Info.7.

Results:

A total of 142cases was reported at LSE region. The incidence was 38,6 cases/100,000 inhabitants ,almost 2 times higher than the annual incidence recorded in Morocco between 2000 and 2016. Two cases were hospitalized with chronic form(spondylopathy). The most affected age group was 15-69 years old (73%), with a female/ male ratio 1:1. Two cases have been confirmed positive for Brucella Bovis Abortis. The consumption of unpasteurized milk was notified in 123 cases (87%). The epidemic curve shows a persistant and commun source. The outbreak is due to the consumption of unpasteurized dairy products according to the local eating behavior. The geospatial repartition of cases was around the main boulevard of Laayoune city, where is located the dairy industry.

Conclusions:

Brucellosis is a real public health problem in Morocco which require the instauration of "One heath" concept, and the education of the population to minimize exposure to the unpasteurized milk.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Human brucellosis, Outbreak, South Morocco

ABSTRACT ID: 307

PRESENTED BY: Hind Majidi / hind.majidi222@gmail.com

8.5. Late breaker: From local to national to international: Salmonella enteritidis outbreak in a Chinese restAurant linked via Whole Genome Sequencing (WGS) to European outbreak

Natalie Wright [1]

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Background:

All salmonellae isolated in NHS laboratories in England are sent to the Public Health England (PHE) reference laboratory for WGS – a form of DNA profiling which provides information on the degree to which different strains of microorganisms are genetically related, and is therefore helpful in determining whether cases are likely to be linked. In May 2018, PHE in Birmingham was notified of 25 confirmed cases of Salmonella enteritidis, all of which were epidemiologically linked to a Chinese restaurant in Birmingham.

Methods:

Epidemiological, environmental and microbiological investigations were conducted in the management of the outbreak locally, as well as the swift implementation of control measures. Microbiologically, faecal samples were first identified as Salmonella species at local NHS laboratories, and were subsequently sent to the reference laboratory for further serotyping and WGS. WGS results were examined in the context of an international database of Salmonella enteritidis strains.

Results:

All 25 cases were within the same 5 – single nucleotide polymorphism (SNP) cluster (1.2.3.18.359.360.%), and 23 shared the same identical SNP-address (1.2.3.18.359.360.9922). A previous (2016) international investigation into this same 5 SNP cluster had identified numerous egg-laying chicken farms in Poland as the source of contaminated eggs exported throughout the EU. This local outbreak then formed part of the international investigation into the strain's re- emergence.

Conclusions:

WGS techniques ultimately enabled this local outbreak of Salmonella at a restaurant in Birmingham, to be linked to an international investigation into the re-emergence of a particular strain of Salmonella enteritidis, known to be associated with contaminated eggs exported from Poland. This represents an exciting step forward in the use of genotyping to quickly establish links between seemingly locally-confined outbreaks and large-scale investigations.

Subject: Novel methods in microbiology (e.g. new diagnostic tools)

Keywords: Salmonella / whole genome sequencing / outbreak / eggs / food-borne

ABSTRACT ID: 607

PRESENTED BY: Natalie Wright / natwright18@hotmail.com

Parallel Session 9
DAY 2, Thursday, 22. November 2018
11:00-12:40

Vaccine-preventable diseases(2): vaccine effectiveness

Moderator

Susan Hahné

Abstracts

9.1. Effectiveness of one dose of acellular pertussis vaccine in hospitalised infants in six EU/EEA countries: preliminary results of the ECDC PERTINENT project, 2016-2018

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Background:

PERTINENT, Pertussis in Infants European Network, is an active surveillance system including 41 hospitals from six EU/EEA countries (https://sites.google.com/a/epiconcept.fr/pertinent). PERTINENT aims at measuring vaccine effectiveness (VE) against pertussis in hospitalised infants aged <1year.

Methods:

From December 2015 to April 2018, hospitals recruited infants presenting with pertussis-compatible symptoms. Cases were vaccine-eligible hospitalised infants testing positive for Bordetella pertussis by PCR or culture; controls were those testing negative to all Bordetella spp. For each vaccine dose, we defined an infant as being vaccinated if he/she had received the corresponding dose >14 days before symptoms onset. We calculated pooled VE as 100*(1-odds ratio of vaccination) adjusted by site, onset date in quarters and age-group (2, 3, 4, ≥5months).

Results:

Of 1735 recruited infants, we included 160 cases and 539 controls eligible for vaccination. The median-age was 3.9 months for cases and 4.6 months for controls (p=0.009). The median-weight at birth was 3220g for cases and 3170g for controls (p=0.6). Thirty-eight cases (24%) had received one pertussis vaccine dose, 31 (19%) two doses and 7 (4%) three doses. Among controls, 165 (31%) had received one dose, 167 (31%) two doses and 25 (5%) three doses. One-dose VE was 61% (95%CI: 29-79) among infants aged <1year (n=469) and 47% (95%CI: -2-72) among those in the age-group targeted by the first dose as defined in each country (n=411).

Conclusions:

Our results suggest a good one-dose VE in infants aged <1year. However, this age-group includes older infants that have not received the scheduled second dose. When restricting to the one-dose age-group, VE estimate is imprecise due to small sample size. Further recruitment will result in a larger sample size enabling VE calculation for each dose.

Subject: Surveillance

Keywords: Whooping cough,P ertussis vaccine, Public Health Surveillance, Burden of Disease

ABSTRACT ID: 429

PRESENTED BY: Lore Merdrignac / l.merdrignac@epiconcept.fr

9.2. Effectiveness of the 23-valent pneumococcal polysaccharide vaccine against invasive pneumococcal disease in older adults by high risk conditions type: Results of SpIDnet/I-MOVE+ multicentre study,

Camelia Savulescu [1]

P. Valentiner-Branth [2], J. Mereckiene [3], B. Winje [4], P. Ciruela [5], P. Latasa [6], M. Guevara [7], R. Carragher [8], T. Dalby [9], M. Corcoran [10], D. Vestrheim [11], C. Munoz-Almagro [12], J. Sanz [13], J. Castilla [14], A. Smith [15], E. Colzani [16], L. Pastore Celentano [17], G. Hanquet [18], A. SpIDnet/I-MOVE+ group [19]

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Background:

Twenty-three-valent polysaccharide (PPSV23) and 13-valent pneumococcal conjugate (PCV13) vaccines are licensed for the prevention of invasive pneumococcal disease (IPD) in the elderly. PPSV23 vaccination is recommended in all sites (8-69% uptake) and PCV13 in two sites for persons with high-risk conditions (<5% uptake). We measured the PPSV23 effectiveness in adults 65+ year-olds against IPD by type of high-risk conditions, pooling surveillance data from seven European sites.

Methods:

Using notifications between 2012 and 2016, we compared the vaccination status of cases of IPD caused by PPSV23 serotypes to that of nonPPSV23 IPD (controls) stratified by high-risk condition type: none, immunocompetent and immunocompromising high-risk conditions. We defined PPSV23 vaccination as having received at least one dose. We computed PPSV23 pooled effectiveness as (1 – vaccination odds ratio)*100 and confidence intervals (95%CI), adjusted for site, age group, sex, and notification year.

Results:

We included 1955 cases and 856 controls. In the analyses restricted to IPD with no high-risk conditions (n=849) and immunocompetent high-risk conditions (n=1329), cases were younger than controls (p=0.002, p=0.016, respectively), and less likely to present with meningitis (p=0.037, p=0.001, respectively). There was no difference between cases andcontrols for the IPD with immunocompromising conditions (n=633). PPSV23 effectiveness was 55% (95%CI: 29-71), 37% (95%CI: 18-52), 7% (95%CI: -33; 34) for IPD with none, immunocompetent and immunocompromising high-risk conditions, respectively (p Mantel-Haenzsel test of homogeneity=0.018).

Conclusions:

Our findings suggest that the type of high-risk condition modifies the PPSV23 effectiveness against IPD caused by PPV23 serotypes. Effectiveness was higher among healthy older adults and lower among older adults with immunocompromising conditions. PPSV23 effectiveness by type of high-risk condition should be taken into account when defining pneumococcal vaccination strategies for older adults.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

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

ABSTRACT ID: 220

PRESENTED BY: Camelia Savulescu / c.savulescu@epiconcept.fr

9.3. Invasive pneumococcal disease in Tuscany region, Italy: integrating multiple data sources to estimate underreporting and underdiagnosis

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Background:

Invasive pneumococcal disease (IPD) is a vaccine-preventable disease characterized by isolation ofStreptococcus Pneumoniae in normally sterile sites, usually presenting as meningitis or sepsis. Since 2007 Italy has implemented an IPD national surveillance system (IPD NSS). This system, however, suffers from high rates of underreporting. This study aims to estimate the level of underreporting and underdiagnosis of IPD in 2016 in Tuscany (Italy) integrating data from IPD NSS, Tuscany regional microbiological surveillance and hospitalization discharge records.

Methods:

To estimate IPD cases in Tuscany in 2016, we collected: 1) notifications to IPD NSS 2) microbiological surveillance records of positive cultures for S. Pneumoniae from normally sterile sites 3) hospitalization records with IPD-related ICD9 codes in discharge diagnoses. We performed data linkage on the three databases to obtain the number of IPD single cases and calculated underreporting rate. We performed a preliminary three-source log-linear capture–recapture analysis to estimate the occurrence of undiagnosed IPD cases.

Results:

We found 74 IPD cases in IPD NSS, 130 in the regional microbiological surveillance, 321 in hospitalization discharge records. After data-linkage, a total of 403 single cases were identified (59% male, mean age 69,1). An underreporting rate of 81,6% was found. Incidence of disease from diagnosed cases was 10,7/100.000 inhabitants. A preliminary capture–recapture analysis suggested that at least one third of IPD cases were not diagnosed in our population.

Conclusions:

This study shows ongoing weaknesses in the IPD surveillance system in Tuscany with substantial underreporting and underdiagnosis. Integration of available data sources may be a useful approach to complement surveillance and provide decision-makers with better information to plan effective control strategies against IPD.

Subject: Surveillance

Keywords: Invasive pneumococcal disease,evaluation of surveillance,vaccine preventable diseases,capture-recapture analysis

ABSTRACT ID: 388

PRESENTED BY: Filippo Quattrone / filippo.quattrone@med.unipi.it

9.4. Invasive pneumococcal disease caused by serotypes 3 and 19A in older adults of 10 European countries after six years of childhood PCV10/13 vaccination

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Background:

SpIDnet/I-MOVE+ European network conducts surveillance for invasive pneumococcal disease (IPD) in adults ≥65 year- olds at 13 sites (10 countries). Since 2010-11, childhood pneumococcal conjugate vaccination (PCV) is implemented with PCV13 in six sites, PCV10 in two and both PCV10/13 in five. We assessed the dynamics of IPD caused by two highly prevalent serotypes in older adults, 3 and 19A (contained in PCV13), to inform decision-making on PCV13 vaccination policies in that age group.

Methods:

We calculated IPD incidence rate ratios (IRR) in ≥65 year-olds, by site, comparing the last PCV10/13 year (2016) to 2009 (pre-PCV10/13). We computed pooled IRR and 95% confidence intervals (CI) using random-effects meta-analysis, and the changes in incidence as (1-IRR)*100.

Results:

After six years of childhood PCV10/13 programme, the incidence of serotype 3 IPD in older adults increased 16% (95%CI:-4 to 41) in all sites; it decreased until 2014 and then increased in the six PCV13 sites (+1%; -12 to 17) and increased 54% (12 to 112) in the four sites using PCV10. The incidence of serotype 19A IPD declined by 23% (-42 to 58) in all sites, with a 49% (21 to 66) decline in PCV13 sites and a 147% (8 to 463) increase in sites using PCV10. In 2016, serotypes 3 and 19A caused 19% IPD in all sites and represented 71% of PCV13 cases.

Conclusions:

In 2016, serotypes 3 and 19A represented the majority of PCV13 IPD in older adults. Childhood PCV13 vaccination showed no indirect effect on serotype 3 IPD but serotype 19A incidence halved after six PCV13 years. In sites using PCV10, both serotypes increased significantly over that period. Decisions on elderly vaccination should account for childhood PCV vaccination.

Subject: Surveillance

Keywords: pneumococcal vaccine, vaccine impact, surveillance, pneumococcal serotypes, elderly

ABSTRACT ID: 490

PRESENTED BY: Germaine Hanquet / ghanquet@skynet.be

9.5. Late breaker: Vaccination policy towards the tail of the diphtheria outbreak among Rohingya population in Cox's Bazar, Bangladesh – challenges and way forward

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Background:

Unprecedented diphtheria outbreak began among largely unvaccinated, displaced Rohingya population in Bangladesh in November 2017. The aim of this study was to assess the interventions and subsequent outbreak evolution.

Methods:

All diphtheria patients were submitted to the WHO surveillance database (EWARS) between 8 November, 2017 and 31 August, 2018, analysed for vaccination status, clinical presentation and laboratory testing (PCR). Three diphtheria vaccination campaigns targeting children <15 years were undertaken in the camps between weeks 50/2017 and 12/2018. For incidence risk ratio (IRR) comparisons, probable case-patients were defined as having respiratory symptoms and pseudomembrane, reference patients had respiratory symptoms only, excluding lymphadenopathy.

Results:

Altogether 8156 diphtheria patients were reported, with currently 10–20 cases per week (August 2018). Crude vaccination coverage was 88% – 110% after three vaccination rounds. More females (67%, 894/1335) and 15 years or older patients (51%, 686/1334) were identified after the vaccination campaigns. Only 21% (268/1279) patient samples were confirmed positive by PCR. Probable case-patients (2892) were more likely (IRR 1.20; 95% CI 1.10–1.31) to have had a contact with a case compared to reference patients (3571). Comparing probable case-patients with reference patients, the level of protection increased with one (IRR 0.82; 95% CI 0.73–0.92), two (IRR 0.84; 95% CI 0.74–0.94) or three (IRR 0.59; 95% CI 0.50–0.69) vaccine doses received.

Conclusions:

The diphtheria outbreak among Rohingya was controlled by stringent vaccination campaigns, clinical management and contact tracing. For the tail of the outbreak, routine and contact vaccination will be reinforced with remaining cases and clusters. We recommend vaccinating all children <5 years under routine EPI and consider vaccinating 15–49 year old females as exit strategy to end the outbreak.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Diphtheria Toxoid, Disease Outbreaks, Public Health Surveillance, Vaccination, Bangladesh

ABSTRACT ID: 575

PRESENTED BY: Katri Jalava / katriyalava@gmail.com

Parallel Session Abstracts

Parallel Session 10
DAY 2, Thursday, 22. November 2018
14:30-15:30

Vaccine-preventable diseases(3): developments and methods

Moderator

Gérard Krause

Abstracts

10.1. Evaluating vaccination programmes for policy decisions by using population-based registers–example of reductions in the total disease burden due to infant pneumococcal conjugate vaccination in Finland

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Background:

The full effects of vaccines can generally only be assessed after large-scale introductions. Impact on rare outcomes (including adverse events), long-term effects, and indirect effects require large populations with high vaccine uptake and sufficient follow-up, rarely feasible in clinical trials. Ten-valent PCV was introduced in infant vaccination schedule in 2010. We evaluated the national vaccination programme’s (NVP) total long-term population effect.

Methods:

The cohort eligible for PCV10 NVP (children born 06/2010-09/2016) was compared with a season and age-matched (age 3-78 months) reference cohort (born 06/2002-09/2008) before NVP introduction. PCV10 first-dose uptake was estimated to be 95.5% in 2015. Age-stratified adult populations were followed-up to assess indirect effects during 2004-2016. Data on relevant outcomes were obtained from national registers: culture-confirmed invasive pneumococcal disease (IPD) from National Infectious Diseases Register, ICD-10-coded non-laboratory-confirmed IPD and hospital-diagnosed pneumonia from hospital discharge register, and for children, tympanostomy tube placements (TTP) from national hospital discharge register and antimicrobial purchases from the Social Insurance Institution as surrogates for otitis.

Results:

In vaccine-eligible infants, the largest relative reductions (79%) were seen for culture-confirmed IPD. However, the absolute reductions were substantial for more common outcomes, such as antimicrobial purchases (25391 per 100000 person- years, compared to 34 for IPD). In the elderly, relative reductions due to the indirect effects were small (16% for IPD and 5% for pneumonia), but the absolute reductions (7 and 145 per 100000 person-years, respectively) were considerable for pneumonia.

Conclusions:

In the Finnish setting, non-bacteraemic endpoints cover the vast majority of the vaccine-preventable disease incidence in the vaccine-eligible children as well as in the elderly. The indirect effects of the infant vaccination programme have major implications regarding the adult vaccination recommendations.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: Streptococcus pneumoniae,Pneumococcal Conjugate Vaccine,Conjugate vaccines,Pneumococcal Infections,Pneumococcal Vaccines,Policy Making

ABSTRACT ID: 360

PRESENTED BY: Arto A. Palmu / arto.palmu@thl.fi

10.2. Development of recombinant human anti-diphtheria toxin neutralizing antibody for diphtheria therapy

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Background:

Diphtheria is a disease caused by toxigenic strains of Corynebacterium spp. that produce a toxin (diphtheria toxin, DT). The disease can be controlled by immunization and is therefore rare in countries with sufficient immunization coverage. However, diphtheria is a significant health problem in countries with poor immunization coverage or disrupted immunization programs. Even in countries where the disease is well controlled there is a need to maintain a stockpile of therapeutic diphtheria antitoxin (DAT) for management of sporadic or imported cases. Currently, diphtheria is treated with DAT which is scarcely supplied and frequently unavailable to patients. The aim of the project is to develop human monoclonal antibodies against DT. The long term goal is the replacement of equine DAT sera with a recombinant antibody product produced in cell culture to ensure that stockpiles are maintained in a way that DAT therapy is accessible to countries, inside and outside of Europe.

Methods:

In the DATMAB project human antibody fragments (scFv) were generated by phage display against DT using naïve and immune antibody gene libraries. The antibody generation and development follows the 3Rs rules to replace, reduce and refine animal experiments.

Results:

Several antibodies were generated and demonstrated significant toxin neutralization activity.

A promising lead candidate was found. This IgG interacts with the receptor binding domain of DT and has a neutralizing potency of approximately 200 IU/mg. It will be further characterized regarding stability and long term storage.

Conclusions:

It was demonstrated, that it is possible to generate fully human monoclonal anti-diphtheria toxin neutralizing IgGs. The long term goal is to generate a recombinant product that is widely available for stockpile and use in Europe to replace equine DAT sera.

Subject: Microbiology

Keywords: Diphtheria, Diphtheria Antitoxin, Single-Chain Antibodies, Monoclonal Antibodies, Therapeutics

ABSTRACT ID: 154

PRESENTED BY: Esther Wenzel / esther.wenzel@tu-braunschweig.de

10.3. Controlling the developing Meningitis W outbreak in the Netherlands; insights from model-based infectious disease data analysis

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Background:

There is a developing Neisseria meningitidis W (MenW) outbreak in The Netherlands. As an outbreak response the 14-months dose of the Men-C vaccine will be replaced with the Men-ACWY vaccine, and adolescents aged 13/14 years will be offered Men-ACWY vaccination. Our aim is to obtain a ‘ball park’ estimate for the impact of the adolescent-dose on population wide MenW transmission before its introduction late 2018, and explore the impact of a catch-up campaign including those aged 15 to 18 years.

Methods:

We estimate the epidemic growth over 2016-2017, and convert this to a reproduction number (Rn). Based on the observed incidence (ages 5-79 years), and assuming a constant case:carrier ratio, we assess the reduction of Rn due to vaccination. We assume a coverage of 85% and a vaccine protection of 95% with a low waning rate.

Results : In 2016-2017, Rn was 1.5 (95% Confidence Interval: 1.2-1.7). The estimated impact of vaccinating 14 year olds would reduce Rn to 1.4 (low: 1.1 high: 1.7) in 2019, and to 1.0 (low: 0.7 high: 1.3) in 2025. Implementing a catch-up campaign would reduce Rn to 1.1 (low 0.8 high 1.3) in 2019 and to an Rn of 1.0 (low 0.7 high 1.3) in 2020. The results are sensitive to changes in the vaccine parameters and uptake, the exact bounds of age-groups, and the assumptions on the duration of carriage and the case:carrier ratio.

Conclusions:

When vaccinating only the 14 years old, it requires around seven years to bring the reproduction number down to around one. Including a catch-up campaign of 15-18 year olds would bring Rn down to one in around two years, considerably earlier.

Subject: Modelling, bioinformatics and other biostatistical methods

Keywords: Vaccination; Adolescent; Neisseria; Herd immunity

ABSTRACT ID: 476

PRESENTED BY: Albert Jan van Hoek / albert.jan.van.hoek@rivm.nl

Parallel Session 11
DAY 2, Thursday, 22. November 2018
14:30-15:30

HIV, sexually transmitted infections and viral hepatitis (1): epidemiology and surveillance

Moderator

Andrew Amato

Abstracts

11.1. Concurrent outbreaks of extensively-resistant Shigella sonnei and Shigella flexneri in men who have sex with men, Melbourne Australia

CANCELLED

11.2. Risk behaviours of homeless people who inject drugs during an outbreak of hepatitis C, Northern Ireland, 2016-2017

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Background:

From July-August 2016, four homeless people who inject drugs (PWID) with recently acquired hepatitis C (HCV) infection, including one acute case, were reported in one city in Northern Ireland. A multidisciplinary team including homeless and addiction services investigated to identify and interrupt transmission chains.

Methods : Cases were PWID clients of homeless hostels in the affected city with laboratory-confirmed HCV infection between July 2016 and December 2017. Recent cases were defined as negative test within the previous year, or reported injecting for less than one year; acute cases had tested negative within previous six months. Contacts in the injecting networks of cases were identified for testing. Selected HCV-positive specimens were referred to the reference laboratory for phylogenetic analysis. From July-December 2017, we interviewed PWID giving consent to elicit risk behaviours.

Results:

During the investigation, 156 PWID were tested and 45 (29%) cases identified, including 7 (16%) recent and 13 (29%) acute infections. 4/6 specimens were genotype 1A with two different lineages. 68 PWID, including 12 cases, were interviewed. All reported using heroin, with 76% injecting once or more daily. Respondents reported sharing spoons (58%) and filters (53%), but also needles (27%) and syringes (29%). Most (94%) used needle exchange services, but 18% reported insufficient clean equipment. More cases than non-cases used public toilets for injecting (83% vs. 43%, p=0.01) and were currently homeless (91% vs. 64%, p=0.08).

Conclusions:

Laboratory analysis indicated a predominantly genotype 1A cluster with multiple transmission chains. Cases were more likely to inject in public spaces, but all respondents indicated concerning risk behaviours. We recommend active surveillance with ongoing testing, expanding existing harm reduction programmes, including needle exchange, and access to relevant services including substitution therapy.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: hepatitis C,disease outbreaks,addictive behaviour, risk-taking, harm reduction

ABSTRACT ID: 14

PRESENTED BY: Anna Maisa / anna.maisa@gmail.com

11.3. Hidden in plain sight, MSM engaging in ‚chemsex' as an emerging risk group for STI/HIV

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Background:

Evidence suggests that men who have sex with men (MSM) are increasingly using drugs during sex (‘chemsex’). Chemsex probably contributes to the high incidence of STI/HIV among MSM. The current study uniquely used STI/HIV laboratory test results to assess the association between chemsex and STI/HIV.

Methods:

From January 2018, 356 MSM visiting two Dutch STI clinics were recruited for an online questionnaire about chemsex, polydrug-use, risky sexual practices, risky drug administration, and needs for harm reduction. Questionnaire data were linked to patients’ most recent STI/HIV laboratory test results. Chi-squared tests were used to study associations between chemsex and STI/HIV. The study is on-going.

Results:

Chemsex <6 months was reported by 55% (136/248) of MSM (median age 35 years), of whom 42% reported chemsex in the past week. Poppers (80%), XTC (48%) and GHB/GBL (47%) were most commonly used. Less than 5% used crystal meth or mephedrone. Polydrug-use was reported by 62%; sharing snorting tubes by 26%; injection of drugs by 4%; sharing needles by none. Condomless anal intercourse during chemsex was reported by 41%. In total, 20% had a recent STI/HIV diagnosis, this was higher in chemsex-MSM (27%) than in non-chemsex-MSM (14%, p=0.01). In total, 19% were known HIV-positive MSM of whom 78% reported chemsex versus 50% in HIV-negative MSM (p<0.01). Fifty-four percent of HIV-negative chemsex-MSM would use Pre-Exposure Prophylaxis (PrEP) when available.

Conclusions:

Over half of MSM participating in the study used drugs during sex, and this was associated with recently diagnosed STI/HIV and HIV positive status. This indicates that awareness among STI care providers and tailored care are needed. Half of HIV-negative chemsex-MSM were interested in using PrEP, indicating the need for implementing innovative harm reduction.

Subject: Surveillance

Keywords: Chemsex,Men who have sex with men,Human Immunodeficiency Virus (HIV),Sexually Transmitted Infections (STI),Pre-Exposure Prophylaxis (PrEP)

ABSTRACT ID: 155

PRESENTED BY: Ymke J Evers / ymke.evers@ggdzl.nl

Parallel Session 12
DAY 2, Thursday, 22. November 2018
14:30-15:30

Food- and waterborne diseases and zoonoses (4): epidemiology and surveillance 2

Moderator

Steen Ethelberg

Abstracts

12.1. Effects of reduced typing coverage for routine Salmonella surveillance in France

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Background:

Whole-genome sequencing (WGS) is becoming more affordable and allows for high-resolution subtyping of pathogens. In 2016, the French National Reference Center for Salmonella (FNRCS) switched from serotyping to WGS as a primary method for routine surveillance of human Salmonella cases. While the new typing method based on WGS proved itself extremely useful for detection of clustered cases and outbreak investigations, budget constraints only allowed to sequence around 60% of samples received at the FNRCS each year.

Methods:

We propose an algorithm to reconstruct full serotype distribution from the partially observed number of samples each week. Based on this algorithm, we were able to sample epidemic curves for each serotype, run outbreak detection algorithms and declare an alert if the frequency of detected outbreaks exceeds a pre-defined threshold. We tested performance of outbreak detection methods on partially observed data by comparing it with outbreak detection results for fully serotyped data, which were assumed to be a gold standard.

Results:

Our results show that for random selection of 60% of samples sensitivity and positive predictive value (PPV) of outbreak detection drop to 0.6 and 0.4, respectively. In contrast, for the sample limiting scheme both sensitivity and PPV were around 0.9. We also looked at the long-term effects of reduced typing and showed that they were negligible compared to the choice of a sampling scheme.

Conclusions:

We explored the performance of outbreak detection algorithms in the case of surveillance systems with reduced typing coverage. This work has important practical implications for surveillance of Salmonella in France. All available samples should be analysed by either WGS or classical serotyping to ensure the balance between discriminatory power and timeliness of outbreak investigations.

Subject: Surveillance

Keywords: Salmonella,surveillance,typing,outbreak detection

ABSTRACT ID: 300

PRESENTED BY: Mikhail Churakov / mikhail.churakov@gmail.com

12.2. Decreasing seroprevalence of Toxoplasma infection amongst pregnant women in France: is it time to change the screening policy?

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Background:

Toxoplasmosis during pregnancy can result in congenital anomalies or foetal death. In France, early antenatal screening with subsequent monthly screening of seronegative women has been recommended since 1978. We investigated trends in Toxoplasma infection seroprevalence amongst pregnant women in France between 1995 and 2016, to inform ongoing debate on the current policy.

Methods : We used data from the National Perinatal Survey, which collected sociodemographic information through self- administered questionnaires from all women giving birth over a one-week period in 1995, 2003, 2010 and 2016. Serological results were extracted from medical records and linked with questionnaire responses. Women were seropositive if IgG or IgM Toxoplasma antibodies were detected. We calculated adjusted prevalence ratios (aPR) by sociodemographic factors using Poisson regression, stratified by nationality and survey year.

Results:

Toxoplasma serology was available for 55,923/57,879 (96%) women over all four surveys. Amongst French women, seroprevalence decreased from 54.3% in 1995 to 31.3% in 2016 (p<0.001), and similarly amongst women from North Africa (51.5% to 39.9%; p<0.001). In all surveys, seroprevalence amongst French women was higher in those over 35 years (aPR=1.5; 95%CI 1.4-1.7) and in women in French overseas territories (aPR=1.8; 95%CI 1.6-2.0), Paris (aPR=1.2; 95%CI 1.1-1.3) and Southwestern regions (aPR=1.2; 95%CI 1.1-1.4) compared to central regions.

Conclusions:

Toxoplasma infection seroprevalence amongst pregnant women experienced a relative decrease of 42% in 21 years. Higher prevalences amongst older women may reflect higher risk of exposure in the past. Persistent geographical differences may reflect dietary or environmental differences. While pregnant women are more susceptible to toxoplasmosis, the current risk of infection might be lower, suggesting that continued intensive screening may not be cost-effective. French health authorities should reevaluate the screening policy considering these results.

Subject: Burden of disease

Keywords: Toxoplasmosis, Toxoplasma gondii, Seroepidemiologic Studies, Pregnant women

ABSTRACT ID: 42

PRESENTED BY: Eve Robinson / eveprobinson@gmail.com

12.3. "Sickenin' in the rain" - increased risk of gastrointestinal and respiratory infections after urban pluvial flooding

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Background:

Climate change models show increasing extreme rainfall events in the Northern Hemisphere leading to increased urban pluvial flooding events. Urban flooding often causes surface run-off and overflows of combined sewage systems contaminating floodwater with several gastrointestinal/respiratory pathogens. Increased flooding events may therefore increase the risk for acute gastroenteritis (AGE) and acute respiratory infection (ARI). We studied the relationship between exposure to pluvial floodwater and AGE/ARI.

Methods:

We performed a retrospective, cross-sectional survey in 699 households (1656 participants) to assess self- reported AGE/ARI in relation to floodwater exposure during a 2-week period following documented pluvial flooding at 13 locations in the Netherlands. Multivariable generalized estimating equations (GEE) regression analysis was used, accounting for the clustered data structure and assessing potential effects of the type of exposure to floodwater on AGE/ARI risk.

Results:

Contact with floodwater was significantly associated with AGE (OR 5.10, 95%CI:2.43–10.67) and ARI (OR 4.05, 95%CI:2.39–6.84). The risk factors with highest ORs for AGE and ARI, while adjusting for age, sex, season and chronic diseases, were water droplets in the mouth (only AGE, OR 3.08, 95%CI:1.12-8.43) and feet/leg contact (only ARI, OR 2.42, 95%CI:1.53-3.81), performing post-flooding cleaning operations (OR 8.55, 95%CI:3.49–20.94) and cycling through floodwater (only AGE, OR 2.26, 95%CI:1.02-5.02). Although unfrequently reported, playing/running and splashing in floodwater (OR 12.12, 95%CI:2.85–51.65) and feet/leg contact (OR 8.09, 95%CI:1.48–44.33) were risk factors for children's AGE.

Conclusions:

Direct exposure to pluvial floodwater increases significantly AGE/ARI risks. Since pluvial flooding events will increase in the future, also in high-income countries there is a need for flood-proof solutions in urban development and increased awareness among stakeholders and the public about the associated health risks.

Subject: International health and migration

Keywords: Urban flooding, exposure, climate change, AGE, ARI

ABSTRACT ID: 74

PRESENTED BY: Annemieke Mulder / annemieke.mulder@rivm.nl

Parallel Session 13
DAY 2, Thursday, 22. November 2018
17:00-18:40

Antimicrobial resistance

Moderator

Jan Walter

Abstracts

13.1. Antimicrobial resistance in Aspergillus fumigatus isolated February to September 2017 from clinical specimens in Lyon, France

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Background:

Triazole antifungals are the first line therapy for invasive aspergillosis, commonly caused byAspergillus fumigatus. Since 1997, triazole resistance by mutations in the lanosterol 14a-demethylase (cyp51A) gene are increasingly reported, leading to recommendations for susceptibility testing of triazoles by the European Centre for Disease Prevention and Control. Our main objective was to assess the burden of Aspergillus isolates with azole resistance from clinical specimens in Lyon.

Methods:

A retrospective study was conducted covering February to September 2017 analysing A.fumigatus isolates from bronchoalveolar lavage, bronchial aspirate and sputum samples of patients attending the inpatient and outpatient wards of the Pulmonary Medicine. Minimum inhibitory concentrations (MICs) were determined using E-test reagent strips for itraconazole, voriconazole, posaconazole, isavuconazole as well as amphotericin B. MICs were determined after 24 and/or 48h. Resistance was defined by EUCAST clinical breakpoints. Molecular resistance mechanisms were identified by sequencing of cyp51A with promoter region.

Results:

A total of 203 isolates of A.fumigatus from 182 patients were analysed. Prevalence of azole-resistance among these patients was 2.2%. In total, four isolates with resistance were detected: two strains against itraconazole/posaconazole/isavuconazole and another two against all four triazoles. Out of these four strains, three presented silent polymorphisms in an intronic part of cyp51A and one presented simultaneously the F46Y, M172V and E427K mutations.

Conclusions:

Azole-multiresistant A.fumigatus strains are causing infections in pulmonary medicine patients in Lyon, including resistance against all first line therapy triazoles. No known fungicide-driven mutation was found but non-cyp51A related mechanisms need to be investigated. In the wake of a global rise in azole-resistance our findings emphasize the diversity of underlying molecular mechanisms as well as the importance for susceptibility testing before treatment.

Subject: Burden of disease

Keywords: azole resistance, fungal infections, antifungals, Aspergillus fumigatus, aspergillosis

ABSTRACT ID: 160

PRESENTED BY: Rolf Kramer / kramer-rolf@gmx.de

13.2. OXA-48-producing Enterobacteriales detected in Irish seawater, 2017

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Background:

The rapid dissemination of carbapenemase-producing Enterobacteriales (CPE) is a major public health concern. Recreational waters are potential reservoirs of antimicrobial resistant bacteria/genes. This study aimed to examine seawater for the presence of CPE.

Methods:

Seawater sampling took place at a recreational beach on eight occasions (May-November 2017). Each sample (30L) was filtered using the CapE large volume filtration system. Wastewater samples (pre-treatment and post-treatment) were obtained from a nearby secondary wastewater treatment plant, on five occasions (June-November 2017). All samples were examined for CPE. Whole genome sequencing of confirmed CPE was carried out (Illumina). Isolate genomes were hosted in a BIGSdb database, and analyses was performed using multiple web-based tools.

Results:

OXA-48-producing ST131 Escherichia coli was detected in a seawater sample collected in May 2017. Analyses indicated that the blaOXA-48 gene was chromosomally integrated, due to the detection of a 21.8kb fragment consistent with TN6237. This isolate was found to be harbouring blaCTX-M-27 and five virulence genes. pMLST revealed the presence of four plasmid replicon types.

OXA-48-producing ST101 Klebsiella pneumoniae was detected in a seawater sample collected in August 2017. This isolate was harbouring 17 additional resistance genes (including blaCTX-M-15), 21 virulence genes and five plasmid replicon types. This included an IncL/M(pOXA-48) plasmid, which analyses indicated was harbouring the blaOXA-48 gene. CPE was not detected in any other sample (seawater/wastewater).

Conclusions:

The presence of OXA-48-producing Enterobacteriales in recreational water is a concern. OXA-48 is the most prevalent carbapenemase in the Irish healthcare setting. E. coli ST131 and K. pneumoniae ST101 are sequence types of human public health significance. The potential for recreational water to contribute to dissemination of CPE in Europe warrants further study.

Subject: Microbiology

Keywords: antimicrobial resistance, carbapenemase-producing Enterobacteriaceae, recreational water

ABSTRACT ID: 311

PRESENTED BY: Bláthnaid Mahon / b.mahon1@nuigalway.ie

13.3. National surveillance of methicillin-resistant Staphylococcus aureus bacteraemia following the implementation of Whole-Genome Sequencing in England, April-December 2017

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Background:

Previous to the launch of whole genome sequencing (WGS) service in April 2017, combined with the Methicillin-resistant Staphylococcus aureus (MRSA) bacteraemia surveillance system in England, low levels of testing (~40%) have precluded the determination of MRSA clonal distribution.We aimed to assess the impact of the WGS implementation in the new surveillance system, in order to describe MRSA molecular epidemiology.

Methods:

WGS data from national laboratory were matched with enhanced mandatory surveillance data from April to December 2017, using patient identifiers. Cases were classed as community-onset (CO-MRSA) if the specimen date was <3 days otherwise as hospital-onset MRSA (HO-MRSA). MLST clonal complexes (CC),SCCmec type, toxigenic, antibiotic and biocide resistance profiles were derived from WGS results. Isolates were considered multi-drug resistant (MDR) when genotypically resistant to β-lactams and ≥ 2 other classes of antibiotic.

Results:

Overall 602 MRSA bacteraemia cases were reported to mandatory surveillance system during the study period. CO-MRSA (65%) and male cases were significantly more than HO-MRSA (35%, $p<0.0001$) and female (68% vs 32%; $p<0.0001$), respectively. The median patient age was 69 years (range: 0-102, inter quartile range-IQR-35 years). 464 (77%) isolates were linked to mandatory reports and sequenced, identifying 18 CC, the majority (81%) carried SCCmecIV. The most prevalent clonal complex was CC22 (48%), followed by CC5 (18%). 66% and 22% of isolates were genotypically MDR; 3.6% were mupA+ and 17% encoded qac genes indicating a reduced susceptibility to decolonizing agents.

Conclusions:

The enhanced surveillance system combined with WGS affords detailed molecular epidemiological data for the majority of bacteraemia cases in England, describing the circulating MRSA clones and providing evidence for future public health decision making, including patient management strategies and national policy.

Subject: Surveillance

Keywords: MRSA, surveillance, whole-genome sequencing, WGS

ABSTRACT ID: 243

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

13.4. Burden of infections caused by antibiotic-resistant bacteria in the European Union and the European Economic Area in 2015 using disability-adjusted life years

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Background:

Infections due to antibiotic-resistant bacteria are threatening modern healthcare. Estimating the burden of these infections is an ongoing challenge given the need for good quality data on their incidence, related complications and attributable mortality.

We estimated the burden of infections caused by antibiotic-resistant bacteria of public health concern in European Union and European Economic Area (EU/EEA) countries, measured in number of cases, attributable deaths and, for the first time, in disability-adjusted life years (DALYs).

Methods:

The incidence of infections with 16 bacteria-resistance combinations was estimated from the European Antimicrobial Resistance Surveillance Network (EARS-Net) 2015 data, corrected for population coverage of participating laboratories in each included country. The incidence of bloodstream infections (BSIs) was multiplied by a conversion factor derived from the ECDC point prevalence survey of healthcare-associated infections in European acute care hospitals 2011–2012 to estimate the number of non-BSIs. Disease outcome models for five types of infection were developed based on systematic literature reviews.

Results:

We estimated that 654,175 (95% Uncertainty Interval [UI] 567,332-744,083) antibiotic-resistant bacterial infections occurred in 2015 in the EU/EEA, the majority healthcare-associated. These infections accounted for 32,164 (95% UI 27,640-37,152) attributable deaths and 839,103 (95% UI 738,720-949,377) DALYs. The burden for the EU/EEA was the highest in infants and the elderly, and increased since 2007. This burden was higher in Italy and Greece than in other countries.

Conclusions:

This study applied a novel methodology for estimating the burden of infections with antibiotic-resistant bacteria. The estimated burden for the EU/EEA was higher than that of other infectious diseases, and heterogeneous across countries. These burden estimates based on the best available evidence are now available to public health decision-makers for prioritizing infectious diseases and interventions.

Subject: Burden of disease

Keywords: Antibiotic Resistance, Burden of Illness, Healthcare Associated Infections

ABSTRACT ID: 233

PRESENTED BY: Alessandro Cassini / alessandro.cassini@ecdc.europa.eu

Parallel Session Abstracts

Parallel Session 14
DAY 2, Thursday, 22. November 2018
17:00-18:40

Tuberculosis

Moderator

Loredana Ingrosso

Abstracts

14.1. Implementation of WGS tuberculosis cluster surveillance; rapid identification and robust public health management in the East Midlands, 2017-2018

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Background:

In December 2016 Public Health England introduced routine prospective whole genome sequencing (WGS) of culture confirmed mycobacterium isolates to provide rapid drug resistance and highly discriminatory relatedness cluster data. We implemented a system reviewing WGS tuberculosis (TB) clusters in the East Midlands (EM) in order to identify opportunities for intervention. Preliminary data are described to inform the use of WGS in TB cluster surveillance.

Methods:

Initial epidemiological surveillance and microbiological data were combined nationally and distributed regionally. A WGS TB cluster was defined as isolates from two or more patients within 12 single nucleotide polymorphisms (SNPs). Locally we reviewed clusters on a monthly basis as a multi-disciplinary team. Clusters were described by geography, demographic factors, social risk factors (SRF), epidemiological links, drug resistance, and SNP distance between cases. Local TB clinics were contacted to share WGS relatedness and ascertain further links between cases. All data and decision logs were recorded centrally for long-term cluster management.

Results:

In total, 20 clusters were reviewed in the EM since October 2017; 14 growing and six new clusters. Twelve clusters were actively investigated; combining WGS and detailed epidemiological data identified new leads for contact tracing in four clusters and outbreak control response in one. Two clusters contained multi-drug resistant isolates, and two other clusters had isoniazid resistant isolates. Thirteen clusters comprised of individuals with SRF. On average, clusters were reviewed within a month of the notification of the most recent case.

Conclusions:

A monthly TB cluster review combining WGS and epidemiological data provided a systematic and robust decision making process regarding intervention. We recommend a monthly WGS cluster review system for surveillance and public health management of WGS TB clusters.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: Tuberculosis, Whole Genome Sequencing,Public Health,Contact Tracing,Drug Resistance,Decision Making

ABSTRACT ID: 239

PRESENTED BY: Hikaru Bolt / hikaru.bolt@phe.gov.uk

14.2. Level of none-adherence to anti-tuberculosis treatment and risk factors associated with it among 2014-2015 cohorts of pulmonary tuberculosis adult patients, Bishkek City, Kyrgyz Republic

Ekaterina Maliukova [1]

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Background:

None-adherence to tuberculosis treatment can lead to unfavorable disease outcomes, drug resistance, and further spread of infection to others. In 2016, we conducted a study to identify the magnitude of none-adherence to treatment and its determinants among adult pulmonary tuberculosis patients in Bishkek city. The aim is to provide evidence-based recommendations to improve treatment compliance.

Methods:

In a retrospective cohort study, we enrolled all newly diagnosed pulmonary tuberculosis patients, aged ≥18 years, who started treatment during 2014-2015 (n=919). None-adherents were patients who interrupted treatment for at least 14 consecutive days. We reviewed medical records, interviewed patients regarding disease clinical and treatment details; and other individual's characteristics that could influence adherence to treatment. We used logistic regression to assess the association between the study factors and none-adherence.

Results : Overall, 14% (129/919) of patients were none-adherents. The rate of none-adherence was highest among: men (18% (88/483)), patients >30 years of age (17% (67/405)), and those who live alone (15% (23/154)). The lowest rate, 7% (32/457), was among those with high education (university or college). In multivariate analysis, predictors of none- adherence were: male gender (OR 2.3, 95% CI 1.4-3.9), living alone (OR 1.9, 95% CI 1.1-3.2). There was some evidence that high education was protective against none-adherence (OR 0.6, 95% CI 0.4-1.0).

Conclusions:

A high level of none-adherence exists in the study population, especially among men and those who live alone. Given the protective effect of higher education, better adherence can be achieved by providing health education on the importance of treatment compliance to all, especially to patients who are males or live alone. Educational messages can be

delivered by the medical personal to the patients while they are under treatment.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: tuberculosis, treatment none-adherence, risk factors, Bishkek city, Kyrgyzstan

ABSTRACT ID: 283

PRESENTED BY: Ekaterina Maliukova / katerina.maliukova@gmail.com

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14.3. Isoniazid mono-resistance negatively affects tuberculosis treatment outcomes in Europe

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Background:

Isoniazid (INH) is an essential drug for tuberculosis (TB) treatment and resistance to INH may increase the likelihood of negative treatment outcomes. We aimed to determine the impact of INH mono-resistance on TB treatment success (defined as cured or treatment completed) at 12 and 24 months observation in the European Union/European Economic Area (EU/EEA).

Methods:

We analysed TB cases with available information on treatment outcomes and drug susceptibility testing results (DST) reported from EU/EEA countries to the European Surveillance System (TESSy) between 2002 and 2014. Multilevel logistic regression models were applied to correct for clustering of cases within countries. Independent variables that caused a change in the regression coefficient between INH mono-resistant TB and treatment success of >10% were considered as potential confounders and retained in the final model

Results:

We included 187,370 fully susceptible and 7,578 INH mono-resistant TB cases from twenty-four EU/EEA countries. Treatment was successful at 12 months after diagnosis in 68% of INH mono-resistant and in 76% of fully susceptible TB cases (P<0.01).Treatment success was constant over the reporting years for both INH mono-resistant and fully susceptible TB (trend analysis 2002-2014: P=0.39 and 1.2, respectively). In the final model adjusted for age, geographical origin, microscopy confirmation and previous TB treatment, the odds of treatment success among INH mono- resistant TB were 40% lower compared to fully drug susceptible TB (OR 0.60; 95%CI 0.41-0.86). The impact of INH mono- resistance on treatment success remained significant when evaluating treatment success at the 24-month observation (OR 0.64; 95%CI 0.44-0.92).

Conclusions:

INH mono-resistance affects TB treatment outcome. Further research is needed to assess the effect of different treatment regimens on treatment outcome of cases with INH mono-resistance

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Subject: Surveillance

Keywords: Tuberculosis,Isoniazid mono-resistance ,Treatment outcome,EU,European Surveillance System (TESSy)

ABSTRACT ID: 456

PRESENTED BY: Basel Karo / baselkaro@gmail.com

14.4. Implementation of Whole-genome sequencing of Mycobacterium tuberculosis in a referral TB hospital in Rome: implications for TB control,

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Background:

Characterization of Mycobacterium tuberculosis (MTB) transmission dynamics is essential to progress toward tuberculosis (TB) elimination in low incidence countries. We report the first results of a newly implemented whole-genome sequencing (WGS) programme on the TB strains circulating in the metropolitan area of Rome, which has a TB incidence twice as high compared to the national Italian average and an ethnically diverse patient population

Methods:

MTB strains isolated from patients admitted to a TB reference center between January 2016 and March 2017 were subjected to DNA extraction (CTAB method) and to WGS by Illumina. Sequences were uploaded on SeqSphere+ (Ridom© GmbH) in order to generate a cgMLST-based minimum spanning tree and to identify clusters and on PhyResSE 1.0 for lineage attribution and for identification of mutations correlated with drug-resistance.

Results:

MTB isolates were collected from 209 patients, of which 153 (73.2%) from foreign born (FB) patients, mostly (51%) from Romania. Twenty-nine clusters -mostly belonging to the Haarlem sub-lineage- and involving 81 patients, were identified. Similar proportions of clustering were reported for Italian and foreign born patients (46 vs 36%). 16 (55.2%) clusters included IB and FB patients; 10 (34.5%) included only FB patients from a single country.

Drug-resistance (DR) mutations were found in 12% of the strains, of which 44% were multi-drug resistant (MDR). Differences among IB and FB in the proportions of DR-MDR mutations were not statistically significant. Drug resistance profiles were shared across clusters.

Conclusions:

Despite the short duration of the study and the fact that was conducted in a single center, this study estimated TB recent transmission in approximately one quarter of all TB cases, with a significant mixing between IB and FB.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: tuberculosis, Whole-genome sequencing , clustering, Drug-resistance

ABSTRACT ID: 496

PRESENTED BY: Angela Cannas /

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14.5. Risk factors for delay in initiation of treatment for pulmonary TB: a time-to-event analysis using linked TB surveillance and clinical case review data in the South East of England, 2011-2015

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Background:

Delays in treatment initiation for TB may lead to worse clinical and public health outcomes, and were longer in pulmonary TB (pTB) cases in the South East of England in 2015 than the national average. We aimed to determine factors associated with treatment delays, to guide public health action.

Methods:

We extracted data on clinical characteristics and on documented potential barriers to treatment from all pTB cases with clinical case review data from 2011-2015 and linked these to Enhanced Tuberculosis Surveillance (ETS) data. We excluded cases referred to specialists following screening or contact tracing. We described the distribution of delays from symptom onset to first presentation ('presentation delay'), and from presentation to treatment ('healthcare delay'). We used time-to-event multivariable models to determine the association between socio-demographic and clinical risk factors and delay outcomes, taking area as a random effect.

Results:

We linked 908/997 (91%) cases with clinical case review data to ETS. Median presentation delay was 30 days (LQ-UQ 11-72). Longer presentation delay was associated with mental health co-morbidity ($p=0.007$) and language barriers ($p=0.042$). Median healthcare delay was 40 days (LQ-UQ 13-89), delays in initiating onward referral to TB specialists were the greatest part (26 days (LQ-UQ 4-73)). Longer healthcare delay was associated with negative sputum smear ($p<0.001$), UK residency greater than 2 years or being UK born ($p=0.001$), females ($p=0.005$), and primary care referral in low-incidence districts ($p<0.001$).

Conclusions:

Access to care for vulnerable populations is important to ensure timely presentation. We encourage clinicians to consider TB diagnosis even in cases perceived as low risk. Strategies to increase the yield from sputum smear investigations, and implementation of more rapid diagnostic approaches in smear negative cases, are required.

Subject: Surveillance

Keywords: Tuberculosis, Delay, time-to-event, record linkage

ABSTRACT ID: 224

PRESENTED BY: David James Roberts / david.j.roberts@phe.gov.uk

Parallel Session 15
DAY 2, Thursday, 22. November 2018
17:00-18:40

Vaccine- preventable diseases(4): vaccine uptake and coverage

Moderator

Alma Tostmann

Abstracts

15.1. Direct and indirect effects of the recommendation for routine Rotavirus-vaccination on notified rotavirus cases and vaccine uptake in infants in Germany 2013-2017

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Background:

Routine rotavirus (RV)-vaccination for infants has been recommended in Germany since 08/2013 to reduce severe cases of RV-gastroenteritis (RVGE) in under five-year-olds. We aimed to determine the impact of the recommendation on RVGE- notifications and to assess vaccination coverage.

Methods:

For estimating the RV-vaccination coverage, we used statutory health-insured persons' prescription data (~85% of the population in Germany) of the birth-cohorts 2014-2017 provided by pharmaceutical data-processing centers.

We defined all RVGE-notifications as cases which either met clinical and laboratory or clinical-epidemiological criteria according to national surveillance definitions.

We calculated age-group specific seasonal incidence rates (IR) of RVGE-cases using mandatory notification data. A seasonal RV-year was defined from calendar-week 40 to the following year's calendar-week 39. All RVGE-cases with disease onset of =/> two days after hospitalisation were classified as nosocomial.

Using Poisson regression we calculated incidence rate ratios (IRR) comparing the time-period before RV-vaccine was available or utilized (seasons 2004/05-2007/08) with the period since the recommendation (seasons 2013/14-2016/17).

Results:

The RV-vaccination coverage in infants steadily increased from 59% (birth-cohort 2014) to 81% (birth-cohort 2017). The IR of all RVGE-notifications for the time-period 2004/05-2007/08 was 1332/100,000 person-years in under five-year-olds and 26/100,000 person-years in those ineligible for vaccination. Since the recommendation IRs of all RVGE-notifications, RVGE- outpatient cases, RVGE-associated hospitalisation and nosocomial RVGE among under five-year-olds decreased by 65% (IRR=0.35; 95%CI=0.34-0.35), 68% (IRR=0.32; 95%CI=0.31–0.32), 62% (IRR=0.38; 95%CI=0.38–0.39) and 79% (IRR= 0.21; 95%CI=0.20–0.23), respectively. For those ineligible for vaccination the IR of RVGE-notifications decreased by 6% (IRR 0.94; 95%CI=0.93-0.95).

Conclusions:

Our analysis suggests direct benefits of routine RV-vaccination in under five-year-olds and indirect benefits for persons ineligible for vaccination, indicating herd immunity.

However, vaccine uptake should be further increased.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: rotavirus,vaccine, health impact, vaccination coverage, program evaluation

ABSTRACT ID: 238

PRESENTED BY: Adine Marquis / marquisa@rki.de

15.2. Extension of the mandatory vaccination program, perception of the French population

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Background:

France vaccination policy was characterized by the coexistence of eight recommended and three mandatory vaccinations for children under 2 years. However, for all children born after January 1, 2018, all the vaccines are now mandatory. We studied the opinion of the French population about this new mandatory vaccine law and assessed factors associated with a positive opinion.

Methods:

The study was conducted using data collected in the GrippeNet.fr cohort, a crowdsourced study conducted in France. Participants were invited to complete an online questionnaire regarding vaccination. Analyses were standardized on age, gender and level of education of the French population. Univariate and multivariate analyses were performed.

Results:

Overall, 3,222 people participated (response rate 50.5%). After adjustment, 64.5% of the population agreed with the extension of mandatory vaccines, 31.0% did not agree and 6.5% had a neutral opinion. It was considered as a necessary step by 68.7% of the study population, while 33.8% considered it as unsafe for children and 56.9% as authoritarian. Factors significantly associated with a positive opinion about extension of mandatory vaccines were: to trust health professionals or media regarding vaccine topics (OR=4.38; 95% CI [2.25; 8.51]), to think that vaccination benefits the population (7.97; [4.25; 14.96]), to think that the most common vaccination side effects are not severe (3.21; [1.84; 5.60]), to think that vaccines are thoroughly tested (5.0; [3.31; 7.53]) and to have been vaccinated against flu for the current season (2.75; [1.04; 2.21]).

Conclusions:

The French population is rather in favour of the policy expansion of mandatory vaccines for children. The perception seems to depend on the degree of trust in safety and benefits of vaccination.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: Vaccination, Immunization Programs, Mandatory Programs, Infant, France

ABSTRACT ID: 500

PRESENTED BY: Pauline Mathieu / thierry.blanchon@upmc.fr

15.3. Is mandatory vaccination influencing maternal decision to vaccinate children in Slovenia? April-May 2016

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Background: High parental confidence is important to maintain vaccination coverage needed for community-level protection against vaccine preventable diseases. In Slovenia 9 childhood vaccinations are mandatory. We quantified vaccine confidence and hesitancy among mothers in Slovenia and how non-mandatory vaccinations would affect their behavior, to advise on maintaining and improving vaccination coverage.

Methods:

In 2016 we conducted the first nationwide cross-sectional survey among mothers of children <2 years old. The sampling frame included women registered in national Perinatal Information System giving birth in 2014-2015 (N=39,497). Vaccine hesitancy was defined as delay in acceptance/ refusal of vaccines despite availability of vaccination services.

Results:

We sent out 3,854 questionnaires, 44% responded. While 47% (95% confidence interval (CI):44-49%) of mothers were vaccine confident, 34% (95% CI:32-37%) were undecided and 19% (95% CI:17-21%) were not confident. The proportion of vaccine hesitant was 22% (95% CI:20-24%); among vaccine confident 12% (95% CI:10-14%), undecided 21% (95% CI:17-24%) and not confident 50% (95% CI:44-56%). Without mandatory vaccinations 56% (95% CI:54-58%) would still vaccinate; among vaccine confident 79% (95% CI:76-81%), undecided 48% (95% CI:44-52%), and not confident 15% (95% CI:11-19%).

Conclusions:

Less than half of Slovenian mothers were vaccine confident with the majority not hesitating to vaccinate their children. Mandatory vaccination may influence the decision to vaccinate, especially among undecided and not confident mothers. Monitoring and improving vaccination confidence is necessary to diminish reliance on a mandatory system.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: vaccination, Slovenia, survey, mothers, children, parental

ABSTRACT ID: 34

PRESENTED BY: Mario Fafangel / mario.fafangel@nijz.si

15.4. Vaccine hesitancy: low uptake of influenza vaccine among Polish population in Lothian, Scotland

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Background:

All Scottish primary school children are offered annual vaccination with live attenuated intranasal flu vaccine (LAIV). Uptake in Lothian (257 schools, 65,000 children) at 68% is lower than elsewhere in Scotland, with substantial variation between schools.

Although 15% of Scotland's population live in Lothian, it is host to 33% of Scotland's Polish population (27,000 Poles, mainly young people).

We assessed differences in LAIV uptake between Polish and UK born children.

Methods:

Three Edinburgh primary schools with high numbers of Polish children were identified. We matched the school LAIV programme data from 2016 and 2017 with health information systems to highlight different ethnicities. Lothian has high recording of ethnicity on routine datasets and a Polish speaker refined ascertainment by examining the pupil lists for traditional Polish names and surnames. The three schools have approximately 900 children 40% of whom are Polish.

Results:

Of the 906 children in the three schools in 2017, overall uptake was 46%. There was a significant difference between uptake in the 383 Polish children (24%, 95% confidence interval 14 - 34%) and the Scottish children (68%, 95% confidence interval 55 - 82%). Analysis of 2016 data showed a similar pattern.

Consent forms were not returned for 40% of the Polish children versus 27% of the Scottish children. Forms actively declining the LAIV were returned for only 10 Scottish children (5%) compared with 137 (36%) of the Polish children. This is 7 times the Scottish refusal rate and twice the overall.

Conclusions:

Vaccine hesitancy is a well recognised phenomenon within Poland and may now be impacting on Scottish vaccine uptake. The Scottish national immunisation programme is now develpong strategies to actively address this issue

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: vaccination; influenza vaccine; vaccine hesitancy; ethnicity

ABSTRACT ID: 499

PRESENTED BY: Lorna Willocks / lorna.willocks@nhslothian.scot.nhs.uk

15.5. Impact of Italy's law 119/2017 regarding mandatory vaccination seven months since it was enforced: experience in the Apulia region

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Background:

In response to alarming decrease in infant immunization coverage and re-emergence of measles outbreaks, in June 2017, the law 119/2017 in Italy made ten vaccinations compulsory for children and adolescents 0 through 16 years of age. These vaccinations are the four that were already compulsory (diphtheria, tetanus, poliomyelitis and hepatitis B) plus pertussis, Haemophilus influenzae type b, measles, mumps, rubella, and varicella.

We report the impact of the new law in the Apulia region, seven months since it was enforced.

Methods:

We compared vaccination coverage (VC) estimates between 2016 and 2017 (within December 31) for: 3 doses of hexavalent (DTaP-IPV-HBV-Hib), 1 dose of measles (MMR/MMRV), and 1 dose of varicella (MMRV/monovalent V) vaccine among toddlers born in 2014; 4 doses of DTaP-IPV, 2 doses of MMR/MMRV, and 2 doses of MMRV/V among children born in 2009; 5 doses of DTaP and IPV, 2 doses of MMR/MMRV, and 2 doses of MMRV/V among adolescents born in 2001.

Results:

Global vaccines coverage increased during 2016-2017 for 3 doses of DTaP-IPV-HBV-Hib (93.3% to 95.3%=+2%), 1 dose of MMR/MMRV (85.9% to 93%=+7.1%), and 1 dose of MMRV/V (82.4% to 90.5%=+8,1) among toddlers; for 4 doses of DTaP-IPV (83% to 90.1%=+7.1%), 2 doses of MMR/MMRV (79.4% to 87%=+7.6%), and 2 doses of MMRV/V (75.4% to 83,4%=+8%) among children; for 5 doses of DTaP (51.7% to 63.4%=+11.7%), 5 doses of IPV (48.5% to 59.6%=+11.1%), 2 doses of MMR/MMRV (82.2% to 84.1%=+1.9%), and 2 doses of MMRV/V (20.5% to 21.2%=+0.7%) among adolescents.

Conclusions:

Preliminary results from catch-up vaccination under the law 119/2017 in Italy seem to be encouraging; continued efforts are needed to increase vaccine uptake and improve public confidence in national immunization programmes.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: Mandatory vaccination, Vaccination coverage, Children, Adolescent, Italy

ABSTRACT ID: 338

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Parallel Session 16
DAY 3, Friday, 23. NOVEMBER 2018
11:00-12:40

HIV, sexually transmitted infections and viral hepatitis (2): surveillance, screening & intervention

Moderator

Helena de Carvalho Gomes

Abstracts

16.1. Does the German screening policy for Chlamydia trachomatis target those most at risk? – Results from the German health examination survey (DEGS) 2008-2011

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Background:

Chlamydia trachomatis (CT) infections are frequently asymptomatic and can lead to infertility if left untreated in women. As younger age is a risk factor, annual screening of women <25 years is recommended since 2008 in Germany. CT is not notifiable in Germany and national prevalence estimates are not available. We aimed to estimate the prevalence of CT in the general adult population by age and sex to assess if the current recommendations target those most at risk.

Methods:

Urine from adult participants of a representative, nationwide health survey (2008-2011) was tested for CT using PCR. Weighted CT prevalence estimates and 95% confidence intervals (95% CI) were generated.

Results : CT test results were available for 6913/8151 of participants (52% female). The highest prevalence in women was estimated in 18-19 year-olds at 3.6% (95% CI 1.1-11), followed by 1.8% in 20-24 year-olds (95% CI 0.5-5.9). In women 25-29 and 30-34 years, the prevalence estimates were 1.2% (95% CI 0.4-3.5) and 1.5% (95% CI 0.3-7.2) respectively. While no CT infections were found in 18-19 year-old men, prevalences of 3.3% (95% CI 1.4-7.3), 3.5% (95% CI 1.6-7.7) and 2.1% (95% CI 0.5-8.4) were estimated in 20-24, 25-29 and 30-34 year-old men, respectively. CT prevalence estimates decreased in older age groups of both sexes.

Conclusions:

Among women, CT-infection was most prevalent in the age groups targeted by the screening recommendations but as 25-34 year-olds were also affected, increasing the age limit should be considered. With an exception for the 18-19 year- olds, CT prevalence was higher among men than women of the same age. The current German screening recommendation thus misses the men, who may serve as a reservoir for the infection.

Subject: Burden of disease

Keywords: Chlamydia trachomatis, Screening recommendations, National health examination survey, Germany

ABSTRACT ID: 212

PRESENTED BY: Martyna Gassowski / gassowskim@rki.de

16.2. Oropharyngeal testing and positivity at the STI clinic in the past 5 years; testing more and finding even more

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Background:

Oropharyngeal Chlamydia trachomatis(CT) and Neisseria gonorrhoeae(NG) are not routinely tested for in STI clinics. Although oropharyngeal infections are often asymptomatic, they contribute to transmission in the population. Routine systematic oropharyngeal testing was implemented in men who have sex with men (MSM) in 2010, and on behavioral indication in heterosexuals, but it is unknown whether this was successful in practice. Moreover, data on oropharyngeal testing and CT/NG positivity in heterosexuals is limited.

Methods:

Men and women aged >16 years attending our STI-clinic between 2009-2015 were included(n=47317). Specimens were tested using NAATs. Multivariable backward logistic regression analyses were used to test associations with testing and CT/NG positivity. Tested determinants were age, sex, symptoms, number of sex partners and notified by (ex)partner.

Results:

Oropharyngeal testing in heterosexuals increased yearly from 13% in 2009 to 16% in 2015 (OR 1.3, 95%CI 1.2-1.3). In MSM, testing increased from 88% to 98% (OR1.6, 95%CI 1.5-1.8). Oropharyngeal CT positivity varied between 1.0-1.6% in women (54/4198), between 0-1.3% in heterosexual men (13/2226) and between 0.8-1.5% in MSM (79/8158), but was not associated with year of testing. Oropharyngeal NG positivity varied between 1.5-3.4% in women (123/4201), between 0.6-4.1% in heterosexual men (61/2226) and between 2.8-6.4% in MSM (406/8156). Oropharyngeal NG positivity increased with year of testing in heterosexual men (OR 1.2, 95%CI 1.01-1.4) and MSM (OR 1.2 95%CI 1.1-1.2).

Conclusions:

Routine oropharyngeal testing in MSM was successfully implemented in practice. Oropharyngeal CT positivity remained stable after increased oropharyngeal testing in all groups, and in women also for oropharyngeal NG. In heterosexual men and MSM, increased oropharyngeal testing revealed increased oropharyngeal NG positivity. This justifies routine oropharyngeal testing in MSM, and warrants careful monitoring in heterosexuals.

Subject: Surveillance

Keywords: Chlamydia trachomatis, Neisseria gonorrhoeae, Oropharyngeal, Heterosexual, Men who have sex with men, Epidemiology

ABSTRACT ID: 187

PRESENTED BY: Geneviève AFS van Liere / genevieve.vanliere@ggdzl.nl

16.3. Impact of nurse led enhanced monitoring, management and contact tracing intervention for chronic hepatitis B in England, 2015-2017

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Background:

Up to 441,000 people live with chronic hepatitis B in England. Despite national guidance on identification and management of cases and their close contacts, testing rates of close contacts is as low as 43% in high prevalence areas of London. Our study aimed to determine whether a nurse led enhanced management and contact tracing of antenatally screened HBV infected women, and chronically infected individuals improved testing uptake, vaccination and onward referral of close contacts.

Methods:

The study was conducted across Greater Manchester and East of England regions between October 2015 and July 2017. All HBV chronically infected individuals registered with a GP and their close contacts were eligible for recruitment. The proportion of contacts who were tested, vaccinated and referred where appropriate were compared before and after the nurse-led intervention, Baseline and outcome information was collected using questionnaires.

Results:

The intervention improved case referral rates by an additional 14% (from 86% (88/102 cases) to 99.7%; 648/650 cases). The proportion of contacts tested increased from 34% to 72-94% with 18 new cases of HBV diagnosed. Amongst close contacts tested, vaccination rates of at least three doses increased from 77% (43/56) to 93% (452/491) during the study. Similar improvements were observed amongst babies born to chronic HBV positive mothers with the proportion vaccinated with at least four doses increasing from 60% (18/30) to 100% (39/39).

Conclusions:

Our study has shown that nurse led enhanced management greatly improves identification, testing and vaccination of close contacts. The identification of new acute and chronic cases is likely to make the intervention cost effective and local health commissioners should consider providing a nurse led service as part of hepatitis B care pathways.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: hepatitis b,chronic hepatitis b

ABSTRACT ID: 367

PRESENTED BY: Kazim Beebeejaun / kazim.beebeejaun@phe.gov.uk

16.4. Effectiveness of three alternative hepatitis B revaccination series (Fendrix®, Twinrix® and HBVaxPro-40®) in healthy non-responders; an open-label randomised controlled multicentre trial

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Background:

Non-protective immunity after hepatitis B vaccination affects 5 to 30 per cent of healthy adults. Which revaccination schedule is most effective is still unclear. We determined the immunogenicity of 3 different vaccines as measured by antibodies against hepatitis B surface antigen (anti-HBs) in non-responders (NR), which are defined as having an anti-HBs < 10 IU/L after one standard series with a recombinant vaccine against hepatitis B virus.

Methods:

In an open-label multicentre randomised controlled trial, participants were randomised with an allocation ratio of 1:1:1:1 to either repeating initial series (HBVaxPro® 10 µg or Engerix-B® 20 µg) as control, or Twinrix® 20 µg, Fendrix® 20 µg or HBVaxPro® 40 µg. All schedules were identical with intramuscular vaccinations at month 0, 1 and 2. Anti-HBs was measured at 0, 1, 2 and 3 months. Our primary endpoint was the percentage of responders (anti-HBs titre > 10 IU/l) one month after the last revaccination of participants who received at least one dose of vaccine.

Results:

A total of 480 participants were randomised of whom 446 received vaccination in one of the study groups. Of these, 434 had an anti-HBs titre available at month 3. Potential confounders were balanced over all groups except for height of baseline anti-HBs titre. The percentage of responders at month 3 was 68.2% in the control-group, and 81.1%, 90.4% and 87.5%, in the Twinrix®, Fendrix® and HBVaxPro-40®-group, respectively. In a multivariable logistic regression analysis HBVaxPro-40® and Fendrix® induced a higher response compared to the control-group ($P<0.01$) after controlling for baseline anti-HBs titre.

Conclusions:

In healthy non-responders, revaccination with Fendrix® or HBVaxPro-40® resulted in significantly better seroconversion rates and should be considered over standard revaccination schemes.

Subject: Microbiology

Keywords: Randomised controlled trial, Serology,Hepatitis B, Vaccines

ABSTRACT ID: 209

PRESENTED BY: Stijn Raven / stijn.raven@radboudumc.nl

16.5. High positivity of sexually transmitted infections in men who have sex with men in the times of HIV pre-exposure prophylaxis (PrEP) - results of a cross-sectional multicentre study in Germany, 2018

Gyde Steffen [1]

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Background:

Men who have sex with men (MSM) are disproportionally more affected by sexually transmitted infections (STI). However, STI testing in absence of symptoms is currently not covered by German health insurances. Approval of HIV pre-exposure prophylaxis (PrEP) in Germany in 2016 might have influenced sexual behaviour and STI prevalence of MSM. Our aim was to estimate STI positivity and risk factors amongst MSM in Germany to plan effective interventions.

Methods:

We conducted a cross-sectional study in Germany in 2018. Thirteen clinics systematically screened MSM for Chlamydia trachomatis, Neisseria gonorrhea, Mycoplasma genitalium and Trichomonas vaginalis using self-collected rectal and pharyngeal swabs, and urine samples. PCR-based APTIMA® STI-assays were used. We collected information on sociodemographics, HIV-status, clinical symptoms, sexual behaviour and PrEP-use. We calculated prevalence ratios (PR) to identify risk factors and stratified for HIV-status and PrEP-use.

Results:

As of 22/04/2018, 1,199 MSM were included: 50.4% (603/1,199) were HIV-positive, median age was 39 years [range 18-71]. Overall STI positivity was 31.4% (Mycoplasma genitalium=17.8%, Neisseria gonorrhea=9.9%, Chlamydia trachomatis=9.1%, Trichomonas vaginalis=0.1%) and was not significantly higher in HIV-positive participants (PR=1.0;CI95%=0.8-1.1). 66.3% (230/347) of STI-positive participants did not report STI-related symptoms. 30.1% (162/539) of HIV-negative participants currently took PrEP. In PrEP-users, the number of male sexual partners (median 12 vs. 5; $p<0.05$), sex without condom (91.7% vs 65.9%;$p<0.05$), use of party drugs such as liquid ecstasy (42.8% vs. 26.6%;$p<0.05$) within last 6 months and STI positivity (PR=1.8;CI95%=1.4-2.3) were significantly higher.

Conclusions : A high proportion of mainly asymptomatic MSM are positive for STI in Germany. Health insurance covered regular STI screenings of PrEP-users amongst MSM, independent of symptoms, would facilitate early treatment and thereby reduce further spread.

Subject: Burden of disease

Keywords: Sexually Transmitted Diseases, Men Who Have Sex With Men, HIV Pre-Exposure Prophylaxis, Risk Factors

ABSTRACT ID: 324

PRESENTED BY: Gyde Steffen / steffeng@rki.de

Parallel Session 17
DAY 3, Friday, 23. November 2018
11:00-12:40

Influenza and other respiratory viruses(1): epidemiology and surveillance

Moderator

Julien Beauté

Abstracts

17.1. Whole genome analysis of influenza A(H3) viruses detected between 2016-2018 in the scope of EuroEVA/I-MOVE vaccine effectiveness study

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Background:

NGS techniques, allow a much deeper genetic analysis of influenza viruses, compared to traditional Sanger sequencing of hemagglutinin gene. The present study aims to perform phylogenetic and mutational analysis at whole-genome level in order to search for genetic features related to vaccine failure.

Methods:

Nasopharyngeal swabs were collected during 2016/17 and 2017/18 winter seasons, from ILI patients participating in EuroEVA/I-MOVE study. Whole genome sequences were obtained for 179 influenza A(H3) viruses by NGS in a MiSeq platform and subsequent bioinformatics analysis using the web-based platform INSaFLU (https://insaflu.insa.pt/). Additional fine-tune sequence analysis was performed using MEGA-7.

Results:

All sequenced viruses clustered in 2 HA-based genetic groups: 58 (32.4%) in 3C.2a group and 121 (67.6%) in 3C.2a1. Vaccine failure cases were detected in a higher proportion in 3C.2a1 group (20/121, 16.5%) than in 3C.2a (8/58, 13.8%). WGS analysis further revealed intra-subtype reassortments based on the closest genetic relatedness of each viral segment to the representative virus of seasonal A(H3) genetic (sub-)groups, with viruses being distributed in 6 different patterns of genome constellation. The group with all genomic segments most closely related to A/Singapore/INFIMH-16-0019/2016 harboured a higher number of vaccine failure cases (14/69, 20.3%). Despite 16 viruses (from 28 detected in vaccinated cases) presented amino acid substitutions not found in unvaccinated cases, these substitutions revealed a sporadic pattern.

Conclusions:

Vaccine failure cases were not exclusive of any genetic group or reassortment pattern, although they were found in slightly higher proportion among 3C.2a1 viruses and in viruses with all genetic segments mostly similar to A/Singapore/INFIMH-16-0019/2016. The further use of WGS in flu surveillance is essential to better understand genetic determinants of infection and evolutionary dynamics of influenza virus.

Subject: Novel methods in microbiology (e.g. new diagnostic tools)

Keywords: influenza virus, whole genome analysis, vaccine effectiveness, vaccine failure

ABSTRACT ID: 458

PRESENTED BY: Raquel Guiomar / raquel.guiomar@insa.min-saude.pt

17.2. Predicting peak influenza activity in primary and secondary care in Scotland – is the Moving Epidemic Method the way forward?

Diogo F. P. Marques [1]

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Background:

Scotland observed an influenza A(H3N2)-dominated 2017/18 season with healthcare services under pressure. We aimed to predict the peak activity period to inform public health decision-making and resource allocation.

Methods:

We applied the moving epidemic method (MEM) to calculate the epidemic thresholds for the 2017/18 influenza season using primary-care (PC) and secondary-care (SC) virology data from seasons 2010/11-2016/17. The start of season was defined as the week where swab positivity breached the 2017/18 threshold for two or more consecutive weeks. For each previous influenza A(H3N2)-dominated season, we calculated the week of breach of threshold(a); the week of peak in swab positivity(b); and the time to peak from breach of threshold in weeks, including the breach week((b–a)+1). We estimated the predicted peak activity period as the average of the time to peak (in weeks) rounded to the nearest whole number, with a range of +/- 1 week.

Results:

The start of 2017/18 season was week 47 for PC and SC virology data. Based on PC data, the predicted average time to peak was 6 weeks and the predicted peak activity period was between weeks 51-01. Based on SC data, the predicted average time to peak was 5 weeks and the predicted peak activity period was between weeks 50-52. These predictions aligned with current season observations where peaks were observed in week 51 for PC and week 52 for SC virology data.

Conclusions:

We conclude that the MEM applied to virology data is a useful tool to define the start of the influenza season and predict the peak activity period. Due to the pragmatic and low-cost nature of our methods, we recommend the method be evaluated by other countries.

Subject: Surveillance

Keywords: influenza, public health, policy, surveillance

ABSTRACT ID: 139

PRESENTED BY: Diogo F. P. Marques / diogo.marques@nhs.net

17.3. Development of a system of automated analysis and reporting for pandemic influenza severity assessment in England

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Background:

In an influenza pandemic a key requirement is rapid severity assessment and monitoring. This requires continuous analysis of multiple data sources from different levels of the disease pyramid. Microsoft Excel is a commonly used analytical tool but analysis is generally non-reproducible and can be time consuming and error prone. R Markdown allows the integration of computer-readable code with human-readable text for the production of automated reports in various formats. The objective of this work is to develop a system of automated analysis and reporting for pandemic influenza.

Methods:

We reviewed reporting arrangements for all routine epidemiological data sources, including primary and secondary care and mortality, and specified reporting formats and aggregation steps. We developed an outline daily pandemic flu report in R Markdown. We wrote scripts in R to retrieve and analyse the multiple data sources and produce outputs for incorporation into a report. We developed standard operating procedures and peer reviewed the scripts.

Results :

The reports include all elements of severity assessment – transmissibility, seriousness of disease, and impact – along with historical comparisons. The scripts automatically analyse multiple data sources and produce a menu of summary tables and figures. The reports can be adapted by the user who may choose which elements to include, input their own interpretation and generate reports in various formats.

Conclusions:

In a future pandemic, this system of automated analysis and reporting will substantially reduce the analytical burden, reduce the opportunities for error and increase reproducibility and accountability. Pandemic surveillance preparedness plans should include details of descriptive analysis and reporting, and this should be automated as far as possible to free up time for interpretation and communication of results.

Subject: Preparedness

Keywords: Pandemic influenza, Surveillance, Severity assessment, Automated reporting, R, R Markdown

ABSTRACT ID: 248

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

17.4. Previous exposure to natural infection matters - The effect of influenza A infection in 2016/17 on influenza A and B infection in 2017/18 in the Finnish elderly

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Background:

In Finland, the influenza seasons 2016/17+2017/18 caused more cases than observed in previous seasons. Both were characterised by an influenza_A(H3N2) and 2017/18 additionally by a strong influenza_B epidemic. Since the Infectious Diseases Register covers all influenza-positive results of laboratory tests performed in Finland, we aimed to estimate how laboratory-confirmed natural infection with influenza_A in 2016/17 affected the risk of influenza in 2017/18.

Methods: We conducted a register-based cohort study in Finnish 65-100-year-olds. We adjusted the Cox regression analysis for age, sex, presence of chronic diseases, number of hospitalisations in 2016, influenza vaccination in 2017/18 and three previous seasons. We calculated hazard ratios comparing the risk of influenza_A and influenza_B in 2017/18 between those with and without laboratory-confirmed influenza_A in 2016/17.

Results: The cohort comprised 1183512 individuals of which 47.1% were vaccinated in 2017/18. 7401 subjects had confirmed influenza_A in 2016/17. Of those, 14 had influenza_A and 136 influenza_B in 2017/18. In those without previously-confirmed influenza_A, 5945 influenza_A and 5653 influenza_B cases were observed. The corresponding hazard ratios were 0.21 (95%CI: 0.13-0.36) and 2.44 (2.06-2.90).

Conclusions:

Previous exposure to natural infection is difficult to assess in observational studies and often omitted in influenza vaccine effectiveness analyses. Although also we had only incomplete information on past infections leading to exposure misclassification, it seems that previous infection, likely followed by immunity, lowered the risk of detecting infections with a similar influenza_A virus in 2017/18. The increased influenza_B risk among the previous influenza_A cases could be a consequence of this residual immunity against influenza_A and an elevated baseline frailty. The effect of natural infection/ residual immunity should be considered in future study designs and when interpreting the population-level impact of vaccination programmes.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: cohort, effectiveness, influenza, vaccine

ABSTRACT ID: 251

PRESENTED BY: Ulrike Baum / ulrike.baum@thl.fi

17.5. Factors associated with admission to intensive care units (ICUs) and/or death among severe hospitalized confirmed influenza cases, Spain, 2010 – 2018

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Background:

Surveillance of severe hospitalized confirmed influenza cases (SHCIC) provides important information for assessing prevention strategies and health-care planning in Spain. We aimed to identify factors for ICU admission and/or death amongst SHCIC and the effects of influenza vaccinations to guide influenza prevention and control policies.

Methods:

We conducted a retrospective cohort study using SHCIC surveillance data from 2010-11 to 2017-18 influenza seasons. We used multivariable Poisson regression models to estimate the association between ICU admission and/or death and several explanatory variables: sex, age-groups (0-<15, 15-<65, 65-<75 and >=75 years), virus type/subtype, obesity class III (BMI>=40kg/m2), diabetes, immunosuppression, other chronic conditions, pneumonia, co-infection, influenza vaccination status, antiviral treatment, season and region.

Results:

Of 18,759 SHCIC, 5,302 (28.3%) were admitted to ICU and 2,629 (14%) died. Being male (adjusted incidence rate ratio (aIRR) 1.12, 95%-CI=1.05-1.21), age <75 years (aIRR 2.3, 95%-CI=2.1-2.6), A(H1N1)pdm09 or A(H3N2) vs B infection (aIRR 1.4, 95%-CI=1.2-1.6; aIRR 1.3, 95%-CI=1.1-1.4, respectively) and obesity class III (aIRR 1.4, 95%-CI=1.3-1.6) were associated with ICU admission. Age 15-<65, 65-<75 and >=75 years vs 0-<15 years (aIRR 11.3, 95%-CI=5.3-24.0; aIRR 15.8; 95%-CI=7.4-33.8; aIRR 22.9, 95%-CI=10.7-48.8, respectively), A(H1N1)pdm09 vs B infection (aIRR 1.5, 95%-CI=1.2-1.8), liver disease (aIRR 1.8, 95%-CI=1.5-2.1) and immunosuppression (IRR 1.6, 95%-CI=1.4-1.9) were associated with death. Patients with recent influenza vaccination were less likely to be admitted to ICU (aIRR 0.88, 95%-CI=0.81-0.96) and/or die (aIRR 0.92, 95%-CI=0.86-0.99). SHCIC who received antiviral treatment within 48h after symptoms onset were less likely to die (aIRR 0.83, 95%-CI=0.70-0.98).

Conclusions:

We identified groups at higher risk of severe outcome amongst SHCIC. Recently conducted influenza vaccinations and early antiviral treatment were protective for SHCIC and should be recommended especially for those groups with higher risks.

Subject: Surveillance

Keywords: influenza; severe influenza; influenza hospitalizations; influenza surveillance; risk factors

ABSTRACT ID: 251

PRESENTED BY: Concepción Delgado-Sanz / cdelgados@isciii.es

Parallel Session 18
DAY 3, Friday, 23. November 2018
11:00-12:40

Late breakers

Moderator

Alain Moren

Abstracts

18.1. Monitoring the dynamics of public perceptions of meningococcal disease and vaccination: The case of an ongoing outbreak in the Netherlands

Marion de Vries [1]

J. Oliva [2], A. Larrauri [3]

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[2,3] 1. National Centre of Epidemiology, Institute of Health Carlos III, Madrid, Spain 3. CIBER of Epidemiology and Public Health (CIBERESP), Madrid, Spain

Background:

Surveillance of severe hospitalized confirmed influenza cases (SHCIC) provides important information for assessing prevention strategies and health-care planning in Spain. We aimed to identify factors for ICU admission and/or death amongst SHCIC and the effects of influenza vaccinations to guide influenza prevention and control policies.

Methods:

We conducted a retrospective cohort study using SHCIC surveillance data from 2010-11 to 2017-18 influenza seasons. We used multivariable Poisson regression models to estimate the association between ICU admission and/or death and several explanatory variables: sex, age-groups (0-<15, 15-<65, 65-<75 and >=75 years), virus type/subtype, obesity class III (BMI>=40kg/m2), diabetes, immunosuppression, other chronic conditions, pneumonia, co-infection, influenza vaccination status, antiviral treatment, season and region.

Results:

Of 18,759 SHCIC, 5,302 (28.3%) were admitted to ICU and 2,629 (14%) died. Being male (adjusted incidence rate ratio (aIRR) 1.12, 95%-CI=1.05-1.21), age <75 years (aIRR 2.3, 95%-CI=2.1-2.6), A(H1N1)pdm09 or A(H3N2) vs B infection (aIRR 1.4, 95%-CI=1.2-1.6; aIRR 1.3, 95%-CI=1.1-1.4, respectively) and obesity class III (aIRR 1.4, 95%-CI=1.3-1.6) were associated with ICU admission. Age 15-<65, 65-<75 and >=75 years vs 0-<15 years (aIRR 11.3, 95%-CI=5.3-24.0; aIRR 15.8; 95%-CI=7.4-33.8; aIRR 22.9, 95%-CI=10.7-48.8, respectively), A(H1N1)pdm09 vs B infection (aIRR 1.5, 95%-CI=1.2-1.8), liver disease (aIRR 1.8, 95%-CI=1.5-2.1) and immunosuppression (IRR 1.6, 95%-CI=1.4-1.9) were associated with death. Patients with recent influenza vaccination were less likely to be admitted to ICU (aIRR 0.88, 95%-CI=0.81-0.96) and/or die (aIRR 0.92, 95%-CI=0.86-0.99). SHCIC who received antiviral treatment within 48h after symptoms onset were less likely to die (aIRR 0.83, 95%-CI=0.70-0.98).

Conclusions:

We identified groups at higher risk of severe outcome amongst SHCIC. Recently conducted influenza vaccinations and early antiviral treatment were protective for SHCIC and should be recommended especially for those groups with higher risks.

Subject: Surveillance

Keywords: influenza; severe influenza; influenza hospitalizations; influenza surveillance; risk factors

ABSTRACT ID: 566

PRESENTED BY: Marion de Vries / marion.de.vries@rivm.nl

18.2. Detection of two seropositive infections with antibodies to zoonotic Borna disease virus-1 (BoDV-1) in a retrospective serosurvey among 424 veterinarians working in an endemic area in Germany

Hendrik Wilking [1]

D. Tappe [2], C. Frank [3], R. Offergeld [4], C. Wagner-Wiening [5], K. Stark [6], J. Schmidt-Chanasit [7]

[1] Robert Koch-Institut

[2,7] Bernard-Nocht-Institut

[3,4,6] Robert Koch-Institut

[5] Baden-Wuerttemberg State Health Office

Background:

Zoonotic Borna disease virus-1 (BoDV-1) was recently discovered as cause of encephalitis in 6 human patients in Germany. Only one patient survived with serious sequelae. In addition, an organ donor was apparently infected but died of non-neurological causes. BoDV-1 is known to cause neurological disease mainly in horses and sheep. The virus is maintained in bicoloured white-toothed shrew (Crocidura leucodon). Animal disease incidence is focused in South and Central Germany, especially parts of Bavaria. Incidence of infection, transmission pathways and risk factors in humans are completely unresolved. Veterinarians may be disproportionally BoDV-1-exposed through contact to vector or host animals.

Methods:

A newly developed indirect immunofluorescence antibody test (IFAT) was applied for primary testing of human sera for anti-BoDV-1 IgG-antibodies, confirmed by immunoblot assays. Anonymized residual samples from a 2009 serosurvey of veterinarians with interview data on exposures were analyzed.

Results:

The survey included 424 serum samples from Bavaria and neighboring districts. Participants' median age was 40 (18–74) years, 276 (65%) were female. Two (0.5%) participants had positive sera: A 25-29-year-old woman and a 55-59-year-old woman from different regions. Both reported private and occupational contact to various pets and farm animals. Both reported joint pain and one muscle pain, asthma and neurological disease as health complaints. All other sera were clearly negative.

Conclusions:

We found serological evidence that BoDV-1-infections occur, but are rare in areas with highest zoonotic risk and in a group with potentially elevated exposure risk. Likelihood of infection may be equally low or even lower in the general population. As sera had already been anonymized, follow up was not possible. Future BoDV-1-epidemiological studies targeting the general population require large sample sizes to obtain statistically significant results.

Subject: Preparedness

Keywords: Communicable Diseases -Emerging, Viral Diseases, Infectious Encephalitis, Borna Disease, Seroepidemiologic Studies, Risk Factors

ABSTRACT ID: 546

PRESENTED BY: Hendrik Wilking / WilkingH@rki.de

18.3. Outbreak of Legionella non-pneumophila subspecies associated with gardening and usage of commercial bagged soil in Sweden, 2018,

Emma Löf [1]

F. Chereau [2], P. Juréen [3], S. Andersson [4], K. Rizzardi [5], M. Kais [6], A. Tideholm-Nylén [7], S. Kühlmann-Berenzon [8]

[1] European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden; Public Health Agency of Sweden, Solna, Sweden

[2] European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden; Public Health Agency of Sweden, Solna, Sweden

[3,4,5,8] Public Health Agency of Sweden, Solna, Sweden

[6,7] Department of Communicable Disease Control, County of Stockholm, Sweden

Background:

In June 2018, an unusually high number of domestic cases of Legionella non-pneumophila subspecies were reported. Four of 22 early cases were identified with Legionella longbeachae, known from literature to be found in soil. An outbreak investigation was initiated to identify the source and exposures.

Methods:

Cases were defined as domestic laboratory-confirmed cases of Legionella non-pneumophila spp. with symptom onset after 14 May 2018. We conducted a matched case-control study with controls from a national survey panel, matched by sex, age, county and exposure period. We inquired about water exposures, gardening, and soil handling, and computed matched odds ratios (mOR) using conditional logistic regression. Case specimens and soil samples from gardens of cases were analysed for Legionella spp. and by whole genome sequencing.

Results:

By September 7, 38 cases of Legionella non-pneumophila (median age 69, 53% women) from 6/21 counties had been reported. Twenty-five of these cases and 170 controls were included in the study. In univariate analysis, cases were more likely to report gardening (mOR 6.7, 95%CI:0.9-52.5) and using commercial bagged soil (CBS) (mOR=3.8, 95%CI:1.1-13.8) compared to controls. Specific activities associated with Legionella non-pneumophila were: watering CBS with hose/spray (mOR=11.8, 95%CI:2.2-62.1), mixing CBS with other products (mOR=8.2, 95%CI:1.9-34.8), and using CBS in a greenhouse (mOR=10.5, 95%CI:1.7-63.4). Thirty of the 38 cases became laboratory confirmed withLegionella longbeachae. Soil samples were polyclonal for Legionella longbeachae and did not cluster with case isolates.

Conclusions:

Investigations are ongoing. Preliminary analysis showed that handling of CBS, including spraying or hosing, mixing or using CBS in a greenhouse, were associated with Legionella non-pneumophila infection. These findings will inform specific public health recommendations for risk groups.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Legionella non-pneumophila,L. longbeachae,outbreak,case-control study,gardening,soil

ABSTRACT ID: 588

PRESENTED BY: Emma Löf / emma.lof@folkhalsomyndigheten.se

18.4. Second epidemic wave of a large measles outbreak in Italy, 2018, amid vaccination policy changes

Xanthi Andrianou [1]

M. Del Manso [2], A. Bella [3], P. Pezzotti [4], M. Rota [5], A. Filia [6]

[1] European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden; Department of Infectious Diseases, National Health Institute, Rome, Italy

[2,3,4,5,6] Department of Infectious Diseases, National Health Institute, Rome, Italy

Background:

A large measles outbreak started in Italy in 2017. In the first wave (January-December 2017, described elsewhere), >5000 cases including four deaths were reported, mostly in central and northern regions, prompting the introduction of a mandatory vaccination law (up to 16 years of age). Our objectives were to describe the second, ongoing, epidemic wave, and measles vaccination coverage (VC) in Italy.

Methods:

We analyzed measles cases reported to the national surveillance system between 1 January and 31 July 2018. Cases were classified using the EU case definition and described by age-group. National and regional incidence per 1,000,000 was calculated. VC data (2016-2017), collected from the Ministry of Health, were analyzed.

Results:

Overall, 2162 cases were reported (incidence: 61/1,000,000); 75.5% laboratory confirmed and 87% unvaccinated. Sicily (southern Italy; 51% of cases) reported the highest incidence (373/1,000,000). The second highest incidence was reported in another southern region (Calabria, 143/1,000,000). This wave peaked in April 2018 (n=467); the number of cases decreased to 120 in July. The highest incidence occurred in infants <1 year (507/1,000,000). Median age was 25 years. Overall, 56% reported at least one complication; 61.4% were hospitalized. Four deaths occurred. National VC at 2 years of age (one dose) was 91.7% in 2017 (4.4% higher than 2016).

Conclusions:

The second wave of the 2017-2018 measles outbreak in Italy seems less intense than the first and is affecting different geographical areas. As in the first wave and other European outbreaks, high incidence occurred among infants. Control measures included vaccination of susceptible contacts from 6 months of age. The mandatory vaccination law contributed to VC increase in children but additional interventions addressing adult immunity gaps are needed to reach elimination.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: measles, outbreak, Italy ,vaccination

ABSTRACT ID: 592

PRESENTED BY: Xanthi Andrianou / xanthi.andrianou@iss.it

18.5. Exploiting publically available microbial genomic data for detecting linked cases in global outbreaks

Anaïs Painset [1]

C. Amar [2], L. Byrne [3], S. Kanagarajah [4], K. Grant [5], M. Sait [6], J. Gregory [7], M. Easton [8], A. Goncalves Da Silva [9], D. Williamson [10], S. Ballard [11]

[1] Public Health England, London, UK

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[6,9,10,11] Microbiological Diagnostic Unit, Public Health Laboratory, Doherty Institute, University of Melbourne Australia

[7,8] Department of Health and Human Services Victoria, Melbourne, Australia

Background:

Foodborne outbreaks of listeriosis are difficult to investigate due to the low attack rate and long incubation period of this severe but rare systemic infection. Genomic surveillance of Listeria monocytogenes isolates from clinical cases and foods is proving transformational for outbreak investigation by detecting linked cases, identifying contaminated food products and tracing the origin of contamination. This presentation illustrates the power of sharing L. monocytogenes whole genomes sequences (WGS) for improved case ascertainment in global outbreaks of listeriosis.

Methods:

A multicountry European outbreak of listeriosis linked to frozen corn was identified in November 2017 using WGS analysis (1). Public Health England routinely sequences all clinical and food Listeria isolates making them publically available by uploading the sequences to the NCBI Short Read Archive (NCBI BioProject PRJNA248549). Sequences from 4 UK clinical isolates associated with the European Frozen corn outbreak were uploaded to the SRA. The Microbiological Diagnostic Unit (MDU), Public Health laboratory in Melbourne routinely searches public genome databases for isolates that match their domestic clinical isolates.

Results:

During the outbreak investigation in 2018, the MDU identified a WGS match between an isolate from an Australian case of listeriosis and the 4 outbreak associated isolates deposited by PHE. Detailed phylogenetic analysis including outbreak isolates from European countries involved in the outbreak clustered the Australian clinical isolate within 5 SNPs of the European outbreak isolates. Consumption of frozen corn was subsequently confirmed by the Australian case.

Conclusions:

Use of publically available WGS databases empowered the detection of a case of listeriosis outside of the EU that was epidemiologically linked to a European multicountry outbreak associated with frozen corn.

www.efsa.europa.eu/sites/default/files/scientific_output/EN-1448.pdf

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Subject: Novel methods in epidemiology (e.g. digital disease detection, e-health)

Keywords: listeriosis, whole genome sequencing,outbreak

ABSTRACT ID: 602

PRESENTED BY: Anais Painset / Anais.Painset@phe.gov.uk

Parallel Session 19
DAY 3, Friday, 23. November 2018
14:30-15:30

Vaccine- preventable diseases (5): preparedness

Moderator

Katharina Alpers

Abstracts

19.1. Guidance for the governance of public-private collaborations in vaccine post-marketing settings in Europe

Laurence Torcel-Pagnon [1]

V. Bauchau [2], P. Mahy [3], M. Tin Tin Htar [4], M. van der Sande [5], C. Mahé [6], T. Grove Krause [7], A. Charrat [8], F. Simondon [9], X. Kurz [10]

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[2] Vaccine Clinical Safety and Pharmacovigilance, GlaxoSmithKline Vaccines R&D, Wavre, Belgium

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[6,8] Vaccine Epidemiology and Modelling (VEM), Sanofi Pasteur, Lyon, France

[7] Department of infectious Disease Epidemiology, Statens Serum Institut, Denmark

[9] MERIT Research Unit, IRD, Paris, France

[10] Pharmacovigilance & Epidemiology Department, European Medicines Agency, London, UK

Background:

The 2009 pandemic influenza highlighted challenges for vaccine post-marketing monitoring in Europe, particularly the need to strengthen public-private collaborations (PPCs) to improve the collection and analysis of safety and effectiveness data. The ADVANCE consortium (IMI project) comprises public and private stakeholders that have worked together to propose a governance framework for efficient, transparent, and trustworthy PPCs for vaccine post-marketing projects.

Methods:

Based on the results of a landscape analysis and screening of formalised existing governance structures, we identified the components of a governance framework and developed recommendations to support stakeholders willing and able to implement collaborative projects. These proposals were discussed by 70 experts during a workshop to gain from their experience and get advice on their implementation.

Results:

We identified core governance principles and defined five fundamental functions that can be attributed to individual partner organisations or to a committee with representatives from more than one partner organisation: decision-making, scientific advice, quality control and audit, implementation and management, and financial management. We propose a generic governance model with options allowing its adaptation to specific contexts and projects. The advantages and disadvantages of PPCs were also examined. Stakeholders' concerns (e.g. scientific integrity and public trust) were addressed through recommendations about transparent decision-making rules and conflicts of interest management with reference to the ADVANCE and ENCePP codes of conduct.

Conclusions:

No one-size-fits-all solution for PPC governance exists but our recommendations could be used to set-up a tailored-made and fully transparent governance structure to support collaborative projects in the European vaccine post-marketing environment. The next steps will involve field-testing the guidance in real-world collaborations and collecting lessons learnt that can be used to improve it.

Subject: Preparedness

Keywords: Governance,Public-private collaboration,Vaccine post-marketing setting

ABSTRACT ID: 434

PRESENTED BY: Laurence Torcel-Pagnon / laurence.pagnon@sanofi.com

19.2. Getting ahead of the wave: informing public health action through mapping to identify populations at high risk of measles introduction and transmission

Mary Cronin [1]

L. Utsi [2], G. Hughes [3]

[1] Public Health England

[2,3] Public Health England

Background:

In the Yorkshire and Humber region, UK there is a high measles, mumps and rubella routine vaccine uptake (MMR1 93%; MMR2 90%). Despite this, an outbreak of measles involving 35 confirmed cases occurred in its main city in January 2018. The index case was a child returning from Romania. This outbreak highlighted a need to identify populations most susceptible to measles introduction and transmission.

Methods:

A combination of routinely available immunisation and demographic data was used to assess where populations at high risk were located. The count of National Insurance Number (NINo) registrations (January 2012 to September 2017) by small areas (approximately 5,000 persons) was used as a proxy for size of the new migrant population. To identify areas where introduction of measles from a high incidence country was most probable, areas in the top quartile of NINo counts were defined as having a high migrant population. Risk categories were assigned to general practitioner (GP) practices based on both their location in a high migrant area and whether they were in the lowest quartile of MMR vaccine coverage (for those aged 2–18 years).

Results:

Of the 713 GP practices in the region, 129 (18.1%) were in a high migrant area with a low MMR vaccine coverage, 131 (18.4%) were in a high migrant risk category (only) and 46 (6.5%) in a low vaccine coverage risk category (only).

Conclusions:

The maps are being used by local public health teams to pro-actively target resources to higher risk GP practices to increase vaccine uptake. This approach enables guided pre-emptive action to prevent future outbreaks of measles in Yorkshire and Humber, demonstrating it to be a beneficial tool.

Subject: Toolkits

Keywords: measles, mapping,vaccination uptake,targeting resources

ABSTRACT ID: 355

PRESENTED BY: Mary Cronin / mcb.cronin@gmail.com

19.3. ADVANCE system testing: vaccine benefit studies by using multi-country electronic health data - An example on pertussis vaccination

Myint Tin Tin Htar [1]

M. de Ridder [2], T. Braeye [3], A. Correa [4], S. de Lusignan [5], T. Duarte-Salles [6], C. Huerta [7], E. Martin [8], L. Tramontan [9], G. Danieli [10], G. Picelli [11], N. van der Maas [12], K. Berensci [13], . Arnheim-Dahlstrom [14], U. Heininger [15], H. Emborg [16], D. Weibel [17], K. Bollaerts [18], L. Titievsky [19], V. Bauchau [20], M. Sturkenboom [21]

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Methods:

We conducted a retrospective cohort analysis in children receiving wP or aP vaccine between 1990-2015 in 7 databases from four countries: Denmark: AUH & SSI, Spain: SIDIAP & BIFAP, UK: THIN & RCGP RSC, Italy: Pedianet. The outcomes of interest were confirmed or suspected pertussis, pneumonia and generalized convulsions within 30 days and death within 90 days of pertussis onset. IRs were calculated in periods 14 days after each dose to 14 days after the following dose, as ratio of number of cases and person time.

Results:

The study cohort comprised 2.9 million children ≤ 5 years old. Data on aP vaccination were available in all databases while only 4 held data on wP vaccination. The IR (/105 person-years) for pertussis ranged between 0.15 (95% CI: 0.12; 0.19) and 1.15 (95% CI: 1.07; 1.23). Its trends over calendar time were coherent with surveillance databases, showing external validity. IR decreased with number of vaccine doses received (0.40-2.83 after one dose of aP and 0.03-0.68 after three doses). Complications in pertussis breakthrough cases were rare and their relative risks comparing pertussis to non- pertussis cases could not be reliably estimated.

Conclusions:

Based on this proof of concept study we demonstrated the feasibility of estimating IR of pertussis using the ADVANCE distributed network system. Inclusion of more data sources could provide additional power to estimate risks for complications in pertussis breakthrough cases.

Subject: Preparedness

Keywords: Immunization, Incidence, Pertussis, data network, electronic health care databases

ABSTRACT ID: 484

PRESENTED BY: Myint Tin Tin Htar / myint.tintinhtar@pfizer.com

Parallel Session 20
DAY 3, Friday, 23. November 2018
14:30-15:30

Influenza and other respiratory viruses

Moderator

Richard Pebody

Abstracts

20.1. 2017–18 Vaccine effectiveness against influenza A(H3N2) and lineage mismatched influenza B in older adults: Results from the I-MOVE+ hospital network

Angela MC Rose [1]

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[24] Spain, Navarra, Italy, France, Romania, The Netherlands, Portugal, Finland, Croatia, Lithuania

Background:

The predominant circulating influenza virus in the 2017–18 season was B/Yamagata, followed by A(H1N1)pdm09 and A(H3N2). Circulating and trivalent vaccine viruses were similar for influenza A but mismatched for B (with B/Victoria lineage in the vaccine). The I-MOVE+ hospital network conducted a multicentre test-negative case control study in 30 hospitals in 10 European countries to measure influenza vaccine effectiveness (IVE) against influenza A(H3N2) and B among older adults.

Methods:

Hospital teams swabbed patients aged ≥65 years admitted with recent onset (≤7 days) of severe acute respiratory infection and collected information on demographics, influenza vaccination status and underlying conditions. Cases were patients RT-PCR positive for influenza A(H3N2) or B and controls those negative for any influenza virus. Using logistic regression, we measured IVE against influenza A(H3N2) and B, adjusted for study site, chronic conditions, age and date of onset.

Results:

We included 2962 patients (1704 controls, 818 influenza B cases and 301 A(H3N2)). Of 1421/1448 (98%) vaccinated patients with known vaccine type, three received quadrivalent vaccine (0.2%). Adjusted IVE against A(H3N2) was 29% (95%CI:7–46) overall, 39% (95%CI: 8–59) in those aged 65–79 and 27% (95%CI: 3–46) in those ≥80 years. Adjusted IVE against B was 34% (95%CI: 20–46) overall, 42% (95%CI: 24–56) in 65–79-year-olds and 20% (95%CI: -16–45) in those ≥80.

Conclusions : Our results suggest low IVE against influenza A(H3N2) among elderly hospitalised patients. IVE against influenza B was similar to that for A(H3N2), despite a vaccine and circulating B lineage mismatch, suggesting some cross- protection. We reinforce the importance of influenza vaccination in older adults as, even when IVE is low, it remains preventive against severe influenza.

Subject: Surveillance

Keywords: Influenza A(H3N2), Influenza B ,vaccine effectiveness, hospital, Europe,elderly, case-control

ABSTRACT ID: 350

PRESENTED BY: Angela MC Rose / demerararose@gmail.com

20.2. High live-attenuated influenza vaccine effectiveness against influenza B in two-year-olds, 2017/18, Finland

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Background:

In Finland, children aged 0.5-2 years are eligible for free seasonal influenza vaccination since 2007. Since 2015, parents can choose for their two-year-old between a trivalent inactivated (IIV3) and quadrivalent live-attenuated (LAIV4) influenza vaccine without recommended preference. The 2017/18 season was characterised by early circulating influenza B-Yamagata (mismatch with IIV3, match with LAIV4) and later circulating A(H3N2) viruses. The aim of this study was to estimate the effect of vaccination with IIV3 and LAIV4 in 2017/18 in two-year-olds.

Methods:

We conducted a register-based cohort study using Cox regression adjusted for age and sex to estimate the risk of laboratory-confirmed influenza_A and B in the birth cohort 2015. In two separate analyses, the exposure was either IIV3 or LAIV4 and children vaccinated with the other vaccine were censored. We estimated hazard ratios (HRs) comparing the risk of influenza between vaccinated and unvaccinated and calculated vaccine effectiveness as 1-HR.

Results:

The cohort comprised 55566 children of which 21.7% were vaccinated with LAIV4 and 9.2% with IIV3. Based on 224 influenza_A (59 LAIV4 vaccinated, 19 IIV3) and 215 influenza_B (11 LAIV4, 25 IIV3) cases, HRs for LAIV4 were estimated at 1.324 (95%CI: 0.977; 1.793) and 0.204 (0.111; 0.375) and for IIV3 at 1.037 (0.642; 1.676) and 1.102 (0.724; 1.102) against influenza_A and B, respectively. Vaccine effectiveness of LAIV4 against influenza_B was 79.6% (95%CI: 62.5%; 88.9%).

Conclusions:

These findings suggest that during an influenza season with circulating influenza_B virus not included in IIV3, LAIV4 provides broader protection to young children. However, in terms of protection against influenza_A(H3N2) both vaccines were observed to perform equally. The national recommendation for 2018/19 is to use a quadrivalent influenza vaccine, without preference for IIV4 or LAIV4.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: cohort, effectiveness, influenza, vaccine

ABSTRACT ID: 345

PRESENTED BY: Ulrike Baum / ulrike.baum@thl.fi

20.3. Cost-effectiveness analysis of seasonal influenza vaccination strategies targeting children and/or the elderly in 6 European countries and regions,

Frank Sandmann [1]

E. Van Leeuwen [2], P. De Boer [3], I. Casado [4], J. Castilla [5], L. Domegan [6], A. Gherasim [7], M. Hooiveld [8], I. Kislaya [9], A. Larrauri [10], A. Machado [11], D. Marques [12], I. Martínez-Baz [13], C. Mazagatos-Ateca [14], J. McMenamin [15], J. Murray [16], B. Nunes [17], J. O'Donnell [18], W. van der Hoek [19], R. Pebody [20], M. Baguelin [21], O. behalf of the I-MOVE+ Work Package 5 participants [22]

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[22] The project has received funding from the European Union's Horizon 2020 programme

Background:

Seasonal influenza vaccination programmes in most European countries currently target primarily the elderly and risk- groups using non-adjuvanted non-high-dose trivalent vaccines. As part of the Integrated Monitoring of Vaccines in Europe (I- MOVE+) project, which focused on reducing influenza disease burden in the elderly, we explored the incremental cost- effectiveness of 12 seasonal influenza vaccination strategies for children (aged 4-16 years) and/or the elderly (≥ 65 years) in Ireland, Navarra, The Netherlands, Portugal, Scotland, and Spain.

Methods:

We used a dynamic-transmission model to infer seasonal influenza transmission per setting based on primary care surveillance and virological data from at least 4 seasons. We estimated costs and quality-adjusted life years (QALYs) from the provider perspective over one average season when moving to an "improved" (adjuvanted or high-dose) trivalent (iTIV) or a non-adjuvanted non-high-dose quadrivalent vaccine (QIV) for the elderly; adopting paediatric vaccination with the quadrivalent vaccine at an uptake of 25%, 50%, or 75%; or combining either strategy for the elderly with either paediatric strategy. We discounted QALYs lost from premature mortality uniformly at 3%, and converted costs to 2017 EUR.

Results:

Across settings, moving the elderly to iTIV was non-dominated and cost-saving only in Portugal. The additional costs-per- QALY of the paediatric vaccinations ranged from cost-saving (Navarra, Netherlands) to €9,423/QALY (Scotland). Afterwards, combining paediatric vaccination with iTIV for the elderly ranged between cost-saving (Portugal) and €109,995/QALY (Spain). Combining paediatric vaccination with QIV for the elderly was non-dominated only in Spain (€90,514/QALY). All other strategies, including the base case, were (extendedly) dominated.

Conclusions:

Subject to assumptions regarding the vaccine prices, moving the elderly to iTIV is the optimal strategy in Portugal; otherwise, paediatric vaccination is the most cost-effective strategy.

Subject: Burden of disease

Keywords: influenza, vaccination, mathematical model, economic evaluation, public health, policy

ABSTRACT ID: 394

PRESENTED BY: Frank Sandmann / Frank.Sandmann@phe.gov.uk

Parallel Session 21
DAY 3, Friday, 23. November 2018
14:30-15:30

Emerging and vector-borne diseases (2)

Moderator

Sooria Balasegaram

Abstracts

21.1. Whole genome sequence analysis reveals a novel cluster of strains with a unique amino acid substitution pattern, responsible for the recent Italian-2017 and Pakistani-2016 Chikungunya virus outbreaks

Erika Lindh [1]

C. Argentini [2], G. Venturi [3], C. Fortuna [4], G. Faggioni [5], E. Benedetti [6], A. Amendola [7], G. Marsili [8], F. Lista [9], G. Rezza [10], M. Remoli [11]

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Background:

Chikungunya virus (CHIKV) is a mosquito-borne pathogen that causes substantial health and economic burdens in the populations affected. In 2017, Italy experienced a CHIKV outbreak that spread in Lazio and caused a secondary outbreak in Calabria, with a final case number of 436. The virus was of the Indian Ocean lineage (IOL) and lacked the E1 A226V mutation, a hallmark for efficient transmission by the Aedes albopictus vector. To understand the underlying genetic and molecular features of the outbreak virus, we sequenced the whole genomes of our isolates.

Methods:

Viruses from mosquito pools (n=2) and samples from viremic patients (n=9) were isolated in cell culture and sequenced using the Illumina platform. We identified amino acid sequence mutations and constructed Maximum likelihood phylogenies based on the complete coding sequence of our CHIKV isolates and reference strains.

Results :

Eight CHIKV genomes were successfully assembled and used for sequence analysis. All genomes shared high sequence identity, pointing at one introduction event. Amino acid sequence analyses revealed a distinct substitution pattern in the Italian-2017 viruses (including mutations in nsP4, E1 and E2), that was partly shared with the Pakistani-2016 outbreak viruses. Evolutionary analyses indicate that these two recent outbreaks and several travel-associated viruses form a cluster of rapidly emerging Indian origin IOL viruses.

Conclusions:

Since the establishment of Ae. albopictus in Italy, the risk of local CHIKV transmission has become substantial. Our analyses show that the 2017 Italian outbreak virus belongs to a cluster of CHIKVs with a dispersion and transmission potential demonstrated by a number of recent outbreaks. Their emergence calls for enhanced monitoring and strengthened preparedness measures, including vector control programs and raised awareness among GPs, in countries at risk.

Subject: Microbiology

Keywords: Chikungunya virus,arbovirus,emerging viral disease,molecular epidemiology

ABSTRACT ID: 206

PRESENTED BY: Erika Lindh / erika.lindh@helsinki.fi

21.2. The epidemic risks from new mosquito borne diseases in Greece in economic terms

Antonios Kolimenakis [1]

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Background: The growing presence of the invasive Asian tiger mosquito (Ae. albopictus) in Greece is associated with greater risks to public health due to the transmission of emerging infectious diseases such as Dengue, Chikungunya and Zika virus. The present study aims to evaluate the economic impact of possible disease outbreaks in terms of post-epidemic costs and to assess the economic efficiency of prevention strategies in Greece.

Methods:

Analysis is based on hypothetical post-epidemic control scenarios and their associated costs. Control costs are based on market prices. Estimated disease costs for imported cases of Dengue, Chikungunya and Zika in Greece from 2013 to 2017 are based on the cost of illness approach. Results from a choice experiment (CE) survey conducted in Athens (2015) are used to evaluate citizens‘ willingness to pay (WTP) for the implementation of prevention programmes targeting at the reduction of health impacts from the Asian tiger mosquito.

Results : Prevention and control costs could increase from the current 0.90 €/ household to a post-epidemic control cost of approximately 25 €/ household. The average cost of one imported disease case is almost 2900€ and could rise significantly in the case of epidemic outbreaks. On the other hand, as found in the CE survey, Athens‘ residents are willing to pay about 15€/year/households for targeted prevention programmes.

Conclusions:

A response vector management plan for diseases transmitted by Ae. albopictus has already been implemented nationally by law. However, the economic interpretation of various outbreak scenarios is of utmost importance for the design of public health policies, taking into account the various socioeconomic challenges in Southern Europe.

Subject: Burden of disease

Keywords: cost of illness, control costs, epidemic response, Asian tiger mosquito

ABSTRACT ID: 237

PRESENTED BY: Antonios Kolimenakis / akolimenakis@gmail.com

21.3. Zika virus in Pregnancy: a retrospective case control study, French Polynesia, 2013-2016

Lorenzo Subissi [1]

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Background:

In 2013-2014, French Polynesia suffered an outbreak of Zika virus (ZIKV). In 2015, a microcephaly outbreak, later associated to ZIKV, was reported in Brazil. Congenital Zika syndrome refers to the spectrum of neurological abnormalities seen in infants infected in utero. Hence, we retrospectively investigated the association of a cluster of neurological defects with the ZIKV outbreak in French Polynesia.

Methods:

Using a case control study, we defined cases as any neurological birth defect or termination of pregnancy of unknown etiology, born between February 2014 and May 2015. For each case, five age and time-matched controls, defined as infants born without birth defects, were recruited from the main hospital of French Polynesia, where 60% of deliveries occur. Mothers completed a face-to-face questionnaire on socioeconomic characteristics, clinical symptoms (rash, fever, conjunctivitis, headache, joint pain, muscle pain) and environmental and chemical exposures. Infection by ZIKV was determined by the detection of anti-ZIKV Neutralizing antibodies using microseroneutralization tests in serum of mothers collected between 11 to 24 months after childbirth. We built two logistic regression models using two exposures (seropositivity, and a categorical variable, divided in: no infection, asymptomatic infection, and symptomatic infection during pregnancy).

Results:

From January to August 2016, we recruited 21 cases and 102 controls. Adjusting for maternal socio-economic status, we found an association between congenital defects with both maternal ZIKV seropositivity (time of infection unknown) (aOR 7.07, 95%CI 0.86-58.3, p=0.02) and symptomatic ZIKV infection during pregnancy (aOR 7·19, 95%CI 1·37-37·2, p=0.04).

Conclusions:

This study revealed that ZIKV of the Asian lineage was neurovirulent and able to cause birth defects before hitting Brazil. Pregnant women should continue avoiding unnecessary travel to Zika virus endemic areas.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: Zika virus infection, Congenital Zika syndrome, Child health,Pacific

ABSTRACT ID: 110

PRESENTED BY: Lorenzo Subissi / lorenzo.subissi@sciensano.be

Poster Abstracts

Poster Abstracts

MODERATED POSTER SESSION A
DAY 1, Wednesday 21. November 2018
15:40-16:40

Track 1: Antimicrobial resistance and healthcare-associated infections: Intervention and assessment

Moderator:
Outi Lyytikäinen

Abstracts

1.1. No association between human antibacterial consumption and incidence of ESBL-producing Escherichia coli and Clostridium difficile infections in Finland: Findings from an ecological study,

Timothee Dub [1]

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Background:

In Finland, during 2010-2016, incidence of invasive Extended Spectrum Beta Lactamase-producing Escherichia coli (ESBL-E.coli) infections significantly increased from 0.48 to 0.85 cases per 1000. Clostridium difficile (C.difficile) remained stable nationwide, but with major regional variation (0.32-2.10 cases per 1000). As human antibacterial consumption influences emergence of antimicrobial resistance, we investigated whether it was associated with their incidence.

Methods:

We obtained wholesale data from 2010-2016 on number of packages by products from the Finnish Medicine Agency; and data on ESBL-E.coli and C.difficile infections from the National Infectious Disease Register. We classified products according to their anatomical therapeutic classification (ATC) and calculated annual Daily Defined Dose (DDD) per day per 1000 inhabitants, nationally and regionally (n=21). We assessed consumption trends over time trough linear regression using years as explanatory and annual antibacterial consumption as dependent variables and looked for correlations between consumption and incidence of ESBL-E.coli and C.difficile infections.

Results:

Nationally, consumption of antibacterials for systemic use (ATC code J01) significantly decreased from 21.9 to 19.1 DDD per day per 1000 inhabitants during 2010-2016 (p-value‹ 0.05) and in 17 regions out of 21. We found a negative correlation between annual consumption of antibacterials for systemic use, and ESBL E.coli incidence: r [CI95%] = -0.48 [-0.61 - -0.32] and no correlation with C.difficile: r [CI95%] = 0.00 [-0.19 - 0.18].

Conclusions:

Antibacterial consumption was surprisingly negatively correlated to ESBL-E.coli infections and did not explain in itself the incidence of C.difficile. Links between individual actual use of antibacterials both, in the community and in-hospital, along with other factors which remain to be identified, and the occurrence of these infections require further investigation.

Subject: Surveillance

Keywords: Antibacterial consumption,Finland,Extended Spectrum Beta Lactamase-producing Escherichia coli,Clostridium difficile,Antibacterials for systemic use

ABSTRACT ID: 105

PRESENTED BY: Timothee Dub / timothee.dub@thl.fi

1.2. Quantifying the transmission dynamics of MRSA in the community and healthcare settings in a low-prevalence country: an individual-based modelling study

Francesco Di Ruscio [1]

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[7] Department of Infectious Disease Epidemiology and Modelling, Norwegian Institute of Public Health, Oslo, Norway; Department of Biostatistics, Institute of Basic Medical Sciences, University of Oslo, Oslo, Norway

Background:

Methicillin-resistant Staphylococcus aureus (MRSA) is a major multi-drug-resistant pathogen in healthcare settings worldwide with increasing occurrence in the community. A clearer understanding of key factors driving the current change as well as of the role of community transmission and pre-admission exposure on the epidemiology within healthcare facilities is needed.

Methods:

The epidemiology of MRSA was studied by means of an individual-based model realistically reproducing the socio-demographic structure of the population in the community, hospitals and nursing homes in Norway. Transmission parameters were calibrated on the number of infections reported in the Norwegian national registry within 2008-2015.

Results:

We estimated an effective reproduction number of 0.71 (95%CI: 0.46-0.93). We found an almost two-fold rise of the average prevalence of MRSA carriage in the eight years of the study period, both in the community (0.36% of the population in 2015, 95%CI: 0.22-0.54%) and in hospitals (0.97% of all in-patients in 2015, 95%CI: 0.60-1.44%), driven by the rising import of cases. Households accounted for two-thirds of all MRSA transmissions in Norway; the remainder occurred in hospitals, with a negligible contribution of nursing homes. However, colonizations acquired in hospital were responsible for 47% (95%CI: 35-63%) of all infections and for the majority of those developed within nursing homes.

Conclusions:

The import of cases acquired abroad is driving the increase of MRSA prevalence in Norway, primarily through household transmission; however, transmission within hospitals is still the driver of infection among hospital patients. Our findings suggest households as a target of potential preventive strategies in the community and emphasize the importance of a coordinated global plan to reduce the global level of antibiotic resistance, thereby mitigating the international spread of resistant pathogens.

Subject: Modelling, bioinformatics and other biostatistical methods

Keywords: Methicillin-Resistant Staphylococcus aureus,Agent-Based Modeling,Mathematical Model,Antibiotic Resistance,Pathogen Transmission,Epidemiologic Determinants

ABSTRACT ID: 389

PRESENTED BY: Francesco Di Ruscio / frdr@fhi.no

1.3. Being a carrier of Multidrug Resistant Micro-organisms in daily life: the perspective of the patient

Sabiena Feenstra [1]

R. Eilers [2], M. Haverkate [3], A. Timen [4]

[1] RIVM

[2,3,4] RIVM

Background:

Carriers of multidrug resistant micro-organisms (MDRO) encounter isolation measures in case of admission in hospitals. For example, they are being taken care of in single patient rooms, and/or by HCW wearing full protective equipment. At home, carriers are not required to take additional measures in their daily life activities. However, being a carrier in daily life could have an impact. The aim of this study is to explore the experiences of carriers in daily life.

Methods:

In total, 13 in-depth interviews were performed, mostly involving carriers of MRSA but also resistant Klebsiella and E.coli in the Netherlands.

Results:

Preliminary results show that the diagnosis came as a shock. Specifically, questions on how they became carrier caused a lot of distress. Participants did not mind being a carrier nor the MDRO itself; however they experienced negative consequences with great impact on different aspects in their life. First, the social interaction with others: participants stated that they were avoided and questioned whether they should come into contact with others because they were afraid to transmit the bacteria. Second, all participants that were admitted in hospital expressed negative experiences with the isolation measures. It made them feel lonely, abandoned and dirty. Moreover, information provision or guidance was lacking during the hospital stay as well as when going back home. Participants who received more information and guidance felt less distressed.

Conclusions:

Carriers were left with many questions in their daily life activities when being dismissed from the hospital. These concern mostly the risks of infecting their family members and other contacts. Using these insights, tailored training and information material for patients and healthcare workers can be developed.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: antibiotic resistance, impact daily life, experiences

ABSTRACT ID: 112

PRESENTED BY: Sabiena Feenstra / renske.eilers@rivm.nl

1.4. Evaluation of Colistin Susceptibility Directly from Blood Cultures - A Novel Flow Cytometric Protocol

Daniela Fonseca e Silva

R. Teixeira-Santos [2], A. Silva-Dias [3], S. Costa-de-Oliveira [4], I. Martins-Oliveira [5], M. Ramos [6], A. Rodrigues [7], C. Pina-Vaz [8]

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Background:

Colistin (CS), recently reintroduced in clinical practice, constitutes the last resort for treating infections caused by multidrug-resistant (MDR) bacteria. Classical susceptibility tests are laborious, time-consuming and technical issues have been reported. The present study intends to develop a flow cytometric method that can easily and quickly analyze bacteria extracted directly from blood cultures (BC) samples and qualitative evaluate the susceptibility for CS.

Methods:

25 BC were spiked with well characterized bacteria including recommended AST control strains (11Enterobacteriaceae, 12Pseudomonasspp. and 2Acinetobacterspp.), inoculated with human blood and incubated until flag positive. Bacteria extracted from BC, were inoculated in FASTinov® gramneg kit containing CS in variable concentrations and a fluorescent dye that detect cell membrane lesion; after incubation (1h), the susceptibility of CS was analyzed by AccuriTMC6 Flow Cytometer. The comparison between the new protocol and susceptibility previous determined according to EUCAST and CLSI was performed. In order to check the accuracy of this new method, error rates [minor (mE), major (ME) and very major (VME)] and categorical agreement (CA) were calculated.

Results:

The time-to-result of flow cytometric protocol was significantly shorter than routine methodologies (2h vs. 24 h), potentially allowing an earlier therapy.Cytometric data showed a high agreement (1.00) with susceptibility determined according to CLSI and EUCAST protocols. No systematic errors were found either minor, major or very major rates.These results validate the method to be used in laboratory for measuring with a good precision and accuracy (sensitivity and specificity of1.00).

Conclusions:

We hereby presented a new and fast flow cytometric protocol which revealed to be an excellent tool for evaluation of CS susceptibility directly from BC samples, with high agreement with broth microdilution reference method.

Subject: Novel methods in microbiology (e.g. new diagnostic tools)

Keywords: colistin, polimyxin, flow-cytometry, blood cultures, MDR microorganisms

ABSTRACT ID: 466

PRESENTED BY: Daniela Fonseca e Silva / daniela.sfsilva@gmail.com

1.5. Evaluation of FASTinov® kit for antimicrobial susceptibility testing on gram positive cocci,

Inês Martins-Oliveira [1]

R. Teixeira-Santos [2], A. Silva-Dias [3], S. Costa-Oliveira [4], A. Rodrigues [5], C. Pina-Vaz [6]

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Background:
Bloodstream infections represent a critical healthcare condition associated to high mortality and morbidity. Increasing rates of antimicrobial resistance and the late laboratorial answer regarding the AST turns urgent the need of rapid diagnostic tests. In this study, the performance of the FASTinov® grampos kit was evaluated directly on positive blood cultures in a time-to-result (TTR) of 2 hours.

Methods:
Blood cultures bottles (aerobic and anaerobic) (BD) were spiked with 52 well characterized bacteria and 10 quality control strains, including 36 Enterococcus sp. and 36 Staphylococcus sp., inoculated with human blood and incubated until obtaining a positive flag. Bacteria were extracted from blood, inoculated in the grampos kit and incubated for 1h; afterwards, the microplate containing the main antimicrobial drugs (for Enterococcus: ampicillin, penicillin, vancomycin, erythromycin, linezolid and gentamicin high concentration; for Staphylococcus: penicillin, cefoxitin, vancomycin, gentamicin, ciprofloxacin, erythromycin and linezolid) and the previously optimized fluorescent dyes, was analyzed by the BD AccuriTM C6 Plus Flow Cytometer. The results were interpreted in a dedicated software according EUCAST and CLSI protocols. In order to check the validity of FASTinov® grampos kit, the error rates and categorical agreement (CA) were calculated.

Results:
The overall CA between grampos kit and broth microdilution was 90% for EUCAST and CLSI protocols. The highest CA was observed for penicillin, vancomycin and linezolid (100%), followed by ampicillin (94%). The rate for major discrepancies was 9% for both protocols; there were not detected very major discrepancies for all tested drugs.

Conclusions:
FASTinov® gram positive kit provided fast and reliable results regarding Enterococcus and Staphylococcus sp., improving turn round time in bloodstream infections, thus allowing early target therapy and an effective antimicrobial stewardship.

Subject: Novel methods in microbiology (e.g. new diagnostic tools)

Keywords: Antimicrobial susceptibility testing,Flow cytometry,Enterococcus sp.,Staphylococcus sp.

ABSTRACT ID: 445

PRESENTED BY: Inês Martins-Oliveira / ioliveira@fastinov.com

Track 2: Emerging and vector-borne diseases (1)

Moderator:

Christian Winter

Abstracts

2.1. Surveillance of imported malaria in Denmark using a digitalized national microbiology database

Lasse S. Vestergaard [1]

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[4,5] Department of Infectious Disease Epidemiology & Prevention, Statens Serum Institut, Copenhagen, Denmark 6 Representatives from all clinical microbiology laboratories in Denmark

Background:

The national surveillance system for imported malaria in Denmark relies on mandatory case information reported from local clinical microbiology laboratories to the national malaria reference laboratory at Statens Serum Institut. The current system is however vulnerable to incomplete and missing case reports, and delays in reporting. To improve reporting completeness and timeliness we developed a digitalized surveillance system based on the Danish Microbiology Database (MiBa). MiBa includes electronic copies of all microbiological reports generated in Denmark.

Methods:

A computerized algorithm was developed to retrieve records in MiBa on malaria tests, including patient identification, type of Plasmodium species, test method used, and information on travel history. To validate the completeness of the system, all data reported in 2016 were retrieved and compared to information reported manually from all Danish laboratories, and discrepancies investigated.

Results:

The current manual system reported 101 malaria cases in 2016. The MiBa based system did not miss any of these cases, as it identified a total of 111 cases (60 P. falciparum, 45 P. vivax, 6 P. ovale, 2 P. malariae and 1 unknown species), thus 10% more cases than officially reported. However, the mandatory information on the patient's travel history was available only in 35 (32%) of the electronic reports found in MiBa.

Conclusions : The use of the digitalized data retrieval system shows a problem of underreporting of imported malaria cases in the official notification system. The MiBa based digital surveillance system provides a more complete and timely reporting of imported malaria. However, a system to ensure inclusion of travel history information in the electronic malaria reports from the laboratories must be developed.

Subject: Novel methods in epidemiology (e.g. digital disease detection, e-health)

Keywords: Imported malaria, surveillance, digital reporting, microbiology database, Denmark

ABSTRACT ID: 381

PRESENTED BY: Lasse S. Vestergaard / lav@ssi.dk

2.2. Prevalence of Candida auris in patients admitted to intensive care units in England,

Ashley Sharp [1]

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Background:

Candida auris is an emerging multi-drug resistant fungal pathogen associated with bloodstream, wound, and other infections, especially in critically ill patients. C. auris is difficult to eradicate from hospitals, with prolonged outbreaks reported globally. In England, 225 cases have been reported since 2013 (164 colonisations and 61 infections including 31 candidaemias) across 22 hospitals, with three significant outbreaks in specialist units. MALDI-TOF or genotypic methods are generally required for effective C. auris identification. Currently, English hospitals are advised to consider admission screening based on local risk assessment. We piloted universal screening of adults admitted to intensive care units (ICU) to estimate the admission prevalence in the ICU population and inform public health guidance.

Methods:

Eight geographically dispersed ICUs, serving ethnically diverse populations reflective of the worldwide distribution ofC. auris, were selected for inclusion in the study. Multi-body-site screening was used including nose, throat, axilla, perineum, rectal, and catheter urine (where available) for all adult (18+) admissions, between May 2017 and March 2018. C. auris identification was performed using Chromogenic agar and MALDI-TOF.

Results:

In total 881 adults were screened. All C. auris screens were negative (95% CI: 0.00-0.42%). Data linkage and descriptive analysis will be completed by June 2018 to obtain clinical and demographic information about the cohort tested and compare with national indicators.

Conclusions:

Based on the low prevalence, we would not recommend universal screening in ICUs in England. Hospitals should continue to screen high-risk individuals (e.g. previously colonised) in high-risk settings (e.g. ICUs). All invasive Candida infections and isolates from normally sterile sites should be identified to species level. Further research is needed to characterise risk factors for C. auris colonisation and disease.

Subject: Surveillance

Keywords: Candida auris,Screening,Prevalence,Intensive care

ABSTRACT ID: 162

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2.3. Molecular characterization of Enterovirus in children hospitalized with severe acute respiratory infection in Northern Italy (2014-2017),

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Background:

The emergence of several Enterovirus (EV) types, such as EV-D68, EV-C105 and Coxsackievirus (CV) A21, in severe illnesses – including severe acute respiratory infections (SARI) - is a major public health concern. This study aimed at investigating the EV types in children hospitalized with SARI in Northern Italy

Methods:

Between 2014 and 2017, respiratory samples were collected from 2,468 children <15 years hospitalized with SARI at University hospital in Milan. Specimens were tested for EV-RNA presence by multiplex real-time PCR (AnyplexTMII, RV16-Detection, Seegene). EV-positive samples were then analysed by real-time RT-PCR assay specific for EV-D68; EV- D68 negative specimens were molecularly characterized by partial sequencing (~400 nt.) of VP1/2A gene.

Results:

EV-RNA was detected in 9% (222/2468) of SARIs and mainly (80%; 171/222) in children <3 years. 142 EV- strains were molecularly analysed. EV-D68 was the predominant types detected in 15.5% of SARIs, almost exclusively in 2016. Overall, 22 EV types were recognized with a remarkable heterogeneity in distribution; EVs species B (49.3%) circulated more frequently than EV-D (28%), EV-A (20%) and EV-C (2.7%). EV-A (including 7 EV types) were more frequently detected in children <3 years while EV-B (including 12 EV types) in those aged 4-15 years. Species D and C included only one (EV-D68) and two (EV-A71, CV-A21) types, respectively. Emerging EVs were identified: six cases of CV- A6 (from Oct-2014 to June-2015), one case of EV-C105 (March-2015), one of EV-A71 (June-2016) and one of CV-A21 (Feb-2017).

Conclusions:

Molecular characterization of EVs from children with SARIs allowed drawing up the epidemiological picture of circulating EVs in Italy, identifying an outbreak of EV-D68 in 2016 as well as the circulation of several emerging EV types with epidemic potential.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Enterovirus; molecular characterization; EV-D68 outbreak; emerging viruses.

ABSTRACT ID: 196

PRESENTED BY: Laura Pellegrinelli / laura.pellegrinelli@unimi.it

2.4. Increased risk of invasive group A streptococcal disease in the household contacts of scarlet fever cases in England, 2011-2016

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Background:

Scarlet fever incidence in England and Wales increased sharply from 8.2 to 33.2 per 100,000 between 2013 and 2016, reaching its highest rate in almost 50 years. The risk of secondary invasive group A streptococcal (iGAS) disease following a scarlet fever case in the same household is unknown. We estimated this risk to determine whether public health action is required to protect contacts.

Methods:

Scarlet fever notifications in England with onset between 01/01/2011 and 31/12/2016 were matched by residential address to confirmed iGAS infections up 01/03/2017. Household clusters were defined as iGAS diagnoses within 60 days following scarlet fever onset in another household member. Numbers of household contacts were estimated from Office for National Statistics Labour Force survey data. We calculated crude and age-specific rates of iGAS infection in contacts and compared this to background rates.

Results:

Twelve iGAS cases were identified among an estimated 189,684 household contacts of 73,456 scarlet fever cases. All occurred after March 2014. The median interval between cases was 20.5 days (range 3-54). All scarlet fever cases within clusters were ≤10 years. The risk of iGAS infection in household scarlet fever contacts was 38.5 per 100,000 person-years, 12 times higher compared to the background rate (RR=12.16; 95% CI 6.9-21.4). The majority of iGAS cases were in parents although risk was highest in household contacts aged 11-17 years (RR=40.7; 5.7-290.3) and ≥75 years (RR=128.0; 18.0-909.0).

Conclusions:

We identified an elevated risk of iGAS among household contacts of scarlet fever. We recommend frontline healthcare professionals and household contacts receive information to facilitate early medical assessment and initiation of potentially life-saving treatment.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: scarlet fever,invasive group A streptococcal infection, household cluster,England

ABSTRACT ID: 92

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2.5. Six year experience of detection and investigation of possible MERS-CoV cases, England, 2012-2018

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Background: Surveillance of novel Middle East Respiratory Syndrome coronavirus (MERS-CoV) infection has been undertaken in the UK since the first laboratory confirmed case was reported in 2012. This study presents the results in England from 2012 to 2018.

Methods:

Local health protection teams report possible cases that meet the criteria in the national investigation algorithm to the national case and outbreak management system (HPZone) with a minimum dataset including demographics, clinical symptoms, travel and contact history, and results of laboratory testing. All laboratory results are submitted to the national respiratory DataMart database.

Results:

In total, 1,176 possible cases were investigated between September 2012 and April 2018. The majority had returned from KSA (52.9%) followed by UAE (27.5%). Four cases were laboratory confirmed (2 imported cases and 2 associated indigenously acquired cases) and 1,172 tested negative for MERS-CoV. Of the 1,176 possible cases, 55.1% were male, 42.5% female and 2.4% gender unknown; 40.1% were aged 45-64 years, 27.6% were 15-44 years and 26.4% were 65+. More cases were investigated after Hajj when pilgrims returned to UK. Laboratory confirmed alternative diagnoses were available for 474 possible cases: influenza virus (alone or as a co-infection with other pathogens) was commonest (n=255, 53.8%), followed by rhinovirus, alone or as a co-infection with other pathogens (n=123, 25.9%), adenovirus and/or other respiratory viruses including hMPV, parainfluenza and RSV (n=73, 15.4%), and legionella (n=14, 3.0%).

Conclusions:

The UK started its MERS-CoV surveillance in 2012. Four confirmed cases were reported in 2012/2013 but none since. Testing peaked annually around the Hajj season and 40.3% of all cases had alternative diagnoses identified, mainly influenza. Transmission of MERS-CoV continues in the Middle East and on-going vigilance is required.

Subject: Surveillance

Keywords: Middle East Respiratory Syndrome , MERS-CoV, surveillance, England

ABSTRACT ID: 149

PRESENTED BY: Hongxin Zhao / Hongxin.Zhao@phe.gov.uk

2.6. Emerging Shiga-toxin-producing E. coli serogroup O80 associated hemolytic and uremic syndrome in France, 2013-2016: differences with other serogroups

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Background:

Shiga toxin-producing Escherichia coli (STEC) associated haemolytic-uremic syndrome (HUS) is the main cause of acute renal failure in children. In 2015, STEC O80 became the predominant serogroup in France. Its reservoir remains unknown. Our aim was to generate hypotheses on potential sources of STEC O80 infection.

Methods:

We used French pediatric HUS surveillance 2013-16 data, and compared characteristics and exposures of STEC O80 cases with those of cases of STEC O157 or other STEC serogroups (case-case study). We calculated crude and adjusted odds ratios (aOR) using logistic regression.

Results:

STEC was isolated from 153/521 (29%) reported HUS cases: 45 serogroup O80, 46 serogroup O157 and 62 other serogroups, with median ages of 1.1, 4.0 and 1.8 years, respectively. By 2015/2016, O80 cases were distributed all over mainland France, while O157 cases were mainly reported in Western France. O80 cases were more likely to live next to a wood (OR 9.8; 95%CI 1.0-122) and less likely to consume ground beef (aOR 0.14; 95%CI 0.02-0.80) than O157 cases. STEC O80 cases were less likely to report previous contact with a person with diarrhea or HUS than O157 cases (aOR 0.13; 95%CI 0.02-0.78) or cases of other serogroups (aOR 0.14; 95%CI 0.04-0.51).

Conclusions:

Differences in age, geographical distribution and exposures between STEC O80 cases and other serogroups suggest the existence of different sources, reservoirs and transmission routes. Those differences underscore the need to include additional exposures in the enhanced HUS surveillance, and conduct animal and analytical/ecological studies to identify the sources/reservoirs and transmission routes of STEC O80 infections.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Shiga-Toxigenic Escherichia coli/epidemiology; Hemolytic-Uremic Syndrome/epidemiology; Enterohemorrhagic Escherichia coli; France/epidemiology; Disease Outbreaks; Disease Notification/statistics & numerical data; Serogroup; Escherichia coli Infections/transmission

ABSTRACT ID: 275

PRESENTED BY: Brecht Ingelbeen / brechtingelbeen@gmail.com

Track 3: Food- and waterborne diseases and zoonoses (1): Epidemiology- Salmonellosis

Moderator:

Samantha Bracebridge

Abstracts

3.1. Salmonella outbreak linked to a rural butcher shop with unusually severe clinical presentation, February-March 2018, Northeast England

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Background:

On 14/02/2018, we observed an increase of salmonella cases in a small area of North East England with three cases reporting links to a local butcher. An outbreak control team investigated the outbreak to identify the source of the infection, implement control measures, and prevent further cases.

Methods:

We defined cases as individuals developing diarrhoea after 21/01/2018, who had laboratory-confirmed Salmonella typhimurium within a unique 5-single nucleotide polymorphism (SNP) outbreak cluster, and links to the local area. We performed a case-control study with controls recruited by case nomination and systematic digit dialling. Exposures were determined by telephone interviews and cases compared with controls using logistic regression analysis. We undertook an environmental investigation, including food sampling.

Results:

We identified 28 cases with onset dates across a 3-week period, median age 61 years, 64% male. Ten cases were hospitalised (36%), two had invasive infections and two died. Twenty four cases (86%) reported a link to the butcher. Five cases were identified solely by whole genome sequencing. In the analytical study we compared 14 cases with 23 controls and found cases were 17 times more likely to have consumed cooked meat from the local butcher (OR17; 95% CI:1.1–260; p=0.04). S.Typhimurium (within the 5-SNP outbreak cluster) was isolated in cooked meat from the butcher.

Conclusions:

We report a Salmonella outbreak with an unusually severe clinical picture. Epidemiological and microbiological investigations suggest a likely association with ready-to-eat foods supplied by a local butcher. A relatively large number of cases were affected despite the rurality of the implicated premises. The investigation demonstrated the benefits of timely sequencing information. Difficulties with control selection hampered this investigation, highlighting the need for novel methods of control selection.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Salmonella ,Outbreak investigation ,Whole genome sequencing

ABSTRACT ID: 361

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3.2. Countrywide outbreak of salmonellosis (Salmonella Bareilly) confirmed by whole genome sequencing in the Czech Republic, 2017-2018

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Background:

In August 2017, an increased incidence of Salmonella enterica serovar Bareilly (SB) was identified by the national reporting system (EPIDAT) and the National Reference Laboratory for Salmonellosis (NRL). Aim of our study was to confirm the outbreak and identify the source.

Methods:

For descriptive analysis, cases were defined as A02 (ICD-10 classification) with laboratory confirmed SB reported in EPIDAT and/or NRL from July 2017, in the Czech Republic. NRL isolates were selected for molecular typing to cover period of July 2017 – February 2018 and all 14 geographical regions of the Czech Republic. Pulse field gel electrophoresis (PFGE) and whole genome sequencing (WGS, provided by ECDC, SNP analysis) were used to identify relationship between SB isolates from NRL. Hypothesis generating questionnaire adapted to local conditions was used to identify suspected vehicle/source. Seven poultry SB strains (all detected in period 2016-2017 in food chain by national veterinary and food authorities) were typed by PFGE.

Results:

As of March 2018, in all 14 regions 225 SB cases were identified, peaked in October 2017. Thirty out of 35 SB isolates from August 2017-February 2018 analysed by PFGE shared identical Xba-I pulsotype. WGS analysis of 16 SB strains with this pulsotype showed close relationship (11 indistinguishable, 5 within 1-5 SNPs).

In February 2018, regional epidemiologists interviewed 14 outbreak cases. All 14 (100%) respondents bought food from grocery chains, ate chicken, eggs, ham, and yogurt. The outbreak pulsotype was not detected in the poultry SB isolates.

Conclusions:

One countrywide outbreak of Salmonella Bareilly was confirmed by combination of molecular typing methods (PFGE and WGS). Common source was not identified yet. Timely application of trawling questionnaire and better communication between stakeholders is recommended.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: countrywide outbreak,Salmonella serovar Bareilly,PFGE,WGS

ABSTRACT ID: 125

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3.3. Second Salmonella Agona outbreak associated with an infant milk production facility in France, 2017; 12 years after the first

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Background:

Salmonella Agona is an uncommon cause of salmonellosis in infants in France, although in 2005 an outbreak associated with infant milk products manufactured in a single facility occurred. In November 2017, the National Reference Center (NRC) for Salmonella identified eight isolates from infants over eight days. We investigated to identify the extent of the outbreak and a possible common exposure.

Methods:

We defined a case as an infant with symptom onset after 1 January 2017 and a Salmonella Agona isolate within the outbreak cluster on whole genome sequencing (WGS). Caregivers of 37 cases were interviewed on exposures. WGS was performed on all Salmonella Agona isolates received by the NRC in 2017 (n=96), eight isolates from the 2005 outbreak, and all other Salmonella Agona isolates from infants since 2000 (n=98).

Results : We identified 38 cases (median age 4 months; 58% female) across France. Symptoms onset was in April 2017 for one, and between August and December 2017 for all others. Preceding onset, 36 cases (97.3%) consumed infant milk products manufactured at the same facility implicated in 2005. Phylogenetic analysis revealed 2017 and 2005 outbreak isolates, and 27 isolates received between 2010 and 2016 clustered within 20 single-nucleotide-polymorphisms.

Conclusions:

Prompt epidemiological and traceback investigation suggested a single facility producing infant milk products as the source of the outbreak. This allowed for rapid control measures to be implemented including the recall of implicated products, alerting caregivers of product consumers, and alerting international authorities. Retrospective WGS determined a link with the 2005 outbreak. This, and the identification of interepidemic cases suggest the persistence of the pathogen in the facility for 12 years. Environmental investigations are ongoing to identify the source of contamination.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Salmonella, Salmonella infections, disease outbreaks, whole genome sequencing, infant formula

ABSTRACT ID: 41

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3.4. A prolonged outbreak of monophasic Salmonella Typhimurium with environmental contamination in Norway, August 2017

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Background:

On 15 September 2017, we detected a geographically widespread cluster of six monophasic Salmonella Typhimurium isolates sharing a rare multi locus variable tandem repeat analysis type. We investigated the outbreak to determine the source and implement control measures.

Methods:

We defined a case as a person with a laboratory confirmed infection with the outbreak strain after 15 August 2017. We interviewed cases for hypothesis generation and descriptive epidemiological investigation. We conducted an inspection of the implicated café and collected environmental specimens between 22 September and 23 October 2017. We performed whole genome sequencing (WGS) with core and accessory genome multilocus sequence typing of 4,128 genes on the human and environmental isolates.

Results:

Twenty-one cases residing in ten municipalities were identified, aged 17-60 years (median 27), of whom 13 (62%) were women. Date of symptom onset ranged from 23 August to 18 November 2017. Median incubation period was 6 days (range 0-16 days), which increased as the outbreak progressed. Cases reported consuming different food or drink at the same Oslo airport café. Inspections identified weaknesses in hygiene routines. WGS showed <=3 allele differences between the human (n=21) and environmental (n=5) isolates independent of origin.

Conclusions : Epidemiological investigation identified an Oslo airport café as the source of this widespread outbreak. WGS linked the cases to café environmental isolates. Case distribution by symptom onset date suggests that a point source was introduced in mid-August, followed by continued environmental contamination. Progressively longer incubation periods were likely due to increasingly low dose exposure. Control measures, including kitchen refurbishment and temporary closure, failed to eliminate the environmental source. We recommend strengthened hygiene measures in case of established environmental contamination during an outbreak.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: outbreak, foodborne disease,Salmonella Typhimurium,whole genome sequencing,Norway

ABSTRACT ID: 114

PRESENTED BY: Lotta Siira / ols@fhi.no

3.5. A Salmonellosis outbreak caused by Italian truffle salami, Stockholm 2018

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Background:

In January 2018, an increase of monophasic Salmonella Typhimurium was observed at the Stockholm County Medical Officer. An investigation was started in collaboration with the Environmental Health Administration, Stockholm municipality, to identify the source and prevent further cases.

Methods:

Cases were electronically reported from clinicians and laboratories upon diagnosis. Isolates were typed with Multiple Locus Variable Number Tandem Repeat Analysis (MLVA) at the Public Health Agency of Sweden. A case of Salmonella serogroup BO with disease onset after 15-11-2017, residing in Stockholm County was defined as suspected case, and was confirmed if the isolates were monophasic Salmonella Typhimurium MLVA 3-10-10-N-211. Suspected cases in Stockholm County were interviewed through trawling questionnaires/telephone regarding food exposures and events. Suspected food items were collected and analysed for Salmonella.

Results:

Fifteen cases were confirmed, date of onset ranged from November-March. Seven were male and the median age was 30 (range 1-76). Questionnaires and interviews revealed that all cases had consumed Italian truffle salami sold by the same deli. Five samples of salami were analysed; 3 from the batch that cases had consumed and two from a later batch. The outbreak strain was detected in one sample from a salami saved by a case. The deli had sold 275 kg of the salami during November-December 2017. Three additional cases from other parts of Sweden were linked to this outbreak.

Conclusions:

Truffle salami from the deli was the likely source of this outbreak. All salamis were sold before the outbreak was detected. The deli was the only known distributor in Europe, but a recall was published in the RASFF portal on 30-01-2018. Consumers should be aware of salami as a risk product for salmonella.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: food-borne,surveillance,salmonella,salami,outbreak

ABSTRACT ID: 344

PRESENTED BY: Joanna Nederby Öhd / joanna.nederby-ohd@sll.se

Track 4: Food- and waterborne diseases and zoonoses (2): Surveillance

Moderator:

Alicia Barrasa

Abstracts

4.1. Compliance with water advisories following water interruptions in the municipality of Baerum, Norway

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Background:

During January–September 2017, Baerum municipality sent 6238 notifications through SMS following 153 interruptions of water service. Advice to residents included storing water in advance and boiling tap water before consumption. We performed a cross-sectional study to investigate awareness and compliance among residents who had received water advisories.

Methods:

We collected information regarding demographics, advices received and compliance through an online questionnaire. The questionnaire was distributed to all 2764 residents that had received water advisories during the last 10 months prior to the study. We conducted descriptive analysis and we calculated odds ratios (OR) using logistic regression in order to identify associations of compliance and awareness with demographic characteristics.

Results:

From 611 respondents (response rate 22%) to the survey, 327 (54%) were women; median age 53 (range 16-86). The awareness rate of the notice was 67% since 412 reported remembering having received a notice. From those 412, 273 (67%) reported remembering the advice of storing water in advance and 269 (66%) the boil water advise. Compliance rate to either of those two recommendations was 85%, but when the lower awareness rate was factored in, the effective compliance rate was calculated to be 57%. The respondent's compliance and awareness with the advices was independent of age, education, household type. Awareness of the notice was independent of sex but compliance was lower among men (OR 0.53, 95%CI 0.29-0.96).

Conclusions:

Awareness was suboptimal among residents who had received water advisories but compliance among those who remembered the advices was high. This study points out the need to improve the distribution, phrasing and content of the water advisory notices in order to achieve greater awareness and compliance.

Subject: Preparedness

Keywords: Boil water advisories, complience, consumer communication, water supply, water outages

ABSTRACT ID: 470

PRESENTED BY: Susanne Hyllestad / susanne.hyllestad@fhi.no

4.2. Epidemiology of Campylobacter in Ireland 2004-2016: What has changed?

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Background:

Campylobacter is the most common notifiable cause of bacterial gastroenteritis in Ireland. However, epidemiological information is limited. We aim to describe campylobacter epidemiology in Ireland, propose enhancements to current surveillance and identify targeted future studies.

Methods:

We described notified cases of campylobacteriosis (2004-2016) by age, sex, area of notification, patient type and outcome. We used negative binomial regression to estimate incidence rate ratios (IRR) and adjusted IRR (aIRR) by sex, age-group and area of notification. We undertook interrupted time series analysis by age-group incorporating terms for trend and for period (2004-2010 and 2011-2016).

Results:

There were 27,034 cases of campylobacteriosis notified between 2004 and 2016. Crude annual incidence ranged from 36.2 to 44.4 per 100,000 population between 2004 and 2010 with higher incidences of 49.8 to 54.4 per 100,000 population between 2011 and 2016. Overall, the incidence was higher in males (aIRR 1.14, 95% confidence intervals (CI) 1.07-1.22), in those <5 years compared with the lowest incidence age-group (45-64 years) (aIRR 5.08, 95%CI 4.58-5.63) and in all other areas compared with the North-East area (aIRR range 1.24-3.18, p-values ≤0.002). For all age-groups, significant increases in trend-adjusted case numbers of 30-44% (p-values <0.006) were detected after 2011. In addition, increasing trends of 3-6% per annum (p-values<0.012) were detected in age-groups ≥45 years but not in younger age groups.

Conclusions :

An apparent stepped increase in campylobacteriosis in 2011 is noted in cases in all age-groups, with an overall increase in trend identified in those aged ≥45 years. While some of these changes may be due to the transition of regional laboratories from culture-based to molecular-based diagnostic methods, further investigation is required to fully explain the identified changes.

Subject: Surveillance

Keywords: Campylobacter, bacterial gastroenteritis, epidemiology, surveillance

ABSTRACT ID: 129

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4.3. Serogroups and virulence factors in STEC isolates found in food items and human samples in Sweden, 2010-2017

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Background:

Shiga-toxin producing Escherichia coli (STEC) are serious foodborne pathogens with cattle being the main reservoir. Therefore, meat and milk products pose a risk for human infections.The aim of our study was to characterize STEC strains from beef and in-line milk filters and compare them to human isolates. The results will provide insights into the risk associated with consumption of beef and raw milk products in Sweden.

Methods:

STEC isolates from beef (28) and in-line milk filters (36) from Swedish dairy farms collected by the Swedish Food Agency (2010/11, 2015) were analysed through whole genome sequencing (WGS) and compared to human isolates (2210) submitted to the Swedish Public Health Agency 2010-2017. Serogroups and virulence genes (stx1, stx2, eae) were identified and analysis of single nucleotide polymorphisms (SNP) was performed on WGS results.

Results:

Twenty-three serogroups were detected from beef and milk filters, 18 of those were also identified in humans. Most prevalent serogroups were O145 and O26 (7.8% each), which were also common in humans (4.2% and 19.4%). stx1 prevalence was similar in milk filter (47.4%) and human isolates (43.3%), stx2 only (59.1%) or together with stx1 (36.4%) dominated in beef isolates (35.1% and 18.5% in humans). eae distribution differed between milk filter (41.7%), beef (17.9%) and human isolates (71.5%). One milk filter isolate (2015) was related to four human cases in 2017 (32 SNPs difference) but no epidemiological link was found.

Conclusions:

The isolate categories share several serogroups but vary in virulence gene distribution. No genotyping link was detected, concluding that our food isolates were not associated with human infections. Nevertheless, further monitoring is needed for risk assessment of human infections coming from food-associated strains.

Subject: Microbiology

Keywords: Shiga-Toxigenic Escherichia coli, Virulence, Foodborne Diseases, Transmission, Sequence Analysis

ABSTRACT ID: 420

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4.4. What factors are associated with non-travel enteric fever (typhoid and paratyphoid) in England and Wales 2006 to 2016?

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Background:

Although non-travel cases of enteric fever comprise a minority in England and Wales, they reflect local transmission. We describe non-travel cases between 2006 and 2016 to investigate associated factors.

Methods:

Using the national surveillance database, non-travel cases were defined as cases without travel to an endemic area or travelled with onset >60 days from return or assessed as UK acquired by public health authorities.

Cases were laboratory confirmed and some isolates had whole genome sequencing (WGS). Describing non-travel cases, including quintile of socio- economic deprivation based on residence, variables with a p-value<0.2 in single variable analysis were brought to a multivariable logistic regression model.

Results:

Of 4500 cases, 351 cases had not travelled, 14 had >60 days onset and 20 were assessed cases.

Non-travel cases varied after 2006 (18%; N=82/455) from 11% (N=53/488; 2011) to 5% (N=18/378; 2012,); mean 8%.

Most non-travel cases were Pakistani (25%), Indian (23%) and Other Asian (17%) ethnicity, and were born in an endemic country (56%), similar to travel cases. Most were symptomatic; 370 (96%), 15 were carriers. Of 414 cases in WGS clusters, 74(18%) were non-travel cases.

In multivariable analysis, White British and Black African/Caribbean ethnicities had a higher odds being non-travel cases (adjusted OR aOR:2.9, 95%CI:1.4-5.7; and aOR:3.4, 95%CI:1.6-7.2 respectively) compared to Other/mixed. Cases in the most deprived quintiles showed higher odds (1st quintile, aOR:2.2, 95%CI:1.3-3.8; 2nd quintile: aOR:2.0, 95%CI:1.3-3.4 compared to 5th) as were cases with Salmonella typhi isolated (aOR:1.7, 95%CI:1.3-2.1) compared to Salmonella paratyphi.

Of 414 cases in WGS clusters, 74(18%) were non-travel cases.

Conclusions:

The disproportionate ethnic and socioeconomic differences require further analysis. We recommend investigation of non- travel cases by epidemiological questionnaires, contact tracing and sequencing to elucidate transmission.

Subject: Burden of disease

Keywords: Enteric fever Salmonella

ABSTRACT ID: 402

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4.5. Investigations of Listeria monocytogenes serogroup IVb, multi-locus sequence type 6 cluster in Finland, 2017-2018

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Background:

Whole genome sequencing (WGS) has been performed on patient isolates since 2015 and is not routinely used on food isolates in Finland. Nine invasive Listeria monocytogenes (Lm) multi-locus sequence type (MLST) 6 cases were detected, January-September 2017. The cluster was reported to Epidemic Intelligence Information System (EPIS). We describe the epidemiological and laboratory investigations of the outbreak in Finland.

Methods:

Case was defined as person with isolated invasive Lm serogroup IVb, MLST 6. Lm isolates were sequenced by MiSeq, illumina and a core genome MLST scheme with >1500 targets used for comparison by Ridom SeqSphere. Serogroup and multilocus sequence type were retrieved from sequence data. Food consumption data was collected by standard questionnaire from patients or their relatives. The cases from 2018 were re-interviewed for corn consumption. WGS was performed on isolates from five frozen corn batches since investigations pointed to corn as possible source.

Results:

October 2016-March 2018, 21 cases were detected in Finland. Median age of the cases was 69 (range 22-92) and 71% were women. Of the cases, 2 died within 30 days of sampling and 12/21 (57%) were interviewed. No common exposure was identified. In January 2018, a RASFF alert was notified due to Lm >100 CFU/g detected in frozen corn sampled at a Finnish food business operator. Four Lm isolates from the frozen corn product clustered closely with cases' isolates (1-3 allele difference). One case had eaten frozen corn of the same brand without heating. Cases were also found in other European countries.

Conclusions:

Further investigations with other affected countries are required to control the outbreak. More WGS data of Lm in foods and humans must be collected to assist epidemiological investigations.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Listeria monocytogenes, whole genome sequencing, outbreak, corn

ABSTRACT ID: 365

PRESENTED BY: Jenni Luukkanen / jenni.luukkanen@thl.fi

4.6. Risk of enteropathogenic protozoa infection in asymptomatic school children and their families and teachers in Leganés, Madrid (Spain), November 2017- March 2018

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Background:

Enteropathogenic protozoa Giardia duodenalis, Cryptosporidium spp. and Blastocystis spp. contribute to intestinal disorders and cognitive and developmental impairments in childhood. Blastocystis has been associated with irritable bowel syndrome and food intolerances. This study investigates schools to estimate the asymptomatic carriage of enteropathogenic protozoa in Spain.

Methods:

We performed a cross-sectional study in schools in Leganés, inviting children (4-14 years), their siblings 0-16 years, parents and teachers. We collected stool samples and demographics; excluding symptomatic individuals, defined as diarrhoea in the past week (N=43). We analysed samples with Real-Time PCR and (semi-)nested PCR. Positive samples were sequenced and genotyped. We calculated carriage and odds ratios (aOR) adjusted for family clusters with logistic regression.

Results:

School response rates varied between 15-47%. After exclusion, we studied 623 individuals from 491 families or teachers. The carriage risk for any protozoa was 21%, 95% Confidence interval (95%CI):18-25%, (N=133); Blastocystis: 13% 95%CI:11-16% (N=81); G. duodenalis: 9% 95%CI:7-12% (N=55); Cryptosporidium: 3% 95%CI:2-5% (N=18). One person was infected with all three protozoa, 19 had two protozoa, only seven had another family member with infection. The odds of Blastocystis infection increased with age; 6-9 years: aOR 2.8 (95%CI:1.5-5.1); 10-16 years: aOR 3.5 (95%CI:1.6-7.7), >30 years: aOR 6.1 (95%CI:2.0-18.5); compared to 0-5 years. The odds of Cryptosporidium infection increased in females (aOR 3.9, 95%CI:1.2-12.5) compared to males and children 10-16 years (aOR 5.4 95%CI:1.5-19.1) compared to 0-5 years.

Conclusions:

We detected sizeable asymptomatic infection, increasing with age, in those accepting screening. Considering possible implications, we reiterate the importance of good hygiene measures throughout all ages to protect from protozoal infections. Furthermore, we recommend further testing and analytical studies to deduce associated risk factors and outcomes.

Subject: Microbiology

Keywords: Giardia duodenalis, Cryptosporidium spp, Blastocystis spp., asymptomatic infection

ABSTRACT ID: 371

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Track 5: Influenza, TB and other respiratory viruses (1): Surveillance, Incidence and Burden

Moderator:

Marta Valenciano

Abstracts

5.1. Evaluation of ECDC Influenza-like illness (ILI) case definition to detect respiratory syncytial virus (RSV) infection through the Influenza Surveillance System in Portugal

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Background:

One of the main challenges for the implementation of a global Respiratory syncytial virus (RSV) surveillance system is the lack of a suitable case definition for RSV disease. In Portugal, RSV cases are detected through the Influenza Surveillance System (ISS) using the ECDC Influenza-like illness (ILI) case definition. The aim of this study was to evaluate the suitability of this case definition to detect RSV infections in Portugal.

Methods:

We conducted a retrospective and observational cross-sectional study of 4,711 cases with individual clinical symptoms and laboratory-confirmed result for respiratory virus between October 2010 and May 2017. Association between clinical characteristics and RSV detection using bivariate and multinomial logistic regression was carried out. The ILI case definition accuracy was assessed by its sensitivity, specificity, and area under the receiver operating characteristic curve (AUC). A 0.05 significance level was accepted.

Results:

A total of 141 (3%) samples were laboratory-confirmed RSV positive cases, being highly significant ($P < 0.0001$) among children less than 5 years old (12/141,8.5%) and adults more than 65 years old (32/141,23%). Cough (OR=2.71;95CI1.19-6.18) and difficulty breathing (OR=2.16;95CI1.53-3.06) were best predictors for RSV infections. However, fever or feverishness (OR=0.4;95CI0.27-0.59), headache (OR=0.65;95CI0.46-0.93) and myalgia (OR=0.34;95CI0.23-0.5) were negatively associated with RSV disease although were significantly associated with influenza positive cases (RRR=3.62; 95CI2.95-4.45, RRR=1.53;95CI1.33-1.75, and, RRR=1.95;95CI1.61-2.37, respectively). The ILI case definition was not significant and showed a sensitivity of 80.9% (73.4-87), specificity of 19.7% (18.6-20.9) and an AUC of 0.623.

Conclusions:

We demonstrated that ILI case definition was not accurate for RSV detection in Portugal. Therefore, the case definition should be adapted within the ISS or a specific RSV surveillance system should be implemented in Portugal.

Subject: Surveillance

Keywords: Respiratory syncytial virus, influenza-like illness, case definition, surveillance

ABSTRACT ID: 108

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5.2. Performance of ECDC ILI case definition and ICPC R80 code for influenza surveillance based on the Portuguese Influenza Surveillance System

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Background:

Swift and accurate identification of influenza epidemics can reduce epidemic-related morbimortality and economic burden. It relies upon a sensitive and specific influenza-like illness(ILI) case definition. The impact depends on the virus subtype, individual age group and vaccination status. In this study we took advantage of the Portuguese Influenza Surveillance System(ISS) database to study the clinical factors associated with the laboratory confirmed diagnosis of influenza and to assess and compare the performance of the two main case definitions used in Portugal: the European Centre for Disease Prevention and Control(ECDC) ILI case definition and the International Classification of Primary Care(ICPC) R80 code.

Methods:

We conducted a retrospective, observational cross-sectional study using the ISS database of 6,769 cases with individual clinical symptoms of both case definitions, vaccination status and a nasopharyngeal swab result with virus subtype collected between October 2010 and April 2017. The performance of both case definitions were assessed by their sensitivity, specificity and area under the receiver operating characteristic curve(AUC). We tested the association between a positive result for influenza infection and sex, vaccination status and clinical symptoms stratified by age group using logistic regression. The significance level was 0.05.

Results:

Cases corresponded mostly to the 18-64 years-old group(mean 39.9±21.2) and non-vaccinated adults(86.4%). The ECDC ILI case definition was the most sensitive(84.1%). The ICPC R80 code was the most specific(47.6%), with the highest AUC(0.551). The most associated symptoms with a positive result were fever(OR:4.16; 95CI:3.38-5.12), cough(OR:3.17; 95CI:2.57-3.90) and shivers(OR:1.98; 95CI:1.71-2.28) while the sudden onset of symptoms was not associated significantly.

Conclusions:

We suggest using the most sensitive case definition complemented with a specific laboratory test since case definitions per se are not accurate enough to predict influenza infection.

Subject: Surveillance

Keywords: Human Influenza,Public Health Surveillance,Europe,Sentinel Surveillance

ABSTRACT ID: 61

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5.3. Burden of respiratory syncytial virus associated hospitalisation in the first year of life in a major urban city, Lyon, France 2010 to 2016

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Background:

Evaluation of burden and costs of RSV-associated hospitalisation (RsvH) in a major metropolitan area is of prime importance to guide future vaccine policies. We aimed to describe RsvH incidence, factors associated with RsvH and direct medical costs of annual RsvH in the first year of life.

Methods:

We conducted a retrospective study on a cohort of newborns (2012 to 2016) from a catchment area of approximately 1.1 million inhabitants using public hospital registry data from the Hospices Civils de Lyon. A case was defined as a laboratory confirmed RSV-infection with hospitalisation occurring in the first year of life. Hospital costs were estimated based on the French version of Diagnosis Related Groups. Case numbers per year were compared using Fisher's exact test. Key variables were used for descriptive epidemiology (Pearson's chi-squared test) and multivariate logistic regression.

Results:

Overall, 663 cases in 45,820 children were identified. We observed a mean annual incidence of 14.5 (95% CI 13.4–15.6) per 1000 newborns. The factors independently associated with RsvH were being born during the RSV season (OR=4.48; 95% CI: 3.83–5.25), prematurity (OR=2.25; 95% CI: 1.85–2.73), and living in areas with lower income (OR=1.40; 95% CI: 1.20–1.64). The average cost per birth cohort of 10,000, was estimated at 662 k€ annually and was increasing according to month-of-birth (1.417 k€ for those born during the RSV season) and prematurity (2.909 k€).

Conclusions:

Being born during the RSV season and prematurity are the two main risk factors that should be target as a priority by the national immunisation program. Moreover monitoring of public birth cohorts may allow surveillance of RsvH in a practical and cost-efficient manner.

Subject: Surveillance

Keywords: Respiratory Syncytial Virus; RSV-associated hospitalisation, Bronchiolitis, Acute Respiratory Infections, Burden of disease, Healthcare Cost-Analysis

ABSTRACT ID: 64

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5.4. The incidence of symptomatic infection with influenza virus in the Netherlands 2011/2012 to 2016/2017, estimated using Bayesian evidence synthesis

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Background:

Due to differences in the circulation of influenza viruses, distribution and antigenic drift of A subtypes and B lineages, and susceptibility to infection in the population, the incidence of symptomatic infection – and disease burden – can vary widely between seasons and age-groups. Because incidence cannot be directly measured at the population level, our goal was to estimate symptomatic infection incidence stratified by season, age-group, and influenza virus A subtype and B lineage through statistical modelling.

Methods:

Using Bayesian evidence synthesis methodology to combine sentinel surveillance data on influenza-like illness (ILI), virus detections in sampled ILI cases, and data on healthcare-seeking behaviour, we estimated the population-level incidence of symptomatic influenza virus infection in the Netherlands for the six seasons 2011/2012 through 2016/2017.

Results:

The age-aggregated incidence of symptomatic infection with any influenza virus was estimated at 6.6 per 1,000 persons (95% uncertainty interval (UI): 4.8-9.0) for season 2011/2012, 33.5 (95% UI: 28.5-39.3) for 2012/2013, 8.2 (95% UI: 5.7-11.7) for 2013/2014, 37.4 (95% UI: 31.9-43.4) for 2014/2015, 37.1 (95% UI: 31.5-43.6) for 2015/2016, and 26.7 (95% UI: 21.9-32.4) for season 2016/2017. There was substantial variation between age-groups (highest incidence for the age- group ‹5 years and relatively low incidence for 65+ years). Incidence was highest in the seasons in which both an A subtype and a B lineage were dominant contributors.

Conclusions:

Combining season-specific syndromic surveillance, virological testing, and data on healthcare-seeking behaviour within an evidence synthesis framework allows the estimation – with appropriately quantified uncertainty – of the incidence of symptomatic influenza virus infection. These estimates provide valuable insight into the variation in influenza epidemics across seasons, by virus subtype and lineage, and between age-groups.

Subject: Modelling, bioinformatics and other biostatistical methods

Keywords: influenza virus, incidence, syndromic surveillance,Bayesian

ABSTRACT ID: 157

PRESENTED BY: Scott McDonald / scott.mcdonald@rivm.nl

5.5. Real-time mortality attributed to seasonal influenza in Spain, 2012-13 to 2017-18

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Background:

Significant excess all-cause mortality is often observed during winter seasons, mainly among the elderly. Our objective was to estimate the influenza-attributable mortality (IAM) in Spain during the seasons 2012-13 to 2017-18 to monitor the impact of seasonal influenza epidemics on the population.

Methods:

IAM was estimated using the FluMOMO model, a multiplicative Poisson regression time-series model, corrected for trend and seasonality. Weekly all-cause deaths were obtained from computerized civil registers that include 92% of the Spanish population. Influenza activity was included in the model as the Goldstein index (weekly influenza-like illness rates multiplied by laboratory positivity rates), and adjusted for a possible confounding effect of extreme ambient temperatures obtained from National Oceanic and Atmospheric Administration. IAM rates per 100,000 population were calculated for total population and by age-groups (0-4, 5-14, 15-64 and >64 years), using national population data and linearly interpolated.

Results:

Higher IAM rates for >64 years were estimated for 2014-15 (221.7, 95%-CI: 205.4-218.0) and 2016-17 (158.4, 95%-CI: 152.6 -164.2) in which A(H3N2) virus was dominant, and for 2017-18 (144.2, 95%CI: 138.6-149.8) when B and A(H3N2) viruses were co-circulating. The highest IAM rate for the 15-64 age-group was observed in season 2017-18 (4.0, 95%-CI: 3.8-4.2). And for all ages, seasons 2014-15, 2016-17 and 2017-18 yielded the following higher IAM rates: 40.6 (95%-CI: 39.3-41.9); 30.1 (95%-CI: 28.9-32.1) and 31.0 (95%-CI: 29.8-32.2), respectively.

Conclusions:

As in other European countries, most influenza-attributed deaths occurred during A(H3N2) dominant seasons and among the elderly. The FluMOMO model, based on daily mortality and routine influenza surveillance data, allows reliable real-time estimations of IAM, which helps to evaluate the impact of control measures such as influenza vaccination programmes.

Subject: Burden of disease

Keywords: Influenza; Influenza surveillance; Mortality; Poisson regression; Public health surveillance; Time series

ABSTRACT ID: 198

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5.6. Contrasting socioeconomic differences in acute infectious diseases in the Netherlands

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Background: Socioeconomic inequalities in health are generally well studied, but not for acute infectious diseases. We aimed to assess socioeconomic differences in incidence and general practice consultation rates for five common acute infectious disease syndromes in adults in the Netherlands, in order to generate hypotheses and possible prevention strategies to reduce health inequalities.

Methods:

Data were collected by a year-round repeated cross-sectional health survey. Adults aged 25 and older were asked if they had experienced acute upper or lower respiratory tract infection (URTI and LRTI), acute otitis media (AOM), urinary tract infection (UTI) or gastro-enteritis (GE) in the previous two months. If so, participants were asked whether they had consulted their general practitioner and if they had been unable to work. Socioeconomic status was defined as the highest obtained formal education. Logistic regression models, including different sets of covariates, were used to explore possible mediation and confounding.

Results: People with a high SES experienced more URTI (OR 1.33; 95%CI 1.24-1.42), while lower SES was a risk factor for LRTI (OR 2.07 (1.64-2.61)), AOM (OR 1.67 (1.35-2.07)) and UTI (OR 2.09 (1.77-2.47)). After adjustment for several possible mediators, the higher odds of URTI in participants with high or middle compared to lower SES remained significant. For all infectious diseases, GP consultation rates increased by 10-20% with decreasing SES. No SES differences were found in inability to work due to the infection.

Conclusions:

Significant and contrasting associations were observed between SES and acute infectious diseases. The relationship between SES and GP consultation rates was similar across the five diseases. This study shows that notable socioeconomic inequalities in health and care seeking behaviors exist for common acute infectious diseases in the Netherlands.

Subject: Burden of disease

Keywords: health inequalities, general practice

ABSTRACT ID: 37

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Track 6: Sexually transmitted infections (1): Chlamydia, Syphilis and Neisseria Gonorrhoeae

Moderator:

Viviane Bremer

Abstracts

6.1. Descriptive analysis of syphilis reinfections in Dublin from 2010 to 2017

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Background:

Persons with syphilis reinfections, including those who are asymptomatic, may play an important role in transmission of sypilis and other STIs. Reinfections became notifiable in Ireland in January 2014. This study aimed to describe the epidemiology of laboratory confirmed cases of syphilis reinfections among adults attending two STIs clinics in Dublin detected between 2010 and 2017.

Methods:

A standardised review and descriptive analysis of the electronic medical records was made of all patients matching the syphilis reinfection definition: an episode of syphilis (symptomatic and/or asymptomatic) in a person who presents with an equal or more than 4-fold increase in RPR (Rapid Plasma Reagin) titre, at least 12 weeks after the completion of effective treatment for a previous syphilis episode that resulted in an equal or more than 4-fold decrease in RPR.

Results:

During 8 year period, 1891 syphilis cases were laboratory confirmed, of which 217 were reinfections (11%; 95%CI 10-13%) most of them (53%) occurring in 2016 and 2017. The median age was 40 years (range 26-83) and majority (99%) were male. 64% were men reporting to have sex with men (MSM), 73% were HIV positive and 39% were diagnosed with at least one other STI. 88% of the cases had one reinfection and 12% had between two and four. The group with more than one reinfection had a higher proportion of diagnosed with other STIs (60%) compared to the group with only one reinfection (34%, $p<0.05$).

Conclusions:

Syphilis reinfections are an increasing public health problem. Further analysis will be needed in order to identify high risk groups and implement appropriate preventive measures to avoid transmission of syphilis and other STIs.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: Syphilis, MSM, sexual transmitted infections, reinfections,HIV

ABSTRACT ID: 222

PRESENTED BY: Natalia Redondo / nataliasevillano@yahoo.es

6.2. The burden of resistant Neisseria gonorrhoeae in the EU/EEA

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Background:

Gonorrhoea is the second most commonly reported bacterial STI in Europe with 75349 confirmed cases reported in 2016. It poses a serious and growing public health threat due to increasing trends, emerging resistance and limited treatment options. We estimated the burden of antimicrobial resistant Neisseria gonorrhoeae in the European Union and European Economic Area (EU/EEA).

Methods:

Average proportions of resistant isolates to ciprofloxacin, azithromycin, cefixime and ceftriaxone between 2013 and 2016 by gender, age and sexual orientation from the European Gonococcal Antimicrobial Surveillance Programme (Euro-GASP) were applied to the number of notified cases in 2016 adjusted for under-reporting (multiplication factor: 1.01 – 3.86). Countries not reporting comprehensive data were assumed to have the mean EU/EEA notification rate for 2016.

Results:

In 2016, we estimated between 50,294 and 192,213 cases were resistant to at least one antimicrobial. Ciprofloxacin- resistance (average 1,100 resistant isolates in Euro-GASP data – 50% resistance) contributed most with between 47,300 and 180,773 cases; 1,552 – 5,934 cases were estimated to be resistant to cefixime (Euro-GASP: 57 resistant isolates – 2.6%); 6,227 – 23,797 resistant to azithromycin (Euro-GASP: 156 resistant isolates – 7%) and 68-260 cases resistant to ceftriaxone (Euro-GASP: three resistant isolates - $<1\%$). The largest burden was estimated among 25-34 year-old men with between 9,463 and 36,166 cases resistant to at least one antimicrobial.

Conclusions:

Assuming Euro-GASP data are representative of resistance in the EU/EEA, large numbers of gonorrhoea cases were resistant in 2016. Even when the proportion of resistance is small, this could imply hundreds of unreported resistant cases, with implications for future control of emerging resistance. Strict adherence to European treatment guidelines is essential for gonorrhoea control.

Subject: Burden of disease

Keywords: Gonorrhoea,Antimicrobial Resistance,burden of disease

ABSTRACT ID: 443

PRESENTED BY: Gianfranco Spiteri / gianfranco.spiteri@ecdc.europa.eu

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6.3. Enhanced surveillance of a long term outbreak of gonorrhoea with high-level resistance to azithromycin in England since 2014

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Background:

Cases of gonorrhoea were initially identified at the end of 2014 among young heterosexuals living in deprived areas in Leeds. The outbreak spread across England and into sexual networks of men who have sex with men (MSM) as the outbreak progressed. Cases among MSM were first identified in November 2015 mainly from a sexual health clinic in London serving a large MSM population. Enhanced surveillance was undertaken in order to provide information on cases in near real time and for some information not routinely collected.

Methods:

Enhanced surveillance for all cases between November 2014 and December 2017 was undertaken to collect information on risk factors, sites of infection, test of cure, and partners. Data was collected using a secure online survey tool and entered by Genito Urinary Medicine clinic staff.

Results:

111 laboratory confirmed cases of high-level azithromycin resistant Neisseria gonorrhoeae were identified in England between November 2014 and March 2018. No specific risk factors (E.g. mobile phone apps or meeting venues) were identified by the surveillance. The majority of the reported sexual partners were not contactable as further details were not disclosed or were unknown to the case.

Conclusions:

Enhanced surveillance provided evidence that transmission of HL-AziR has continued in England since November 2014. The lack of epidemiological links between cases could indicate that there has been significant under-diagnosis of cases. However, despite the lack of epidemiological links the geographic clustering at the start of the outbreak suggested that the cases are part of a discrete outbreak. This has been confirmed by Whole Genome Sequencing. Problems in contacting sexual partners are likely to have further contributed to sustained transmission of this resistant infection.

Subject: Surveillance

Keywords: gonorrhoea, Enhanced surveillance, high-level azithromycin resistant

ABSTRACT ID: 245

PRESENTED BY: Adrian Wensley / adrian.wensley@phe.gov.uk

6.4. Emergence of a new clade of multidrug resistant Neisseria gonorrhoeae in Budapest, Hungary, 2016-2017

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Background:

The Euro-GASP survey in 2009-2010 revealed that G1407 and G225 were the prevalent NG-MAST genogroups of Neisseria gonorrhoeae (NG) in Europe, associated with antibiotic resistance. In our previous study, G1407 was also prevalent and associated with decreased susceptibility to cefixime and azithromycin in Hungary between 2012-2014. We aimed to investigate the changes in molecular epidemiology and genetic alterations associated with antibiotic resistance among the multidrug resistant (MDR) NG isolates in Hungary, in 2016-2017.

Methods:

Non-duplicate NG isolates from patients visiting any of six sentinel Dermatology and Venereology clinics in Budapest were included. Sequence data of MDR-NG isolates (resistant to ciprofloxacin, azythromycin and cefixime/ceftriaxon) from whole genome sequencing (WGS) were used for molecular epidemiological analysis (NG multi-antigen sequence typing (NG- MAST), MLST and phylogenomic) by WGS Analysis (www.wgsa.net), and for antibiotic resistance analysis by NG-STAR tools.

Results:

Ten NG isolates (7/94 in 2016, 3/71 in 2017) from male patients (median age 26 years, range 25-45y) showed MDR phenotype (ciprofloxacin, azithromycin and cefixime resistance). One isolate from 2016 belonged to G1407 NG- MAST-type, ST1901 MLST-type and ST756 NG-STAR-type (penA type XXXV mosaic; mtrR -35A; ponA L421P; gyrA S91F,D95G; parC S87R), while all remaining isolates (originating from March 2016 to August 2017) belonged to one clade with G13876, ST7363 and ST771 NG-STAR-type (penA type X mosaic, mtrR G45D, ponA L421P, gyrA S91F,D95N; parC S87R,S88P; 23S rRNA C2611T).

Conclusions:

Phylogenomic analysis showed that one main clade comprised 90% of the MDR-NG isolates in this study. Despite the phenotypical susceptibility to ceftriaxone, based on the genomic data ceftriaxon resistance also could be predicted. The emergence of this new clade is of major public health concern and was notified to the ECDC.

Subject: Microbiology

Keywords: Neisseria gonorrhoeae, Antibiotic resistance, DNA Sequencing, Sexually Transmitted Diseases, Molecular epidemiology

ABSTRACT ID: 374

PRESENTED BY: Ákos Tóth / toth.akos@oki.antsz.hu

6.5. Novel culture-free genotyping of Neisseria gonorrhoeae vastly improves surveillance by overcoming high failure rate and cross-reactivity in extra-genital sample

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Background:

Resistance of Neisseria gonorrhoeae (NG) is increasing for a wide range of antibiotics. Therefore, surveillance of circulating strains is important. Current genotyping methods rely on bacterial culture which typically is only performed from one anatomical site and frequently fails. In this study, we developed a culture-free genotyping method that is compatible with the NG multiantigen sequence typing (NG-MAST) database. Furthermore, we aimed to gain insight in the frequency of patients infected with distinct NG strains at separate anatomical sites.

Methods:

Specific primers for both PCR targets por and tbpB were designed using Clustal Omega and Basic Local Alignment Search Tool. Technical validation of the culture-free NG-MAST was performed, assessing the specificity, concordance and clinical application. Next, paired samples from concurrent NG infections at separate anatomical sites of 80 consultations (70 patients) were analysed.

Results:

The method was validated and demonstrated that 90.2% (185/205) of clinical samples could be genotyped without cross- reactivity with non-gonoccocal Neisseria species. Applying culture-free NG-MAST to the paired samples revealed a high percentage (25.0%) of consultations with distinct NG strains at separate anatomical sites. In 3 samples, the notorious genogroup G1407, linked with ceftriaxone resistance in NG, was observed. In 2/3 samples this genogroup was not identified using culture-derived NG-MAST.

Conclusions:

Culture-free NG-MAST is three-fold more sensitive (90.2%) compared to culture-derived NG-MAST (28.8%). This novel NG-specific typing method overcomes the cross-reactivity with commensal Neisseria species in extra-genital samples and revealed distinct NG strains currently missed in culture-derived surveillance. Including extra-genital and concurrent NG samples in surveillance could limit dissemination of multi-drug resistant NG strains. Furthermore, characterisation of extra- genital NG infections is important, as these sites may act as a reservoir for acquisition of antimicrobial resistance.

Subject: Novel methods in microbiology (e.g. new diagnostic tools)

Keywords: Neisseria, genotyping,surveillance,concurrent infections,gonorrhoeae

ABSTRACT ID: 416

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6.6. Late breaker: Lymphogranuloma venereum in men who have sex with men in Malta in 2018: an emerging problem

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Methods:

We conducted a retrospective review of data from 01/01/2018 and 30/06/2018 at the Genitourinary Clinic (GUC) to identify Ct positive samples from MSM. Rectal swabs were sent abroad for genotyping. Cases were defined as persons with laboratory confirmed Ct genotypes L1-L3 by polymerase chain reaction (PCR). Cases were treated with doxycycline 100 mg twice daily for 21 days. Identified sexual partners were advised to visit the GUC for testing.

Results:

Of 40 positive Ct rectum swabs and one urine sample, 11 (27%) were LGV positive. All LGV cases engaged in condomless sex (CLS) and five (45%) had concomitant STI infection, including two newly diagnosed with HIV. Six (55%) were symptomatic and four (36%) were foreign nationals. Six (55%) were part of three small group sex and chemsex clusters. Six identified sexual contacts from the group sex clusters were LGV negative. Of four preserved samples from LGV cases genotyped, all were genotype L2b.

Conclusions:

The emergence of LGV in Malta follows similar patterns to other countries with cases among MSM reporting frequent STI co-infections and high risk behaviours including CLS, group sex and chemsex. Awareness of LGV should be raised among clinicians, laboratories and particularly MSM through community engagement. Behavioural surveillance is needed to understand the prevalence of risk behaviours and monitor interventions. Capacity to conduct local genotyping of Ct positive samples should be considered in Malta for rapid diagnosis and early treatment.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Lymphogranuloma venereum, Malta, Disease Outbreaks, Men who have sex with men

ABSTRACT ID: 571

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Track 7: Zoonosis

Moderator:

Carmen Varela Santos

Abstracts

7.1. Public perceptions towards health authorities' risk communication and response in a large regional outbreak of Q fever in South-Limburg, the Netherlands

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Background:

In early 2009, a dairy-goat farm in South Limburg, the Netherlands, reported a massive wave of Coxiella burnetii–related livestock abortions. This was followed by high numbers of human Q fever infections. We assessed the general public information perception towards health authorities' risk communication and response measures taken, and its willingness to comply with the authorities' advice on useful preventive measures.

Methods:

Based on a cross-sectional survey (May-July 2012), we approached three groups in the outbreak area: members of the general public who had not been tested for Q fever (n=189), individuals who had tested negative (n=144), and patients who had tested positive (n=152). The response varied from 20% to 76%. Determinants of public information perception and compliance included test status (untested as reference), risk perception, self-efficacy, and trust towards general practitioners, the public health service, municipal and/or national authorities.

Results:

Overall, 64% (n=312) felt insufficiently informed. This public information perception was associated with higher age (aOR:2.2, 95%CI:1.0-4.5), positive test status (aOR:3.9, 95%CI:1.9-7.9), low self-efficacy (aOR:3.5, 95%CI:1.3-9.6), and low trust towards GPs (aOR:4.5, 95%CI:2.0-10.0) and authorities (aOR:6.4, 95%CI:1.6-25.8). Compliance was only associated with high risk perception (aOR:17.7, 95%CI:1.6-202.3).

Most participants had low self-efficacy (65%) and low trust towards authorities' risk communication and response (59%). Participants expressed a desire for more comprehensive (48%), timely (56%), clear (57%), and personalized (33%) information.

Conclusions:

In general, the public's perception of being insufficiently informed indicates the need for research. Public information perception varied between groups with different test status. Our findings show that public health preparedness and response towards future outbreaks of infectious diseases should include efforts to improve risk communication, and take into account self-efficacy and trust among the general public.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: Q Fever, Coxiella burnetii, Surveys and Questionnaires, Communicable Disease Control

ABSTRACT ID: 140

PRESENTED BY: Jeanne Heil / jeanne.heil@ggdzl.nl

7.2. Human exposure to H5N8 highly pathogenic avian influenza virus in the Netherlands, 2016 – 2017

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Background:

Since 2010, H5N8 highly pathogenic avian influenza (HPAI) virus has been detected in wild birds and on poultry farms in the Eurasian and North American region. So far, no transmission of H5N8 to humans has been detected in symptomatic patients after poultry contact. We initiated a prospective cohort study to investigate the zoonotic potential of H5N8.

Methods:

We conducted our study among persons working or living on a H5N8-infected poultry farm in the Netherlands from November 2016 through March 2017. Within two days after confirmation of poultry infection, we collected a finger-prick dried blood-spot sample (fpDBS) and collected data on socio-demographics, bird exposure, influenza-related symptoms and use of personal protective equipment (PPE) from study participants. Further fpDBSs and symptom data were collected four weeks later (T4). We used a protein microarray to test fpDBSs for IgG antibodies against the hemagglutinin subunit HA1 of seasonal and avian influenza viruses. We calculated relative risks (RR) for association between exposures and symptoms.

Results:

Twenty-two persons from 10 different farm outbreaks participated. Direct contact with infected birds (14 persons, RR0.9; 0.2-4.1), and absence of PPE (13 persons, RR0.5; 0.1-2.2) were not associated with influenza-related symptoms at T4. One person showed a >4-fold titer increase against subtype H5, but also a >4-fold titer increase against multiple other subtypes. None of eight other participants with a >4-fold titer increase against one or more other subtypes did so for H5.

Conclusions : We found no evidence that direct contact with H5N8-infected birds is associated with influenza-related symptoms. One participant showed a generalized immunological response to multiple influenza virus subtypes, including H5. Further research is warranted to determine this response could represent a specific response against H5N8.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: avian influenza,zoonoses,risk,farm outbreaks,H5N8,the Netherlands

ABSTRACT ID: 102

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7.3. Impact of Rev-1 vaccination of sheep and goats on human brucellosis in the Republic of Macedonia

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Background:

Brucellosis is a zoonotic disease whose elimination as endemic disease in humans requires an elimination and eradication among the animals in the country. Measures and activities for prevention of brucellosis are primarily within the competence of veterinary service, but nearby routine cooperation between the two departments - Health and Veterinary with a timely information and coordination of activities are of primary importance for putting this zoonosis under control.

Methods:

Retrospective study based on the epidemiological reports and official data on brucellosis cases from the Institute for Public Health of the Republic of Macedonia and a review of the relevant literature.

Results:

From 2001 to 2014, a total of 3706 human brucellosis cases were reported in R. Macedonia, with a mean annual incidence rate of 12,96/100.000. The highest morbidity rate during this period was recorded in 2008 (490 cases and an incidence rate of 24/100.000), and the lowest one in 2013 (36 cases and an incidence rate of 1,8 /100.000). In 2008, a Rev- 1 vaccination of sheep and goats was introduced which resulted with a decrease of incidence on animal brucellosis. There is a strong positive correlation between the number of infected animals and humans ($r = 0,77$, $p < 0,05$) for the period from 2001 to 2014.

Conclusions:

Crucial results have been achieved with the measures taken by the veterinary activities, resulting in a continuous and significant decline of diseases among the people, and certainly the most important is the introduction of vaccination in sheep and goats in 2008. Although the number of patients with brucellosis has been in continuous decline, some areas of the Republic remain as regions with constant presence of brucellosis.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Brucellosis,Republic of Macedonia

ABSTRACT ID: 78

PRESENTED BY: Svetlana Popovska Kljuseva / svetlanapopovska@yahoo.com

7.4. The burden of disease of Q-fever: a meta-analysis with individual patient data up to nine years after acute infection

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Background:

The largest Q-fever outbreak to date took place in the Netherlands between 2007 and 2010, with 4107 registered cases. Many studies regarding the impact of Q-fever (i.e. quality of life (QoL), fatigue, physical and social functioning) from onset of illness up to nine years after acute infection were performed. The aim of this study was to analyse the course of the burden of disease in three patient groups: Q-fever fatigue syndrome (QFS), chronic Q-fever, and other (not further specified) Q- fever patients.

Methods :

A patient level pooled multilevel analysis was performed on original data from eight studies. Levels of QoL (Nijmegen Clinical Screening Instrument), fatigue (Checklist Individual Strength), physical functioning (Sickness Impact Profile) and social functioning (Short Form 36) were measured using identical validated questionnaires across the studies.

Results :

Data included 4309 observations of 2675 individual Q-fever patients classified as 228 QFS patients, 135 chronic Q-fever patients, and 2312 other Q-fever patients. Results showed that in the first years following the acute Q-fever infection, disease burden was highest among QFS patients, and remained high, with no significant changes over time. In chronic Q- fever patients, levels of QoL, fatigue, and physical functioning worsened significantly over time. In contrast, all outcomes among other Q-fever patients (86% of patients) improved significantly over time.

Conclusions:

The disease burden of Q-fever differs greatly between QFS, chronic Q-fever and other Q-fever patients. Among chronic Q- fever patients, levels of QoL, fatigue and physical functioning continue to worsen over time, while QFS patients report a continued high burden of disease. However, the overall majority of patients, belonging to the group other Q-fever, showed significant improvements over time.

Subject: Burden of disease

Keywords: Q fever, zoonoses, health status, meta-analysis, time

ABSTRACT ID: 415

PRESENTED BY: Cornelia HM van Jaarsveld / Ellen.vanJaarsveld@radboudumc.nl

7.5. Epidemiology of animal bites and animal rabies in Jordan, 2010-2017

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Background:

Rabies continues to be a major public health problem worldwide. Multiple factors contribute to high morbidity and mortality due to animal bites. This study aimed to describe the epidemiology of animal bites and animal rabies in Jordan during the period from 2010 to September 2017.

Methods:

A descriptive surveillance-based study was conducted. The study included all data about animal bites and animal rabies from the national surveillance system for the period 2010- September 2017. The characteristics of the reported animal bites were described according to gender, age, geographic area, year, and type of the animal bites. The incidence rate of animal bites was calculated per 100,000 population.

Results : A total of 34857 animal bites were reported during the period (2010-september 2017). The number of cases increased from 2936 in 2010 with an incidence rate of 46.6 per 100,000 populations to 5221 in 2016 with an incidence rate of 53.3 per 100,000 population. In all years, the number of cases peaked in the period from June to September. About 54% of cases were in the central region, 42% in the north, and 4% in the south. About 75% of animal bite victims were males and 46% were older than 20 years. Of the 210 suspected animal rabies, 141 (67.1%) animals tested positive. Of those, 39.7% and 24.8% were dogs and cows, respectively. Other animals tested positive included donkeys (9.2%), goats (8.5%), horses (7%), sheep (6.4%), and other (4.4%). Of all human victims, six patients were diagnosed with rabies (3 in 2017).

Conclusions :

Animal bites continue to be a problem in Jordan. Efforts to protect people against animal bites are essential for preventing rabies.

Subject: Burden of disease

Keywords: Animal bites, rabies, Epidemiology, Jordan

ABSTRACT ID: 495

PRESENTED BY: Mohammad Alrawahnih / dr.rawahnih@yahoo.com

7.6. A Case of Rabies Leads to Prophylaxis for Others Exposed, Balkh Province, Afghanistan, 2016

CANCELLED

Poster Abstracts

Track 8: Vaccine- preventable diseases (1): Implementation and modelling

Moderator:

Tanya Melillo

Abstracts

8.1. Agent-based modeling of influenza dynamics in Russian cities: the role of spatial heterogeneity and background immunity levels

Vasiliy Leonenko [1]

G. Bobashev [2]

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Background:

Influenza, being one of the most widespread diseases, still draws much attention from the researchers. One of the important questions is how the changes in contact patterns and levels of background immunity affect the epidemic dynamics. In the presented work we address this matter by calibrating an agent-based model of influenza dynamics to data for Saint Petersburg, Russia.

Methods:

Our approach combines three interlinked components: (1) a synthetic population of Saint Petersburg, created by the authors; (2) an agent-based microsimulation model of influenza dynamics implemented via open-source framework FRED (Grefenstette et al., 2013); (3) micro and macro data (namely, weekly incidence of acute respiratory infections and background immunity levels obtained via laboratory analysis) provided by Russian Influenza Research Institute. For comparison purposes, we also use an age-structured compartmental influenza model calibrated to the same data (Leonenko, Bobashev, in press).

Results:

The simulation results demonstrate the ability of our agent-based model to reproduce the overall flu incidence dynamics in Saint Petersburg coherent to actual disease incidence and to assess the number of new influenza cases on a finer scale compared to the compartmental model. We show that variations in background immunity significantly affects the disease dynamics in urban settings, and the immunity levels cannot be assessed directly via laboratory analysis.

Conclusions:

In this work, we showed that the agent-based approach is more efficient compared to the compartmental modeling when targeted influenza control measures are to be planned. Also, to correctly assess the background immunity levels in the population, which is crucial for influenza dynamics prediction, a combination of laboratory analysis and retrospective modeling is required.

Subject: Modelling, bioinformatics and other biostatistical methods

Keywords: influenza, agent-based model, background immunity, FRED,synthetic populations

ABSTRACT ID: 431

PRESENTED BY: Vasiliy Leonenko / vnleonenko@yandex.ru

8.2. Risk assessment and cost impact of adverse events during pandemic influenza vaccinations

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Background:

One of the main public health interventions available for pandemic response are pandemic influenza vaccines, which are crucial for a pandemic influenza preparedness planning. Nonetheless, the challenges for developing an optimal pandemic vaccine response include taking into account the uncertainty about the timing, severity, and speed of spread of a novel virus; together with the commercial availability of pandemic vaccine. Moreover, there is the potential risk of serious adverse events associated with pandemic vaccination that may have a substantial financial and economic impact.

Methods:

We performed a scenario based risk assessment of adverse events during pandemic influenza vaccination campaigns. We used narcolepsy as a “worst case” adverse event and analysed the effect of pandemic vaccination duration, rate, target, and timing on both pandemic influenza infection incidence and number of adverse events. Disease incidence for each scenario was estimated using an epidemiological model. For each scenario we calculated both the quality-adjusted life-year (QALY) gain due to vaccination and the estimated QALY loss due to adverse effects.

Results:

Overall, the scenario-based analysis showed that only duration and vaccination target in terms of age group (and vaccination rate) influenced the total number of adverse events. Nonetheless, the QALY gains from pandemic vaccination generally outweigh the QALYs lost due to the adverse events, unless the vaccination was started very late in the pandemic wave.

Conclusions:

While QALYs gained from pandemic vaccination in general outweigh the QALYs lost, a crucial consideration is the timing of vaccination. If vaccination starts very late during the pandemic then it can be more beneficial to not vaccinate broadly on a population-level due to the increased risk of adverse events from vaccination.

Subject: Modelling, bioinformatics and other biostatistical methods

Keywords: influenza, vaccination, adverse event, mathematical model, economic evaluation, public health

ABSTRACT ID: 118

PRESENTED BY: Edwin van Leeuwen / edwinvanl@gmail.com

8.3. Quantile regression for seroprevalence study of pertussis comparing Norway and Sweden, 2012-2013

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Poster Abstracts

Background:

Levels of pertussis antibodies (anti-PT) vary with age due to e.g. vaccination, waning effect and exposure. In 2012, Sweden and Norway vaccinated the 4th dose against pertussis at 5-6 years and 7-8 years, respectively; and a catch-up dose was administered in Sweden at 9-11 years. To obtain a picture of how anti-PT varied with age, we fitted quantile regressions to the median and 90th percentile.

Methods:

In 2012-2013, 3618 specimens were collected from laboratories in Sweden and 3058 in Norway, from individuals 2-100 years old. A harmonized in house IgG-anti-PT ELISA was used in both countries. For each country, fitted non-parametric quantile regression with age as covariate with smoothing parameter (lambda=2). Fitted curves were plotted with 95% confidence intervals. Results were age-standardized to the 2012 Swedish population.

Results:

We obtained a profile over the span of ages for the median and for the 90th percentile of anti-PT IgG of each country. Both median curves showed peaks at the different ages of vaccination. Two to four years after the last vaccination the median curves were constant at around 6 IU/ml (Sweden) and 8 IU/ml (Norway), and the 90th percentile at 30 IU/ml. For Norway there was also an increase of IgG-anti-PT among those between 15 to 25 years in the 90th percentile.

Conclusions:

The quantile regression models produced IgG-anti-PT profiles over all ages and had the advantage to be independent of cut-offs and age groups, and were easy to interpret. With this method we were able to identify patterns such as the higher seroprevalence among young adults in Norway. Based on the present results, future plans include detailed analysis of waning immunity after vaccination.

Subject: Modelling, bioinformatics and other biostatistical methods

Keywords: Whooping Cough ,Prevalence,Vaccination,Seroepidemiologic Studies

ABSTRACT ID: 480

PRESENTED BY: Ilias Galanis / sharon.kuhlmann-b@folkhalsomyndigheten.se

8.4. Knowledge, attitudes and practice related to maternal pertussis vaccination: study among public health nurses and midwives in Finland

Jana Prattingerová [1]

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Background:

Pertussis is a vaccine-preventable disease with potentially severe consequences for newborns. In response to increased incidence, many countries have modified their immunisation strategy including the introduction of maternal immunisation to protect newborns. In Finland, pertussis incidence is relatively low. In preparation for the possibly increasing incidence and the need to introduce maternal vaccination, we aimed to assess the awareness of pertussis and vaccination during pregnancy among public health nurses and midwives.

Methods:

Between December 2017 and February 2018, we conducted a prospective semi-quantitative knowledge, attitude and practice (KAP) online survey among a convenience sample of public health nurses and midwives recruited through adverts in a professional journal. We used descriptive statistics and logistic regression to assess the impact of demographic and KAP-related variables on intent to recommend pertussis vaccine during pregnancy.

Results:

Of 253 survey participants (median age, 41 years), 91% were public health nurses. Most of them knew the current Finnish epidemiology and vaccine recommendations for pregnant women (76 and 79 %, respectively), but only 18 % were aware of pertussis fatalities. Among participants, 87% reported their intentions to recommend pertussis vaccine to pregnant women, 40% had received a pertussis booster themselves. In the multivariate analysis, factors associated with intention to recommend vaccination were knowledge of vaccine recommendations (OR, 2.87; 95%Cl, 1.16-7.13), favorable risk-benefit belief (OR, 5.33; 95%CI, 2.23-12.75) and personal choice of adult booster (OR, 3.06; 95%Cl, 1.07-8.72). Other variables were not significantly associated with willingness to recommend the vaccine.

Conclusions:

Nurses and midwives play a vital role in ensuring that pregnant women are able to make an informed choice on vaccination. Gaps in their knowledge should be addressed prior to introduction of maternal vaccination.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: pertussis,survey,vaccination,pregnancy

ABSTRACT ID: 6

PRESENTED BY: Jana Prattingerová / jana.prattingerova@gmail.com

8.5. ADVANCE system testing: benefit-risk analysis of a marketed vaccine using MCDA and cohort modelling

Kaatje Bollaerts [1]

E. Ledent [2], T. de Smedt [3], D. Weibel [4], H. Emborg [5], K. Berensci [6], A. Correa [7], G. Danieli [8], T. Duarte-Salles [9], C. Huerta [10], E. Martin [11], G. Picelli [12], L. Tramontan [13]

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Background:

The Accelerated Development of VAccine beNefit-risk Collaboration in Europe (IMI-ADVANCE) is a public private collaboration aiming to develop a system for benefit-risk (B/R) monitoring of vaccines using European electronic healthcare (EHR) databases. Proof of concept (POC) studies were designed for system testing. With this POC, we aim testing B/R methods for vaccines. The test case was the comparison of the B/R profiles of whole-cell (wP) and acellular pertussis (aP) formulations in children (‹6years).

Methods:

We used multi-criterion decision analyses (MCDA) to structure the B/R assessment combined with cohort modelling to build the B/R effects table. In the cohort model, we simulated the number of events within 2 hypothetical cohorts of 106 children from birth to age 6 years: one cohort received wP, the other aP. The benefits were pertussis and complications. The risks were febrile convulsions, fever, hypotonic-hyporesponsive episodes, injection site reactions and persistent crying. The model parameters were informed using EHR data from Denmark (SSI), Spain (BIFAP – SIDIAP), Italy (Pedianet) and the UK (RCGP – THIN). Preferences were elicited from medical experts and combined with the cohort modelling results to obtain B/R scores.

Results:

Incidence and relative risk estimates from EHR databases could be used to inform the cohort model, of which the results were easily combined with preference weights to obtain B/R scores. Conditional on our model assumptions and preference weights, the BR scores were 84.3% (95% CI: 64.6 – 99.1) and 58.4% (95% CI 24.5 – 97.5) for wP and aP.

Powered by TCPDF (www.tcpdf.org)

Conclusions:

B/R methodology and estimates obtained from EHR databases can be successfully used for B/R assessment of vaccines. This study was for system testing and not to inform decisions on pertussis vaccination.

Subject: Preparedness

Keywords: benefit-risk assessment, vaccines, methodological study, Europe

ABSTRACT ID: 465

PRESENTED BY: Kaatje Bollaerts / kaatje.bollaerts@p-95.com

8.6. ADVANCE system testing: Feasibility of using a network of health data bases for vaccine safety studies: an example on pertussis vaccination

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Background:

The Accelerated Development of Vaccine benefit-risk Collaboration in Europe (ADVANCE) is developing and testing a system for rapid benefit-risk monitoring of vaccines using health care databases in Europe, under a multi-stakeholder framework. The system was tested comparing incidence rates (IR) of events of interest (EI) between whole cell- (wP) and acellular- (aP) pertussis vaccines, in children, to feed a test-case benefit/risk analysis.

Methods:

The study population were children aged 1 month to ‹6 years, during 2001-2016, in 7 health care databases (i.e., Italy (Pedianet), Spain (SIDIAP & BIFAP) and UK (THIN & RCGP), DK (AUH & SSI). IRs and incidence rate ratios (IRRs) of EIs were estimated in outcome specific risk windows following wP and aP vaccination and in non-risk periods, using common protocol and analytics. IRs and IRRs were pooled using random-effects meta-analyses.

Results:

In a study population of 5.9 Million children the overall (i.e., risk plus non-risk periods) IR per 1000 PY varied between 0.5 and 3.1 for cutaneous reactions (ISR), 8.5 - 491.0 for fever, 0.01 - 0.44 for somnolence, 2.4-22.1 for persistent crying, 2.6-14.2 for febrile convulsion, and between 0.2 and 1.5 for hypotonic hyperresponsive episode (HHE). IRs were similar across similar databases but differed between based on where outcome is captures (primary or secondary care). The risk for febrile convulsions, fever, ISR, persistent crying, and somnolence was slightly higher for wP than aP during 1stdose risk period. The IRR and IR were consistent with available literature and expert feedback.

Conclusions:

Based on this proof of concept study we demonstrated the feasibility of generating reliable vaccine safety data using the ADVANCE distributed network system.

Poster Abstracts

Subject: Preparedness

Keywords: Immunization, Post-licensure vaccine safety, multi-center observational studies, data network, electronic health care databases

ABSTRACT ID: 462

PRESENTED BY: Daniel Weibel / weibeldaniel@gmail.com

MODERATED POSTER SESSION B
DAY 2: Thursday, 22 November 2018
15:40-16:40

Track 9: Antimicrobial resistance (Epidemiology and Surveillance)

Moderator:

Alessandro Cassini

Abstracts

9.1. Outbreak of a rare type of Methicillin-resistant Staphylococcus aureus (MRSA) among teenagers and their families in a small community in Norway, 2016-2017

Cecilia Wolff [1]

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Background:

MRSA is a notifiable disease in Norway with 2,338 cases notified in 2016. Community outbreaks are occasionally reported, but not routinely investigated. In May 2017, the Norwegian reference laboratory for MRSA detected a cluster of a rare type of MRSA from mainly adolescent patients in one municipality, which were sampled from February to May 2017. There was no known epidemiological link. Our aims were to identify the transmission route and develop a tool for investigating community outbreaks of resistant bacteria.

Methods:

We used the Norwegian Surveillance System for Communicable Diseases to find cases with the rare type PVL- positive MRSA CC398, spa-type t034. All such isolates in 2016 and 2017 from this municipality were whole-genome sequenced (WGS). For the case interviews, we developed a questionnaire with semi-open questions covering school, employment, organised and non-organised activities, and social networks.

Results:

The outbreak included twelve cases from five families: five male teenagers, three three-to-six-year-old children (two males), and four adults (two males). Cases presented with superficial wounds or skin abscesses. Samples were taken from 16/08/2016 to 17/06/2017 and WGS confirmed close relatedness of the isolates (<=6 single nucleotide polymorphisms). Interviews with parents of four families revealed epidemiological links between all five families via their social network and schools.

Conclusions:

Awareness of and testing for MRSA increased, and the outbreak did not extend any further into the community. Local authorities and NIPH agreed that no community-focused actions were needed. This is the first MRSA community outbreak investigated by NIPH through a combination of surveillance information, WGS and case interviews. We recommend this approach for future community outbreaks of multi-drug resistant organisms known to be transmitted via contacts.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Methicillin-Resistant Staphylococcus aureus, Disease Outbreaks, Surveys and Questionnaires, Whole Genome Sequencing, Norway

ABSTRACT ID: 39

PRESENTED BY: Cecilia Wolff / cecilia.mia.wolff@fhi.no

9.2. Epidemiology of carbapenemase-producing bacteria in England, 2016–2018: results from the national enhanced surveillance system

Rachel Freeman [1]

D. Ironmonger [2], K. Hopkins [3], R. Puleston [4], B. Muller-Pebody [5], R. Hope [6], S. Hopkins [7], A. Johnson [8], N. Woodford [9], I. Oliver [10]

[1] Public Health England

[2,3,4,5,6,7,8,9,10] Public Health England

Background:

In May 2015, following an increase in reported cases, Public Health England launched an enhanced surveillance system to electronically capture data on patients infected/colonised with carbapenemase-producing Gram- negative bacteria. Our study aimed to identify high risk groups to inform infection prevention and control interventions.

Methods: Cases were defined as patients with a carbapenemase-producing organism isolated from a screening or clinical specimen in England between April 2016–March 2018. Cases were de-duplicated by patient, bacterial species, specimen site and resistance mechanism for each year of surveillance.

Results:

There were 3953 cases reported via the system. 1786 (45.2%) patients were female and 2163 (54.7%) were male. The median age of patients was 69.5 years. Most cases were hospital inpatients (3436, 86.9%). Enhanced fields including foreign travel and clinical specialty were poorly completed (14% and 21%, respectively).

The majority of organisms reported were from screening specimens (3151, 79.7%), with 798 clinical specimens recorded (20.2%). The most common clinical specimen types were urine (330, 41.4%), blood (102, 12.8%) and sputum (57, 7.1%). Carbapenemase enzymes were identified in 15 different genera. The most common species were Klebsiella pneumoniae (1424, 36.0%) and Escherichia coli (1119, 28.3%). Nine resistance mechanisms were identified; OXA-48-like enzymes were the most frequently identified (2076, 60.4%), followed by NDM (904, 22.9%) and KPC (890, 22.5%).

Conclusions:

The enhanced surveillance system is voluntary and poor completion of enhanced data fields is limiting our ability to identify high risk patient groups to inform public health action. However, the system does capture comprehensive patient demographic data and functions as an electronic referral system. Future work will involve data linkage to allow us to identify groups at greater risk and focus control and prevention efforts.

Subject: Surveillance

Keywords: carbapenemase; surveillance; epidemiology

ABSTRACT ID: 225

PRESENTED BY: Rachel Freeman / rachel.freeman@phe.gov.uk

9.3. Two regional outbreaks of Carbapenemase producing Klebsiella pneumoniae ST512, Finland, 2013-ongoing

Janko van Beek [1]

K. Räisänen [2], M. Broas [3], J. Kauranen [4], A. Kähkölä [5], J. Laine [6], E. Mustonen [7], T. Nurkkala [8], T. Puhto [9], J. Sinkkonen [10], S. Torvinen [11], T. Vornanen [12], R. Vuento [13], J. Jalava [14], O. Lyytikäinen [15]

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Background:

Carbapenemase-producing Enterobacteriaceae (CPE) are rare in Finland, 5-34 cases annually. Clusters of Klebsiella pneumoniae were detected by routine surveillance using whole genome sequencing (WGS). The objective was to investigate transmission chains and to evaluate screening policies to stop further transmission.

Methods:

Cases were defined as persons with K. pneumoniae KPC-3 ST512 strain detected in Finland from August 2013 to April 2018. We collected epidemiological information of the cases and data on screening specimens obtained from patients and environment. WGS was performed on all K. pneumoniae cultures using Illumina MiSeq platform and data was analysed using Ridom SeqShere software and K. pneumoniae cgMLST schema.

Results:

Nineteen cases were found in five hospitals. Genetic analysis showed two clusters: two closely-related (less than 10 allele difference) cases in Tampere university hospital and 17 in four other hospitals (Oulu n=3, Kemi n=8, Kajaani n=1, Rovaniemi n=5). The index case in Tampere university hospital was transferred from an Italian hospital. The travel history of the first patient in Oulu university hospital remained unknown. Epidemiological investigation identified previously unnoticed case transfer from Oulu university hospital to Kajaani and Rovaniemi hospitals, but not to Kemi hospital. Onwards transmission was identified in all hospitals, except in Kajaani. Despite extensive screening of exposed patients and environment, only two new cases in Kemi hospital were found and one positive isolation room in Tampere university hospital.

Conclusions:

This outbreak was mostly related to domestic case transfer between hospitals and most of the cases were found by examining clinical specimens. This study shows that CPE surveillance using WGS and collaboration between hospitals are crucial to identify outbreaks and transmission chains. Identification of patients at risk for screening needs further evaluation.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: CPE, outbreak,Finland,Klebsiella pneumoniae,Carbapenemase

ABSTRACT ID: 106

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

9.4. First report of macrolide-resistant Mycoplasma pneumoniae in adults with community-acquired pneumonia in Italy

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[5] Department of Medical and Surgical Sciences - University of Foggia

Background:

Mycoplasma pneumoniae is a common cause of community-acquired pneumonia (CAP). This cross-sectional study aimed to determine the prevalence of macrolide-resistant M. pneumoniae strains in adults with CAP.

Methods:

A convenience series of 234 adult hospitalised and non-hospitalised subjects who were diagnosed with CAP in January 2013 to April 2015 in South Italy was enrolled. Respiratory samples were subjected to real-time PCR. InM. pneumoniae-positive samples, domain V of 23S rRNA was sequenced to detect resistance-conferring point mutations. P1 major adhesion protein typing and multiple loci variable-number tandem repeat analysis (MLVA) were also performed.

Results:

Of the 234 samples, 15 (6.4%) were positive for M. pneumoniae. Three of these (20.0%) had a macrolide-resistant genotype: two and one had A2063G and A2064G, respectively. Fourteen of the 15 strains were subtyped: half had subtype 1 and half had subtype 2. Eight strains underwent MLVA profiling: one each had the J, A, and Z type. The remainder were unclassifiable.

Conclusions:

This novel discovery of macrolide-resistant M. pneumoniae strains in adults with CAP in Italy suggests that there may be increasing circulation of these strains in the population. To facilitate rapid optimization of the antibiotic strategy in Italy, macrolide resistance should be monitored by a surveillance system that is based on molecular methods.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Mycoplasma pneumoniae,Macrolide-resistant Mycoplasma pneumoniae,community-acquired pneumonia

ABSTRACT ID: 447

PRESENTED BY: Daniela Loconsole / loconsole.daniela@libero.it

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9.5. Cryptococcosis: Molecular types and drug susceptibility of German clinical isolates (2011-2017)

Regina Selb [1]

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Background:

Cryptococcosis is the most common fungal infection of the central nervous system worldwide, resulting in 181.000 deaths annually. In Germany, 50-60 cases are diagnosed each year. Molecular typing suggests that the pathogen can be imported or acquired locally. In vitro resistance to antifungals is emerging, with up to 34% of clinical isolates resistant to first line agents in some countries. Currently, data on antimicrobial susceptibility of German isolates are unavailable. We determined the frequency of antimicrobial resistance and the molecular epidemiology of German clinical isolates collected between 2011 and 2017 to evaluate the need for routine screening.

Methods:

We performed susceptibility testing (CLSI microdilution) of 105 C. neoformans var. grubii isolates regarding the antimycotic agents Fluconazole, 5-Flycytosine, Amphotericin, Voriconazole, Posaconazole, and the drug candidate Sertraline. Resistance to Fluconazole and 5-Flucytosine was defined at a minimal inhibitory concentration (MIC) >8µg/ml. Furthermore, we assessed phylogenetic relationships by MLST according to the International Society for Human and Animal Mycology consensus scheme.

Results:

In MLST, 63% of sequences clustered with reference isolates associated with autochthonous infection in previous studies. Within this cluster we identified one isolate with in vitro resistance to both Fluconazole (MIC 16 µg/ml) and 5-Flucytosine (MIC 64 µg/ml) from a patient with relapsed infection. Another isolate with resistance to Fluconazole only (MIC 16 µg/ml) displayed a sequence type previously associated to an Asian origin. MICs for sertraline were in range with previous reports (MIC90 = 8 µg/ml).

Conclusions:

Antimycotic resistance in Germany is rare, pertaining to <2% of C. neoformans var. grubii isolates collected between 2011 and 2017. We recommend drug resistance screening for patients with travel history and for those with relapse. Sertraline shows promising in vitro activity.

Subject: International health and migration

Keywords: Cryptococcus, Cryptococcosis, Drug Resistance Fungal, Multilocus Sequence Typing, Antifungal Agents, Drug Resistance Multiple Fungal

ABSTRACT ID: 107

PRESENTED BY: Regina Selb / SelbR@rki.de

Track 10: Emerging and vector-borne diseases (2): International health

Moderator:

Ioannis Karagiannis

Abstracts

10.1. Ongoing high morbidity and mortality due to infectious diseases in Walikale territory, Democratic Republic of the Congo (DRC) 2017

Eve Robinson [1]

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Background:

In 2012, Médicins Sans Frontières recommenced activities in Walikale territory, DRC, in response to renewed conflict and largescale population displacement. In 2013, the crude mortality rate (CMR) was 1.2 deaths per 10,000 persons/day, above the emergency threshold of 1. In late 2017, after a period of relative stability, we undertook a morbidity and mortality survey to reassess the health status of the population to inform ongoing operations.

Methods:

We performed a two-stage cluster survey. We selected villages using probability proportional to size and households using a random walk procedure. We interviewed consenting household heads on self-reported morbidity and mortality, healthcare use, vaccination status, and bednet availability within the household. We calculated CMR and under- five mortality rate (U5MR) as deaths per 10,000 persons/day using the mid-period population and a recall period of 324 days.

Results : The sample included 5,711 persons in 794 households. In 89.3% of households at least one person was ill in the previous fortnight, and

57.5% sought healthcare. Care was not sought due to cost in 58.3% of the cases. Malaria was the most frequently reported illness (56.7%) amongst the last ill household member. Coverage of measles-containing-vaccine was 61.9% in under-fives. Universal bednet coverage (1 bednet/2 people) was reported from 17.4% of households. The CMR and U5MR were 0.98 (95%-CI 0.78-1.23) and 1.29 (95%-CI 0.82-2.00), respectively. The most frequent causes of death were malaria (31.1%), diarrhoea (14.6%) and respiratory infections (7.9%).

Conclusions:

Mortality in Walikale has decreased to just below emergency thresholds, but morbidity and mortality remains high for preventable infectious diseases. These findings reinforce the need to increase access to basic primary and secondary healthcare, and optimize preventive interventions such as vaccinations and bednet distributions.

Subject: International health and migration

Keywords: Democratic Republic of the Congo, Health survey, morbidity, mortality, vaccination coverage, mosquitoe nets

ABSTRACT ID: 325

PRESENTED BY: Eve Robinson / eveprobinson@gmail.com

10.2. Implementing WHO's Early Warning, Alert and Response System (EWARS) for outbreak detection during the Rohingya Crisis, Bangladesh 2017-2018

Basel Karo [1]

C. Haskew [2]

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Background:

Since August 2017, violence in Myanmar's Rakhine State has driven more than 500,000 Rohingya across the border into Cox's Bazar, Bangladesh. The WHO's Early Warning, Alerts and Response System EWARS is a web-based system designed to enhance disease surveillance and outbreaks detection in emergency settings. We aim to describe the implementation of EWARS in the Rohingya refugee settlements in Cox's Bazar

Methods:

On 1 January 2018, WHO deployed EWARS out of a box which contains mobile phones, laptops and a local server to collect reports and manage disease data. Health facilities were enrolled and trained as reporting sites for EWARS in the first week. Based on burden and epidemic potential, the case management team involving WHO, Ministry of Health, and humanitarian partners defined thirteen reportable diseases/syndromes and their alert thresholds

Results:

From January through February, 157 health facilities run by 23 humanitarian partners were enrolled in EWARS, covering a total of 728,786 (84%) Rohingya refugees. On average, 70% of the health facilities submitted their reports in EWARS weekly. During the same period, 103 alerts were triggered by health facilities across the settlements. After verification and risk assessment, we identified two outbreaks from alerts; acute jaundice syndrome (AJS) (17 alerts; 944 cases) and measles (27 alerts; 864 cases). Mapping alerts in EWARS provided information on age and geographical distribution of cases which helped the measles vaccination campaign, and the field investigation and sample collection for AJS

Conclusions : EWARS provided a functional and simple, portable surveillance system in the emergency setting by detecting outbreaks, and provided targeted information. We recommend implementing EWARS in the early stage of a crisis for timely detection and response to outbreaks

Subject: Novel methods in epidemiology (e.g. digital disease detection, e-health)

Keywords: outbreaks detection,emergency settings; ,Rohingya Crisis, EWARS, portable surveillance system

ABSTRACT ID: 133

PRESENTED BY: Basel Karo / baselkaro@gmail.com

10.3. The Epidemic Intelligence from Open Sources (EIOS) Initiative: A collaboration to improve and support global epidemic intelligence through event-based surveillance and information sharing

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Background:

Event-base surveillance (EBS) complements indicator-based surveillance, increasing sensitivity and timeliness for informed response. The growth of open source information provides unprecedented

opportunities for EBS, but increases the effort required to identify relevant information. The EIOS initiative is a collaboration between the World Health Organization (WHO) and key public health

stakeholders performing EBS. Its goal is to save lives through a unified, all-hazards, One Health approach for early detection and assessment of public health risks, supported by a state of the art Web-based system for monitoring open source information.

Methods:

The EIOS system is developed with the European Commission's Joint Research Centre. It collates articles from a broad range of publicly available sources including media and official sites. It runs a series of

modules to filter, categorize and de-duplicate articles. Users can securely interact with the data,

perform EBS activities and selectively share information. The system's enhancement is user-driven and

informed by monitoring and evaluation activities.

Results:

In November 2017, WHO released the first version of EIOS for evaluation, granting access to 121 users from 13 institutions working on human, animal and plant health. The EIOS system screens over 300,000

articles per day from 8,600 sources in 68 languages in 216 countries/ territories of which an average of

16,500 articles are tagged and displayed on EIOS. The fist evaluation confirmed the system's value and

identified key areas for improvement.

Conclusions:

The EIOS initiative connects experts involved in public health and standardize the approaches to EBS. The EIOS system will be further enhanced, but already significantly improves EBS, facilitates information

sharing within and across organisations, nurtures expert communities and creates environments for

rapid detection and verification of public health risks.

Subject: Surveillance

Keywords: Event-based surveillance, detection, open source information, all hazard, One-health, information sharing

ABSTRACT ID: 294

PRESENTED BY: Emilie Johanna Peron / perone@who.int

10.4. Enhanced Completeness of Digital Surveillance Outbreak Response Management and Analysis System (SORMAS) versus Conventional Surveillance for Lassa fever and Meningitis Outbreaks in Nigeria 2017/2018

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Background:

Nigeria experienced an outbreak of cerebrospinal meningitis (CSM) from December 2017 to May 2018 and one of Lassa Fever (LF) from January to May 2018. Conventional surveillance (CS) within the Integrated Disease Surveillance and Response (IDSR) consists of paper case forms completed at district level and sent via state health department to the national level for transferal into excel database. We deployed the mobile and web-based Surveillance and Outbreak Response Management and Analysis System (SORMAS) in 3/12 and 3/18 States affected most by CSM and LF respectively. This study compares completeness in SORMAS versus CS.

Methods:

SORMAS deployment included a 4-day training of all Disease Surveillance Notification Officers (DSNO) at state- level and district-level who were equipped with smart tablets. We performed chi-square tests with R to compare differences in data completeness between SORMAS and CS for vaccination status and occupation

Results:

For CSM, vaccination status was available for 51% (148/291) in SORMAS versus 3% (34/1139) in CS [OR=33.63, CI 95%, 22.29-50.76]. For occupation, completeness was 89% (259/291) in SORMAS versus 19% (211/1139) in CS [OR= 35.59 CI 95%, 23.94-52.92] for CSM, and 71% (17/24) versus 22% (256/1154) [OR= 8.52, CI 95%, 3.49-20.77] for LF.

Conclusions:

Completeness was significantly higher for cases assessed via SORMAS than via conventional surveillance in IDSR most likely due to improved user friendliness and early digitalization in SORMAS.

Subject: Novel methods in epidemiology (e.g. digital disease detection, e-health)

Keywords: Systematic evaluation,Surveillance ,Outbreak,CSM,Lassa fever,eHealth,mHealth,SORMAS,Data quality

ABSTRACT ID: 292

PRESENTED BY: Bernard Silenou Chawo / daniel.tom-aba@helmholtz-hzi.de

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10.5. Descriptive epidemiology of a large outbreak of Diphtheria among Forcibly Displaced Myanmar Nationals, Bangladesh, 2017-2018

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Background:

Following intercommunal violence in August 2017, there was an influx of over 650,000 Rohingya refugees from Myanmar to Cox's Bazar, Bangladesh. In early November 2017, an outbreak of diphtheria began among this immunologically naïve refugee population, something not previously described in the published literature.

Methods:

Patients were linelisted by organisations operating treatment facilities, and these were used to generate descriptive epidemiological analyses of the outbreak. A probable case was defined as a person with an upper respiratory tract illness with laryngitis or nasopharyngitis or tonsillitis AND sore throat or difficulty swallowing and an adherent membrane/ pseudomembrane OR gross cervical lymphadenopathy. Confirmed cases were those positive for toxigenic C. diphtheriae strain by a multiplex assay.

Poster Abstracts

Results:

Between 8 November 2017 and 31 August 2018, 7068 cases were notified (271 confirmed, 3625 probable, 3172 suspected), 71.5% of whom were aged under 15 years and 55.6% of whom were female. There were 43 deaths (case fatality ratio 0.6%). The overall attack rate was 115.3/10000 population. Sore throat (93.7%) and fever (86.4%) were the most common symptoms, while pseudomembrane (35.3%) and gross cervical lympadenopathy (31%) were the most common signs. Of 4279 cases with known vaccination status, 2198 (51.4%) were vaccinated. 5320 (64.9%) patients were treated with antibiotics, while 1476 (18.0%) were treated with DAT.

Conclusions:

This large outbreak occurred among a population that had been chronically underserved prior to their arrival in Bangladesh, among whom the risk of various outbreaks of vaccine-preventable diseases was high. The data presented here were used for real-time forecasting of vaccine and anti-toxin requirements, which were facing a global shortage due to the limited global stockpile and concurrent diphtheria outbreaks in Yemen, Venezuela and Indonesia.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Diphtheria, Refugees, Disease Outbreaks, Bangladesh

ABSTRACT ID: 322

PRESENTED BY: Jonathan Polonsky / polonskyj@who.int

10.6. Vaccine-preventable diseases among asylum-seekers in Germany between 2015-2017

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Background:

Between 2015 and 2017, more than 1.4 million asylum seekers (AS) were registered in Germany. It is policy to vaccinate AS according to the national immunization schedule, depending on vaccination status. However, data on the implementation of this policy are lacking. Our objective was to analyse notification data of vaccine-preventable diseases (VPDs) among AS aged <25 years over time to identify any increased risk of acquiring VPDs in Germany.

Methods:

Cases of VPDs reported to the Robert Koch-Institute between September 2015 and September 2017 were described regarding age group, sex and country of origin. We calculated the proportion of VPDs among all notified cases, both in AS and non-asylum seekers (NAS) and assessed the proportion of VPDs over time.

Results:

In total, 4.993 VPD-cases were notified among AS. Two thirds of VPD-cases in AS were male. Most originated from Syria, Afghanistan or Iraq. The proportion of VPDs was significantly higher in AS compared to NAS (64% vs.42%). Chicken pox and rotavirus-gastroenteritis were most commonly notified VPDs among children <5 years. Chicken pox accounted for a markedly higher proportion among AS compared to NAS (36% vs. 15%). Between the maximum and minimum number of reported cases during the observation period, the proportion of VPDs in AS decreased from 82% to 43% while in NAS it decreased from 23% to 19%.

Conclusions:

VPDs represent a high proportion of all notified infectious diseases, both among AS and NAS; still VPDs are more common among AS. This might be due to insufficient vaccination coverage, but differences in consultation and diagnostic testing are also likely. Vaccination coverage data are urgently needed to better identify needs and to guide vaccination activities.

Subject: International health and migration

Keywords: Varicella, vaccine, immunization, notification, asylum seekers

ABSTRACT ID: 442

PRESENTED BY: Alexandra Sarah Lang / LangAl@rki.de

Track 11: Food- and waterborne diseases and zoonoses (3): Hepatitis and viral infection

Moderator:

Thibaut Jombart

Abstracts

11.1. Sources and risk factors for acute hepatitis E in the Netherlands

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Background:

The number of hepatitis E patients has recently increased in the Netherlands, as in other European countries. Although swine are known as main reservoir for hepatitis E virus (HEV), the exact transmission routes of HEV are currently unknown.

Methods :

A case control study (2015-2017) was performed to identify sources and risk factors for acute HEV infections in the Netherlands. A questionnaire on potential risk factors for HEV exposure, health and socio-demographics was completed by 376 patients with laboratory-confirmed (HEV serology IgM and/or PCR positive) acute hepatitis E, and 1534 population controls matched for age, gender and region of residence.

Results:

Patients with acute hepatitis E were more likely than population controls to report consumption of traditional Dutch dry raw pork sausages which are generally consumed sliced unheated on bread: “cervelaat” (aOR 2.0; 95%CI 1.4-2.7), “sliced sausage” (aOR 1.9; 95%CI 1.3-2.6), “farmer sausage” (aOR 1.8; 95%CI 1.3-2.4). 72% of patients reported consumption of at least one of these dry raw pork sausages, compared to 46% of controls (aOR 3.0; 95%CI 2.2-4.1). Working with a septic tank was a risk factor (aOR 6.9; 95%CI 1.2-40.8), reported by 4 patients and 4 controls. Patients reported more comorbidity such as preexisting liver disease (aOR 3.8; 95%CI 2.0-7.1) or diabetes (aOR 2.1; 95%CI 1.4-3.2).

Conclusions:

Consumption of several dry raw pork sausages seems to be the prominent transmission route of HEV from pigs to humans. The prevalence and infectivity of HEV in these products should be investigated, as well as the production methods and origin of HEV-contamination within these sausages, e.g. small amounts of pork liver. Although not frequently reported, contact with contaminated water was a risk factor.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Hepatitis E, Risk Factors, Zoonoses, Netherlands

ABSTRACT ID: 197

PRESENTED BY: Anna Tulen / lola.tulen@rivm.nl

11.2. Risk factors for autochthonous Hepatitis E in Germany

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Background:

Notified cases of Hepatitis E have increased 40-fold during the last 10 years in Germany. While it is known that the consumption of undercooked pork and pork products is an important risk factor for symptomatic infections, it is unclear which specific food items and non-alimentary exposures play a role. The objective of this study was to assess risk factors for autochthonous hepatitis E in Germany.

Methods:

We conducted a case-control study using symptomatic hepatitis E cases reported to local health departments between 01/2012 and 01/2014 and population controls individually matched on sex, age group and area of living (4:1). Demographic, clinical and exposure data within two months before disease onset were collected in semi-standardised telephone interviews. Univariable and stepwise conditional logistic regression analysis (cutoff: $p<0.05$) were used to calculate matched odds ratios (mOR).

Results:

In total, 270 cases and 1168 controls were included in the analysis (mean age 53 years and 61% men in both groups). Exposures associated with disease in the final model were consumption of undercooked pork liver, pork meat and wild boar meat, frankfurters and liver sausage, raw vegetables and occupational contact with waste water [all mORs between 1.9 and 5.5, p-values<0.03]. Various host factors, such as pre-existing liver disease, were also significantly associated with disease.

Conclusions:

Consumption of various pork products, including items that are specifically marketed as ready-to-eat appear to be the main risk factor for autochthonous hepatitis E in Germany but host factors may greatly modify this risk. A review of existing consumer recommendations and production methods may be indicated. The role of boiled sausages and raw vegetables needs further research.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: hepatitis E, epidemiology, risk factors, zoonosis, foodborne infections

ABSTRACT ID: 349

PRESENTED BY: Mirko Faber / faberm@rki.de

11.3. Emergence of Hepatitis E virus in Belgium, 2010-2016

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Background:

Indigenously acquired hepatitis E virus (HEV) infections, mostly of genotype 3, have increased in the last decade in many European countries. In a 2011 Belgian study in swines, 3f was the predominant subtype. Little is known about main HEV subtypes circulating in humans and how they spread in Belgium. To better understand them, we describe the epidemiological trends of HEV infections since 2010, with a focus on phylotype dynamics.

Methods:

We used molecular and epidemiological data from the National Reference Centre (NRC). Suspected patients were patients for whom clinicians requested either HEV serology and/or HEV polymerase chain reaction (PCR). Confirmed cases were IgM- and/or PCR-positive individuals. We targeted a stretch of 348 nucleotides within HEV ORF2 genomic region using Sanger sequencing.

Results:

HEV incidence increased from 0.23 (2010), to 0.74 per 100,000 inhabitants (2016). The confirmation ratio (confirmed cases/suspected patients) dropped from 8.1% (2010) to 3.4% (2014), and increased again to 4.8% (2016). Genotyping was performed on 148/306 PCR-positive samples (48.0%). Among those, 89.3% were genotype (G)3, followed by 8.8% of G1 and 1.3% of G4. G3 viruses were mainly 3f, 3c and 3e. G3c cases increased significantly, from one (2010) to 21 cases (2016), whereas other G3 subtypes remained stable or showed milder increase (3f).

Conclusions:

The continuous increase in reported suspected cases, together with an increasing laboratory confirmation ratio ,suggests an increased infection pressure from 2014 onwards in Belgium.

Sequencing analyses revealed that HEV phylotypes circulating in humans are similar to those infecting Belgian swines, possibly suggesting transmission to humans from pigs. Studies to detect HEV in food products are urgently warranted to shape recommendations for high risk groups (e.g. immunocompromised).

Subject: Surveillance

Keywords: hepatitis, zoonosis, surveillance, epidemiology, foodborne disease

ABSTRACT ID: 111

PRESENTED BY: Lorenzo Subissi / lorenzo.subissi@sciensano.be

Poster Abstracts

11.4. Relevance of sex ratio in the early detection of a foodborne hepatitis A outbreak in a context of epidemic among men who have sex with men, Bordeaux, France, June-July 2017

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Background:

In mid-July 2017, eight hepatitis A cases were notified over a single week to the health agency of Bordeaux, in the context of European epidemic among men who have sex with men (MSM). This increase of the notification associated to a balanced sex-ratio of 1 was suggestive of a distinct outbreak. We launched an investigation to identify all the cases, a common source, and to respond specifically.

Methods:

A case was defined as a person from the district of Bordeaux with hepatitis A associated with the VRD_521_V3 variant, and onset of symptoms in June or July 2017. The strain was a variant with a single nucleotide substitution of the prototype strain VRD_521_2016 found in the MSM epidemic. We used a standardized questionnaire to collect personal characteristics and exposures of the cases.

Results:

Eighteen cases were identified. The sex ratio was 1 and the mean age 41. Ten cases were hospitalized without complications. Twelve cases lived in neighbouring cities of Bordeaux. Among the 18 cases, sixteen had frequented the same restaurant, one identified himself as MSM, and one was without risk exposure. The index case, not interviewed, was a cook in the restaurant.

Conclusions:

We reported a foodborne hepatitis A outbreak in the general population. Strain description was essential for the case definition. The sex ratio proved to be a relevant surveillance indicator to detect this outbreak early in the context of the large epidemic among MSM. Furthermore, this outbreak was a public health opportunity to promote vaccination and hygiene among food handlers.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Hepatitis A, Disease Outbreaks, Sex Ratio, Genotype, Homosexuality

ABSTRACT ID: 396

PRESENTED BY: Yann Lambert / patrick.rolland@santepubliquefrance.fr

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11.5. Improving preparedness to respond to cross-border hepatitis A outbreaks in the European Union/European Economic Area: towards comparable sequencing of hepatitis A virus

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Background:

Sequence-based typing of hepatitis A virus (HAV) is an important tool for outbreak detection, investigation and surveillance. To promote harmonised procedures, better preparedness for outbreak investigations and effective response to multi- country outbreaks, the European Centre for Disease Prevention and Control (ECDC) mapped HAV sequencing and related surveillance practices in 2014 and 2016.

Methods:

In 2014 and 2016, ECDC sent two on-line surveys to public health institutes or their collaborating centres in EU/EEA countries to identify molecular surveillance procedures and to assess progress in HAV sequencing and related surveillance practices. The responses of the EU/EEA countries were compared and analysed descriptively.

Results:

In 2014, 23/30 EU/EEA countries participated, compared to 27/30 in 2016. For the 23 countries participating in both surveys, 14 procedural instances of progress were observed when comparing responses received in 2016 with those from 2014. In 2016, three additional countries reported central collection and storage of their HAV samples (n=15), and introduced a referral system (n=14). Two more countries started sequencing of HAV samples (n=17). Variation existed in laboratory sequencing practices, particularly in amplicon length, but all countries sequenced an overlapping fragment in the VP1-2a region, as proposed in the HAVNet protocol. Two more countries initiated collaborations with the food sector (n=13) and four more countries joined HAVNet (n=15).

Conclusions:

The survey results demonstrate that many EU/EEA countries have a good capacity for sequence-based typing of HAV and progress towards preparedness for effective response to HAV threats has been made. Still, typing practices are variable. To fully utilize sequencing techniques for strengthening preparedness and accelerating public health responses, EU/EEA countries should consider fully harmonising the amplified regions and enhance collaboration across sectors.

Poster Abstracts

Subject: Preparedness

Keywords: Hepatitis A virus, Sequence Analysis, European Union, Surveys and Questionnaires, Foodborne Diseases, Capacity Building

ABSTRACT ID: 407

PRESENTED BY: Theresa Enkirch / theresa.enkirch@gmail.com

11.6. Echovirus type 6 transmission clusters in the Netherlands and the role of environmental surveillance in early warning

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Background:

Echovirus type 6 (E6) is one of the most frequently detected enterovirus serotypes in Europe and is associated with meningitis outbreaks. In the Netherlands, it is identified through clinical and environmental enterovirus surveillance (CEVS and EEVS). We aim to identify E6 transmission clusters and to assess the role of EEVS in surveillance and early warning of E6, in order to inform control activities.

Methods:

We included all E6 strains identified from CEVS and EEVS, from 2007 to 2016. CEVS samples were from patients with enterovirus-like illness. EEVS samples came from sewage water of pre-specified sampling points. E6 strains were described by month and 4-digit postal code. Phylogenetic E6 clusters were detected using pairwise distances in genetic VP1 sequences. We identified transmission clusters using a combined pairwise distance in time, place and phylogeny dimensions.

Results:

E6 was identified in 157 of 3,506 CEVS clinical episodes and 92 of 1,067 EEVS samples. Increased E6 circulation was observed in 2009 and from 2014 onwards. Eight phylogenetic clusters were identified; five included both CEVS and EEVS strains. Among these, identification in EEVS did not consistently precede CEVS. One cluster was dominant until 2014, but genetic diversity increased thereafter. Of fourteen identified transmission clusters, six included both EEVS and CEVS; in two of them, EEVS identification preceded CEVS identification. Transmission clusters were consistent with phylogenetic clusters, and with previous outbreak reports.

Conclusions:

Algorithms using combined time-place-phylogeny data allowed identification of clusters not detected by any of these variables alone. EEVS identified strains circulating in the population, but EEVS samples did not systematically precede clinical case surveillance, limiting EEVS usefulness for early warning in a context where E6 is endemic.

Subject: Surveillance

Keywords: enterovirus, environmental surveillance, Echo-6, cluster detection

ABSTRACT ID: 32

PRESENTED BY: Susana Monge / susana.monge@rivm.nl

Track 12: Food- and waterborne diseases and zoonoses (4): Epidemiology and Outbreaks 1

Moderator:

Giri Shankar

Abstracts

12.1. An outbreak of toxin-producing Clostridium perfringens following a Mother’s day lunch, UK, March 2018

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Background:

In March 2018 approximately twenty cases of gastrointestinal illness were reported among diners who had eaten a Mother’s Day lunch served at the same restaurant in Yorkshire, UK. We investigated to describe the outbreak, determine the source of infection and to implement control measures.

Methods:

A retrospective case-control study was performed. A case was defined as an individual with diarrhoea within 3 days after eating the Mother’s day lunch. A control was defined as an individual who had eaten the Mother’s day lunch but had not experienced diarrhoea. Environmental inspection and microbiological sampling of cases, the kitchen environment and food leftovers was undertaken. All individual food items listed on the set lunch menu were considered as potential sources of infection. An online questionnaire was used to collect information. Single variable and multivariable analysis was undertaken.

Results:

A total of 32 cases were identified with eight confirmed as toxin-positive Clostridium perfringens. Environmental investigation identified that the beef served for the lunch did not reach acceptable temperatures during the cooking process and was held at a warm temperature prior to service. Enterotoxigenic C. perfringens isolated from the beef was genetically indistinguishable from that isolated from human samples by molecular typing. Beef was identified as the most likely source of exposure (odds ratio 12.2, 95% confidence interval 3.3–47.9; $p<0.01$).

Conclusions:

The results of this investigation strongly indicate that the beef was the probable source of infection. The combination of epidemiological, environmental and microbiological findings all contribute to the confidence of this finding. Evidence from the investigation enabled effective communication to the restaurant and assurance that beef would be cooked and stored appropriately in the future.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Clostridium perfringens, case-control,outbreak

ABSTRACT ID: 357

PRESENTED BY: Mary Cronin / mcb.cronin@gmail.com

12.2. Non-foodborne outbreak of acute gastroenteritis among German guests in a self-catering youth accommodation in Austria, March 2017

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Background:

In March 2017, a school group of 51 students and 16 adults from North Rhine-Westphalia (Germany) visited Austria and stayed in self-catering accommodation. During the trip, over half of participants experienced acute gastroenteritis. We investigated the outbreak to identify the source of infection, and to derive recommendations for prevention of illness on school trips.

Methods:

A case was defined as a participant of the school trip, who experienced vomiting or diarrhea from 13 March. We conducted a retrospective cohort study collecting information on clinical symptoms, food consumption and risk exposures using a self- administered online questionnaire. We calculated attack rates (AR) and risk ratios. Stool samples of some hospitalised cases were analysed.

Results:

Of the 44 participants who completed the questionnaire, 35 met the case definition (AR=80%). 27 were students (AR=61%) and 8 were adults (AR=80%). The predominant symptom was vomiting (91% of cases). Of the 16 cases hospitalised, norovirus was confirmed in four stool samples. Investigators learned that on the second day of the trip, a student vomited in a corridor connected to several rooms; the outbreak peaked two days later, at which point ill members of the group were separated from the well. The questionnaire responses did not reveal a significant food exposure or another risk factor.

Conclusions:

A foodborne source was unlikely in this outbreak. The presumed vehicle was rapid and extensive spread of norovirus after the first case vomited on the premises. We recommended immediate separation of participants with symptoms of gastroenteritis. Responsible adults should contact local health authorities directly, for the earliest possible implementation of control measures. Furthermore, we recommend training of adult chaperones on appropriate response to gastroenteric infections, and control measures.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Disease outbreaks, Norwalk Virus, Cohort studies, Students, Prevention and control

ABSTRACT ID: 44

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

12.3. First reported outbreak of enteroinvasive Escherichia coli O96:H19 in Sweden

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Background:

In mid-November 2017, a local Public Health Authority was notified that more than 20 individuals had developed severe diarrhoea after attending a conference venue in Halland county, Sweden. An outbreak investigation was initiated to identify the causative pathogen and prevent further transmission.

Methods:

Persons attending the venue from November 8-10 were invited to complete an online questionnaire to identify food exposures. Cases were visitors and staff, who had consumed food at the venue and subsequently experienced gastrointestinal illness. Stool samples were collected by local healthcare providers and analysed by PCR for enteric pathogens.

Results:

Of 554 potential respondents, 398 (72%) replied; 83 reported gastrointestinal symptoms. Women had higher attack rates than men (24.6% versus 15.6%, RR 1.58 p=0.029). Attendees at lunch November 9th had highest risk for illness (RR 3.02, 95%CI: 1.51-6.04). Leafy greens (rocket, baby spinach and mixed salad) were included in 8/8 of the food items with the highest risk ratios for illness (RR 1.47 to 1.96). Local food authorities conducted traceback of leafy greens, but none of these food items were available for testing.

Five stool samples were PCR-positive for the ipaH gene, and whole genome sequencing of three isolates indicated O96:H19 enteroinvasive E. coli (EIEC) with ST99.

Conclusions:

This is the first time EIEC has been associated with an outbreak in Sweden; epidemiological results suggested leafy greens as the source. The same serotype and sequence type were reported from outbreaks in Italy in 2012 and the United Kingdom in 2014, with vegetables implicated as the vehicle. In Sweden, EIEC has been considered a travellers' disease, but this outbreak shows that EIEC should be considered in domestic outbreaks of gastroenteritis.

Poster Abstracts

Subject: 121

Keywords: Field epidemiology (e.g. outbreak investigations)

ABSTRACT ID: EIEC, outbreak investigation, E. coli

PRESENTED BY: Emma Löf / emma.lof@folkhalsomyndigheten.se

12.4. Multi-country outbreak of listeriosis due to Listeria monocytogenes, multi-locus sequence type 6, infections probably linked to frozen corn, European Union 2015–2018

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Background:

On 3 November 2017, Finland reported on the Epidemic Intelligence Information System (EPIS) a national human cluster of Listeria monocytogenes (Lm) since 2016, verified by whole genome sequencing (WGS). The later verification of a multi- country outbreak by WGS triggered the European Union (EU)-wide investigation to find the source.

Methods:

Confirmed outbreak cases were defined as patients with symptom onset since 01/01/2015 and with Lm isolate ≤7 allelic differences from the representative Finnish outbreak strain using core genome multilocus sequence typing (cgMLST). National standard questionnaires were used for patient interviews. Non-human Lm isolates matching the outbreak strain were searched to perform a joint cgMLST analysis, and food tracing back/forward exercises were performed at EU level.

Results:

Between 01/12/2015 and 31/03/2018, 42 cases were detected in five countries; in Finland (n=20), United Kingdom (n=9), Sweden (n=7), Denmark (n=4) and Austria (n=2). Fifteen cases were hospitalised and eight were fatal. Five food isolates (three from frozen corn and two from frozen vegetable mixes with corn) and one environmental Lm isolate matching the outbreak strain were detected in Austria, Finland, France and Sweden (2016–01/2018). The only common food item in these samples was corn. Corn exposure was not investigated in all national questionnaires. After new and re-interviews, 10/18 cases recalled consumption or possible consumption of corn. Preliminary traceability of the food/environmental samples pointed to a common origin in Hungary.

Conclusions:

This multi-country outbreak highlights the importance of cross-sectoral collaboration in particular to identify unusual source of outbreaks. It emphasized the value of WGS for hypothesis generation. Standard listeriosis questionnaires should capture information on vegetable consumption including corn. Further investigations are needed to verify the contamination point in the food chain.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Listeria monocytogenes, Listeriosis, Disease Outbreaks, Foodborne Diseases, Whole Genome Sequencing, Corn

ABSTRACT ID: 109

PRESENTED BY: Margot Einöder-Moreno / Margot.Einoder-Moreno@ecdc.europa.eu

12.5. Outbreak Investigation of Shigellosis Diarrhoea in Baudh District of Odisha-India 2016

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Background:

Background: Shigellosis is endemic in developing countries, estimated to cause 80 million cases of bloody diarrhoea including 0.7 million deaths annually. Odisha has reported four shigellosis outbreaks in year 2014-2015. In May 2016, an outbreak of shigellosis diarrhoea was reported in Baudh district, Odisha. We investigated the outbreak to identify risk factors and recommend control measures.

Methods:

Methods: We defined a case as diarrheal illness (› 3 loose stools per day) in a person in Baunsuni village from May 1 – 15, 2016 We conducted active surveillance through house to house survey and conducted a 1:2 unmatched case control study to assess risk factors. We defined a control as a person staying at least two houses from a case without diarrheal illness. Faecal swabs and water specimen were collected and processed for culture at Regional Medical and Research Centre laboratory, Bhubaneswar.

Results:

Results: We identified 70 cases (60% female; median age 30 years [range 8-75 years]) with an attack rate of 3%. Consumption of overnight stored water rice (OR = 15, 95% CI = 4.76 – 47.21), fish (OR = 3.07, 95% CI = 2.25-4.19) and green leafy vegetables (OR = 3.1, 95% CI = 2.25-4.19) were risk factors associated with shigellosis. Two of four faecal specimens showed Shigella flexneri growth. E coli was isolated in all water specimens indicating fecal contamination. All specimens were negative for Salmonella and Vibrio species.

Conclusions:

Conclusion: This outbreak could be associated with food borne transmission and water contamination. Personal hygiene, frequent handwashing and proper food handling practice should be stressed among household to reduce food borne transmission. Improved water storage with disinfection could reduce future potential outbreaks

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Shigella, Odisha, India

ABSTRACT ID: 5

PRESENTED BY: Priyakanta Nayak / priyakantanayak@gmail.com

12.6. Large outbreak of human campylobacteriosis linked to domestic chicken production, Sweden 2016-2017

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Background:

From September 2016 to May 2017, 6612 domestic campylobacteriosis cases were reported in Sweden, compared to an annual average of 3440 cases in 2009-2013. Laboratory investigation indicated Swedish broilers as the source. After the outbreak, we used surveillance data to quantify the number of cases attributable to the outbreak, and identify differences in demographics and severity of illness during the outbreak compared to endemic periods, to inform ongoing disease control activities.

Methods:

We included domestic campylobacteriosis cases reported in Sweden, with onset from March 2009 to February 2018. Time series were used to predict monthly number of cases in 2016-2017, by modeling data from an endemic period (2009-2013). Outbreak duration and magnitude were estimated by comparing predicted and observed number of cases. We compared case demographics (age, gender) for the endemic and outbreak periods. We retrieved information on mortality within 30 days after onset, and calculated standardized mortality ratios (SMR) with 95% confidence intervals (95%CI) for the endemic and outbreak periods, using Swedish population mortality as reference.

Results:

The outbreak lasted from August 2016 until May 2017, and caused 5147 excess cases. More women were affected (48% versus 44%, p-value<0.001), and cases were older (mean age of 47 versus 42 years, p-value<0.001) during the outbreak compared to the endemic period. SMR were similar for both periods (2.2 [95%CI:1.1-3.8] and 2.2 [95%CI:1.4-3.4]).

Conclusions:

We estimated that 5147 cases above the endemic baseline were attributable to the outbreak, but mortality in excess of endemic levels was not observed. Our results reinforce the importance of maintaining low levels of Campylobacter colonization in the broiler production industry, and will be used to estimate the disease burden and cost of the outbreak.

Subject: Burden of disease

Keywords: campylobacteriosis, domestic,time series analysis

ABSTRACT ID: 13

PRESENTED BY: Fanny Chereau / fanny.chereau@free.fr

Track 13: Healthcare-associated infections (1): Epidemiology and Surveillance

Moderator:

Sophie Gubbels

Abstracts

13.1. An outbreak of adenoviral keratoconjunctivitis in a hospital setting, Slovenia, August – October 2017

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Background:

On 30th August 2017, the National Laboratory reported an increased number of conjunctival swabs with isolated adenovirus to the National Institute of Public Health. Swabs were taken in the Ophthalmology Department (OD) of the University Medical Centre Maribor. An investigation was initiated to determine the scope and source of a possible outbreak and implement control measures.

Methods:

We defined a primary case as any person with clinically diagnosed keratoconjunctivitis or laboratory-confirmed adenovirus keratoconjunctivitis, with a previous hospitalisation or outpatient examination in the OD, from 1st August. Secondary cases had an epidemiologic link to a primary case. We reviewed available medical records of all cases. Conjunctival swabs were tested for adenovirus with RT-PCR, with subtyping on selected positive samples. Hand swabs had been requested previously from healthcare workers (HCW) to detect bacterial contamination. We reviewed infection control procedures in the OD.

Results:

We identified 63 cases (50 primary, 13 secondary) starting 9th August, peaking 18th August and ending 7th October. 41/43 conjunctival swabs tested positive for adenovirus. Subtyping of 7 isolates showed subtype HAdV-8. A HCW in the OD was identified as the possible index case. Hand swabs from HCWs taken 17th-31st August showed heavy bacterial contamination. Control measures (changing hand disinfectant, cohorting outpatients, using single-use eye drops) were implemented. After hand hygiene training 12th September, no HCW hand swabs showed heavy contamination. The outbreak was declared over 22nd October.

Conclusions:

This is the first reported outbreak of adenoviral keratoconjunctivitis in a hospital setting in Slovenia. To prevent future outbreaks, the hospital was advised to immediately exclude any HCW with keratoconjunctivitis from work and implement control measures. Supplementary hand hygiene training may have contributed to containment of the outbreak.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: adenovirus, adenoviral keratoconjunctivitis, outbreak, hospital setting, Slovenia

ABSTRACT ID: 132

PRESENTED BY: Sanja Vuzem / sanja.vuzem@nijz.si

13.2. Nosocomial Staphylococcus aureus bloodstream infections in Finland, 1999-2017

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Background:

Staphylococcus aureus (SA) is one of the most common pathogens causing bloodstream infections (BSI) in Finland, and the burden of SA-BSI has continuously increased. SA-BSIs are known to be often healthcare-associated and thus potentially preventable. We analyzed the Finnish Hospital Infection Program data regarding nosocomial SA-BSIs to identify patient groups at risk and to better target prevention strategies for BSIs.

Methods:

Hospital-wide surveillance data on nosocomial BSIs from 1999-2017 were reviewed. We assessed annual overall BSI and SA-BSI rates, and risk factors for SA-BSI. BSIs with an identified infection focus other than vascular lines were categorized as secondary, and the rest primary.

Results: We identified a total of 23,247 BSIs (0.49 BSIs/1,000 patient-days). Of those, 3,944 (17%; proportion by year, 11-21%) were caused by SA (0.08 SA-BSIs/1,000 patient-days); 1,846 (47%) were primary SA-BSIs. Of all patients with SA-BSIs, 82% were treated outside of intensive care units (ICU) and 30% had a central vascular catheter (CVC). We identified preceding surgery (RR 1.13; CI95%, 1.07-1.20) and chronic haemodialysis (RR 2.58; CI95%, 2.42-2.75) as risk factors for SA-BSI. Of the patients with secondary SA-BSIs, 59% had preceding surgery. Haemodialysis (RR 3.22; CI95%, 2.98-3.49) increased risk also for primary SA-BSI; surgery (RR 0.75; CI95%, 0.68-0.82) , CVC use (RR 0.76; CI95%, 0.70-0.83) and ICU care (RR 0.87; CI95%, 0.80-0.97) seemed to decrease the risk for primary SA-BSIs.

Conclusions: SA-BSIs were common in non-ICU wards and in patients without CVCs. Peripheral lines might act as a source for SA-BSI, and since they are very commonly used, cause a significant burden of SA-BSI. The implementation of infection prevention guidelines regarding vascular catheters, covering also peripheral lines, should be reinforced in non-ICU wards.

Subject: Surveillance

Keywords: bloodstream infection, staphylococcus aureus, nosocomial, vascular line

ABSTRACT ID: 368

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13.3. Specific characteristics of healthcare-associated infection (HAI)-outbreaks - results from the national surveillance system in Germany, 2012-2017

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Background:

In Germany an estimated 400.000-600.000 inpatients are affected by healthcare-associated infections (HAIs) annually. Since 2011, Germany has been collecting nationwide surveillance data on HAI-outbreaks, which we analysed to better understand the burden and characteristics of inpatient HAI-outbreaks for improving prevention strategies.

Methods:

The surveillance system contains information on cases, fatalities, pathogens, antimicrobial resistance (AMR, as defined by the local public health authority) and ward type. We included all outbreaks affecting ≥2 inpatients that were reported 2012-2017. We stratified data by pathogen type and ward. We used chi-square and Fisher‘s exact tests.

Results: A median of 909 HAI-outbreaks [range 489-1,121] comprising 6,591 inpatients [range 5,213-8,598] were reported annually. Overall, 80.1% (3,867/4,830) of HAI-outbreaks were caused by viruses, 16.1% (778/4,830) by bacteria and 3.8% (185/4,830) by other pathogens. Outbreak with bacteria included fewer persons than those with viruses (median 4 [2-76] vs. 6 [2-136], $p<0.05$), but case fatality was higher (7.1% vs 0.3%, $p<0.05$). 239(39.9%) of bacterial HAI-outbreaks occurred in adult intensive care units (ICUs), 163 (27.1%) in non-intensive care units (non-ICUs) and 67 (11.2%) in neonatal ICUs (NICUs). Mainly reported outbreak-pathogens were Clostridium difficile (49.1%) and methicillin-resistant Staphylococcus aureus (MRSA, 23.3%) in non-ICUs, MRSA (19.7%) and vancomycin-resistant Enterococci (15.9%) in ICUs, and carbapenem-resistant Klebsiella pneumoniae and MRSA in NICUs (both 13.4%). Overall proportion of AMR outbreak-pathogens increased from 40.7% (2012) to 62.1% (2017) ($p<0.05$).

Conclusions: HAI-outbreaks cause a considerable disease burden in Germany. Early case detection during bacterial HAI- outbreaks and rapidly implemented infection control measures adapted to pathogen spectrum in different ward types could decrease transmission and case fatality. High proportion of AMR outbreak-pathogens and its increase over time suggests that further research is needed to explore preventive options.

Poster Abstracts

Subject: Surveillance

Keywords: surveillance,healthcare-associated infections,outbreaks

ABSTRACT ID: 395

PRESENTED BY: Gyde Steffen / steffeng@rki.de

13.4. Possible underreporting and misclassification of healthcare-associated Legionnaires' disease cases in the EU/EEA

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Background:

Healthcare-associated Legionnaires' disease (HALD) is a known cause of pneumonia outbreaks. LD surveillance in the European Union and the European Economic Area (EU/EEA) countries is based on passive reporting which is prone to underreporting. This study aimed to assess the extent of possible HALD underreporting to ECDC by matching cases collected through different data sources.

Methods:

We compiled HALD cases reported to three modules of the Healthcare-Associated Infections Surveillance Network (HAI- Net): the Point prevalence surveys (PPSs) of healthcare-associated infections (HAIs) in acute care hospitals of 2011–12 and 2016–17, the PPSs of HAIs in long-term care facilities of 2010, 2013 and 2016–17 and the surveillance of HAIs in intensive care units (ICUs) for 2008–16. We matched these cases with European Legionnaires' disease surveillance network (ELDSNet) data for 2008–17 on country, age, and sex. We defined cases as probable match when onset dates matched and as possible match if onset dates were less than 15 days apart.

Results:

Of the 32 HALD cases identified in HAI-Net data, 18 (56.3%) could not be matched with ELDSNet data and 14 (43.7%) matched with 30 cases in ELDSNet data, of which 29 (96.7%) were possible matches and one (3.3%) a probable match. Of the 14 matched cases in HAI-Net data, 12 (85.7%) were identified in ICUs participating in HAI-Net and two (14.3%) in acute care hospitals participating in the PPS. Of the 30 cases in ELDSNet data, four (13.3%) were reported as HAI.

Conclusions:

Most LD cases captured by HAI-Net were not in ELDSNet data, suggesting substantial underreporting of HALD in ELDSNet. We will further explore the identified matches to confirm possible misclassification of cases.

Subject: Legionnaires' disease; Surveillance; Healthcare; Europe

Keywords: Surveillance

ABSTRACT ID: 432

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13.5. Epidemiology and risk factors of community-associated Clostridium difficile infections in Northern Ireland, 2012-2016

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Background:

Community-associated Clostridium difficile infection (CA-CDI) represents almost half of all CDI in Northern Ireland, yet the understanding of the epidemiology of these infections is limited. We aimed to identify risk factors for CA-CDI for future interventions.

Methods:

We used population-based surveillance data from 2012-2016 to describe socio-demographic factors and outcome (mortality) for all CA (hospital onset <=2 days after admission or community onset >4 weeks after hospitalisation, n=1303) and hospital-associated (HA, community onset within 4 weeks after hospital discharge or hospital onset >2days following hospitalisation, n=1356) CDI. Of these, 483 CA- and 287 HA-CDI cases with disease community onset were routinely administered a paper questionnaire on potential risk factors (socio-demographic, healthcare contact, selected medication use, travel history, and infant contact); the data were used for a case-case study. We used logistic regression models for univariate and multivariable analysis.

Results:

Compared to HA-CDI, CA-CDI cases had higher odds of being female (AOR 1.4, CI 1.15-1.73; $p<0.001$), and living in rural rather than urban settlement (AOR 1.5, 95% CI 1.1-2.1; $p=0.05$). CDI-specific death within 30 days was lower in CA-CDI than HA-CDI (7% vs. 11%, $p<0.001$). There was no statistically significant difference between CA and HA-CDI for most risk factors, such as gastric acid suppressants use and antimicrobial therapy in the four weeks prior to CDI (50% vs. 55%, $p=0.11$ and 18% vs. 20%, $p=0.5$, respectively).

Conclusions: CA-CDI cases are more likely to be female and live in rural settlements. However, our analysis of community onset cases suggests that risk factors for HA-CDI may be equally important for CA-CDI. Opportunities to safely reduce antibiotic and gastric acid suppressants use should be investigated in all healthcare settings.

Subject: Surveillance

Keywords: Clostridium difficile, community-associated infections, hospital-associated infections,enhanced surveillance

ABSTRACT ID: 15

PRESENTED BY: Anna Maisa / anna.maisa@gmail.com

Poster Abstracts

13.6. Sex/gender analysis within Cochrane reviews of medical device related infections

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Background:

The use of medical devices such as catheters, mechanical ventilators, and gastric tubes, among others commonly leads to healthcare-associated infections (HAIs). These HAIs increase morbidity, mortality and healthcare costs and their control continues to be an unresolved issue worldwide. Evidence suggests that medical device infections show sex/gender differences (SGBA), but these differences are not considered in studies. We aim to describe the extent to which sex/gender based analysis (SGBA) is considered in Cochrane reviews of medical device related infections in the healthcare setting.

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 medical device related infections. 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 35 included reviews showed that SGBA was insufficient. The reviews met very few SGAT- SR criteria. Sex and gender terms were used interchangeably in the included reviews. The background described the relevance of sex/gender to the review question in 6/35 (17%) reviews. The inclusion/exclusion criteria for studies in the reviews never considered sex/gender differences. Data were never disaggregated by sex. There were subgroup analyses by sex completed in only 3/35 (9%) reviews, and only 2/35 (6%) reviews highlighted any sex/gender differences as research gaps.

Conclusions:

SGBA is absent in Cochrane reviews on prevention of medical device related 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.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: medical devices,sex,gender,cochrane,health infections

ABSTRACT ID: 204

PRESENTED BY: Abelardo Fernández Chávez / elenastallings.pubhealth@gmail.com

Track 14: Sexually transmitted infections (2), HIV and Viral Hepatitis: Surveillance

Moderator:

Gianfranco Spiteri

Abstracts

14.1. Identifying missed opportunities for HIV testing to address late diagnosis of HIV in the East of England

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Background:

Reducing the number of people diagnosed at a late stage of HIV infection is a key public health priority in England. In the East of England the proportion of new HIV diagnoses considered late (defined as having a CD4 count <350 cells/mm3 at diagnosis) is significantly higher than the England average.

Implementation of existing HIV testing guidelines is a crucial element in tackling late HIV diagnosis. Utilising national guidelines, we created a HIV dashboard to identify missed opportunities for testing.

Methods:

Key indicators were chosen from the 2016 NICE guidance and populated using national data sources and local intelligence, with values categorised as red, amber or green (from worse to better).

Data were provided at local authority, East of England and national levels to highlight variation in practice and provide benchmarking to facilitate improvement.

Gaps in the offer and coverage of HIV testing were highlighted.

Results:

Eleven key indicators were chosen for inclusion in the dashboard.

Potential missed opportunities for HIV testing were identified in two key settings. Within specialist sexual health services HIV testing coverage ranged from 69% to 86% with variation by population group, and within tuberculosis services ranged from 13% to 100%.

The dashboard was presented at a meeting of the East of England local authority sexual health commissioners and further work was agreed to investigate the variation in these settings in more detail (results to be presented).

Conclusions:

The HIV dashboard has proven useful for highlighting areas where local authorities are doing well and where there is room for improvement.

The dashboard should be used for systematically tracking key indicators, with the results presented regularly at appropriate meetings leading to suitable public health action.

Subject: Surveillance

Keywords: HIV,Delayed Diagnosis,Public Health,Sexual Health

ABSTRACT ID: 166

PRESENTED BY: Ashley Popay / ashley.popay@phe.gov.uk

14.2. Laboratory results of HIV-syphilis co-infection in Bavaria 2010-2017

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Background:

HIV and syphilis are both sexually transmitted diseases (STD) associated with similar risk factors. Moreover, syphilis may increase the risk of HIV acquisition by causing genital ulcers, while HIV could affect the presentation, diagnosis, disease progression and therapy of syphilis. Both are anonymously notifiable directly to the Robert Koch Institute (RKI) with the voluntary inclusion of co-infections. The HIV co-infection among syphilis notification was 4.7 % and 6.3 % in 2014 and 2015, respectively. The aim of the study was to investigate the extent of the underreporting of co-infections, by analyzing routine laboratory tests performed at the Bavarian Health and Food Safety Authority (LGL).

Methods:

All serum samples tested for HIV and/or syphilis at the LGL 2010-2017 were analysed, excluding samples from asylum- seeker screening, material of inadequate quality, quality assurance samples, and duplicates within 4 weeks. Positivity, notification and co-infection rates were calculated using STATA 12.

Results:

Out of 290 000 samples 51-55% were from Local Health Authorities (LHA) and 44-47% from penitentiaries. All were tested for HIV and 30% for syphilis. Samples from penitentiaries were significantly more often tested for syphilis, but more syphilis- samples from LHA were positive. Due to low numbers varied the co-infection rate over the years (2.78-12.12%). Underreporting in at least 4 years was evident. No difference in co-infection rates among LHA and penitentiaries was observed.

Conclusions:

Both LHA and penitentiaries had 2010-2017 higher co-infection compared to the notified rates for 2014 or 2015, and in individual years the laboratory-based co-infection rate in Bavaria could be twice as high. We would recommend a higher uptake of syphilis laboratory tests, especially during STD consultation hours at the LHA and for patients diagnosed with HIV.

Subject: Surveillance

Keywords: HIV,syphilis,co-infection,underreporting

ABSTRACT ID: 221

PRESENTED BY: Durdica Marosevic / djurdjica.marosevic@gmail.com

14.3. Evaluation of the hepatitis B enhanced surveillance system in Ireland

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Background:

Enhanced surveillance for hepatitis B cases in Ireland was established in 2005. It geographically covers all eight health service executive regions and is part of the electronic, national notifiable infectious disease surveillance system, CIDR. We aimed to evaluate the surveillance system focusing on; completeness, timeliness, acceptability and simplicity, identified by the surveillance team as important attributes.

Methods:

We extracted electronic information on all notified hepatitis B cases from 2012 to 2016 to evaluate data quality and timeliness (acute cases only). We used international sero-prevalence studies and census data to estimate the expected number of cases in Ireland, and we distributed an on-line questionnaire to stakeholders to evaluate the simplicity and acceptability of the system.

Results:

The system differentiates between acute and chronic cases with 97% of cases assigned appropriate disease status. Data completeness for chosen variables was better for acute cases (71%-95%) compared with chronic (32%-62%). Only 33% of acute cases were notified to the system within four days of laboratory result date while 29% had incorrect dates reported. Approximately 50%-57% of the expected number of hepatitis B cases was reported to the system. The majority of questionnaire respondents found the system acceptable (90%) and easy to use (69%), but suggested matching paper enhanced surveillance information exactly to electronic hepatitis B surveillance fields, having fewer fields to complete and removing duplicate fields.

Conclusions :

The hepatitis B surveillance system, while comprehensive, does not fulfil all of its objectives. We recommend improved reporting timeliness for acute cases, better data collection for chronic cases, implementation of existing hepatitis B screening guidance to ensure that notified cases are representative of hepatitis B in Ireland and streamlining the system as suggested by stakeholders.

Subject: Surveillance

Keywords: hepatitis B, surveillance,Ireland,communicable disease

ABSTRACT ID: 77

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Poster Abstracts

14.4. Foreign-born men who have sex with men at excess risk of infection during hepatitis A outbreak in Berlin 2017

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Background:

There have been numerous recent hepatitis A virus (HAV) outbreaks affecting MSM, with 4101 confirmed cases across 22 European countries (Jan'16-Nov'17). We investigated an outbreak in Berlin, (onset Nov'16) to determine factors associated with complete HAV vaccination and infection in MSM.

Methods:

Inclusion criteria were MSM, age $>=$18years and attending specialist primary healthcare (HIV/infectious disease). We collected information on cases (notified Nov'16-May'17) through detailed questionnaires. We conducted an anonymous cross-sectional survey to determine vaccination status in MSM attending specialist primary healthcare for any reason.

From the cross-sectional survey we calculated HAV vaccine coverage and conducted multivariable analysis for factors associated with complete HAV vaccination. We then compared the cross-sectional survey cohort to cases using multivariable analysis to identify associations with case-status.

Results:

There were 756 MSM in the cross-sectional survey, 32.0% (n=242) had complete and 34.8% (n=263) partial HAV vaccination. Complete HAV vaccination was less likely among foreign-born (aOR: 0.39, 95%CIs: 0.25-0.63; $p<0.001$) and more likely if hepatitis B (HBV) vaccination (aOR: 2.04, 95%CIs: 1.19-3.51; $p=0.01$) or HIV positivity (aOR: 1.83, 95%CIs: 1.22-2.75; $p=0.001$) was reported. There were 27 cases available for comparison. Cases were more likely to be foreign- born (aOR:5.08; 95% CIs:1.69-15.29; $p<=0.01$) and to report HBV vaccination but no HAV vaccination (compared to neither vaccination) (aOR:4.47; 95%CIs:1.17-17.06; $p<0.05$).

Conclusions:

MSM who were provided with HBV vaccination may represent a higher risk population and it is essential that MSM are routinely offered combined HAV and HBV vaccination. Physicians and MSM should be alerted to the need to review vaccination status and initiate or complete HAV vaccination. It is essential to tailor interventions to the needs of foreign-born both in terms of vaccination and infection prevention.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Vaccination, Hepatitis A, Outbreak

ABSTRACT ID: 340

PRESENTED BY: Janine Thoulass / j9ct@yahoo.co.uk

14.5. Can the observed increase of hepatitis B cases in Germany since 2015 be explained by screening of asylum seekers?

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Background:

Germany had experienced a peak of asylum seeker (AS) influx in 2015, mostly males <40 years from hepatitis B (HBV) intermediate and high endemic countries. Information on AS status has been collected in the surveillance system since 09/2015. Three federal states with 23% of the German population routinely screened for HBV among AS. We investigated the influence of the screening on HBV notifications to support interpretation.

Methods:

We compared HBV surveillance data from 2010-2013 (baseline) with 2015-2016 excluding 2014 due to the beginning of AS influx. Cases with provided AS status were defined as AS cases (ASC), all others as non-AS cases (non- ASC). Using Poisson regression, we estimated the increase above the mean HBV case number (baseline) for excess-non- ASC in 2015-2016. We calculated number of ASC and excess-non-ASC in 2015-2016 and their proportion by federal state. To estimate the extent of ASC misclassified as non-ASC, we compared baseline proportion of males <40 years with ASC and excess-non-ASC in 2015-2016 using chi-square-test.

Results:

HBV cases increased from 1,855 (mean baseline) to 3,873 (2015) and 3,466 (2016), with 869 (2015) and 1,034 (2016) ASC and 946 (2015) and 464 (2016) excess-non-ASC. Seventy-three percent of ASC and 57% of excess-non-ASC were notified in federal states with screening. Seventy percent of ASC (2015-2016; $p<0.01$) and 60% (2015; $p<0.01$) or 42% (2016; $p<0.01$) of excess-non-ASC were males <40 years compared to 20% (baseline).

Conclusions: Demographic and geographical distributions suggest that the increase of HBV cases is attributable to screening of AS to a higher extent than available surveillance data indicates. Therefore, completeness of AS information should be improved by raising awareness amongst clinicians and staff of notifying laboratories and local public health authorities.

Subject: Surveillance

Keywords: Hepatitis B, Refugees, Germany, Epidemiologic Surveillance

ABSTRACT ID: 231

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Track 15: Influenza, TB and other respiratory viruses (2): Vaccination and interventions

Moderator:

Louise Coole

Abstracts

15.1. Previous vaccination and viral genetic variation effects over the 2016-17 influenza vaccine in Spain

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Background: The Spanish 2016-17 influenza season was dominated by A(H3N2). We evaluated the effect of the previous vaccination over the 2016-17 Influenza vaccine effectiveness (IVE) in preventing mild and severe influenza, considering the genetic variation of the circulating A(H3N2)

Methods:

Using a case-control test-negative design, we estimated the IVE against mild influenza for all ages in primary healthcare (cycEVA study) and in influenza hospitalized elderly (IMOVE+ study). We evaluated IVE for those vaccinated only in 2016-17, only in 2015-16 and both seasons, using not vaccinated as reference. A(H3N2) strains were genetically characterized by analysing the hemagglutinin gene sequence

Results:

We recruited 1019 patients (602 cases) in cycEVA and 906 patients (337 cases) in IMOVE+, and characterized 342 and 99 strains, respectively. We grouped the identified mutations in antigenically less relevant (LRM) or potentially relevant mutations (PRM). IVE against mild influenza for those vaccinated only in 2016-17 and in both seasons was 86% (95%CI: 46; 97) vs. 33% (95%CI: -65; 73) (p=0.037) against LRM, and 79% (95%CI: 5; 96) vs. -22% (95%CI: -183; 48) (p=0.034) against PRM. For the same categories, IVE against severe influenza was 77% (95%CI: -5; 95) vs. 55% (95%CI: 17; 76) (p=0.396) respectively, against LRM and 80% (95%CI: -60; 98) vs. 39% (95%IC: -29; 71) (p=0.289) against PRM

Conclusions:

Against mild A(H3N2) influenza, we found a possible negative interference of the previous vaccination over the protective effect of the 2016-17 influenza vaccine, especially against PRM. Against severe A(H3N2) influenza in elderly, previous season vaccine did not interfere the current vaccine´s effect, disregard of the viral mutations. We underline the importance of influenza vaccination in elderly for preventing severe influenza, with a considerable impact in public health

Subject: Surveillance

Keywords: influenza vaccine, previous vaccination, influenza A(H3N2), viral mutations

ABSTRACT ID: 366

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15.2. Lower treatment completion among tuberculosis patients with diabetes in London, 2016-2017

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Background:

Diabetes is a known risk factor for poor outcomes for patients with tuberculosis (TB). We aimed to characterise patients with diabetes and determine the effect of diabetes on tuberculosis treatment completion.

Methods:

We conducted a retrospective cohort study of adult patients notified to the London Tuberculosis Register in 2016 and 2017. Characteristics of patients with diabetes were compared with other TB patients. We performed logistic regression with treatment completion at 12 months since notification as the outcome, adjusting for demographic characteristics, social risk factors, and the use of directly observed therapy. Patients with drug-resistant or central nervous system/miliary disease were excluded from all analysis of outcomes.

Results:

Of 4,322 TB patients, 10% (435) had diabetes. Compared to those without, patients with diabetes were older (median age 60 versus 36 years), more likely to be born outside the UK (87% versus 79%), more likely to be of South Asian ethnicity (50% versus 36%), and less likely to be of black African ethnicity (11% versus 22%).

At 12 months, patients with diabetes were less likely to have completed treatment (76% versus 88%), and more likely to have died (9.5% versus 2.4%) or stopped treatment (3.3% versus 1.0%).

We included 2,497 patients in the regression model, of whom 11% (268) had diabetes. Patients with diabetes had higher odds of not completing treatment at 12 months compared to those without (odds ratio 1.5, 95% confidence interval 1.1 to 2.2).

Conclusions:

Diabetes is a common comorbidity affecting one in ten TB patients in London. Patients with diabetes were less likely to complete treatment at 12 months. The reasons for this should be further explored to find opportunities to improve outcomes among these patients.

Subject: Surveillance

Keywords: tuberculosis, diabetes mellitus, london, retrospective studies, logistic models, comorbidity

ABSTRACT ID: 255

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15.3. Effectiveness of the 2017/18 trivalent and tetravalent influenza vaccines against influenza B in children and adolescents in Germany

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Background:

In Germany, the majority of influenza viruses detected in the current season were type B. According to the National Reference Centre for influenza, B/Yamagata lineage viruses, which are included in the seasonal tetravalent but not in the trivalent vaccines, have greatly outnumbered those of the B/Victoria lineage. We estimated the effectiveness (VE) of the tetravalent (IV4) and trivalent influenza vaccines (IIV3) in preventing laboratory-confirmed influenza B cases among children.

Methods:

From week 49/2017 to 17/2018, sentinel paediatricians swabbed acute respiratory illness (ARI) patients for testing of influenza viruses by PCR. We compared influenza B cases and influenza-negative controls. We estimated trivalent and tetravalent vaccine specific VE against influenza B 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 live or inactivated vaccines.

Results:

Of 1,584 included patients, 30% (n = 471) were positive for influenza B. In children aged 2-6 years VE estimates for IIV3 and IV4 were 55% (95% CI: -32-84) and 66% (95% CI: -168-96) respectively. Among children aged 7-17 years the adjusted VE for IIV3 was 27% (95% CI: -25-58%) and for IV4 76% (95% CI: 13-94%). IV4 VE in 2-17-year-old children was 74% (95% CI: 22-91) and IIV3 VE 35% (95% CI: -3.6-59).

Conclusions:

Our study indicates a low preventive effect of trivalent and a high preventive effect of tetravalent vaccines against influenza B among 2-17-year-old children in 2017/18. These differences were expected, because dominant B/Yamagata viruses were only included in tetravalent vaccines. Cross-protection might explain some effectiveness of trivalent vaccines as a result of vaccination against B/Victoria virus.

Subject: Surveillance

Keywords: influenza, vaccine effectiveness, preventione & control, surveillance

ABSTRACT ID: 408

PRESENTED BY: Carina Helmeke / carina.helmeke@sachsen-anhalt.de

15.4. Influenza B vaccine effectiveness in the trivalent vaccine B/lineage-mismatched 2017/18 influenza season in Europe: investigating cross- protection and changes in VE over time

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Background:

Vaccine effectiveness against influenza B (VE_B) in seasons with trivalent vaccine and circulating B/lineage match/mismatch can contribute to decision-making for the move to quadrivalent inactivated influenza vaccines. In the I- MOVE primary care multicentre case-control study, VE_B varied between 40%-55% in three post-pandemic seasons with good lineage-match, but was only 4% in the mismatched 2015/16 season with B/Yamagata in the trivalent vaccine and B/Victoria circulating. In 2017/18, 99% of B was B/Yamagata, whereas B/Victoria trivalent vaccines were predominantly used in I-MOVE participating countries.

Methods:

Using a test-negative design, we calculated VE_B in 2017/18, adjusting for age, sex, chronic conditions, onset time and study site. We measured VE_B by age-group, calendar time (early: October-December, peak: January, late: February-April) overall and stratified by days since vaccination.

Results:

We included 4,630 influenza B cases and 5,656 controls.

VE _B was 24% (95%CI: 12-35%), 41% (12-60%), 21% (2-36%) and 28% (6-45%) overall and among 0-14, 15-64 and >=65 years respectively.

VE_B was 42% (95%CI: 14-61), 24% (3-40) and 18% (-4 to 35) in early, peak and late season, respectively.

Among those vaccinated <90 days before onset, VE_B was 41% (95%CI: 12-61), 27% (5-44) and 31% (-3 to 54) in early, peak and late season, respectively.

Among those vaccinated >=90 days before onset, VE_B was 48% (95% CI -208 to 91), 5% (-52 to 41) and 10% (-18 to 32) in early, peak and late season, respectively.

Conclusions:

In this mismatched season, VE_B was moderate, suggesting some lineage cross-protection. This cross- protection seems to decrease over the season; waning immunity (time since vaccination) may not explain this. The interplay between previous vaccinations and infections and B/lineage-mismatch warrants further investigation to understand the dynamics of cross-protection.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

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

ABSTRACT ID: 321

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15.5. 2017/18 European influenza season: Disparate I-MOVE multicentre case control study estimates with A(H1N1), A(H3N2) and trivalent vaccine lineage-mismatched B/Yamagata influenza viruses circulating

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Background: In 2017/18 we conducted a multicentre test-negative case-control study using I-MOVE sentinel GP networks in 11 EU countries to measure vaccine effectiveness (VE) against influenza A(H1N1)pdm09, A(H3N2) and B. Countries predominantly used trivalent vaccine, containing A/Michigan/45/2015 (H1N1)pdm09, A/Hong Kong/4801/2014 (H3N2) and B/Brisbane/60/2008-like virus (B/Victoria lineage).

Methods:

We compared odds of vaccination between influenza virus type/subtype positive and negative patients. We calculated VE, adjusted for study site and potential confounders (age, sex, onset time, presence of chronic conditions). We stratified VE by age-group (0-14, 15-64, >=65 years).

Eight countries genetically characterised a random selection of influenza viruses; six countries determined lineage on all influenza B viruses.

Results:

We included 13046 ILI patients among whom 1923, 732 and 4630 were A(H1N1)pdm09, A(H3N2) and B positive, respectively. 79/1159 vaccinated patients (6.8%) received quadrivalent vaccine.

All 35 characterised A(H1N1)pdm09 viruses belonged to the vaccine-virus clade. Sixty percent (32/53) of all characterised A(H3N2) viruses belonged to the vaccine-virus clade, 40% to the A/Singapore/INFIMH-16-0019/2016 3C.2a1 subclade.

Among 2644 B viruses systematically selected for lineage identification, 2605 (99%) belonged to the trivalent vaccine- mismatched B/Yamagata lineage.

VE against A(H1N1)pdm09 was 59% (95%CI: 47-69) overall; from 51% (15-64 years) to 65% (0-14 years). VE against A(H3N2) was 13% (95%CI: -15 to 35) overall; from -10% (>=65 years) to 34% (15-64 years). VE against B was 24% (95%CI: 12-35); from 21% (15-64 years) to 41% (0-14 years).

Conclusions:

The 2017/18 VE against A(H1N1)pdm09 was higher overall and by age-group than VE against A(H3N2) and B. VE against vaccine lineage-mismatched B suggests some cross-protection. As in previous seasons, we observed low VE against A(H3N2), particularly among the elderly, where influenza burden is high.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

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

ABSTRACT ID: 302

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15.6. Seasonal influenza vaccination in 2017/18 and two previous seasons lowered the risk of influenza B in 2017/18 in the elderly, a Finnish cohort study

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Background:

The 2017/18 influenza season was characterised by an approximate balance of influenza_A and influenza_B viruses in Finnish elderly. Of the circulating A(H3N2) subtype and B-Yamagata lineage, the latter was not included in the trivalent inactivated influenza vaccine (IIV3). We aimed to analyse the effect of IIV3 on influenza_B in the elderly taking into account vaccinations given since 2012/13.

Methods:

We conducted a register-based cohort study using Cox regression to estimate the risk of laboratory-confirmed influenza_B in 2017/18 in 65-100-year-olds in Finland. Six variables describing each subject's vaccination status in 2012/13-2017/18, plus age, sex, presence of chronic diseases, and number of hospitalisations in 2016 were included all together in one model.

Results:

The cohort comprised 1183512 individuals of which 47.1% were vaccinated in 2017/18, 46.2% in 2016/17, 40.9% in 2015/16, and 38.8% never since 2012/13. We counted 5789 influenza_B cases in 2017/18. The hazard ratio comparing the vaccinated in 2017/18 to the unvaccinated in 2017/18 was 0.75 (95%CI: 0.69-0.80). In analogy, the hazard ratios for vaccination in the other five seasons were estimated at 0.92 (0.85-1.00) for 2016/17, 0.80 (0.74-0.86) for 2015/16, 1.03 (0.95-1.12) for 2014/15, 1.05 (0.96-1.15) for 2013/14 and 1.05 (0.96-1.14) for 2012/13.

Conclusions:

Despite the potential mismatch of circulating and vaccine antigens in 2017/18 (and 2016/17), IIV3 protected against influenza_B suggesting the presence of cross-protection between the B-Victoria and B-Yamagata lineage. Interestingly, also the last IIV3 composition including Yamagata from 2015/16 still had a beneficial effect indicating vaccine-induced immunity might persist over several seasons. These findings support further use of IIV3 and repeat vaccination in the elderly. The potential interaction between different or identical vaccine antigens used in different seasons must yet be investigated and understood.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: cohort, effectiveness, influenza, vaccine

ABSTRACT ID: 332

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Track 16: Vaccine- preventable diseases (2): Epidemiology and Surveillance

Moderator:

Jussi Sane

Abstracts

16.1. Were mistakes in vaccination management responsible for an outbreak of measles in the district Eichsfeld, Thuringia, Germany in autumn 2016?

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Background:

During a measles outbreak in 2016 affecting the district Eichsfeld, Thuringia, many cases were observed in individuals with a record of two or even more different measles-mumps-rubella (MMR) vaccinations. The goal of our investigation was to analyse the cause of the assumed vaccination failures.

Methods:

We analysed surveillance data, collected details on vaccination of affected individuals and their contacts, tested patient samples for measles virus specific parameters, conducted a cohort study and revised the management of vaccine storage and application in a doctor's practice.

Results:

From October to December 2016, 23 individuals 6 to 53 years old contracted measles. Primary vaccination failure was determined for 13 of 16 adults vaccinated according to the recommendation of the German standing committee on vaccination (STIKO). All 13 cases had been vaccinated with different lots and vaccine formulation vaccines of the MMR vaccine during a 20 years period in the same doctor's practice. Individuals, who had been vaccinated exclusively in the practice, had a 18-fold increased risk of contracting measles than individuals that had received the immunisation also in other institutions (RR 17,8; 95% CI 5,8-54,9). An evaluation of the storage and the application of the vaccines revealed minor shortcomings and deficiencies but no systematic failure.

Conclusions:

Though systematic mistakes with respect to vaccination management were not observed during this recent outbreak, our findings indicate that the high number of affected people displaying a primary vaccination failure must be attributed to faults with respect to storage and application of the light- and temperature sensitive vaccine in a certain doctor's practice. Our results underline once again the necessity of a correct storage and use of live vaccines.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: measles, vaccination,cohort study,vaccination failure

ABSTRACT ID: 351

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16.2. Large outbreak of measles in Nouvelle-Aquitaine Region, France, due to low vaccine coverage, November 2017 to March 2018

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Background:

Following the 2008-2012 epidemic, only sporadic measles cases were reported in Nouvelle-Aquitaine region (NA). In December 2017, clinicians notified four measles cases among Bordeaux University students. Simultaneously we observed an increase of measles cases in the same district. We conducted an investigation to describe the outbreak, identify clusters and stop further transmission.

Methods:

We included all cases reported in the mandatory notification system who lived in NA and developed rash onset after 29 October 2017: clinical cases (possible), cases with epidemiological link to a laboratory-confirmed case (probable) and laboratory-confirmed cases (confirmed). We interviewed cases to identify contacts at risk and detect clusters in high risk groups. Clusters were defined as at least three cases including one confirmed case in settings with high number of susceptibles and/or people at risk to develop complications.

Results:

As of 30 April 2018, we identified 1,025 cases (440 possible, 180 probable, 405 confirmed). The cumulative incidence rate in NA was 17.2/100,000 population and reached 38.4/100,000 in the biggest district. Fifty-three percent were males and 60% were older than 15 years. Eighty-three percent were not vaccinated against measles as recommended. 218 cases required hospitalisation (21%), 83 suffered from complications (8%) and one died. We identified 18 clusters (184 cases) among students, healthcare workers and vulnerable social population. We informed healthcare professionals and the public and ran catch-up and post-exposure vaccination campaigns.

Conclusions:

This outbreak has occurred and spread within France due to low measles vaccine coverage resulting in an increasing pool of susceptible individuals - despite current vaccination recommendations. Measles infection may have severe complications resulting in long-term sequelae or death, and outbreaks should be prevented through vaccination coverage above herd immunity threshold.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: measles, outbreak, vaccination, students, healthcare

ABSTRACT ID: 218

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16.3. Epidemiology of Invasive Meningococcal Disease (IMD) in Greece during 2006-2016

Anastasia Flountzi [1]

T. Georgakopoulou [2], S. Balasegaram [3], K. Kesanopoulos [4], A. Xirogianni [5], A. Papandreou [6], P. Mavraganis [7], G. Tzanakaki and the Greek Meningitis study group [8]

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Background:

Greece has included Meningococcal C vaccine from 2005, replaced by Meningococcal ACWY vaccine in 2011 in the national vaccination programme for children. Meningococcal B vaccine is not recommended in the programme but available privately. Herein, we describe the epidemiology of invasive meningococcal disease (IMD) in Greece during the period 2006-2016.

Methods:

Combined data from notified and laboratory confirmed IMD cases were obtained from the two national centres. Laboratory identification and typing was undertaken by conventional and molecular methods. Data were analysed by incidence, serogroup/genogroup, age-specific trends, and case fatality.

Results:

796 IMD cases were notified; 721(91%) confirmed. Annual incidence per 100.000 for confirmed cases decreased from 0.91 (100 cases in 2006)

to a low of 0.46 (51 cases in 2011) and remained stable to 2016 (0.47, 51 cases). A similar trend was observed in most age groups, especially in 0-4 years: 7.7 (2006) to 2.7 (2011) and 2.9 (2016), except for adults (>20yrs), where incidence increased from 0.21 (19 cases 2006) to 0.32 (28 cases 2016). Overall, case fatality was 6.5% (52/796); annual range 2%-13%.

Among 658 typable cases, MenB was predominant, 80%, (annual range 65-92%) in all ages; however, a similar decline in Men B incidence from 5.3 (2006) to 2.7 (2016) was observed in the 0-4 years group. A low proportion was observed throughout for MenC; 5% (annual range 0-13%), MenY; 2% (0-6%), MenW and MenA; 1% each (0-4%).

Conclusions:

Over 11 years, the annual incidence of IMD declined by 50%, especially in the 0-4 years age group and consequently for type MenB. We recommend continuous surveillance as assessing trends are important for reviewing and planning future vaccine policies.

Subject: Surveillance

Keywords: Epidemiology, Invasive Meningococcal Disease,vaccination

ABSTRACT ID: 191

PRESENTED BY: Anastasia Flountzi / fanastasia@hotmail.com

16.4. A measles outbreak in Ireland, 2017: Low vaccination coverage at subnational level challenges the elimination goal

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Background:

Ireland has made progress to meet the European target for measles elimination in recent years, and had interrupted endemic transmission for 24 months by the end of 2016. In October 2017, a measles outbreak in two adjacent regions in Ireland was investigated in order to implement control measures and prevent further cases.

Methods:

We applied the national measles case definition, for persons resident in outbreak areas between October-December 2017, conducted case finding, and carried out descriptive analysis. Confirmed cases were genotyped. Childhood immunisation uptake data were obtained from routine surveillance.

Results:

Overall, 186 suspect measles cases were investigated; 22 were confirmed, and none were known to be imported. Cases occurred in Dublin (n=13) and in the North-East region (n=9); 45% of cases were male, and 45% from minority ethnic groups. Median age was 11 years (range: 1month-57years), and 45% were >=16 years old.

Of 17 cases eligible for routine vaccination, 12 (71%) had none or unknown MMR vaccination history (58% >=16 years of age and 50% minority ethnic groups). Half of the cases (n=11) were hospitalised, 64% were <=2 years of age; no deaths occurred. All genotyped cases (n=19) were B3. MMR1 uptake was 92% nationally, but 89% in the affected Dublin area.

Conclusions:

The outbreak was contained through intensified vaccination and engagement with stakeholders. However, it highlights that pockets of insufficiently immunised populations continue to exist amongst teenagers, adults and minority ethnic communities in the Dublin area. Awareness needs to be raised amongst healthcare professionals of the possibility of measles in such groups to ensure timely and appropriate case management. To achieve measles elimination, supplementary immunisation activities are required, to reach these groups with low MMR uptake.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Measles-Mumps-Rubella vaccine,Immunisation,Measles elimination,Outbreak

ABSTRACT ID: 84

PRESENTED BY: Annalisa Quattrocchi / annalisaquattrocchi@hotmail.com

16.5 Investigation of Measles Outbreak in Dehdadi district, Balkh Province, Afghanistan, Dec 2016 - Sep 2017

CANCELLED

16.6. Late breaker: Very high case fatality rate of serogroup W invasive meningococcal disease in teenagers in 2018, the Netherlands

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Background:

The incidence of serogroup W invasive meningococcal disease (IMD-W) is increasing in the Netherlands, with an annual incidence of 0.02/100,000 before 2015 and an incidence of 0.7/100,000 in 2018 (up to August). Since 2015, 17% of IMD-W cases died. Given the high case-fatality rate (CFR), we studied characteristics associated with mortality in teenagers.

Methods:

The Netherlands has a comprehensive surveillance system for IMD including clinical, epidemiological, and microbiological data. Cases diagnosed from January 2015 to August 2018 were included in the analysis. CFRs within 14-24 year olds were calculated by year and characteristics were compared between deceased and surviving cases. Symptoms at disease onset were only known for 2017 and 2018 cases.

Results:

Forty-six IMD-W cases among 14-24 year olds were reported. The CFR was 0% (0/1) in 2015, 17% (2/12) in 2016, 21% (4/19) in 2017 and 54% (7/13) in 2018 (ptrend=0.04). Only one of the cases had an underlying condition. All deceased cases had septicaemia/septic shock versus 43% (13/30) of the surviving cases ($p<0.01$). Of the deceased cases, 56% (5/9) had diarrhea at disease onset versus 10% (2/21) of the surviving cases ($p<0.01$). None of the deceased cases had petechiae and one had neck stiffness (11%) versus four (19%, $p=0.16$) and four (19%, $p=0.59$) of the surviving cases, respectively. Finetype was P1.5,2:F1-1 in 85% (34/40) of cases and did not differ by outcome status ($p=0.18$).

Conclusions:

The CFR of IMD-W among teenagers increased during the outbreak and is currently very high. Diarrhea at disease onset and septicaemia/septic shock were associated with mortality. The meningococcal-ACWY vaccination campaign among 14-18 year olds, which starts in October 2018, will hopefully prevent further deaths of IMD-W in the coming years.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: invasive meningococcal disease, case fatality rate,outbreak,serogroup W

ABSTRACT ID: 612

PRESENTED BY: Mirjam Knol / mirjam.knol@rivm.nl

MODERATED POSTER SESSION C
DAY 3: Friday, 23 November 2018
15:40-16:40

Track 17: Food- and waterborne diseases and zoonoses (5): Epidemiology and Outbreaks 2

Moderator:

Emmanuel Robesyn

Abstracts

17.1. Use of a case-case comparison study for the investigation of an outbreak of Salmonella Typhimurium 1,4 [5],12:i:- in Central Greece, August 2017

Theofilos Papadopoulos [1]

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Background:

Following intercommunal violence in August 2017, there was an influx of over 650,000 Rohingya refugees from Myanmar to Cox‘s Bazar, Bangladesh. In early November 2017, an outbreak of diphtheria began among this immunologically naïve refugee population, something not previously described in the published literature.

Methods:

Patients were linelisted by organisations operating treatment facilities, and these were used to generate descriptive epidemiological analyses of the outbreak. A probable case was defined as a person with an upper respiratory tract illness with laryngitis or nasopharyngitis or tonsillitis AND sore throat or difficulty swallowing and an adherent membrane/pseudomembrane OR gross cervical lymphadenopathy. Confirmed cases were those positive for toxigenic C. diphtheriae strain by a multiplex assay.

Results:

Between 8 November 2017 and 31 August 2018, 7068 cases were notified (271 confirmed, 3625 probable, 3172 suspected), 71.5% of whom were aged under 15 years and 55.6% of whom were female. There were 43 deaths (case fatality ratio 0.6%). The overall attack rate was 115.3/10000 population. Sore throat (93.7%) and fever (86.4%) were the most common symptoms, while pseudomembrane (35.3%) and gross cervical lympadenopathy (31%) were the most common signs. Of 4279 cases with known vaccination status, 2198 (51.4%) were vaccinated. 5320 (64.9%) patients were treated with antibiotics, while 1476 (18.0%) were treated with DAT.

Conclusions:

This large outbreak occurred among a population that had been chronically underserved prior to their arrival in Bangladesh, among whom the risk of various outbreaks of vaccine-preventable diseases was high. The data presented here were used for real-time forecasting of vaccine and anti-toxin requirements, which were facing a global shortage due to the limited global stockpile and concurrent diphtheria outbreaks in Yemen, Venezuela and Indonesia.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Diphtheria, Refugees, Disease Outbreaks, Bangladesh

ABSTRACT ID: 3

PRESENTED BY: Theofilos Papadopoulos / theofilospapadopoulos@hotmail.com

17.2. Freshly pressed grape must as a novel vehicle for infection with Francisella tularensis: an outbreak of oropharyngeal tularemia in autumn 2016, Germany

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Background:

In autumn 2016, an outbreak of oropharyngeal tularemia occurred near the city of Mainz, Rhineland-Palatinate, among participants of a grape collection event with no exposure to hunting or eating game.

Methods:

We conducted a retrospective cohort study among all participants and investigated their activities, food consumption, and the environment to identify and stop the source of the outbreak. Case patients were defined as having symptoms compatible with tularemia up to 21 days after the event and positive serology. We tested food and environmental samples with nucleic acid amplification and culture methods for the presence of F. tularensis as well as suspected food items for mammalian DNA.

Results:

Among 29 participants, we identified six case patients with oropharyngeal tularemia and high titres of IgG and IgM antibodies against F. tularensis. Among all exposures investigated, drinking freshly pressed must was associated with the highest risk of contracting tularemia (adjusted incidence risk ratios 13.5; 95 percent confidence interval, 1.6 to infinity) and accounted for the highest attack rate (six out of eight, 75 percent). DNA of F. tularensis ssp. holarctica was found at a concentration of approximately 1.7x104 genome equivalents per millilitre in secondary products from the same must, as was DNA from wood mice (Apodemus). Environmental investigation revealed the use of a mechanized harvester for this collection and cross-contamination of subsequently harvested grapes of a different collection with the same machinery.

Conclusions:

Study of this outbreak implicated freshly pressed must from mechanically harvested grapes as novel vehicle for food-borne tularemia. It underlines the importance of treating raw food stuffs before consumption.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: outbreak, oropharyngeal tularemia, grape must, Francisella tularensis, Germany

ABSTRACT ID: 400

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

17.3. Investigation of a large hospital outbreak of Legionnaires' disease in Lisbon, Portugal, October to November 2017

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With the collaboration of Administração Regional de Saúde de Lisboa e Vale do Tejo, Lisboa

Background:

One of the largest Legionnaires' disease hospital outbreaks occurred in 2017 in Hospital São Francisco Xavier in Lisbon. We conducted an outbreak investigation to identify the source of the outbreak, time of exposure, and measures to prevent future outbreaks.

Methods:

We obtained data of the cases through the Portuguese Epidemiological Surveillance System based on the outbreak case definition. We genotyped Legionella pneumophila (Lp) from clinical and environmental samples at the National Laboratory using seven-allele standard sequence-based typing and whole-genome sequencing. We obtained data on temperature, wind and humidity from the National Institute of Meteorology.

Results:

We identified 58 hospitalized confirmed cases with pneumonia and positive antigenuria in urine for Lp serogroup 1; five (8.6%) died. The median age was 73 years; 45% were women. All had some risk factor or chronic disease. The first onset of symptoms was on October 27 and last on November 17 2017. In 34 of 43 genotyped patients, an identical genetic profile (serotype 1- ST1) was detected. Among 77 samples taken in the water systems, 19 were positive for Lp, 10 of which were positive for ST1, with a cooling tower identified as the most likely source of infection. Poor manutention of the water distribution system was detected. Poor air circulation and relative humidity values above 90% at 2 meters, and the presence of fog, made the night of October 25- 26 2017 the period of greatest risk for the spread of the disease.

Conclusions:

A cooling tower in the hospital was the most likely source of infection. Meteorological data can assist in investigations of Legionnaires' disease outbreaks. Compliance with the guidelines and regulation on Legionnaires' disease prevention at the hospital were revised.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Legionnaires' disease, Legionella pneumophila, hospital outbreak, field epidemiology, meteorological data

ABSTRACT ID: 127

PRESENTED BY: Alexis Sentís / alexissentis@gmail.com

17.4. Investigating a cluster of Yersinia enterocolitica using Whole Genome Sequencing, United Kingdom, 2017

Thomas Inns [1]

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Background:

Yersinia enterocolitica is a zoonosis which is commonly reported across Europe, with an annual rate of 2.2 cases per 100,000 persons. The rate reported from the United Kingdom is lower (0.1 cases per 100,000) and outbreaks are infrequently reported. In May 2017 Public Health England were notified of a cluster of three Y. enterocolitica positive isolates from Liverpool. An Outbreak Control Team was convened to investigate this cluster of cases and find a possible common source.

Methods:

A case was defined as a person with a laboratory confirmed isolate of Y. enterocolitica, sampled in 2017, resident in Liverpool local authority at the time of sampling. Faecal samples were cultured at the local laboratory and identified using MALDI-TOF. Positive isolates were whole genome sequenced by the Gastrointestinal Bacteria Reference Unit using Illumina HiSeq 2500.

Results:

There were 9 cases, this was significantly greater (p<0.0001) than the average number of cases in this area from the last 10 years. Six cases were female (66.67%) and ages ranged from 20-81 (median 54). Sample dates ranged from 29 April to 01 August 2017. WGS results showed that the 9 isolates did not have a close genetic relationship, relative to the diversity of other Y. enterocolitica isolates.

Conclusions:

This was the first time that WGS was used to investigate a cluster of Y. enterocolitica cases; cases were clustered in time, person and place but WGS results indicate that these cases were not from the same source. This result informed the OCT's decision making and resulted in the investigation being closed.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Epidemiology,Surveillance,WGS,Yersinia

ABSTRACT ID: 130

PRESENTED BY: Thomas Inns / thomas.inns@phe.gov.uk

17.5. Health risks associated with participating in mud and obstacle runs; a prospective cohort study between April and October 2017, the Netherlands

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Background:

Mud and obstacle runs are increasingly popular in the Netherlands. Outbreaks of e.g. gastroenteritis have been reported, however, health risks associated with participating in these events have not been assessed systematically. Our objectives were to identify the incidence of and risk factors for acute gastrointestinal illness (AGI), skin and respiratory complaints and injuries among participants of mud and obstacle runs.

Methods:

We conducted a prospective cohort study among participants of 17 runs in the Netherlands between April – October 2017. We distributed an online survey one week after a run to collect demographical, symptomatic and behavioural data. Stool specimens were collected for microbiological tests. We calculated adjusted odds ratios (aOR) and 95% confidence intervals (95%CI) using multivariable multilevel logistic regression.

Results : Of 2,646 respondents (median age 33 years, 53% males), 3% met our case definition for AGI. Ingesting water (aOR 2.4; 95% CI 1.1-5.2) and mud (aOR 2.6; 95% CI 1.02-6.5) were associated with AGI. 38 respondents participated while having AGI. In total, 4% reported skin complaints, 6% respiratory complaints and 5% injuries. Chronic allergies and illness were respectively associated with respiratory (aOR 1.6; 95% CI 1.04-2.4) and skin complaints (aOR 1.7; 95% CI 1.07-2.8). For injuries no evident risk factors were identified. Of 111 stool specimens, 14 tested positive (sapovirus (n=5) , norovirus (n=4), Shigella spp. (n=1), EHEC (n=1), Campylobacter jejuni (n=1), Giardia lamblia (n=2)), however no clustering was found.

Conclusions:

The overall reported incidence of AGI, skin and respiratory complaints and injuries was low. However subgroups were at increased risk for several complaints. Risks can be further decreased by informing participants to take preventive measures, e.g. not participating when ill and avert ingesting water and mud.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: gastroenteritis, prospective, epidemiology, running

ABSTRACT ID: 202

PRESENTED BY: Elke den Boogert / e.den.boogert@ggdhvb.nl

17.6. Outbreak of gastroenteritis among participants of a survival run in The Netherlands in September 2016

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[4] Department of Primary and Community Care, Radboud university medical centre, Nijmegen, The Netherlands

Background:

In September 2016 a two-day survival run with 1000 participants took place in Udenhout, a town in the south of the Netherlands. An outbreak investigation was initiated after the public health authorities were notified that several participants had developed gastroenteritis in the days following the event.

Methods:

We conducted a retrospective cohort study among survival run participants to identify the source of the gastroenteritis outbreak. We sent an online questionnaire to participants directly, and the link was shared on the Facebook page and website of the survival run. We calculated attack rates and relative risks for several exposures to identify risk factors for developing diarrhea and/or vomiting within 3 days after the run. In addition, stool samples of six participants were tested for common gastrointestinal pathogens.

Results:

A total of 444 people completed the questionnaire. Symptoms of gastroenteritis were reported by 163 study participants (37%). Five participants reported symptoms of gastroenteritis in the week before and three participants during the survival run. Participation on the second day of the run (adjusted relative risk (aRR) 2.4; 95%CI 1.1-5.3), ingesting water (aRR 1.7; 95%CI 1.3-2.3) and ingesting mud (aRR 1.3; 95%CI 1.1-1.6) were identified as risk factors for developing gastroenteritis. Four of six stool samples tested positive for norovirus (different types).

Conclusions:

Our findings indicate that participants with symptoms of gastroenteritis before and during the survival run could have contaminated the track and event area, allowing norovirus to spread through obstacles, water and mud. Participants of such outdoor sports events should be informed about possible health risks and prevention measures, such as do not participate if you have gastroenteritis, to reduce the risk of spreading of infectious diseases.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: epidemiology, disease outbreaks, gastroenteritis, norovirus

ABSTRACT ID: 30

PRESENTED BY: Danielle Oorsprong / d.oorsprong@ggdhvb.nl

Track 18: Food- and waterborne diseases and zoonoses (6): Surveillance systems

Moderator:

Lisa Hansen

Abstracts

18.1. Evaluation of public health interventions for a national outbreak of Salmonella Enteritidis using a combination of epidemiological methods and whole genome sequencing, UK 2018

Matt Edmunds [1]

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Background:

In September 2015, routine whole genome sequencing (WGS) and single nucleotide polymorphism (SNP) typing for Salmonella identified a national outbreak of Salmonella enterica serovar Enteritidis, with cases accruing at a rate of around eight per month. An Incident Management Team (IMT) was formed, and found strong evidence of an association with reptile feeder mice originating from a breeding farm in another EU Member State. In 2016, interventions were introduced and the IMT was put on hold. This study aimed to assess the effectiveness of the interventions that were introduced.

Methods:

In March 2018, an epidemiological analysis was completed on a 5-SNP cluster using data extracted from the national Gastrointestinal Data Warehouse, to compare cases before (Apr-2015- to Mar-2016) and after (Apr-2016 to Feb-2018) the introduction of interventions. Phylogenetic analyses were conducted on a 25-SNP cluster of human and animal isolates received up to November 2017.

Results:

Since April 2014 there had been a total of 427 reported cases; 199 occurred during the pre-intervention period and 228 after. No difference was found between pre- and post-intervention periods for mean age (pre=40.1y, post = 41.2y, p=0.49), proportion of males (pre=48%, post=47%, p=0.23), geographical distribution or incidence of cases per month (pre=8.2, post=7.9, p=0.32). Phylogenetic analysis of 498 isolates suggested there had been no decrease in effective population size and added to the epidemiological evidence indicating that there was a persistent common source of contamination.

Conclusions:

The combination of epidemiological investigation and phylogenetic analysis suggests that interventions have not changed the incidence of cases, nor resolved the likely source. The disease burden of this outbreak is now high, and ongoing work to identify more robust interventions are being be prioritised.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Salmonella Enteritidis, Whole Genome Sequencing, Evaluation

ABSTRACT ID: 298

PRESENTED BY: Matt Edmunds / matt.edmunds@phe.gov.uk

18.2. Effect of culture-independent diagnostic tests on enteric disease surveillance, Wellington, New Zealand

Craig Thornley [1]

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Background:

Population-based surveillance of enteric infections in New Zealand uses direct laboratory reporting of tests indicating pathogen detection in human clinical specimens. Culture-independent diagnostic testing (CIDT) for all community gastroenteritis specimens was introduced in the greater Wellington region, New Zealand, in January 2018. Testing utilises a multiplex PCR panel to detect sequence targets for Shigella/enteroinvasive Escherichia coli (EIEC), Salmonella spp, Campylobacter spp, stx1, stx2, E. coli O157, Giardia intestinalis, Cryptosporidium parvum and C. hominis, and Yersinia spp. This study sought to examine the effect of the changed diagnostic testing on surveillance for notifiable enteric pathogens.

Methods:

Data on enteric disease notifications from the greater Wellington region (a population of approximately 400,000) for the five-year period 2013-2017 were compared with data from 2018 for changes in notification delay, disease incidence, demographics and clinical characteristics of notified cases.

Results:

Following the introduction of CIDT, enteric disease notification delays have been reduced and incidence has increased. Changes in incidence are uneven: notifications of shigellosis (as defined by detection of Shigella/EIEC), yersiniosis, cryptosporidiosis and particularly shigatoxigenic E. coli (STEC) infections have increased markedly, while the incidence of campylobacteriosis, salmonellosis and giardiasis has been relatively unchanged. The majority of STEC notifications do not have O157 detected by PCR, and an increased proportion of notified cases of STEC infection have low- grade symptoms.

Conclusions:

Introduction of CIDT for all community gastroenteritis specimens has apparent advantages for enteric disease surveillance due to reductions in notification delay and greater sensitivity. However, this has also required changes to operating procedures to manage the altered characteristics of notified cases, and has created workload pressure for public health unit staff.

Subject: Surveillance

Keywords: Enteric infections,Surveillance,STEC,PCR

ABSTRACT ID: 512

PRESENTED BY: Craig Thornley / craig.thornley@huttvalleydhb.org.nz

18.3. Description of the norovirus laboratory data to inform a surveillance system in Denmark

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Background:

In Denmark, norovirus infections which are currently not under routine surveillance will likely become statutory notifiable in 2019. We aimed to describe existing norovirus data to inform the implementation of a new laboratory-based surveillance system.

Methods : We identified all norovirus samples registered in the Danish Microbiology Database (MiBa) between 2010- 2017. MiBa collects information from relevant clinical laboratories, including: requesting physician, test results and Personal Identification Number (CPR). The CPR comprises information on patient demographics (date of birth, sex and residence). Cases retested (or with a repeat positive test) within 30 days were excluded as duplicates.

Results:

Data validation indicated that 0.5% of CPR were incorrectly registered and 1% of patient residence addresses were incorrect or absent. Between 2010-2017, a total of 151,656 tests for norovirus were registered with an increasing trend (10,925 in 2010 vs 29,630 in 2017). The proportion of positive samples remained stable each year (average 14%). We identified 14,299 cases, the majority in patients <5 or >70 years old with an increase in incidence in the former (31 per 100,000 in 2010 vs 166 in 2017) and a decrease in the latter (144 vs 72). Most tests were done in the Capital Region (1,131 per 100,000 in the study period), fewest in the Central Region (46 per 100,000). Seasonal variation in norovirus infections was recognized with a strong winter peak (December-February).

Conclusions:

This is the first attempt to collect national analysis of norovirus laboratory data. A laboratory-based surveillance system for norovirus seems feasible. The automated data collection is likely to provide timely and valid information for public health actions. If combined with for instance hospital databases this might assist in identifying and managing outbreaks.

Subject: Surveillance

Keywords: norovirus, Danish Microbiology Database, MiBa, automated data collection, automated incidence monitoring

ABSTRACT ID: 100

PRESENTED BY: Monika Roberta Korcinska / monika.korcinska@gmail.com

18.4. Patient foreign travel information in the Danish National Microbiological Database (MiBa)

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Background:

Patient travel information is important in surveillance of infectious diseases. Information may be gathered by phone interviews of cases but this procedure is cumbersome and expensive. The Danish Microbiology Database (MiBa) nationwide includes copies of all clinical microbiological reports. Until 2018 MiBa rarely included travel information but beginning 1 January 2018 information was gathered as free-text answers to standardized questions, prompted when relevant tests is ordered. In this study, travel information was extracted from free-text answers in order to evaluate completeness and concordance with Salmonella cases in the National Registry of Enteric Pathogens (NREP).

Methods:

Patient travel information at sample level was extracted by a semi-automated algorithm searching for country names. Information was compared to travel information available for cases of Salmonella in NREP between 1 January and 30 April 2018. Data completeness and concordance between MIBA and NREP was evaluated by linking data by the unique person identifier (CPR).

Results:

During January to April 2018 346 cases of Salmonella were recorded in NREP, travel information was available for 249 cases (72 %) of which 156 (45 %) stated foreign travel. Before phone interviews information was available for 140 cases (40 %). MiBa contained travel information for 233 cases (67 %). For cases with travel information (travel, no travel) in both MiBa and NREP agreement was 82% (147/179).

Conclusions:

Extraction of travel information from MiBa was feasible. In comparison with NREP, data completeness in MiBa was 27 percent-points higher before phone interviews and only 5 percent-points lower following phone interviews. Continued investigations will evaluate if phone interviews may be partly or fully omitted leading to savings and timelier gathering of travel information.

Subject: Surveillance

Keywords: Patient travel,Automated Data Collection ,Salmonella

ABSTRACT ID: 437

PRESENTED BY: Karsten D Bjerre/ kadb@ssi.dk

18.5. Can syndromic surveillance systems operating in Public Health England detect subnational outbreaks of Cryptosporidiosis in the West Midlands?

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Background:

Potential benefits of syndromic surveillance systems for gastroenteritis outbreak detection include timeliness of detection and response. The aim of this ecological study was to determine early warning capabilities of syndromic surveillance systems to detect subnational Cryptosporidiosis outbreaks in England and to identify key predictors for use in a statistical algorithm to improve its detection capabilities.

Methods:

We identified Cryptosporidiosis outbreaks of ten or more cases in the West Midlands using case-based surveillance systems and collected daily syndromic surveillance data on diarrhoea and vomiting consultations between 2014 and 2016. Age, gender and geographical distribution of the outbreak cases were described. Time-series graphs of the selected syndromic indicators along with statistical exceedance plots (based on historical data) were visually examined.

Results:

Five Cryptosporidiosis outbreaks were identified, all occurring in visitor attraction centres during spring. Median number of cases was 17 (range: 14 to 30), with a median duration of 19 days (range: 9 to 30). Where information on the outbreaks was available, the majority of cases were aged one to ten years, and affected local authorities ranged from three to eight (within and outside the West Midlands). No differences in gender distribution were observed. None of the outbreak periods coincided with changes in trends of syndromic surveillance indicators or triggered a statistical alarm that would have warranted further investigation.

Conclusions:

Syndromic surveillance was not able to detect sub-national Cryptosporidiosis outbreaks. One possible key-predictor identified in our study was age, which may be included in the existing statistical algorithm to improve the sensitivity. Our findings are important for system users as they describe the outbreak detection limits of our current suite of syndromic surveillance systems.

Subject: Surveillance

Keywords: Syndromic Surveillance

ABSTRACT ID: 287

PRESENTED BY: Monique Pereboom / monique.pereboom@phe.gov.uk

18.6. The benefit of whole-genome sequence-based typing in Public Health microbiology: retrospective analysis of human and food-associated L. monocytogenes isolates in Austria, 2017

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Background :

In Austria, all Listeria monocytogenes isolates from food companies are sent to the National Reference Laboratory (NRL). In 2016, Whole Genome Sequencing (WGS)-based typing was introduced for the surveillance of listeriosis at a national level. Here, we aimed to analyze WGS data from clinical, food and environmental L. monocytogenes isolates collected in 2017 to guarantee prompt outbreak detection.

Methods:

A total of 1785 L. monocytogenes isolates were retrieved: 35 corresponded to 32 invasive listeriosis cases and 1750 were non-clinical. All were sequenced using Illumina MiSeq and characterized using a core genome (cg)MLST genotyping scheme. Twenty-two provenance categories were defined for non-clinical isolates according to the corresponding referral form.

Results:

Among the clinical isolates (n=35), only 4 were epidemiologically related belonging to 2 clusters. Cluster 1 (25 isolates, CT1234, ST155) was reported as an outbreak associated to an Austrian meat provider for which cases with the same CT and ST had been recorded in previous years. Cluster 2 (6 isolates, CT4446, ST1) was possibly linked to meat consumption. Also, one isolate was involved in an additional outbreak, which is an ongoing multi-country outbreak (ST6, IVb serotype) linked to the consumption of a frozen vegetable. The most common STs among non-clinical isolates were: ST511 for cheese (30/86) and milk (30/40), ST21 (23/75) for vegetables, ST9 (100/463) for meat and ST121 (43/85) for fish.

Conclusions:

The implementation of WGS-based typing in Austria has improved the detection of new L. monocytogenes outbreaks providing high discriminatory power, reduced costs and speed. This study reveals that unknown infection sources still exist since not all food isolates match the clinical isolates, being an EU coordinated use of WGS methodologies essential to decrease listeriosis burden.

Subject: Microbiology

Keywords: Listeria monocytogenes, invasive listeriosis, whole-genome sequencing, core-genome MLST, outbreak, food isolates,surveillance

ABSTRACT ID: 68

PRESENTED BY: Adriana Cabal / adacabal@gmail.com

Track 19: Healthcare-associated infections (2): Surveillance 2

Moderator:

Lieke Van Alphen

Abstracts

19.1. A single patient infection prevention record for Wales,

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Background:

In Wales, Infection Prevention Teams (IPTs) co-ordinate hospital infection prevention (IP) activities and monitor outcomes through surveillance. Previously, IPTs identified patients with healthcare associated infections (HCAI), recorded risk factors, actions, treatment and advice through electronic/paper/telephone systems, making information difficult to access and standardise. We provided a case management system to improve patient care, aid efficiency, standardise practice and simplify access to data.

Methods:

We purchased a commercial IP case management system, with links to laboratory, administration and surgery information systems. We installed it as a single national system, giving IPTs access to data on patients within their hospitals. Subsets of information are available for national surveillance. We established a user forum to support standardisation of practice, including common alert organisms, minimum data sets and alerts.

Results:

All (19/19) NHS IPT sites have access, viewing data for patients in their hospitals with full patient history, including admissions, organisms identified, advice given in other hospitals previously. Organisms from specified locations e.g. augmented care and defined specimen types e.g. blood cultures are included in a regularly reviewed organism list monitored by all IPTs. Minimum data sets for Clostridium difficile and bacteraemia have been agreed. Admission alerts function within and between hospitals, highlighting high risk admissions e.g. patients with drug resistant organism history and organism clusters within a location or timeframe.

Conclusions:

We have demonstrated that establishment of a national infection prevention system is possible. We anticipate single patient IP records benefitting patient care; access to complete patient histories enriches IPT advice and alerts prompt early intervention. Consistency of national HCAI surveillance data from the system should improve with standardisation of IP practice. A benefits realisation exercise will be conducted following implementation.

Subject: Surveillance

Keywords: infection prevention,HCAI,surveillance

ABSTRACT ID: 97

PRESENTED BY: Mari Morgan / mari.morgan@wales.nhs.uk

19.2. Whole genome sequencing of Streptococcus pyogenes type emm89 from 2013 in Sweden reveals geographically distinct outbreak clusters

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Background:

The number of reported invasive Streptococcus pyogenes infections in Sweden increased in 2012 and led to the initiation of an enhanced program for emm-typing. Data collected since indicate the presence of geographic type- specific clusters. Using whole genome sequencing (WGS) we investigated invasive S. pyogenes emm89 isolates obtained from one year of population-based surveillance in order to explore if an observed cluster is due to sporadic cases or a localized outbreak.

Methods:

The genomes of 81 emm89 isolates collected during 2013 from all but one county were sequenced using Ion Torrent technology. Multilocus sequence type (MLST) was determined by mapping to reference sequences for each loci of the PubMLST S. pyogenes scheme. Whole genome single nucleotide polymorphism (SNP)-analysis was performed for the different sequence types (STs) separately.

Results:

Eighty isolates were ST101 and one was ST407. We detected two geographically distinct genetic clusters of emm89 ST101. Cluster one (n=11) consisted of four isolates with indistinguishable genomes (0 SNP difference), and an additional seven within 3 SNPs. Cluster two (n=7) consisted of five isolates with indistinguishable genomes and two isolates within 5 SNPs. The median age of all cases was 77 years (IQR 23.5) and the median age of cases represented within the clusters were 84 (IQR 13) and 83 (IQR 11) years, respectively.

Conclusions:

WGS of S. pyogenes emm89 isolates from Sweden shows geographically distinct clusters, indicating two previously undetected outbreaks during 2013. By collecting epidemiological data, we are planning to investigate possible epidemiological links between the cases. Our findings show that WGS increases the discriminatory power compared to the conventional typing method and may provide valuable supporting evidence in outbreak investigations and surveillance.

Subject: Microbiology

Keywords: Streptococcus pyogenes, whole genome sequencing, cluster, group A streptococcus

ABSTRACT ID: 95

PRESENTED BY: Nina Lagerqvist /
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19.3. Hip and knee joint infections after joint replacement surgery in Finnish hospitals, 1999-2016

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Background:

Surveillance of surgical site infections (SSI) in orthopedic surgery has been conducted in the Finnish Hospital Infection Program (SIRO) since 1999. Reported SSI rates have increased over time. Both the National Infectious Disease Register and the European prevalence survey of healthcare-associated infections have shown an increase inStaphylococcus aureus (SA) infections in Finland. In order to explore targets for SSI prevention, we aimed to determine whether SA is responsible for the increasing incidence of SSIs.

Methods:

We analyzed data on 157,087 hip and knee primary and revision arthroplasties from 19 hospitals participating in prospective SIRO surveillance during 1999-2016. Cases were patients meeting the EU SSI case definition (superficial and deep incisional, organ/space SSIs). We defined prosthetic joint infection (PJI) to include both deep and organ/space SSIs. For each year, the overall SSI and PJI rates per 100 procedures (%) were calculated. We used binomial regression with a log link to model trends.

Results:

We identified 3,585 SSIs; 2001 were superficial SSIs and 1,584 PJIs (366 deep incisional SSIs, 1,218 organ/space SSIs). The annual overall SSI rate decreased significantly from 4.00% in 2003 to 1.62% in 2014 ($p<0.001$). The trend of PJI rate increased significantly from 0.54% in 2002 to 1.36% in 2016 ($p<0.001$). Of SSIs, 79% (2,848), and 88% (1,401) of PJIs were microbiologically confirmed; 40% of which were caused by SA (range by year, 12-50%).The proportion of PJIs attributable to SA has increased by 3.6% (95% CI: 2.2-5.0%) each year.

Conclusions:

Despite the decreasing trend of overall SSI rate, we found a significant increase in severe infections caused by SA following hip and knee arthroplasty. Evaluation of evidence-based prevention measures implemented for SSIs might be useful.

Subject: Surveillance

Keywords: Surgical site infections, Staphylococcus aureus,Prosthetic joint infection ,Surveillance

ABSTRACT ID: 4

PRESENTED BY: Jana Prattingerová / jana.prattingerova@gmail.com

19.4. Surveillance of M. chimaera invasive infections after cardiac surgery under cardiopulmonary bypass and survey on practices in matters of heater-cooler units (HCUs)

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Background:

In the context of the first European risk assessment about Mycobacterium chimaera invasive infections following cardiac surgery under cardiopulmonary bypass in 2015, two French cases were confirmed. In 2017, we carried out an epidemiological follow-up and an evaluation of practices.

Methods:

We conducted the survey during the period January 2015 - June 2017. It concerned all cardiac surgery services in French hospital. We performed a retrospective surveillance by questionnaire of invasive cardiovascular infections and an evaluation of maintenance practices of HCUs (changing water and disinfection) and microbiological controls of HCUs.

Results:

56 hospitals (participation rate: 92%) participated in the survey. Incidence ratios of patients re-operated for infectious endocarditis were of 0.97 in 2015 and 1.07 in 2016. No case of invasive infection with M. chimaera was identified while an active case finding was carried out in 54% of hospitals.

The current use of 227 HCUs was reported by all services, which corresponds to 5.8 HCUs per 1,000 surgical interventions. The maintenance procedure of HCUs was reportedly following manufacturer's recommendations in 68% of hospitals. Howerver regarding to each step of the maintenance procedure, the overall compliance was of 9%. A large part (86%) of hospitals consider that the manufacturer recommendations were very difficult to apply. Microbiological specimen were collected in

75% of hospitals; 56% of HCUs were contaminated by common bacterial flora and 23% by Mycobacterium avium complex.

Conclusions:

Even if no new case of M. chimaera infection was identified during the study period, the HCUs were frequently contaminated. The applied procedures of maintenance of HCUs were heterogeneous. These results suggest the need for national reflection on recommendations for the maintenance of HCUs.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: Mycobacterium Infections, Bacterial Endocarditis, Epidemiology, Surveillance, Risk Assessment

ABSTRACT ID: 433

PRESENTED BY: Côme Dania / come.daniau@santepubliquefrance.fr

19.5. EuroSCORE developed for predicting operative mortality for patients undergoing isolated coronary artery bypass grafting surgery do not predict surgical site infections in Norway

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Background:

Surgical site infection (SSI) is a serious complication after coronary artery bypass grafting (CABG) and is associated with burden for both patients and health-care system. Hospital-specific incidence of SSI is a national quality indicator in Norway. The EuroSCORE (European System for Cardiac Operative Risk Evaluation), a method for predicting post-operative mortality for patients undergoing cardiac surgery, is included in the Norwegian surveillance system for Health Care-Associated Infections (NOIS). We aimed to determine whether EuroSCORE can predict risk of infection after isolated CABG and thus be useful for risk stratification.

Methods:

We carried out a register-based cohort study using data from NOIS. We included patients who underwent isolated CABG surgery between 2010 – 2017 in five hospitals that reported EuroSCORE. We expressed the incidence of general and deep SSI as the number of infections within 25 days after surgery over the total number of procedures. To evaluate the existence of a relationship between the EuroSCORE and risk of infection, we used ttest, logistic regression and ROC curves.

Results:

In total, 6069 patients were included in the study. A total of 312 (5.1%) SSIs were reported, ranging from 3.8–8.4%, including 68 (1.1%) deep infections. 1262 (21%) observations had missing EuroSCORE. There was no association between EuroSCORE and SSI and the ROC curve indicated that the EuroSCORE cannot predict SSI in general or deep infections after CABG (C-statistics=0.37 and 0.46).

Conclusions:

The lack of association between EuroSCORE and risk of SSIs suggests that EuroSCORE is not useful for risk adjustment. We recommend exploring reasons for differing incidences between hospitals and active use of the data locally and nationally to improve patient safety.

Subject: Surveillance

Keywords: Public Health Surveillance,Coronary Artery Bypass,Surgical Wound Infection,incidence

ABSTRACT ID: 148

PRESENTED BY: Laura Espenhain / laura_espenhain@hotmail.com

19.6. Attributable mortality and excess length of stay due to surgical site infections following cholecystectomy, European Union/European Economic Area (EU/EEA), 2009-2015

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Background:

Since 2008, ECDC has collated surveillance data on surgical site infections (SSIs), including SSIs following cholecystectomy, a common surgical procedure in the EU/EEA. In this study, we estimated the attributable mortality and excess length of stay (LOS) due to SSIs following cholecystectomy using EU/EEA surveillance data.

Methods:

We included SSIs diagnosed during hospital stay from seven countries collecting cholecystectomy data. To estimate the attributable mortality prior to discharge in patients with an SSI, we used a retrospective cohort analysis, matching patients with SSI with patients without SSI (controls). We matched patients using surgical procedure subtype, laparoscopic/open procedure, year, hospital, SSI risk index, followed by nearest neighbour propensity score matching for age, gender and LOS (until discharge or onset of SSI). We calculated the attributable mortality and excess LOS as the difference between matched patients.

Results:

Data were available on 29,942 cholecystectomies and 274 (0.9%) in-hospital SSIs. We successfully matched 252 patients with an SSI with 252 controls. Mortality in patients with an SSI was 8.7% (22/252) compared with 3.6% (9/252) in matched controls, resulting in an overall attributable mortality of 5.2% (95% confidence interval (CI) 0.6-9.7%). The attributable mortality of SSI was 4.0% (95%CI -2.4-10.4%) for laparoscopic procedures and 6.9% (95%CI -0.6-12.5%) for open procedures. The median LOS was 15.5 days [Interquartile range (IQR) 10-23] for patients with an SSI and 6 days [IQR 4-9] for the controls; an excess LOS of 9.5 days.

Conclusions:

In our study, SSIs following cholecystectomy led to increased mortality and LOS, although our analysis is limited by full patient risk profiles not being available. Adherence to international guidelines on SSI prevention is recommended to reduce the frequency of SSIs and associated mortality.

Subject: Surveillance

Keywords: Cholecystectomy,Surgical Wound Infection,Mortality

ABSTRACT ID: 369

PRESENTED BY: Tommi Kärki / tommi.karki@ecdc.europa.eu

Track 20: Sexually transmitted infections (3): Intervention

Moderator:

Aura Andreasen

Abstracts

20.1. Spontaneous clearance of urogenital, anorectal and oropharyngeal Chlamydia trachomatis and Neisseria gonorrhoeae in women, MSM and heterosexual men visiting the STI clinic,

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Background:

Chlamydia trachomatis(CT) and Neisseria gonorrhoeae(NG) infections can clear without treatment. Despite the high prevalence of anorectal infections in both men who have sex with men (MSM) and women, studies on anorectal clearance are scarce. Moreover it is unknown whether bacterial load affects urogenital and anorectal CT clearance. Here, CT and NG clearance is assessed in three anatomic sites of men and women.

Methods:

CT and NG positive MSM, heterosexual men and women >18 years of age who attended our STI clinic underwent a repeat PCR test when returning for treatment between 2011-2013 (480 consultations). Real-time PCR was used to quantify CT OmpA-gene copies/ml (log10 transformed). Clearance rates were calculated; for CT multivariable logistic regression was used to evaluate predictors for clearance.

Results:

CT clearance was 9.1%(10/110) for urine, 6.8%(20/292) for vaginal swabs, 12.7%(8/63) for anorectal swabs (i.e., 4.0%(1/25) in MSM and 18.4%(7/38) in women) and 57.1%(4/7) for oropharyngeal swabs. For NG this was 33.3%(2/6), 28.6%(2/7), 20.0%(2/10), and 27.3%(6/22) respectively. The number of days between tests (mean 11,SD 6) was not associated with clearance. Lower bacterial load in the screening sample was the only predictor for CT clearance (urine samples; 1.2 versus 2.6 CT/ml,P=0.001, vaginal swabs; 2.1 versus 5.2 CT/ml,P<0.0001, anorectal swabs; 2.0 versus 3.7 CT/ml,P=0.002).

Conclusions:

This study reports the largest number of anorectal infections tested for CT and NG clearance to date. Spontaneous clearance in all sample types in men and women is substantial with between 7-57% for CT, and between 20-33% for NG (low absolute numbers). CT clearance was associated with a lower load in the screening sample. Insight in viability of CT and NG infections is needed for further interpretation of these results.

Subject: Microbiology

Keywords: Chlamydia trachomatis,Neisseria gonorrhoea,Sexually transmitted infections (STIs),STI clinic,Bacterial load,Microbiology

ABSTRACT ID: 188

PRESENTED BY: Geneviève AFS van Liere / genevieve.vanliere@ggdzl.nl

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20.2. Post-exposure prophylaxis for HIV after sexual exposure is a marker of future risk of sexually transmitted infections among heterosexual STI clinic attendees

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Background:

Post-exposure prophylaxis following sexual exposure (PEPSE) is a marker of subsequent HIV and sexually transmitted infections (STI) in men who have sex with men (MSM). We investigated if the association between PEPSE and future STI acquisition also applied to heterosexuals.

Methods:

We extracted data from the GUMCAD STI Surveillance System on heterosexuals aged >15 years who attended an STI clinic in England in 2014/2015. We identified two groups: those prescribed PEPSE and those not, and selected the day of PEPSE prescription or a random attendance as the respective baseline attendances. Inclusion criteria at baseline were HIV- negativity, no known PEPSE in the prior year, and ≥1 full HIV/STI screen 43-365 days during follow-up. We compared the two groups in terms of: a) sociodemographic differences at baseline using

Pearson's chi-squared test, b) incidence and hazard rate of HIV/STIs (HIV, chlamydia, gonorrhoea, syphilis) within 43-365 days of baseline using Cox regression modelling (adjusting for gender, age, ethnicity, and number of HIV/STI screens during follow-up), and c) time to HIV/STI diagnosis using Kaplan-Meier analysis.

Results:

Among 254,868 eligible heterosexuals, 600 (2.4%) received PEPSE. A higher proportion of individuals given PEPSE were male, >24 years old, Black/Asian, and had multiple HIV/STI screens during follow-up (all p<0.01). HIV/STI incidence was 5.1 per 100 person-years (95% confidence interval: 5.0-5.2) in the non-PEPSE group and 8.6 (95%CI: 6.0-12.4) in the PEPSE group. The adjusted hazard ratio for an STI diagnosis was 1.9 (95%CI: 1.3-2.8; p<0.001).

Conclusions:

Heterosexuals receiving PEPSE are at higher risk of subsequent HIV/STI acquisition, suggesting sustained risk behaviour for up to a year following prescription. Heterosexuals using PEPSE may benefit from additional risk prevention interventions, such as motivational interviewing or PrEP.

Subject: Surveillance

Keywords: Post-Exposure Prophylaxis, England, Kaplan-Meier Estimates, Proportional Hazards Models, HIV Infections, Heterosexuals,Sexually Transmitted Infections

ABSTRACT ID: 481

PRESENTED BY: Paula Blomquist / paula.blomquist@phe.gov.uk

20.3. Success factors for vaccination completion in a targeted hepatitis B vaccination program directed at people using hard drugs

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Background:

To prevent people who use hard drugs (PWUD) from getting infected with hepatitis B virus (HBV), targeted vaccination strategies are necessary. The aim of this study is to give an overview of the activities directed at PWUD in a decentralised vaccination program in the Netherlands and report on factors associated with completion of a standard series of three vaccinations against HBV.

Methods:

Data were used from PWUD who were immunised against hepatitis B between 2002 and 2011 in the Netherlands. A standard series of three vaccinations (at months 0, 1 and 6) was offered at inclusion and continued if serological markers for past or chronic HBV infection were absent. A logistic regression analysis was performed with completion of a vaccination series (i.e. at least three vaccinations) as a dependent variable.

Results:

The program reached 18.054 PWUD. Of the 15.746 participants eligible for vaccination (i.e. neither a carrier of hepatitis B, nor immune to hepatitis B), 9.089 (58%) completed a series of three hepatitis B vaccinations. Factors associated with a higher completion rate of a vaccination series (P<0.01) were start of vaccination in the earlier years of the program, higher age, female gender, intravenous drug use, vaccine administration by addiction care centres and flexibility in location of vaccine delivery.

Conclusions:

Despite using a standard HBV vaccination schedule and no financial incentives, reasonable vaccination completion was achieved among PWUD. Our results suggest that flexibility in location of vaccination and administration of vaccines by healthcare workers with sustainable contact with PWUD could improve vaccination programs for this risk-group.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: Hepatitis B, Vaccination, Drug users, Public Health

ABSTRACT ID: 27

PRESENTED BY: Stijn Raven / stijn.raven@radboudumc.nl

20.4. Uptake and Acceptability of Pre-exposure prophylaxis (PrEP) for HIV in Wales, March 2018

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Background:

Pre-exposure prophylaxis for HIV (PrEP) provision started in sexual health clinics in Wales in July 2017. We assess the uptake and acceptability of PrEP in the first 6 months of roll-out.

Methods:

Data were collected through the existing Sexual Health in Wales Surveillance System (SWS). PrEP codes were added to SWS to capture eligibility, outcome of the offer of PrEP, and reasons for declining. Eligibility categories were defined based on nationally agreed criteria (e.g.: men who have sex with men (MSM) who report condomless anal intercourse (CAI) in the past 3 months and affirm likelihood of CAI in the next 3 months; partners of HIV positive individuals not known to be virally suppressed who anticipate condomless intercourse).

Results:

In six months, 516 people were eligible and 296 started PrEP (57%). Ten did not start PrEP because of medical contraindication, and 157 initially declined it.

Of the 157 people who declined, 88 had reported reason(s): 50 (57%) did not believe themselves at risk, 21 (24%) preferred using other protection, 15 (17%) mentioned side effects concerns, 8 (9%) did not want medication, and 2 (2%) did not want monitoring.

Most eligible people (96%, 494/516) were MSM. These represent 17% of all reported MSM attending during the same period.

Of those who started PrEP, 290/296 (98%) were MSM (10% of MSM attendees).

Conclusions:

Despite encouraging uptake of PrEP amongst those eligible, the fact that the main reason for decline was self-perception as “no-risk” is of concern given the eligibility criteria. This warrants further analyses on STI/HIV outcomes of this cohort, and a closer look at reasons for decline. Interventions to improve self-perception of risk may help decision making around PrEP use.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: HIV, Pre-Exposure Prophylaxis, Wales, Intervention, Uptake, Acceptability

ABSTRACT ID: 117

PRESENTED BY: Laia Fina / laia.fina@wales.nhs.uk

20.5. Cardiovascular disease (CVD) risk factors in a local population of HIV positive patients

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Background:

Besides the well-established risk factors for CVD, HIV patients have additional risk due to dyslipidemia resulting from the infection and its treatment. Our objective was to identify the most significant risk factors for CVD amongst HIV patients in Malta.

Methods:

This was a retrospective observational study. Data collected from medical notes included demographics, CVD risk factors, development of CVD and type of antiretroviral treatment (ART).

HIV viral load and lipid profiles at time of diagnosis and last visit were obtained. The Framingham Risk Score (FRS) was also calculated at both visits to determine the 10-year cardiovascular risk.

Results:

Of the 101 patients, 77 were males. Mean age at diagnosis was 38.2 years and mean follow-up duration was 8.2 years. 38 were current smokers and 8 were diabetic.

There was no significant correlation between development of CVD and gender, hypertension, smoking or alcohol. However, there was a strong association between baseline LDL and diabetes ($p=0.008$) and between both these variables and CVD ($p=<0.01$). Mean FRS score was significantly higher in patients who developed CVD ($p=0.001$).

We found no significant relationship between CVD and viral suppression ($p=0.634$) or when comparing CVD rates between the two commonest ART combinations; NRTI/NNRTI and NRTI/PI ($p=0.695$).

Conclusions:

Our findings confirm diabetes and elevated LDL as important CVD risk factors even in HIV patients. Furthermore, FRS appears to be a reliable screening tool in this population.

As HIV life expectancy improves, morbidity and mortality resulting from CVD is likely to increase. Hence, identifying those at highest risk and addressing their modifiable risk factors is of utmost importance.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: HIV infections, risk factors, cardiovascular diseases, diabetes mellitus, reverse transcriptase inhibitors, life expectancy

ABSTRACT ID: 373

PRESENTED BY: Sarah Vella / smv2610@gmail.com

Track 21: Vaccine- preventable diseases (3): Burden of disease

Moderator:

Frantiska Hruba

Abstracts

21.1. Rationale of maintaining the first dose of MMR at 18 months in Sweden

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Background:

The child health programme in Sweden includes routine visits at 12 and 18 months. At the 12-month visit, medical staff give hexavalent and pneumococcal vaccines and conduct a medical examination. The first dose of vaccine against measles, mumps and rubella (MMR1) has been offered at 18 months since 1982. Measles and rubella have been eliminated and mumps is under control. Children born today receive lower levels of maternal antibodies than in the pre-vaccine era and concerns were raised about the risk of measles infection before their first vaccination, especially during travels abroad. Therefore we analysed factors of importance for deciding at which age to offer MMR1 within the Swedish national vaccination programme.

Methods:

We analysed registry data and performed literature reviews, interviews and surveys to gather necessary information. Two groups of key national professionals reviewed the results and provided feedback in facilitated workshops.

Results:

In the last ten years, 3,8 cases of measles were reported annually among children below 18 months; mumps and rubella cases were rare. MMR1 vaccination coverage consistently exceeded 95% since 2006. The response to MMR-vaccination improves also during the second year of life. Health-care staff are reluctant to overload the comprehensive 12-month visit and, like parents, hesitant to give three shots at once. Introducing an additional routine visit, e.g. at 15 months, would cost approximately 2 million Euro annually, but the gains in immunity would be very small.

Conclusions:

Based on the results, it was decided to maintain MMR1 at 18 months, to ensure good long-term immunity in the population and balance the child health care services. However, children travelling abroad should receive their first dose earlier, due to increased risk of infection.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: measles mumps rubella immunization programme

ABSTRACT ID: 333

PRESENTED BY: Hélène Englund / helene.englund@folkhalsomyndigheten.se

21.2. Increasing incidence of notified cases of Herpes zoster in the German federal state of Brandenburg 2009 to 2017

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Background:

Population based incidence estimates for herpes zoster [HZ] are rare. Brandenburg was the first German federal state introducing mandatory notification of HZ in 2009 to monitor the effects of the varicella vaccination, recommended in Germany since 2004, on HZ incidence. In this study we describe surveillance data of HZ in Brandenburg to foster understanding of the burden of this vaccine preventable disease.

Methods:

We analysed HZ notifications from all 18 districts (2010-2017) to assess HZ incidence, its overall and age-specific trends, age and spatial distributions and the proportion of hospitalized cases. Fitting a negative binominal regression model, we determined time, age- and locations-specific risk ratios [IRR] per year. Additionally, we analysed nationwide data from the varicella sentinel system [VSS] (2013-2016) and Brandenburg hospital diagnosis data [HD] (2010-2016).

Results:

Notifications increased steadily from 260 to 1,827 cases with age-standardized annual incidence rising from 18 to 139 per 100,000 inhabitants. Cases occurred in all age groups and the age-related incidence increased with age, peaking in the age-group >80 years. Among notified cases 190/7,881 (2.4%) were hospitalized due to HZ. Incidence increased in both sexes, all districts and nearly all 5-year-age groups (overall IRR=1.3, 95% confidence interval [95%CI]=1.28-1.39), except in the age group 5-9 years (IRR=0.92, 95% CI=0.81-1.05, n=73). Furthermore, incidence increased in VSS data (overall IRR 1.07, 95%CI=1.04-1.10) and Brandenburg HD data (overall IRR=1.08, 95%CI=1.06-1.09).

Conclusions:

HZ comprises a high disease burden in Brandenburg. The observed increase in surveillance data might be influenced by the progressing implementation of mandatory notification. However, trends in VSS and HD strongly indicate a true increase in HZ incidence. We recommend the analysis of statutory health insurance data to further support these findings.

Subject: Burden of disease

Keywords: herpes zoster,statutory surveillance,Brandenburg,burden of disease,varicella vaccination,VZV,Germany,shingles

ABSTRACT ID: 314

PRESENTED BY: Benjamin Tittmann / tittmannb@rki.de

21.3. Disease burden of neonatal invasive Group B Streptococcal infection in the Netherlands

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Background:

Neonatal invasive infection with Group B Streptococcus (Streptococcus agalactiae, GBS) is a rare but serious disease. Children infected with GBS during birth or in the neonatal period can present with meningitis and/or sepsis. Maternal GBS vaccines are in development, but not yet on the market. To prepare for future introduction of maternal GBS vaccine, we aimed to estimate the current disease burden of neonatal invasive GBS infection in the Netherlands.

Methods:

We constructed a disease progression model, based on national data, literature and expert consultation, using the Burden of Communicable

Diseases in Europe methodology. Probabilities of neurodevelopmental impairment were derived from literature and national data. Annual numbers of cases were derived from the register of the National Reference Laboratory for Bacterial Meningitis, adjusted for underreporting. Disease burden was expressed in disability-adjusted life years, combining mortality and morbidity due to neonatal GBS disease.

Results:

Incidence of neonatal invasive GBS disease has risen steadily in the period 1996-2016. Preliminary study results give an average estimate of 776 (95% CI 640-922) DALY per year in the Netherlands, corresponding to 4.6 DALY per 100,000 population. This estimate comprises disease burden due to acute illness (sepsis/meningitis), neonatal death and neurodevelopmental impairment. This estimate is comparable to the annual estimated burden due to meningococcal disease or invasive H. influenzae infection in the Netherlands in 2016. At the conference, we will present the final estimates of the disease burden of neonatal invasive GBS infection in the Netherlands.

Conclusions:

Neonatal invasive GBS infections cause a significant and potentially vaccine-preventable disease burden in the Netherlands. More research is needed to extend our model to include cost of illness and societal burden.

Subject: Burden of disease

Keywords: Streptococcus agalactiae,neonatal sepsis,bacterial meningitis

ABSTRACT ID: 38

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

21.4. Assessing the burden of congenital rubella syndrome in Europe: A review of methods towards verifying elimination

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Background:

The completeness of European national congenital rubella syndrome (CRS) surveillance data does not meet WHO- recommended standards for rubella elimination verification. Supplemental CRS burden assessment methods are required to enable more accurate case reporting. With the aim of developing a generic protocol for retrospective CRS case identification in EU/EEA countries, we performed an extensive literature review of CRS burden assessment methods.

Methods:

We used the PubMed search engine to retrieve peer-reviewed articles reporting on CRS burden assessments using case counts or incidence calculations published up to April 2017. We excluded seroprevalence studies and those based solely on routine surveillance data. We summarised study characteristics and CRS burden assessment methodologies, including prospective vs retrospective study type, study population, inclusion criteria, case definitions and data sources used.

Results : We identified 771 articles reporting CRS burden assessments, published between July 1964 and March 2017. Thirty-six papers remained after applying exclusion criteria, 26 (72%) of which were of retrospective design. Twelve (33%) studies explicitly reported using WHO or EU case definitions. Data sources documented in retrospective studies were maternity and tertiary hospital records (n=10), laboratory registers (n=3), birth records (n=1), birth defect registries (n=2), pregnancy termination records (n=2), surveys (n=7), surveillance data (n=10), insurance and health system data (n=1), literature review (n=4), and immunisation programmes (n=1). Nine (35%) studies used a combination of data sources. Where evaluated (n=4), retrospective studies reported higher sensitivity compared to routine surveillance data.

Conclusions:

We suggest that countries measure CRS burden by reviewing maternal and tertiary care records, and supplement this core assessment using optional methods tailored to the country. This adaptable, generic protocol for retrospective CRS burden assessment will support verification of rubella elimination in EU/EEA countries.

Subject: Burden of disease

Keywords: rubella, congenital rubella syndrome, congenital rubella infection, disease burden, literature review

ABSTRACT ID: 343

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21.5. Mortality and causes of death analysis in Rabat commune, 2013-2015

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Background:

Mortality statistics and causes of death play a key role in the general information system relating to the state of health. They are used as a tool for evaluating health systems and evidence-based health policy to determine strategic choices. The aim of our study was to describe the mortality characteristics and causes of death during the 2013-2015 period in the commune of Rabat.

Methods:

We used 2013–2015 data from death certificates registered at the Rabat Communal Office of Hygiene via underlying cause of death. We calculated proportionate mortality ratios (PMRs) and potential years of life lost with a cut-off point at 65 years using Moroccan sex-specific life expectancy for 2014.

Results:

During the 2013-2015 period, the Rabat Commune recorded 20 476 deaths, of which 9 045 were Rabat residents. Cardiovascular diseases were the leading cause of death with 23.2% and were responsible with cancer and diabetes of 53.2% deaths. The ranking vary by sex and age group. The main cause of death was represented by non-communicable diseases group (83.4% of total deaths) followed by communicable diseases (12.8%) and injuries with 3.9%. The number of years of life lost in Rabat population between 2013-2015 amounts to 28 041. The first three diseases responsible of these potential years of life lost (PYLL) were cancer with 12700 PYLL, the external causes 7622 PYLL and male predominance, and circulatory system with 6 282 PYLL.

Conclusions:

In Rabat, the health system is marked by epidemiological transition; a significant mortality related to non-communicable diseases compared to that of communicable disease. Strategic choices must consolidate the prevention and fight against communicable diseases, also deal the emergence of chronic diseases and cancers.

Subject: Burden of disease

Keywords: motality ,underlying cause of death,potential years of life lost ,epidemiological transition

ABSTRACT ID: 504

PRESENTED BY: Hind Wadifi / wadifihind@yahoo.fr

21.6. Analysis of mumps surveillance data of Cairo, Egypt from 2012 to 2017

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Background:

Although two doses of mumps vaccine has been incorporated in Egyptian national childhood vaccination program since 2008, outbreaks have been witnessed in the country. Routine analysis of data is important to know disease burden and detect outbreaks.

Methods:

Reported cases were extracted from National Electronic Disease Surveillance System (NEDSS) from 2012 to 2017. Mumps cases were classified according to criteria of surveillance case definition of national surveillance guidelines into suspected (acute salivary gland swelling unexplained by another more likely diagnosis) and confirmed cases (positive laboratory confirmation for mumps virus). Descriptive analysis was conducted according to age, gender, date, residence, laboratory test and MMR vaccination status.

Results:

In total, 4091 cases registered in Cairo from 2012 to 2017. Diagnosis was laboratory confirmed in 19% of cases, while 79 % were classified as suspected. There was an obvious increase in reported cases in 2012 (772 cases) which reached the peak in 2013 (1,772 cases). The number declined in 2014 (252 cases) and 2015 (168 cases) then increased in 2016 (430) and (697) in 2017. The 5 to ‹15 year age group was the most affected (56 %; 2372 of 4091 cases) followed by 1 to ‹5 age group (874 cases). The least affected age group was ‹ 1 year (41 cases). Males represented 64.2% of cases. Data showed seasonal pattern of disease in October and March. About (13.5%; 550) of cases were documented to be immunized by MMR vaccine.

Conclusions:

Our study showed children at school age were at increased risk for mumps infection we recommend to add more details about vaccination status and number of doses of MMR vaccine were administrated in our national surveillance system.

Subject: Burden of disease

Keywords: Surveillance, Analysis, Mumps, MMR vaccine.

ABSTRACT ID: 492

PRESENTED BY: Hodaallah Yussuf / dr.hodaallah@hotmail.com

Track 22: Vaccine- preventable diseases (4): Vaccine effectiveness

Moderator:

Arnold Bosman

Abstracts

22.1. Seasonal influenza vaccination in French people with diabetes from 2006 to 2015: estimating transition probabilities from nonvaccinated to vaccinated and influencing factors using Markov model

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Background:

People with diabetes are at increased risk of seasonal influenza and its complications. Seasonal influenza vaccination (SIV) is recommended yearly to these patients in most countries. SIV coverage remains far below the target of 75% however and has decreased since the 2009 pandemic.

Over a 10-year period, we aimed to estimate transition probabilities between SIV states (nonvaccinated, NoV / vaccinated, V) and to identify factors that influence these transitions.

Methods:

Among a representative sample of the French National Health Insurance Fund beneficiaries, we identified patients with diabetes <=65 years (n=29,257), followed from 2006 through 2015. We used SIV reimbursement claims, and a time- inhomogeneous Markov model with piecewise constant transition intensities to estimate transition probabilities. Associated factors included demographic characteristics and various health events (e.g., aggravation of diabetes‘ severity, hospitalisation for diabetes or influenza).

Results:

Over the 10-year period, the probability of getting SIV at season n+1 for patients who had already received SIV at season n was 0.83 (V--V transition); the NoV--NoV transition probability was 0.90. The NoV—V transition probability was 0.10 and significantly lower after 2009. The V--NoV transition probability was 0.17 and higher among women and younger patients. Further analyses will explore the influence of health events on these transitions.

Conclusions:

Almost 20% of patients getting SIV during one season will not during the following season. These preliminary results suggest that women and young patients are more prone to irregular SIV. Knowing influence of health events on SIV transition probabilities will help better understand the role of health evolution in SIV and identify moments of patients’ lives that could offer opportunities to make them aware of the benefits of SIV.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: Diabetes Mellitus; Influenza Vaccines; Vaccination; Markov Chains; Follow-Up Studies

ABSTRACT ID: 183

PRESENTED BY: Sébastien Cortaredona / aurelie.bocquier@inserm.fr

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22.2. Epidemiological impact on invasive pneumococcal disease of the 10-valent PCV as part of the Austrian childhood immunisation programme in children and adults, 2009-2017

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Background:

A 10-valent pneumococcal conjugate vaccine (PCV10) with a 2+1 schedule was introduced into the Austrian childhood immunisation programme in 2012. We evaluated the effects on the occurrence of invasive pneumococcal disease (IPD) in the Austrian population using before-after analyses and interrupted time series analyses of national surveillance data.

Methods:

The study period was divided into pre- (2009-2011) and post-vaccination period (2013-2017), regarding 2012 as transition year. We defined vaccine-type (VT)-IPD and PCV10-related type IPDs (6A, 19A) as intervention outcomes and non-VT IPD as control outcome. We calculated the pre-to-post percentage change in the average monthly incidence rate among <5, 5-49 and 50+ years old. In order to control for overall and seasonal trends monthly incidence data of 5-49 and 50+ years old were also analysed using segmented negative binomial regression. We calculated the percentage reduction from the modelled number of cases in the post-period.

Results:

We found a VT-IPD rate reduction of 58% (95% CI: 30%; 74%) among <5 years old and a VT-IPD case reduction of 67% (95% CI: 32%; 84%) among the 50+ years old in the post-period, compared to the pre-period. There was neither a pre-to-post reduction in the second intervention outcome, the 6A-, 19A-ST IPD nor in the non-VT IPDs control outcome. The VT-IPD among 5-49 years old remained unchanged in the post-period.

Conclusions: Our population-based study adds to the evidence on the direct and indirect effectiveness of PCV10 as part of the childhood immunisation programme in reducing VT-IPD in children and adults. Segmented regression proved to be a valuable method for evaluating intervention effects adjusted for time series trends. There was no evidence of cross- protection for serotypes 6A and 19A.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: Pneumococcal Infections, Interrupted Time Series, Regression Analysis, PCV10

ABSTRACT ID: 459

PRESENTED BY: Lukas Richter / lukas.richter@ages.at

22.3. Effectiveness and impact of the 13-valent pneumococcal conjugate vaccine against pneumococcal meningitis in European children under five years of age: results of SpIDnet multicentre study

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Background:

SpIDnet conducts enhanced population-based surveillance for invasive pneumococcal disease in 13 European sites. Using surveillance data on clinical presentation, we measured the effectiveness and impact of 13-valent pneumococcal conjugate vaccine (PCV13) against pneumococcal meningitis (PM) in children under five years-old.

Methods:

To measure PCV13 effectiveness, we compared the vaccination status of PM cases caused by PCV13 serotypes to that of nonPCV13 PM (controls) reported from January 2012 to December 2016. We calculated pooled PCV13 effectiveness as (1-odds ratio)*100, adjusted for age group, underlying conditions, notification year and site. To measure PCV13 impact on PM, we calculated site specific incidence rate ratios (IRR) comparing PM incidence by serotype categories in each of the six PCV13 years to the PCV7 period. We calculated pooled IRRs with 95% confidence intervals (CI) using random effects meta-analysis, and impact as (1-IRR)*100.

Results:

In the PCV13 effectiveness study, we included 45 cases and 325 controls. Serotypes 19A and 7F were the most frequent among cases: 12 (27%) and 8 (18%), respectively. The effectiveness of at least one dose PCV13 was 78% (95%CI: 44-92). All-type PM incidence ranged 1.7-5.1/100,000 in the PCV7 period and 1.1-3.4/100,000 in 2016. Six years after PCV13 introduction, all-type, PCV7 and additional six PCV13 serotype PM incidence decreased by 29% (IRR=0.71, 95%CI: 0.56-0.90), 79% (IRR=0.21, 95%CI: 0.10-0.43) and 87% (IRR=0.13, 95%CI:0.06-0.27), respectively. NonPCV13 PM incidence increased each year up to 79% (IRR=1.79; 95%CI: 1.23-2.61) in 2016.

Conclusions: SpIDnet results suggest a good PCV13 effectiveness and impact of vaccination programmes against PM caused by vaccine serotypes. The increase of nonPCV13 PM incidence indicates serotype replacement. Clinical data are crucial for monitoring the severity of pneumococcal disease and the performance of conjugate vaccines.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

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

ABSTRACT ID: 203

PRESENTED BY: Camelia Savulescu / c.savulescu@epiconcept.fr

22.4. Invasive pneumococcal disease in Latvia six years after PCV10 introduction, 2012-2017

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Background:

In 2010 in Latvia, invasive pneumococcal disease (IPD) became notifiable for physicians and vaccination of infants with 4 doses of 7–valent pneumococcal conjugate vaccine (PCV7) commenced. In 2012, 10–valent pneumococcal conjugate vaccine (PCV10) (3 doses) vaccination was introduced. We analysed IPD surveillance data for trends and impact of vaccine on disease serotypes in order to provide recommendation for further actions prior to changing vaccination policy to PCV13.

Methods:

Laboratory confirmed IPD cases are passively notified to the Centre for Disease Prevention and Control of Latvia by laboratories and clinicians. We calculated incidence by age, sex, case fatality and trend in serotypes.

Results:

From 2012 to 2017, 390 cases of IPD were reported, mean annual incidence 3.3/100,000. The notified incidence remained stable from 2012-2014 (2.7), peaked in 2015 (4.4) and fell to 3.8 in 2017. Riga represented 73% (284/390) notifications yet only 50% of the population. Mean annual incidence was highest in infants (5.6) and in >=65 years (5.5). Incidence was higher in males (26.4) compared to females (13.7) (IR-1.9 CI(1.6-2.4)). Case fatality was 18% (71/390) and 24% (31/127) in cases aged >=65 years.

81% (317/390) of isolates were serotyped. The proportion of PCV10 vaccine serotypes fell from 53% (20/38) in 2012 to 26% (18/68) in 2017 (chi2 test for trend p=.0002). In 2017, 29% (20/68) serotypes were 23-valent pneumococcal polysaccharide vaccine (PPV23) and 28% (19/68) non-vaccine. The same trends are seen stratifying by age groups (5-14, 15-64 years and >=65 years).

Conclusions:

Surveillance data indicate evidence of serotype replacement. Surveillance evaluation should asses the representativeness of notification, especially from outside Riga. Furthermore S. pneumoniae carriage study may be useful to characterise serotype circulation.

Subject: Surveillance

Keywords: invasive pneumococcal disease,serotype replacement,10–valent pneumococcal conjugate vaccine

ABSTRACT ID: 123

PRESENTED BY: Larisa Savrasova / larisa.savrasova@spkc.gov.lv

22.5. Rethinking the efficacy of acellular pertussis vaccines for primary immunization

CANCELLED

22.6. Evidence of vaccine effect on pneumococcal meningitis cases in France: a geographical analysis

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Background: Geographic variation in Invasive Pneumococcal Diseases (IPD) incidence and serotypes distribution were observed before and after pneumococcal conjugate vaccine (PCV) introduction at regional level and between Europe and US. Even if Pneumococcal Meningitis (PM) incidences seems to be less variable compared to other IPD, differences in vaccine coverage and in prevalence of other risk factors could still play a role.

Methods: This paper analyses variability in local annual PM incidences in all départements in metropolitan France from 2001 to 2016 through mixed-effects Poisson model by exploring and quantifying the contribution of local vaccine coverage and the geographical landscape type.

Results:

Vaccine coverage, estimated from Nation Health Insurance reimbursements data, grew every year until reaching an average of 85% in 2016. Even if vaccine coverage varied among geographic units, our data show a consistency of vaccine efficacy resulting from vaccine coverage among all départements. Cumulative effect of vaccine coverage led in 2016 to local PMs reductions from the prevaccine era ranging from 87% (25th percentile) to 91% (75th percentile) for PCV7-vaccine serotypes PMs and from 58% to 63% for only PCV13-vaccine serotype PMs. Serotype replacement phenomena issued from vaccine coverage is more variable and it is recovered only for PCV7 coverage. Nonvaccine-serotype PMs increases from prevaccine era range among geographic units from a percentage of 98% to a percent of 127%. Landscape type is also shown to play a role, begin the presence of mountainous massifs and rural landscapes a protective factor.

Conclusions:

Our analysis allowed to show and quantify the statistical association between vaccination coverage and PMs cases, taking into account the cumulative effect of a growing vaccine coverage and a geographical and temporal random effect.

Subject: Modelling, bioinformatics and other biostatistical methods

Keywords: Pneumococcal Meningitis,Pneumococcal Conjugate Vaccine ,Vaccine Coverage,Mixed-effects Poisson Model,Bayesian Inference,Geographic Variation

ABSTRACT ID: 167

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Track 23: Policy approaches and evaluation

Moderator:

Charmaine Gauci

Abstracts

23.1. A review of evaluations of the Norwegian Surveillance System for Communicable Diseases: Need for a systematic approach

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Background:

The Norwegian Surveillance System for Communicable Diseases (MSIS) was established in 1975 and includes 68 conditions. Notification criteria are based on clinical findings and/or laboratory confirmation. Data are collected to describe disease incidence, detect outbreaks and evaluate the effects of infection control measures. We performed the first review of studies and evaluations of MSIS including conditions covered, surveillance objectives, study rationale, recommendations and their implementation, to inform future prioritization of evaluations and improve follow-up of recommendations.

Methods:

We conducted a literature search in PubMed and the NIPH archives and included all MSIS studies that documented one or more surveillance attributes from the “CDC Guidelines for Evaluating Public Health Surveillance Systems”. We extracted information on the stated aims and objectives, methods, attributes evaluated, findings and recommendations using a standardized data extraction form. We verified if recommendations were then implemented.

Results:

We identified 19 completed studies: nine evaluations, seven epidemiological studies and three quality assessments. Fifteen studies evaluated the surveillance of one notifiable condition, while four evaluated multiple conditions. Surveillance of 42/68 conditions have never been evaluated until April 2018. The most evaluated attributes were completeness (n=17), timeliness (n=10) and representativeness (n=6). Rationale for the evaluation was stated seven out of nine times. Specific recommendations to improve the systems were followed up partly or completely eight out of 16 times.

Conclusions:

We recommend developing a framework for conducting surveillance evaluations of notifiable conditions in MSIS more systematically. This should include clear evaluation rationales and follow up of recommendations.

Subject: Surveillance

Keywords: Surveillance,Evaluations,Infectious Disease Surveillance

ABSTRACT ID: 219

PRESENTED BY: Astrid Løvlie / astrid.louise.lovlie@fhi.no

23.2. Primary diphtheria immunisation for adults using a low dose vaccine: a literature review,

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Background: In Sweden, high-dose diphtheria and tetanus vaccine (DT) is used for primary vaccination of children and until recently also for adults. Due to recent vaccine shortages and increasing adverse reactions against DT with age, a low dose (LD) diphtheria and tetanus vaccine (dT) was used for individuals ≥7 years for primary vaccination. A systematic review of scientific literature was undertaken to identify studies providing evidence on whether three doses of reduced diphtheria toxoid induce sufficient immunity in unvaccinated adults previously not exposed to diphtheria.

Methods:

PubMed, Cinahl and Scopus online articles published between 1921-10/2017 using key words of “adult” or “elderly” and “diphtheria” or “diphtheria toxoid”, combined with “immunisation” or “vaccination” or “vaccine” were evaluated. Additionally, references of identified articles were screened. Main inclusion criteria were immunity status (seronegative: unvaccinated and no previous diphtheria exposure), age (≥7 years) and vaccine dose (≤ 7.5 Lf, minimum of two doses). Identified articles were graded based on evidence and included in a qualitative synthesis.

Results:

3289 records were identified and screened based on titles, resulting in the exclusion of 3064 articles. 147 more articles were excluded after abstract reading. Full-text of 78 articles was evaluated and 15 relevant records included in a qualitative synthesis. Seven studies met the inclusion criteria (total population n=517) demonstrated seroprotection rates between 62.5-100% after three doses of 1.5-7.5 Lf each. The limited record number was mainly due to the difficulty of identifying studies including unvaccinated seronegative individuals.

Conclusions:

Studies about the immunogenicity of reduced diphtheria toxoid for primary vaccination of adults were scarce and with heterogeneity in design. Although findings should be interpreted with caution, they may help guide policy making in Sweden.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: Diphtheria, Vaccination, Immunization, Antigens, Policy

ABSTRACT ID: 341

PRESENTED BY: Theresa Enkirch / theresa.enkirch@gmail.com

23.3. Evaluating the completeness and timeliness of the surveillance system for invasive meningococcal disease (IMD) in the Netherlands, 2004-2016

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Background:

Enhanced surveillance for confirmed cases of invasive meningococcal disease (IMD) was introduced in the Netherlands in 2003, in which reference laboratory data (NRLBM) is linked with notification data (OSIRIS). With an increasing incidence of IMD in the Netherlands since 2015 and implementation of a new vaccination schedule in 2018, the quality of surveillance information is important for public health decision making. Our objective was to describe the system and evaluate it for data completeness and timeliness.

Methods:

Cases reported in the surveillance system from 2004 to 2016 were included. We corrected the database for missing links and described the proportion of cases in each database. For the OSIRIS data, we used information on mortality, vaccination status, country of infection and serogroup as indicators for record completeness. Notification times to regional and national level were calculated using the reported dates available in the OSIRIS database.

Results:

A total of 2,123 cases were reported in the years 2004-2016, of which 1,968 (93%) were reported by the NRLBM and 1,995 (94%) in OSIRIS. Information on mortality, vaccination status and country of infection was available in 99%, 88% and 97% of all cases, respectively. The serogroup was known in 85% of cases overall, and this was significantly higher (92%) in the years 2012-2016. Regional notification of cases occurred within one working day for 86% of cases and 98% were notified nationally within three working days.

Conclusions:

A well performing IMD surveillance system was demonstrated. Serogroup completeness has improved over the years, but underlining the need for reporting to both the clinical and laboratory surveillance remains important to further improve the overall performance in supporting public health response and vaccination policy.

Subject: Surveillance

Keywords: invasive meningococcal disease,surveillance,evaluation,the Netherlands

ABSTRACT ID: 103

PRESENTED BY: Diederik Brandwagt /diederik.brandwagt@rivm.nl

23.4. Impact of school education targeting vaccination on knowledge and intention to vaccinate of 14 year old schoolchildren in Tirol, Austria

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Background: Measles outbreaks are reported every year in Austria. Adolescents are frequently affected who will be the future parents. We investigated the impact of school lectures focusing on vaccine preventable diseases on knowledge, attitudes and intention to vaccinate of children born in 2002 and 2003.

Methods:

Standardized 45 minutes school lectures were organized in randomly selected schools (intervention group). Forty two questions about knowledge, attitudes and intention to vaccinate were obtained through an anonymous online survey at least 6 weeks after the lectures and from control schools. Questions were equally scored within each category and mean values compared using t-tests. Univariate analysis was conducted to identify determinants for not being vaccinated with MMR.

Results:

357 school children participated in the survey of which 36% attended a lecture. They showed higher mean scores of knowledge (11.7 of 21; p=0.04) compared to those who did not (10.6). The intention to vaccinate was highest for tick-borne encephalitis (91.2%), followed by tetanus (88.7%), polio (86.7%) and measles (84.3%). In the intervention group significantly more participants intended to get vaccinated against pertussis (71.8 versus 56.56.6%; p=0.007) compared to the control group. Several determinants were associated with not being vaccinated against measles mumps rubella: lack of a vaccination card (prevalence ratio (PR)=5.92; 95% CI: 3.30-10.65); doubting the success

of vaccinations (PR=5.37; 95% CI: 2.85-10.11); considering vaccinations unnecessary (PR=3.62 ; 95% CI: 1.97-6.64), and not being aware about the effectiveness of MMR (PR=3.76; 95% CI: 1.19-1185).

Conclusions:

Health education in schools has proven to increase knowledge and intention to vaccinate in school aged children. School children should be a target group besides parents. The Austrian Medical Student Association is continuing this activity in future.

Subject: Preparedness

Keywords: Measles, vaccination,health knowledge attitides practices,asolescent behavious, school enrollment

ABSTRACT ID: 320

PRESENTED BY: Peter Kreidl / peter.kreidl@i-med.ac.at

23.5. Immunization policymaking in the EU/EEA Member States: the complexity behind reality

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Background:

With an ever-increasing number of vaccines on the market, boosted by innovation and a worldwide commitment for strengthening efforts towards infectious diseases elimination, the development of national immunization programmes (NIPs) has matured into robust processes where evidence-based methodologies and frameworks have increasingly been adopted. A key role in the decision making and recommending process is played by National Immunisation Technical Advisory Groups (NITAGs).We assessed the current roles and responsibilities of the existing EU\EEA NITAGs in general and specifically in the process of elaborating operational goals and implementation tools for NIPs, using measles as the example of an important vaccine-preventable disease targeted for elimination

Methods:

In this cross-sectional study, conducted from March to May 2016, an electronic questionnaire was sent to representatives of NITAGs or equivalent bodies in each of the 31 EU/EEA Member States.

Results:

Validated responses from all 31 EU/EEA Member States showed that while most of the countries (26 of 31, 84%) have already constituted a NITAG, the roles and responsibilities of existing committees differ from providing recommendations for immunization schedules (24 of 26, 92%) or vaccine implementation/scientific assessment (20 of 26, 77%) to direct involvement in risk-benefit analysis (13 of 26, 50%) or recommendations on research and development directions (3 of 26, 11.5%). Further the operational goals and implementation tools of the measles NIP are diverse within the EU/EEA.

Conclusions:

The roles and responsibilities of existing 26 EU/EEA NITAGs vary across the Region and this is also reflected in the heterogeneity of operational goals and implementation tools currently being used for measles NIPs. Our study supports previous findings about the disparities in NITAGs processes which could potentially also explain the differences in NIPs across Europe.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: Vaccination, Policy, European Union, Measles,NITAG

ABSTRACT ID: 71

PRESENTED BY: Mihai Alexandru Bica / mihaialexandru.bica@curevac.com

23.6. Seasonal influenza vaccine procurement systems in Europe

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Background:

The EMA requires marketing authorization holders to annually estimate brand-specific influenza vaccine effectiveness. Knowledge on procured vaccines could allow to organize the selection of locations for prospective observational studies around brand availability. We describe influenza vaccine procurement systems in Europe in terms of number of procured brands, timeliness and publicly accessible information.

Methods:

A structured survey on procurement systems for the national seasonal influenza vaccination campaign in Europe was administered to public and private sector experts in 2017/2018.

Results :

The survey was completed for 14 countries. Four main procurement systems were identified: public tenders at the a) national level [Denmark, Finland, Netherlands, Norway, Slovenia, Ireland] or b) regional level [Italy, Sweden, Spain], and direct purchase from manufacturers or wholesalers at the clinic level by c) general practitioners [UK-England] or d) pharmacies [Belgium, France, Germany, Greece].

Generally, countries with national tenders procure 1-2 brands for which 1-to-4-year contracts are concluded in quarter 1 (Q1). National tender outcomes are available online or upon request from authorities. Regional procurement differed across countries. In Italy and Spain 2-5 brands are procured regionally, and (mostly) annual contracts are often concluded late (Q3); instead in Sweden, often one brand is procured regionally, through multi-year contracts. Regional tender outcomes are difficult to find in the public domain. Generally, multiple brands are available in countries with direct purchase, but details are not available publicly.

Conclusions:

Timely and publicly accessible information on brand availability in an upcoming influenza season is limited, especially for countries without national or multiyear tenders. Restrictions may apply to use procurement information to select locations for prospective observational studies assessing brand-specific vaccine effectiveness.

Support: EU/EFPIA IMI-2 Joint Undertaking (DRIVE, grant n°77736). www.drive-eu.org. Twitter:@drive_eu.

Subject: Preparedness

Keywords: immunization programs,influenza vaccines,influenza,equipment and supplies,Europe,vaccines

ABSTRACT ID: 200

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Track 24: Late breakers

Moderator:

Aftab Jasir

Abstracts

24.1. Outbreak of influenza B and group A streptococcal co-infection among international travellers on a coach tour of Scottish Highlands & Islands, May 2018

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Background:

In May 2018, Health Protection Scotland was informed of two hospitalised individuals infected with influenza and group A Streptococcus (GAS). Both travelled on an 11-day coach tour of Scottish Highlands & Islands involving multiple tour companies and composed mainly by elderly American Tourists. Due to the unusual nature of the setting (prolonged close contact, existence of co-infection and potential for disease spread among a vulnerable population), an outbreak management team with representatives from UK and USA was rapidly convened.

Methods:

Following the tour, travellers returned to multiple countries/states. Each country conducted contact tracing and risk assessment. Symptomatic travellers were evaluated and treated. Asymptomatic travellers were offered antibiotic chemoprophylaxis (according to national GAS household contact guidance) and provided with advice should symptoms develop within 30 days. Demographic and clinical presentation details were collected. GAS isolates underwent emm typing and whole genome sequencing (WGS). Influenza characterisation was performed.

Results:

Contact tracing identified another five symptomatic individuals among 21 tour travellers (18 from USA and 3 from UK). Clinical presentations included cough, sore throat and bronchitis. Both hospitalised individuals were infected with influenza B-Yamagata and a rare GAS emm type 1.107 (identical WGS). One had invasive GAS infection and required intensive care management. Six asymptomatic travellers received antibiotic chemoprophylaxis. No further transmission was identified outside the coach outbreak. Decontamination instructions were provided to the coach operator.

Conclusions:

This incident was characterised by complex travel arrangements and challenging contact tracing. This investigation highlights the increased transmissibility of influenza/GAS co-infections among close contacts and the importance of international co-operation in managing disease risk. We recommend that countries consider managing contacts in settings with prolonged close contact as per existing GAS household contact guidance.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: influenza, streptococcal infections, disease outbreaks, travel, international cooperation

ABSTRACT ID: 550

PRESENTED BY: Diogo F. P. Marques / diogo.marques@nhs.net

24.2. Investigation of screening sensitivity to improve sample collection during Acinetobacter baumannii outbreaks, 2018

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Background: In 2017/2018 a Carbapenem-resistant Acinetobacter baumannii outbreak with 22 cases occurred in a German surgical hospital department, declared over in June 2018. Official German screening guidelines recommend taking swabs from nose-pharynx and large skin parts, but lack clear guidance for outbreaks. This often caused too little or excessive sampling during the outbreak. Observed fluctuations in screening results could have resulted in late detection or missing of cases. We aimed to retrospectively evaluate screening patterns and sensitivity according to sampled body sites to structure future screening practices.

Methods: A. baumannii was detected using selective culturing and MALDI-TOF. We calculated screening sensitivity for different body sites from 22 confirmed cases assuming patients as positive from first to last positive swab. Sensitivity compared actual laboratory results of collected swabs to this assumed “positive time period” reference. Screening swabs included were collected from axilla, groin, nose, pharynx, anus, and combinations nose-pharynx, axilla-groin.

Results:

In total, 680 screening swabs were collected with a median of 3 swabs per patient and day (range: 1-8). Most frequently sampled body sites were anus (n=193), nose-pharynx (n=185) and axilla-groin (n=176). Screening sensitivity for >=1 positive swab per patient and day irrespective of body site was 72% (95%CI: 64%-78%). Among frequently sampled body sites sensitivity was 59% (95%CI: 51%-67%) for >=1 positive swab from the currently recommended combination of nose-pharynx and axilla groin and 71% (95%CI: 63%-78%) when anal swabs were included additionally.

Conclusions:

Collection of anal swabs in addition to currently recommended axilla-groin/nose-pharynx swabs increased sensitivity while avoiding unnecessary sampling. This should be further investigated as it could improve official recommendations to structure practices and reduce clinic and laboratory work load during already tensed outbreak situations.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: influenza, streptococcal infections, disease outbreaks, travel, international cooperation

ABSTRACT ID: 584

PRESENTED BY: Amrei Krings / kringsa@rki.de

24.3. A large foodborne outbreak of campylobacteriosis linked to schools of Pescara, Italy, May-June 2018

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Background:

In June 2018, more than 100 students and school personnel presented with gastroenteritis symptoms at hospitals in Pescara, Italy. Microbiological analysis confirmed Campylobacter spp. infection. One catering/provider with two cooking centers had prepared lunches for the involved schools. We present results of the investigation and the measures implemented.

Methods:

We performed active case finding in schools and checked hospital admission records using the EU definition for probable and confirmed campylobacteriosis. Cases were compared with controls from the same schools. A detailed questionnaire, with foods served during 28/05/2018-01/06/2018 school lunches, was administered. Additional information on the cooking centers supplying the schools was obtained and food samples tested.

Results:

In total, 222 cases (91.4% aged 3-11 years) from 21 schools were identified with symptom onset: 30/05/2018-06/06/2018 (peak on 01/06/2018); 91 were confirmed. The highest attack rates (AR) were for those having lunch at school on 29/05/2018: 7.8% for all schools and 13.1% for schools supplied by one cooking center. Hundred-seventy-six cases and 62 controls were interviewed. Cases were more likely (OR=4.06 [95% CI: 1.11-15.62]) to have consumed lunch from the cooking center with the highest AR. The most likely exposure was a cheese consumed on 29/05/2018 (OR=2.02 [95% CI: 1.01-4.05]) which tested positive for Campylobacter spp.

Conclusions:

This was the largest Campylobacter outbreak recorded until now in Italy, where approximately 1000 cases are reported yearly. The analysis indicated that one cooking center was more involved in the distribution of the contaminated food. The timely suspension of the catering service and the closure of the schools for summer the week after the start of the outbreak probably prevented further spread. Authorities are reconsidering the school caterers' selection criteria in the region.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Campylobacter,outbreak,schools,Italy,foodborne

ABSTRACT ID: 596

PRESENTED BY: Patrizio Pezzotti / xanthi.andrianou@iss.it

24.4. Spatial analysis as epidemiological investigations tools - the case of toxoplasmosis outbreak in Santa Maria, Rio Grande do Sul, Brazil, 2018

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Background:

In the first half of 2018, a toxoplasmosis outbreak occurred in Santa Maria, southern Brazil and is considered one of the largest in the world. From 15/01 to 08/08/2018, 1,830 cases were reported, of which 1,530 were suspected cases. 647 cases were considered as confirmed/probable (262/385 respectively) by laboratory criteria. This summary describes spatial analysis techniques performed during the outbreak investigation, whose statistical analyses and environmental and laboratory investigations have demonstrated an association with consumption of tap water and green vegetables.

Methods:

Exploratory techniques of global spatial analysis used were: Kernel intensity calculation (Heat maps), Nearest Neighbor Ratio (NNI) and G Function; and local: Ripley‘s K function. Of the confirmed/probable cases, 97.5%(631/647) were residents of the city. It was possible to perform the georeferencing of 76.2% (481/631) of the cases, included in the analyses.

Results: The Kernel map showed the presence of hot zones in the west and central regions of the municipality; G function showed that the clusters of cases did not occur randomly (G=0.30032). The NNI (0.05044; z-score=-39.8406; p- value=‹0.001; expected distance=0.056487; observed distance=0.002849) showed that the cases were clustered in relation to complete spatial randomness. The Ripley K function indicated positive spatial aggregation of cases (L=0.1217). When stratified data were analyzed between probable and confirmed cases, the results were the same.

Conclusions:

Although rarely used in outbreak investigations, spatial analyses have proved to be important tools for the detection of clusters and can be reproduced in other investigations. Analysis of detecting focal clusters was recommended (Diggle Test), which shows aggregation of cases around fixed and space-time points (Knox test), for analysis of clusters of cases in space and time, during the period of the outbreak.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: Epidemiology, outbreak investigation, spatial analysis, spatial cluster

ABSTRACT ID: 517

PRESENTED BY: Camila Ribeiro Silva / camilarsilva@hotmail.com

24.5. Nationwide outbreak of puerperal group A streptococcal infection in the Netherlands

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Background:

Puerperal fever or -sepsis with group A streptococcus (pGAS) is a serious disease which can be healthcare-associated. Surveillance is essential to detect clusters with a common source. In the summer of 2018, a higher than usual number of pGAS notifications was received. We aimed to describe this outbreak and study emm-types involved, in order to generate hypotheses about its cause.

Methods:

pGAS is notifiable in the Netherlands since 2011. In 2016, a change in notification criteria was implemented to include not only sepsis but all fever postpartum with GAS. Emm typing of GAS strains by PCR is not common practice, but requested when epidemiologically linked cases occur.

Results:

In July and August 2018 combined, 28 cases were notified, compared to an average of 6.7 cases in these two months in 2011-2017. Mean age was 31, with a range between 24 and 39. Date of disease onset was a median of 2 days after giving birth, ranging from 0 to 6. All cases survived but one lost her infant due to neonatal GAS infection. Cases were spread across the country. Six isolates from a central region were found to be five different emm types. However, two cases in a hospital in the South had emm-type 102, which has never been reported before in the Netherlands.

Conclusions :

A thus far unexplained increase in puerperal iGAS infections is ongoing in the Netherlands. In two related pGAS cases, the rare emm-type 102 was cultured. Further investigation is ongoing into risk factors for pGAS and to test hypotheses about the cause of this outbreak, such as the emergence of emm-type 102, or a coinciding increase of impetigo among children.

Subject: Field epidemiology (e.g. outbreak investigations)

Keywords: puerperal infection, public health surveillance, Streptococcus pyogenes, perinatal care

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24.6. Implementation of influenza POCT and influenza ward to improve hospital capacity and to reduce costs

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Background:

Seasonal influenza epidemics pose a significant burden on hospital capacity and costs. To increase efficiency of patient care, a clinical pathway was implemented in the 2017/2018 season, including influenza point-of-care testing (POCT) at the Emergency Department (ED) and a temporary influenza ward. We report the results of these implementations comparing the 2017/2018 with the 2016/2017 season.

Poster Abstracts

Methods:

During the 2017/2018 influenza epidemic, a PCR-based POCT for influenza A/B/RSV with a turnaround time of 20 minutes (Cobas Liat, Roche) was placed at the ED of a Dutch tertiary teaching hospital. Nose/throat swabs from patients presenting with acute respiratory infections were tested by ED nurses. If hospitalization was indicated, influenza positive patients were admitted to the 15-beds influenza ward. After a maximum of five days, patients were moved or dismissed.

Results :

In 2016/2017 positive influenza-tests were reported for 189 patients out of 591 (32%) patients, compared to 624/1546 (40%) in 2017/2018. Time from ED presentation to sample collection (3.2 vs 0.8 hrs, $p<0.0001$) and from sample collection to result (18.2 vs 1.0 hrs, $p<0.0001$) significantly decreased. A small reduction was found in patients' time spent on the ED (3.83 vs 3.63 hrs, $p=0.03$).

Costs of the clinical pathway were estimated at €100,000 and savings on €500,000, based on a lower percentage of hospitalized influenza-positive patients (91% vs 73 %, $p=0.0001$) and shorter length of stay (5.86 vs 4.61 hrs, $p=0.0001$).

Conclusions:

Implementing this clinical pathway has a positive effect on hospital capacity and is cost saving because of a decreased diagnostic turnaround times and improved patient flow by less admissions and shorter length of stay. The considerable cost savings can partly be explained by the long-lasting influenza epidemic.

Subject: Implementation science (e.g. integration of research findings and evidence into public health policy and practice; monitoring and evaluation of programmes)

Keywords: Influenza, point-of-care testing, health care costs emergency department, epidemic, clinical pathway

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