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
Table of Contents

<table>
<thead>
<tr>
<th>Page</th>
<th>Section</th>
</tr>
</thead>
<tbody>
<tr>
<td>02</td>
<td>WELCOME</td>
</tr>
<tr>
<td>06</td>
<td>SCIENTIFIC COMMITTEE</td>
</tr>
<tr>
<td>08</td>
<td>ABSTRACT REVIEWERS</td>
</tr>
<tr>
<td>10</td>
<td>INFORMATION STANDS</td>
</tr>
<tr>
<td>14</td>
<td>INVITED SPEAKER BIOGRAPHIES</td>
</tr>
</tbody>
</table>

### PLENARY SESSION ABSTRACTS

<table>
<thead>
<tr>
<th>Page</th>
<th>SESSION</th>
<th>DAY</th>
<th>Time</th>
</tr>
</thead>
<tbody>
<tr>
<td>20</td>
<td>A</td>
<td>Day 1, Wednesday 21 November</td>
<td>9:00-10:30</td>
</tr>
<tr>
<td>20</td>
<td>B</td>
<td>Day 1, Wednesday 21 November</td>
<td>17:00-18:30</td>
</tr>
<tr>
<td>21</td>
<td>C</td>
<td>Day 2, Thursday 22 November</td>
<td>9:00-10:30</td>
</tr>
<tr>
<td>22</td>
<td>D</td>
<td>Day 3, Friday 23 November</td>
<td>9:00-10:30</td>
</tr>
<tr>
<td>23</td>
<td>E</td>
<td>Day 3, Friday 23 November</td>
<td>17:00-18:30</td>
</tr>
</tbody>
</table>

### PARALLEL SESSION ABSTRACTS

<table>
<thead>
<tr>
<th>Page</th>
<th>PROGRAMME</th>
<th>DAY</th>
<th>Time</th>
</tr>
</thead>
<tbody>
<tr>
<td>27</td>
<td>1: Healthcare-associated infections</td>
<td>Day 1, Wednesday 21 November</td>
<td>11:00-12:40</td>
</tr>
<tr>
<td>29</td>
<td>2: Emerging and vector-borne diseases</td>
<td></td>
<td></td>
</tr>
<tr>
<td>32</td>
<td>3: Food- and waterborne diseases and zoonoses: microbiology and whole genome sequencing</td>
<td>Day 1, Wednesday 21 November</td>
<td></td>
</tr>
<tr>
<td>34</td>
<td>4: Food- and waterborne diseases and zoonoses (2): epidemiology and surveillance</td>
<td>Day 1, Wednesday 21 November</td>
<td>14:30-15:30</td>
</tr>
<tr>
<td>36</td>
<td>5: International health and migration</td>
<td></td>
<td></td>
</tr>
<tr>
<td>38</td>
<td>6: Vaccine-preventable diseases (1): epidemiology and surveillance</td>
<td>Day 2, Thursday 22 November</td>
<td>11:00-12:40</td>
</tr>
<tr>
<td>39</td>
<td>7: Cholera</td>
<td></td>
<td></td>
</tr>
<tr>
<td>42</td>
<td>8: Food- and waterborne diseases and zoonoses (3): outbreaks</td>
<td></td>
<td></td>
</tr>
<tr>
<td>44</td>
<td>9: Vaccine-preventable diseases (2): vaccine effectiveness</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
## Table of Contents

<table>
<thead>
<tr>
<th>Page</th>
<th>Parallel Session Programme</th>
<th>Day</th>
<th>Time</th>
</tr>
</thead>
<tbody>
<tr>
<td>48</td>
<td>PARALLEL SESSION 10: Vaccine-preventable diseases (3): developments and methods</td>
<td>DAY 2, Thursday 22 November</td>
<td>14:30-15:30</td>
</tr>
<tr>
<td>49</td>
<td>PARALLEL SESSION 11: HIV, sexually transmitted infections and viral hepatitis (1): epidemiology and surveillance</td>
<td></td>
<td></td>
</tr>
<tr>
<td>51</td>
<td>PARALLEL SESSION 12: Food- and waterborne diseases and zoonoses (4): epidemiology and surveillance</td>
<td></td>
<td></td>
</tr>
<tr>
<td>52</td>
<td>PARALLEL SESSION PROGRAMME</td>
<td>DAY 2, Thursday 22 November</td>
<td>17:00-18:40</td>
</tr>
<tr>
<td>52</td>
<td>PARALLEL SESSION 13: Antimicrobial resistance</td>
<td></td>
<td></td>
</tr>
<tr>
<td>55</td>
<td>PARALLEL SESSION 14: Tuberculosis</td>
<td></td>
<td></td>
</tr>
<tr>
<td>57</td>
<td>PARALLEL SESSION 15: Vaccine-preventable diseases (4): vaccine uptake and coverage</td>
<td></td>
<td></td>
</tr>
<tr>
<td>60</td>
<td>PARALLEL SESSION PROGRAMME</td>
<td>DAY 3, Friday 23 November</td>
<td>11:30-12:40</td>
</tr>
<tr>
<td>60</td>
<td>PARALLEL SESSION 16: HIV, sexually transmitted infections and viral hepatitis (2): surveillance, screening &amp; intervention</td>
<td></td>
<td></td>
</tr>
<tr>
<td>63</td>
<td>PARALLEL SESSION 17: Influenza and other respiratory viruses (1): epidemiology and surveillance</td>
<td></td>
<td></td>
</tr>
<tr>
<td>66</td>
<td>PARALLEL SESSION 18: Late breakers</td>
<td></td>
<td></td>
</tr>
<tr>
<td>68</td>
<td>PARALLEL SESSION PROGRAMME</td>
<td>DAY 3, Friday 23 November</td>
<td>14:30-15:30</td>
</tr>
<tr>
<td>68</td>
<td>PARALLEL SESSION 19: Vaccine-preventable diseases (5): preparedness</td>
<td></td>
<td></td>
</tr>
<tr>
<td>70</td>
<td>PARALLEL SESSION 20: Influenza and other respiratory viruses (2): vaccination</td>
<td></td>
<td></td>
</tr>
<tr>
<td>72</td>
<td>PARALLEL SESSION 21: Emerging and vector-borne diseases (2)</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

### Poster Abstracts

<table>
<thead>
<tr>
<th>Page</th>
<th>Moderated Poster Session A</th>
<th>Day</th>
<th>Time</th>
</tr>
</thead>
<tbody>
<tr>
<td>76</td>
<td>MODERATED POSTER SESSION A</td>
<td>DAY 1, Wednesday 21 November</td>
<td>15:40-16:40</td>
</tr>
<tr>
<td>76</td>
<td>TRACK 1: Antimicrobial resistance and healthcare associated infections: Intervention and assessment</td>
<td></td>
<td></td>
</tr>
<tr>
<td>78</td>
<td>TRACK 2: Emerging and vector-borne diseases (1)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>81</td>
<td>TRACK 3: Food- and waterborne diseases and zoonoses (1): Epidemiology: Salmonellosis</td>
<td></td>
<td></td>
</tr>
<tr>
<td>84</td>
<td>TRACK 4: Food- and waterborne diseases and zoonoses (2): Surveillance</td>
<td></td>
<td></td>
</tr>
<tr>
<td>87</td>
<td>TRACK 5: Influenza, TB and other respiratory viruses (1): Surveillance, Incidence and Burden</td>
<td></td>
<td></td>
</tr>
<tr>
<td>90</td>
<td>TRACK 6: Sexually transmitted infections (1): Chlamydia, Syphilis and Neisseria Gonorrhoeae</td>
<td></td>
<td></td>
</tr>
<tr>
<td>93</td>
<td>TRACK 7: Zoonosis</td>
<td></td>
<td></td>
</tr>
<tr>
<td>96</td>
<td>TRACK 8: Vaccine-preventable diseases (3): Implementation and modelling</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
## Table of Contents

### POSTER ABSTRACTS

<table>
<thead>
<tr>
<th>MODERATED POSTER SESSION B</th>
<th>DAY 2, Thursday 22 November</th>
<th>15.40-16.40</th>
</tr>
</thead>
<tbody>
<tr>
<td>99 TRACK 9: Antimicrobial resistance (Epidemiology and Surveillance)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>101 TRACK 10: Emerging and vector-borne diseases (2): International health</td>
<td></td>
<td></td>
</tr>
<tr>
<td>104 TRACK 11: Food- and waterborne diseases and zoonoses (3): Hepatitis and viral infection</td>
<td></td>
<td></td>
</tr>
<tr>
<td>107 TRACK 12: Food- and waterborne diseases and zoonoses (4): Epidemiology and Outbreaks 1</td>
<td></td>
<td></td>
</tr>
<tr>
<td>113 TRACK 14: Sexually transmitted infections (2), HIV and Viral Hepatitis: Surveillance</td>
<td></td>
<td></td>
</tr>
<tr>
<td>116 TRACK 15: Influenza, TB and other respiratory viruses (2): Vaccination and interventions</td>
<td></td>
<td></td>
</tr>
<tr>
<td>119 TRACK 16: Vaccine-preventable diseases (2): Epidemiology and Surveillance</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>MODERATED POSTER SESSION C</th>
<th>DAY 3, Thursday 23 November</th>
<th>15.40-16.40</th>
</tr>
</thead>
<tbody>
<tr>
<td>122 TRACK 17: Food- and waterborne diseases and zoonoses (5): Epidemiology and Outbreaks 2</td>
<td></td>
<td></td>
</tr>
<tr>
<td>125 TRACK 18: Food- and waterborne diseases and zoonoses (6): Surveillance systems</td>
<td></td>
<td></td>
</tr>
<tr>
<td>131 TRACK 20: Sexually transmitted infections (3): Intervention</td>
<td></td>
<td></td>
</tr>
<tr>
<td>133 TRACK 21: Vaccine-preventable diseases (3): Burden of disease</td>
<td></td>
<td></td>
</tr>
<tr>
<td>136 TRACK 22: Vaccine-preventable diseases (4): Vaccine effectiveness</td>
<td></td>
<td></td>
</tr>
<tr>
<td>140 TRACK 23: Policy approaches and evaluation</td>
<td></td>
<td></td>
</tr>
<tr>
<td>143 TRACK 24: Late breakers</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>INDEX BY SUBJECT</th>
</tr>
</thead>
<tbody>
<tr>
<td>147</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>INDEX BY PRESENTING AUTHOR</th>
</tr>
</thead>
<tbody>
<tr>
<td>151</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>INDEX BY KEYWORD</th>
</tr>
</thead>
<tbody>
<tr>
<td>153</td>
</tr>
</tbody>
</table>
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.

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.

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.

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,
Scientific Committee

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 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 ESMID 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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Emily MacDonald
Hanne Nokleby
Karim Nygård
Pawel Stefanoff
Didrik Frimann Vestrheim

Poland
Janusz Janiec
Magdalena Rosinska
Ewa Sadowy
Information Stands

Eurosurveillance – ECDC

Eurosurveillance is a European peer-reviewed scientific journal devoted to the epidemiology, surveillance, prevention and control of communicable diseases, with a focus on such topics that are of relevance to Europe. It is a weekly online journal, with 50 issues per year published on Thursdays, and features short rapid communications, longer in-depth research articles, surveillance and outbreak reports, reviews and perspective papers, as well as short news items. Timely publication of short authoritative papers on ongoing outbreaks or other relevant public health events is one of the major assets of the journal. Under special circumstances when current events need to be urgently communicated to readers for rapid public health action, e-alerts can be released outside of the regular publishing schedule. Topical compilations of selected articles and special issues are also published in print 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(4) 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.

Public Health Training Section – ECDC

The ECDC Fellowship Programme is a two-year competency-based training with two paths: the field epidemiology path (EPIET) and the public health microbiology path (EUPHEM). After the two-year training, EPIET and EUPHEM graduates are considered experts in applying epidemiological or microbiological methods to provide evidence to guide public health interventions for communicable disease prevention and control.

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


www.eurosurveillance.org
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

www.ecdc.europa.eu
Information Stands

EPIET Alumni Network (EAN)

The 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 of six elected members.

www.epietalumni.net

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 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 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
Information Stands

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.sormas.org.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”

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.

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.
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?”*

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**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-convenor 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.

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**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

<table>
<thead>
<tr>
<th></th>
<th>PLENARY SESSION A</th>
<th>DAY 1, Wednesday 21 November</th>
<th>9:00-10:30</th>
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</thead>
<tbody>
<tr>
<td></td>
<td>PLENARY SESSION B</td>
<td>DAY 1, Wednesday 21 November</td>
<td>17:00-18:30</td>
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<td>PLENARY SESSION C</td>
<td>DAY 2, Thursday 22 November</td>
<td>9:00-10:30</td>
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<td>PLENARY SESSION D</td>
<td>DAY 3, Friday 23 November</td>
<td>9:00-10:30</td>
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<td>PLENARY SESSION E</td>
<td>DAY 3, Friday 23 November</td>
<td>17:00-18:30</td>
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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.
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.

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 UN-AIDS, 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, World Health Organization (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 coordination: 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 coordination: 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

<table>
<thead>
<tr>
<th>Day</th>
<th>Time</th>
<th>Session</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>25</strong></td>
<td></td>
<td>PARALLEL SESSION PROGRAMME Day 1, Wednesday 21 November 11:00-12:40</td>
</tr>
<tr>
<td>27</td>
<td></td>
<td>PARALLEL SESSION 1: Healthcare-associated infections</td>
</tr>
<tr>
<td>29</td>
<td></td>
<td>PARALLEL SESSION 2: Emerging and vector-borne diseases (1)</td>
</tr>
<tr>
<td>32</td>
<td></td>
<td>PARALLEL SESSION 3: Food- and waterborne diseases and zoonoses (1): microbiology and whole genome sequencing</td>
</tr>
<tr>
<td><strong>34</strong></td>
<td></td>
<td>PARALLEL SESSION PROGRAMME Day 1, Wednesday 21 November 14:30-15:30</td>
</tr>
<tr>
<td>34</td>
<td></td>
<td>PARALLEL SESSION 4: Food- and waterborne diseases and zoonoses (2): epidemiology and surveillance 1</td>
</tr>
<tr>
<td>36</td>
<td></td>
<td>PARALLEL SESSION 5: International health and migration</td>
</tr>
<tr>
<td>38</td>
<td></td>
<td>PARALLEL SESSION 6: Vaccine-preventable diseases (1): epidemiology and surveillance</td>
</tr>
<tr>
<td><strong>39</strong></td>
<td></td>
<td>PARALLEL SESSION PROGRAMME Day 2, Thursday 22 November 11:00-12:40</td>
</tr>
<tr>
<td>39</td>
<td></td>
<td>PARALLEL SESSION 7: Cholera</td>
</tr>
<tr>
<td>42</td>
<td></td>
<td>PARALLEL SESSION 8: Food- and water-borne diseases and zoonoses (3): outbreaks</td>
</tr>
<tr>
<td>44</td>
<td></td>
<td>PARALLEL SESSION 9: Vaccine-preventable diseases (2): vaccine effectiveness</td>
</tr>
<tr>
<td><strong>48</strong></td>
<td></td>
<td>PARALLEL SESSION PROGRAMME Day 2, Thursday 22 November 14:30-15:30</td>
</tr>
<tr>
<td>48</td>
<td></td>
<td>PARALLEL SESSION 10: Vaccine-preventable diseases (3): developments and methods</td>
</tr>
<tr>
<td>49</td>
<td></td>
<td>PARALLEL SESSION 11: HIV, sexually transmitted infections and viral hepatitis (1): epidemiology and surveillance</td>
</tr>
<tr>
<td>51</td>
<td></td>
<td>PARALLEL SESSION 12: Food- and waterborne diseases and zoonoses (4): epidemiology and surveillance 2</td>
</tr>
<tr>
<td><strong>52</strong></td>
<td></td>
<td>PARALLEL SESSION PROGRAMME Day 2, Thursday 22 November 17:00-18:40</td>
</tr>
<tr>
<td>52</td>
<td></td>
<td>PARALLEL SESSION 13: Antimicrobial resistance</td>
</tr>
<tr>
<td>55</td>
<td></td>
<td>PARALLEL SESSION 14: Tuberculosis</td>
</tr>
<tr>
<td>57</td>
<td></td>
<td>PARALLEL SESSION 15: Vaccine-preventable diseases (4): vaccine uptake and coverage</td>
</tr>
</tbody>
</table>
Parallel Session Abstracts

<table>
<thead>
<tr>
<th>Session</th>
<th>Title</th>
</tr>
</thead>
<tbody>
<tr>
<td>60</td>
<td>PARALLEL SESSION 16: HIV, sexually transmitted infections and viral hepatitis (2): surveillance, screening &amp; intervention</td>
</tr>
<tr>
<td>63</td>
<td>PARALLEL SESSION 17: Influenza and other respiratory viruses (1): epidemiology and surveillance</td>
</tr>
<tr>
<td>66</td>
<td>PARALLEL SESSION 18: Late breakers</td>
</tr>
<tr>
<td>68</td>
<td>PARALLEL SESSION 19: Vaccine-preventable diseases (5): preparedness</td>
</tr>
<tr>
<td>70</td>
<td>PARALLEL SESSION 20: Influenza and other respiratory viruses (2): vaccination</td>
</tr>
<tr>
<td>72</td>
<td>PARALLEL SESSION 21: Emerging and vector-borne diseases (2)</td>
</tr>
</tbody>
</table>

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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


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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
4,5,6 Department of Infectious Disease Epidemiology and Prevention, Statens Serum Institut, Copenhagen, Denmark
7 Department of Orthopaedic Surgery, Aarhus University Hospital, Danish Society for Hip and Knee Arthroplasty (DSHK).
8 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 of those 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

A. Doble 1, J. Islam 2, G. Hood 3, D. Ashiru-Oredope 4, S. Hopkins 5

1 Public Health England
2, 4, 5 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 (261, 3.9%). 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 modellling McCabe score and linking to datasets that capture Charlson co-morbidity index is planned. Our results provide insight into prescribing practices in secondary care.
Parallel Session Abstracts

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

**María Ganczak**

K. Topczewska 1, M. Budnik-Szymoniuk 1, P. Kalinowski 4

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2 Department of Epidemiology and Management, Pomeranian Medical University, Szczecin, Poland
3 Department of Community Nursing, Nicolaus Copernicus University, Toruń, 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% (both: 39.2%). The most recent PI was caused by a hollow-bore (53.5%). 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% (both: 39.2%). The most recent PI was caused by a hollow-bore (53.5%). The most recent PI was caused by a hollow-bore (53.5%) and will be used to model estimates of inappropriate prescribing to inform the government’s ambition.

**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 interventions, 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 / ganczakz@wp.pl

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

**Laura Esphenhain**

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1 Department of Antibiotic Resistance and Infection Prevention, Norwegian Institute of Public Health
2 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 Esphenhain / aura.espenhain@hotmail.com
Factors associated with Methicillin-Resistant Staphylococcus aureus (MRSA) acquisition rates of wards in a Singapore tertiary hospital: An electronic medical records study

Zaw Myo Tun1
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2 Division of Infectious Diseases, National University Hospital, Singapore
3 Saw Swee Hock School of Public Health, National University of 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-resistant Staphylococcus 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); 2,000 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 = 1.71 (95% CI: 1.22-2.44); 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
2.2. Occupational swine exposure associated with seropositivity for Ascaris suum in veterinarians in Austria, 2017/2018

Karin Taus 1
F. Schmoll 1, H. Auer 1, S. Pekard-Amenitsch 1, F. Allerberger 1, D. Schmid 6

1 Austrian Agency for Health and Food Safety (AGES), Vienna, Austria
2 European Programme for Intervention Epidemiology Training (EPiET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
3 Austrian Agency for Health and Food Safety (AGES), Vienna, Austria
4 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 than other veterinarians. Seropositivity increased with occupational swine exposure to seropositivity 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
Parallel Session Abstracts

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

Laura Bubba 1
E. Broberg 2, A. Jazir 3, H. Harvala 4

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2,3 European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
3,4 Public Health Agency of Sweden

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 young children <3 months of age (4,486/15,617). Most frequently typed EVs and HPeVs in the EU/EEA countries in order to improve recognition by frontline physicians and surveillance for these infections.

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. Coxackievirus 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 1, E. van Straten 1, P. Bjelkmar 4

1 Public Health Agency of Sweden
1-4 Public Health Agency of Sweden

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)
Parallel Session Abstracts

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

**ABSTRACT ID:** 393

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

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**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

I. Fawcett 1, P. Manley 3

1 National Infection Service, Public Health England
2 Yorkshire and Humber Health Protection Team, Public Health England, Leeds, United Kingdom
3 Gastrointestinal Bacterial Reference Unit, Public Health England, London, United Kingdom

**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

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

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3 Gastrointestinal Bacterial Reference Unit, Public Health England, London, United Kingdom
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
Parallel Session Abstracts

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

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M. Saavedra-Campos 1, L. Larkin 1, D. Curtis 1, H. Evans 1, S. Wylie 1, R. Davies 1, J. McCormick 1, J. Lighthill 1, T. Potter 1, M. Chattaway 1, N. Elviss 1, I. Oliver 1

1 Public Health England
2,5,8,10,11 AGES - Austrian Agency for Health and Food Safety
2,3,4,6,7,9,10,11 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 single nucleotide polymorphism linkage cluster of Salmonella Typhimurium, ‘the outbreak strain’ (1.4,3,6,7,9,12,27,32,45,92,121,123), 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 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

1 AGES - Austrian Agency for Health and Food Safety
2,3,4,6,7,9,11 AGES - Austrian Agency for Health and Food Safety
3,4 Department Biological Safety, Federal Institute for Risk Assessment (BfR), Berlin, Germany
6 European Public Health Microbiology Training Programme (EUPHEM), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden

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

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2,3,4,6,7,9 Public Health Agency of Canada, Infectious Disease Prevention and Control Branch, National Microbiology Laboratory, Winnipeg, Canada
4,8,10,12,13,14,15 Public Health Agency of Canada, Infectious Disease Prevention and Control Branch, Centre for Foodborne, Environmental, and Zoonotic Infectious Disease, Guelph, Canada
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

3.6. Impact of whole genome sequencing on food contamination, food safety, foodborne disease, molecular typing, and strengthen evidence to inform food safety policy in Canada.

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

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

Moderator
Daniel Thomas

Lamprini Veneti 1
T. Johansen 1, B. Guzmán-Herrador 1, E. Framstad 4, L. Vold 3

1 Division for Infectious Disease Control and Environmental Health, Norwegian Institute of Public Health
3,5 Division for Infectious Disease Control and Environmental Health, Norwegian Institute of Public Health
4 Norwegian Institute of 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

ABSTRACT ID: 472
PRESENTED BY: Sabine Maritschnik / sabine.maritschnik@ages.at

Keywords:
Whole-genome sequencing, food contamination, food safety, foodborne disease, molecular typing

Parallel Session Abstracts
(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

3.6. Impact of whole genome sequencing on food contamination, food safety, foodborne disease, molecular typing, and strengthen evidence to inform food safety policy in Canada.

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

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

Moderator
Daniel Thomas

Lamprini Veneti 1
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Methods:
We linked MSIS data with data regarding peaks of rodents collected by the Norwegian Institute for Nature Research. We conducted descriptive
Parallel Session Abstracts

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

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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 2005-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:
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 mosquitios. We observed 4-year periodicity (sine-wave p=0.294; cosine-wave p=0.003) 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 tulareemia cases.

Conclusions: The seasonality and multiannual cyclic pattern of tulareemia epidemics were associated with lemming/rodent density cycles, suggesting a 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.

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

Patricia Garvey 1

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2,4,10 Health Service Executive -Health Protection Surveillance Centre, Dublin, Ireland
3,5 Health Service Executive-East, Dublin, Ireland
6 National Salmonella, Shigella and Listeria Reference Laboratory, Galway, Ireland
8 University Hospital Galway, Division of Microbiology, Ireland

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

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
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ABSTRACT ID: 90
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Parallel Session Abstracts

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; gastrointestinal 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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² Centre for Nutrition, Prevention and Health Services, National Institute for Public Health and the Environment (RIVM), Bilthoven the Netherlands

³ A. de Melker ², A. van Hoek ¹, J. Koopsen ², R. de Man ¹, M. Mangen ², H. de Melker ¹, J. Polder ³, A. de Wit ⁴

⁴ Tranzo Scientific Center for Care and Welfare, Tilburg School of Social and Behavioral Sciences, Tilburg University, Tilburg, The Netherlands

⁵ Julius Centre for Health Sciences and Primary Health Care, University Medical Centre Utrecht, the Netherlands

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 20.4% and 20.2% 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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¹ National Centre of Infectious and Parasitic Diseases, Sofia, Bulgaria; National Institute of Public Health - National Institute of Hygiene, Warsaw, Poland; European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden

² National Institute of Public Health - National Institute of Hygiene, Warsaw, Poland; European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden

Background: Migrants are groups at risk for vaccine-preventable diseases. Communication failures may negatively affect the uptake of recommended vaccinations.

Methods: A mixed-methods study was conducted in a refugee camp in Poland. A qualitative component included a long-time employee of the camp and a focus group with asylum-seekers. The quantitative component presented a telephone questionnaire to 96% of the asylum-seekers. This was followed by a random walk-audited survey with a total of 473 migrants.

Results: The results showed that the camp's employees did not possess accurate knowledge about the diseases and the need for vaccination. The questions about the vaccination included basic information that was unsatisfactory. The majority of the migrants stated that they were not vaccinated. The main reasons for non-vaccination were: lack of information about available vaccines, lack of confidence in the system, fear of side effects, and the belief that they had already been vaccinated.

Conclusions: The main issues with vaccination were identified and these will be used to improve communication in the camp. The findings will be applied to other camps in Poland and the European region.
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

Bernhard Silenou Chawo ¹

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² Helmholtz Centre for Infection Research (HZI), Braunschweig Germany; PhD Epidemiology Programme, Hannover Medical School (MHH), Germany
³ 1 Helmholtz Centre for Infection Research (HZI), Braunschweig Germany; German Centre for Infection Research (DZIF), Germany; Hannover Medical School (MHH), Hannover, Germany; Twincentre, Centre for Experimental and Clinical Infections Research, Hanover, Germany

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
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, 41,000 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.

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From 40 different DCC, 896 children participated (response rate 45%; median age 44 months, range 8-80). In 2015, 41,000 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, 41,000 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, 41,000 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.
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=0.02) and 7-8 years (2.0% Sweden, 8.5% Norway, p=0.02).

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-berenzon@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
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5-6 Ministere de la Santé, Kinshasa, Democratic Republic of the Congo
7-8 Institute of Tropical Medicine, Antwerp, Belgium

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

Brecht Ingelbeen

D. Hendrickx 1, M. Van der Sande 1, B. Miwanda 1, H. Vochten 1, M. Mossoko 2, N. Nyakio Kakuusu 2, V. Vanlerberghge 3, J. Jacobs 4, M. Boelaert 4, B. Kebele 5, D. Bomangue Nikoko 6, J. Muyembe-Tanfum 7

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7 Clinical Sciences Department, Institute of Tropical Medicine, Antwerp, Belgium
8 Programme National d’Elimination du Cholera et de lutte contre les autres Maladies Diarrhéiques, Ministry of Public Health, Kinshasa, Democratic Republic of the Congo
9 Clinical Sciences Department, Institute of Tropical Medicine, Antwerp, Belgium
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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@fps.bwh.de
Parallel Session Abstracts

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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

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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: 76.8-84.4), 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’ (59%).

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
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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 were overcrowded with
Parallel Session Abstracts

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

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4 Gastrointestinal Bacteria Reference Unit, Public Health England

Abstracts

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

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 ≥ 1 year 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, 125 (1.8%) Guzamala, 63 (1.0%) Maiduguri, 23 (0.4%) Mafa and 2 (0.03%) from Gongola Local Government Areas. 619 (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, Complex Emergency, Oral Cholera Vaccine, Internally Displaced Person, Acute Watery Diarrhoea, Severe Dehydration, Suspected Cholera Case
ABSTRACT ID: 558
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Parallel Session 8
DAY 2, Thursday, 22. November 2018
11:00-12:40

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

Moderator
Anders Wallensten

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

Simon Packer 1

Kingdom J. Cameron 2, C. Willis 1, C. Amar 2, M. Kennedy 3, J. Turner 2, B. Nozad 2, M. Gobin 2

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2 South West Health Protection Team, Public Health England
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Abstracts

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

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
PRESENTEBy: Luise Müller / lmu@ssi.dk
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 who 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

ABSTRACT ID: 240

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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.
Parallel Session Abstracts

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 142 cases 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 (spondylodiscitis). 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 persistent and common 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: 607
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
B. Sibal 2

1 Health Protection Team, Public Health England
2 Health Protection Team, Public Health England

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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5 Health Protection Surveillance Centre, Dublin, Ireland
6,7,8 NIPH, Prague, Czech Republic
9 Instituto de Salud Pública y Laboral de Navarra, Pamplona, Spain
10 Norwegian Institute of Public Health, Oslo, Norway
11 Institut Pasteur, Paris, France

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

**Camelia Savulescu**


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8. Health Protection Scotland, Glasgow, United Kingdom
9. Temple Street Children's University Hospital, Irish Pneumococcal Reference Laboratory, Dublin, Ireland
10. Hospital Sant Joan de Déu. Barcelona, Spain
11. Scottish Haemophilus, Legionella, Meningococcus and Pneumococcus Reference Laboratory, Glasgow, United Kingdom
12. European Centre for Disease Prevention and Control, Stockholm, Sweden
13. Epiconcept, France

**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 (>65% 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: non, 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=1129), cases were younger than controls (p=0.002, p=0.016, respectively), and less likely to present with meningitis (p=0.037, p=0.003, respectively). There was no difference between cases and controls 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.
immunocompromising high-risk conditions, respectively (p Mantel- Haenszel 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

Filippo Quattroone ¹

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Background:
Invasive pneumococcal disease (IPD) is a vaccine-preventable disease characterized by isolation of Streptococcus Pneumoniae from 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 Quattroone / filippo.quattroone@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

Germaine Hanquet ¹

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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

Subject: Surveillance

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

ABSTRACT ID: 388
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Parallel Session Abstracts

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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%, 894/1333) 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 <15 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
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

Arto A. Palmu


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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

Esther Wenzel

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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 naive 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
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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

Anna Maisa 1
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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
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

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.
### Parallel Session Abstracts

#### 12.3. “Sickenin’ in the rain” - increased risk of gastrointestinal and respiratory infections after urban pluvial flooding

**Annemieke Mulder**

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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.

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**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  
**Abstacts:**

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

**Rolf Kramer**

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**Background:** Triazole antifungals are the first line therapy for invasive aspergillosis, commonly caused by Aspergillus fumigatus. Since 1997, triazole...
resistance by mutations in the lanosterol 14α-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

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

Bláthnaid Mahon ¹

N. Cahill ¹, E. McGrath ¹, L. O’Connor ¹, C. Brehony ¹, M. Mulligan ¹, B. Ruane ¹, A. Varley ¹, M. Cormican ¹, S. Ryan ¹, P. Ryan ¹, C. McFadden ¹, A. Tanaka ¹, P. Hickey ¹, S. Keane ¹, J. Bray ¹, K. Jolley ², M. Maiden ³, D. Morris ⁴

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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 16 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.mahons@nuigalway.ie

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

Laura Bubba ¹

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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 52%; 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 CC2 (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

Alessandro Cassini¹

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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] 567,322–744,489) 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@ecd.europa.eu
Parallel Session Abstracts

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

Tuberculosis

Moderator
Loredana Ingrosso

Abstracts


Hikaru Bolt 1
S. Newitt 2, A. Trindall 3, A. Burkitt 4, J. Davidson 5, P. Monk 6, E. Robinson 7, S. Makki 8

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

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

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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% (32/217)). 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...
Isoniazid mono-resistance negatively affects tuberculosis treatment outcomes in Europe

Basel Karo


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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.

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

Angela Cannas

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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.

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2 Thames Valley Health Protection Team, Public Health England South East, Chilton, UK

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.

ABSTRACT ID: 496
PRESENTED BY: Monica Saneschepisi / monica.saneschepisi@inmi.it

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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J. Koch 2

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2 Department of Infectious Disease Epidemiology, Robert Koch Institute, Berlin
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 ≥2 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 1,372/100,000 person-years in under five-year-olds and 26/100,000 person-years in those ineligible for vaccination. Since the recommendation IRRs 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

Pauline Mathieu

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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 31.3% 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 (5.0; [2.75; 9.06]), 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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V. Učakar 1, A. Kraigher 1

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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

Lorna Willocks 1
D. Gorman 2, K. Bielecki 3, K. Pollock 4, A. Kirollos 5

1 NHS Lothian
2-5 NHS Lothian

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 developing 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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2,3, 4, 5 Department of Medical and Surgical Sciences, University of Foggia, Italy

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/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 varicella (MMRV/V 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.

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
PRESENTED BY: Domenico Martinelli / d.martinelli@unifg.it
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% (OR 6, 95% CI 1.5-1.8). Oropharyngeal CT positivity varied between 1.0-1.6% in women (64/4198), between 0-1.3% in heterosexual men (23/2226) and between 0.8-1.5% in MSM (79/8156), 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% 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.


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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
**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**

**Stijn Raven**

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6. Centre for Infectious Diseases, Leiden University Medical Centre, Leiden, The Netherlands. Department of Internal Medicine, Maasstad Hospital, Rotterdam, the Netherlands.

**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 titre < 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 the 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 62.8% 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

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**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**

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2. Department for Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany
3-4 Labor Krone/Labcon-OWL, Bad Salzuflen, Germany
5 MSM Screening Study group

**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,
Parallel Session Abstracts

Neisseria gonorrhoea, 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 gonorrhoea=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

Raquel Guiomar 1
V. Borges 1, P. Cristóvão 1, I. Costa 1, P. Conde 1, A. Machado 1, A. Rodrigues 1, V. Gomez 1, I. Kislaya 1, B. Nunes 1, J. Gomes 1, P. Pechirra 1

1 National Influenza Reference Laboratory, Infectious Diseases Department, National Institute of Health Dr. Ricardo Jorge, Portugal

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
J. Murray 1, R. Cameron 1, A. Potts 1, J. Bishop 1, B. von Wissmann 1, N. William 1, A. Reynolds 1, C. Robertson 1, J. McMenamin 1

1 Health Protection Scotland
**Parallel Session Abstracts**

64

**1 Field Epidemiology Training Programme, Public Health England**

**M. Sinnathamby 2, C. Obi 3, S. Elgohari 4, R. Pebody 5**

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

**ABSTRACT ID:** 139

**Keywords:** Surveillance

**Subject:** Surveillance

**ABSTRACT ID:** 248

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

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

**Ashley Sharp 1**

M. Sinnathamby 1, C. Obi 1, S. Elgohari 1, R. Pebody 1

1 Field Epidemiology Training Programme, Public Health England

2 National Infection Service, Public Health England

**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:**

It is 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

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### 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

**Ulrike Baum 1**

R. Syrjänen 2, K. Auronen 1, N. Ikonen 5, H. Nohynek 5

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2 Department of Public Health Solutions, National Institute for Health and Welfare, Finland

3 Department of Mathematics and Statistics, University of Turku, Finland

4 Department of Health Security, National Institute for Health and Welfare, Finland

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

Concepción Delgado-Sanz 1
J. Oliva 1, A. Larrauri 1

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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=1.05-1.19), age ≥75 years (aIRR 2.3, 95%-CI=2.1-2.6), A(H1N1)pdm09 vs A(H3N2) 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
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) 1.2, 95%-CI=1.05-1.2), age 75 years (aIRR 2.3, 95%-CI=1.2-1.6), A(H1N1)pdm09 or A(H3N2) vs B infection (aIRR 1.4, 95%-CI=1.1-1.4) and obesity class III (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 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 1, C. Frank 1, R. Offergeld 1, C. Wagner-Wiening 1, K. Stark 1, J. Schmidt-Chanasit 7

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

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
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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=10.5, 95%CI:1.7-63.4). Thirty of the 38 cases became laboratory confirmed with Legionella longbeachae. Soil samples werepolyclonal 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: 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

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

Xanthi Andrianou 1

M. Del Manso 2, A. Bella 2, 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 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), 15000 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 11 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:

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

Anais Painset 1

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

1 Public Health England, London, UK
2,3,4,5 Public Health England, London, UK
6,9,10,11 Microbiological Diagnostic Unit, Public Health Laboratory, Doherty Institute, University of Melbourne Australia
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.

Subject: Field epidemiology (e.g. outbreak investigations)
Keywords: measles, outbreak, Italy, vaccination
ABSTRACT ID: 592
PRESENTED BY: Xanthi Andrianou / xanthi.andrianou@iss.it
Parallel Session Abstracts

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

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2,20 Erasmus University Medical Centre, Rotterdam, The Netherlands
3 Sciensano, Brussels, Belgium
4 University of Surrey, Guildford, UK
6 Institut Universitari d’Investigació en Atenció Primària Jordi Gol (IDIAP Jordi Gol), Barcelona, Spain
2,8 Base de Datos Para la Investigación Farmacoepidemiológica en Atención Primaria (BiFAP), Spanish Agency of Medicines and Medical Devices (AEMPS). Madrid, Spain
5,9,10 Epidemiological Information for Clinical Research from an Italian Network of Family Paediatricians (PEDIANET), Padova, Italy; SoSoTe(Pedianet) Consorzio Arsenal.IT
11 Epidemiological Information for Clinical Research from an Italian Network of Family Paediatricians (PEDIANET), Padova, Italy
12 National Institute for Public Health and the Environment (RIVM), Bilthoven, Netherlands
13 Aarhus University Hospital, Aarhus, Denmark
14 Karolina Institutet, Stockholm, Sweden
### 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.

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**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

1 EpiConcept, Paris, France
2,3 EpiConcept, Paris, France
4 National Centre of Epidemiology, CIBERESP, Institute of Health Carlos III, Spain
5 Navarra Public Health Institute, IdISNA - Navarre Institute for Health Research, Pamplona, Spain
6-8 Istituto Superiore di Sanità, Department of Infectious Disease, Rome, Italy
9-10 Instituto Nacional de Saúde Doutor Ricardo Jorge, Lisbon, Portugal
11-12 National Institute for Health and Welfare, Finland
13 Croatian Institute of Public Health, Zagreb, Croatia
14 Department of Infectious diseases, Lithuanian University of Health Sciences, Kaunas, Lithuania
15 National Centre of Epidemiology, CIBERESP, Institute of Health Carlos III, Spain
16 Navarra Public Health Institute, IdISNA - Navarre Institute for Health Research, Pamplona, Spain; National Centre of Epidemiology, CIBERESP, Institute of Health Carlos III, Spain
17 Inserm, CIC 1414, CHU Rennes, France
18 Cantacuzino Institute, Bucharest, Romania
21 University Hospital for Infectious Diseases, Zagreb, Croatia
22 Department of Health Sciences, Faculty of Medicine, Lund University, Lund, Sweden
24 Spain, Navarra, Italy, France, Romania, The Netherlands, Portugal, Finland, Croatia, Lithuania
Parallel Session Abstracts

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


1 Public Health England (PHE), London, UK
2-21 Public Health England (PHE), London, UK
3 National Institute for Public Health and the Environment (RIVM), Bilthoven, The Netherlands
4-13 Instituto de Salud Pública de Navarra – IdISNA, CIBERESP, Pamplona, Spain
5 CIBERESP, Pamplona, Spain
6 Health Service Executive-Health Protection Surveillance Centre, Dublin, Ireland
7-18 National Centre of Epidemiology, CIBERESP, Institute of Health Carlos III, Spain
8 Nivel (Netherlands Institute for Health Services Research), Utrecht, The Netherlands
9 Instituto Nacional de Saúde Dr. Ricardo Jorge (INSA), Lisbon, Portugal
10-11 Health Protection Scotland (HPS), Glasgow, UK
22 The project has received funding from the European Union’s Horizon 2020 programme

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

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

Ulrike Baum 1

N. Ikonen 1, H. Nohynek 1

1 Department of Public Health Solutions, National Institute for Health and Welfare, Finland
2 Department of Health Security, National Institute for Health and Welfare, Finland

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 (99 LAIV4 vaccinated, 125 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 IVIV or LAIV4.
**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

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**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 1, C. Fortuna 1, G. Faggioni 1, E. Benedetti 1, A. Amendola 1, G. Marsili 1, F. Lista 1, G. Rezza 1, M. Remoli 1

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2,4,6,7,8,10,11 Department of Infectious Disease, Istituto Superiore di Sanità, Rome, Italy  
5,9 Scientific Department, Army Medical Center, Rome, Italy

**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

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**Parallel Session Abstracts**

**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.

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**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 Abstracts

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

Antonios Kolimenakis 1
D. Latinoopoulos 2, C. Richardson 1, K. Bithas 1, A. Michaelakis 1, D. Papachristos 6

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2 School of Spatial Planning and Development, Aristotle University of Thessaloniki, Greece
3-4 Research Institute of Urban Environment and Human Resources, Panteion University
5 Benaki Phytopathological Institute, Department of Entomology and Agricultural Zoology
6 Agricultural Zoology

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


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7-12 World Health Organization, Geneva, Switzerland
13-15 World Health Organization, Western Pacific Regional Office, Manila, The Philippines
16 Materno-fetal and Obstetrics Research Unit, Obstetric Service, Department
17 Department of Infectious Disease Epidemiology, London School of Hygiene and Tropical Medicine, London, UK 15 Centre de Liaison sur l’Intervention et la Prévention Psychosociales (CLIPP), Montreal, Canada
18 Bureau de Veille Sanitaire, Direction de la Santé, Tahiti, French Polynesia

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 socio-
economic 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 into: 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

<table>
<thead>
<tr>
<th>MODERATED POSTER SESSION A</th>
<th>DAY 1, Wednesday 21 November</th>
<th>15.40-16.40</th>
</tr>
</thead>
<tbody>
<tr>
<td>76</td>
<td>TRACK 1: Antimicrobial resistance and healthcare associated infections: Intervention and assessment</td>
<td></td>
</tr>
<tr>
<td>78</td>
<td>TRACK 2: Emerging and vector-borne diseases (1)</td>
<td></td>
</tr>
<tr>
<td>81</td>
<td>TRACK 3: Food- and waterborne diseases and zoonoses (1): Epidemiology - Salmonellosis</td>
<td></td>
</tr>
<tr>
<td>84</td>
<td>TRACK 4: Food- and waterborne diseases and zoonoses (2): Surveillance</td>
<td></td>
</tr>
<tr>
<td>87</td>
<td>TRACK 5: Influenza, TB and other respiratory viruses (1): Surveillance, Incidence and Burden</td>
<td></td>
</tr>
<tr>
<td>90</td>
<td>TRACK 6: Sexually transmitted infections (1): Chlamydia, Syphilis and Neisseria Gonorrhoeae</td>
<td></td>
</tr>
<tr>
<td>93</td>
<td>TRACK 7: Zoonosis</td>
<td></td>
</tr>
<tr>
<td>96</td>
<td>TRACK 8: Vaccine- preventable diseases (1): Implementation and modelling</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>MODERATED POSTER SESSION B</th>
<th>DAY 2, Thursday 22 November</th>
<th>15.40-16.40</th>
</tr>
</thead>
<tbody>
<tr>
<td>99</td>
<td>TRACK 9: Antimicrobial resistance (Epidemiology and Surveillance)</td>
<td></td>
</tr>
<tr>
<td>101</td>
<td>TRACK 10: Emerging and vector-borne diseases (2): International health</td>
<td></td>
</tr>
<tr>
<td>104</td>
<td>TRACK 11: Food- and waterborne diseases and zoonoses (3): Hepatitis and viral infection</td>
<td></td>
</tr>
<tr>
<td>107</td>
<td>TRACK 12: Food- and waterborne diseases and zoonoses (4): Epidemiology and Outbreaks 1</td>
<td></td>
</tr>
<tr>
<td>113</td>
<td>TRACK 14: Sexually transmitted infections (2), HIV and Viral Hepatitis: Surveillance</td>
<td></td>
</tr>
<tr>
<td>116</td>
<td>TRACK 15: Influenza, TB and other respiratory viruses (2): Vaccination and interventions</td>
<td></td>
</tr>
<tr>
<td>119</td>
<td>TRACK 16: Vaccine- preventable diseases (2): Epidemiology and Surveillance</td>
<td></td>
</tr>
</tbody>
</table>

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<thead>
<tr>
<th>MODERATED POSTER SESSION C</th>
<th>DAY 3, Friday 23 November</th>
<th>15.40-16.40</th>
</tr>
</thead>
<tbody>
<tr>
<td>122</td>
<td>TRACK 17: Food- and waterborne diseases and zoonoses (5): Epidemiology and Outbreaks 2</td>
<td></td>
</tr>
<tr>
<td>125</td>
<td>TRACK 18: Food- and waterborne diseases and zoonoses (6): Surveillance systems</td>
<td></td>
</tr>
<tr>
<td>131</td>
<td>TRACK 20: Sexually transmitted infections (3): Intervention</td>
<td></td>
</tr>
<tr>
<td>133</td>
<td>TRACK 21: Vaccine- preventable diseases (3): Burden of disease</td>
<td></td>
</tr>
<tr>
<td>136</td>
<td>TRACK 22: Vaccine- preventable diseases (4): Vaccine effectiveness</td>
<td></td>
</tr>
<tr>
<td>140</td>
<td>TRACK 23: Policy approaches and evaluation</td>
<td></td>
</tr>
<tr>
<td>143</td>
<td>TRACK 24: Late breakers</td>
<td></td>
</tr>
</tbody>
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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
E. Sarvikivi 1, T. Möttönen 1, T. Voipio 1, J. Ollgren 1, O. Lyytikäinen 6

1 Department of Health Security, National Institute for Health and Welfare (THL), Helsinki, Finland; 6 Finnish Medicines Agency (Fimea), Helsinki, Finland

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 through 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
G. Guzzetta 1, J. Vildershøj Bjørnholm 2, T. Leegaard 2, A. Moen 2, S. Merler 2, B. Freiesleben de Blasio 5

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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 com-
**Poster Abstracts**

**1.3. Being a carrier of Multidrug Resistant Micro-organisms in daily life: the perspective of the patient**

Sabiena Feenstra ¹
R. Eilers ¹, 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:** 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:** Sabiena Feenstra / renske.eilers@rivm.nl

**1.4. Evaluation of Colistin Susceptibility Directly from Blood Cultures - A Novel Flow Cytometric Protocol**

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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 (11 Enterobacteriaceae, 12 Pseudomonasspp. and 2 Acinetobacter spp.), 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 AccuriTM C6 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. 24h), 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 of 1.00).

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, polymyxin, flow-cytometry, blood cultures, MDR microorganisms
ABSTRACT ID: 445
PRESENTED BY: Inês Martins-Oliveira / ioliveira@fastinov.com

1.5. Evaluation of FASTinov® kit for antimicrobial susceptibility testing on gram positive cocci,

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Background:
Bloodstream infections represent a critical healthcare condition associated with high mortality and morbidity. Increasing rates of antimicrobial resistance and the late laboratory 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 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, cephalixin, 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

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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.
Poster Abstracts

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,

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6 London North West Healthcare Trust
7 Royal Free London NHS Foundation Trust
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10 Public Health Laboratory, London, Public Health England
11 Royal Brompton Hospital

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 candidaemia) 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 Coxackievirus (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 type 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 (18%), EV-A (20%) and EV-C (0.7%). 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.
Poster Abstracts

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; Hemolytic-Uremic Syndrome; Enterohemorrhagic Escherichia coli; Disease Outbreaks; Disease Notification; Serogroup; Escherichia coli Infections

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.
Poster Abstracts

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 (OR=17; 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
PRESENTED BY: Nicola Love / nicola.love@phe.gov.uk

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). Aims 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 34 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
PRESENTED BY: Klára Labská / klara.labska@szu.cz

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.
3.4. A prolonged outbreak of monophasic Salmonella Typhimurium with environmental contamination in Norway, August 2017

Lotta Siira 1

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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 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=58).

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.

3.5. A Salmonellosis outbreak caused by Italian truffle salami, Stockholm 2018

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4 3. Public Health Agency of Sweden
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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 Administra-
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Susanne Hyllestad 1

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, advice 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 442, 273 (67%) reported remembering the advice of storing water in advance and 269 (66%) the boil water advice. 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 advice was independent of age, education, household type. Awareness of the notice was independent of sex but compliance was lower among women (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 advice 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, compliance, 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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4 Health Protection Surveillance Centre, Dublin, Ireland. Subject : Surveillance

ABSTRACT ID: 467
Poster Abstracts

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 15 years compared with the lowest incidence age-group (45-64 years) (aIRR 5.08, 95%CI 4.38-5.63) 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 socioeconomic 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 4,500 cases, 351 cases had not travelled, 14 had 160 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 (1-2 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

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**4.6. Risk of enteropathogenic protozoa infection in asymptomatic school children and their families in Leganés, Madrid (Spain), November 2017- March 2018**

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**Background:**

Entero-pathogenic protozoa Giardia duodenalis, Cryptosporidium spp. and Blastocystis spp. contribute to intestinal disorders and cognitive and developmental impairments in childhood. Blastocystis has been as-
Poster Abstracts

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); 130 years: aOR 6.1 (95%CI:2.0-18.3); 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 (I): 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;95CI:1.9-6.18) and difficulty breathing (OR=2.16;95CI:1.5-5.1) were best predictors for RSV infections. However, fever or feverishness (OR=0.49;95CI:0.7-0.9) and myalgia (OR=0.34;95CI:0.2-0.5) were negatively associated with RSV disease although were significantly associated with influenza positive cases (RRR=1.62; 95CI:1.4-1.9, RRR=1.53;95CI:1.3-1.8, and, RRR=1.95;95CI:1.7-2.3, 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%) and the ICPC R80 code was the most specific (47.6%), with the highest AUC (0.55). The most associated symptoms with a positive result were fever (OR: 4.16; 95CI: 3.38-5.12) and 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
PRESENTED BY: Pedro Pinto-Leite / pedro.cspl@gmail.com

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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Poster Abstracts

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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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 ILL 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 15 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
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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: 205.4-238.0) and 2016-17 (158.4, 95%-CI: 152.6-164.2) in which A(H3N2) virus was dominant, and for 2017-18 (146.2, 95%-CI: 138.6-153.8) 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.

6.1. Descriptive analysis of syphilis reinfections in Dublin from 2010 to 2017

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Abstracts
Poster Abstracts

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 75,349 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-resistant (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 25-35 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

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.
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, azithromycin 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, ST1961 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; 235r rRNA C261S).

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 ceftriaxone resistance also could be predicted. The emergence of this new clade is of major public health concern and was notified to the ECDC.

Subject: Surveillance
Keywords: gonorrhoea, Enhanced surveillance, high-level azithromycin resistant

ABSTRACT ID: 245
PRESENTED BY: Adrian Wensley / adrian.wensley@phe.gov.uk
Poster Abstracts

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.
Poster Abstracts

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: 102
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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, RRs: 0.2-4.1), and absence of PPE (13 persons, RRs: 0.1-2.2) were not associated with influenza-related symptoms at T4. One person showed a 14-fold titer increase against subtype H5, but also a 14-fold titer increase against multiple other subtypes. None of eight other participants with a 14-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

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. 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 in incidence of sheep and goats. 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.
**Poster Abstracts**

**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:** Cornelia HM van Jaarsveld / Ellen.vanJaarsveld@radboudumc.nl

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**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 4399 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
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**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 1936 in 2010 with an incidence rate of 33.9 per 100,000 populations to 5221 in 2016 with an incidence rate of 54.3 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 between 20 and 40 years of age. Of the 2896 suspected animal rabies, 141 (6.1%) 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
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**7.6. A Case of Rabies Leads to Prophylaxis for Others Exposed, Balkh Province, Afghanistan, 2016**

**CANCELLED**
8.1. Agent-based modeling of influenza dynamics in Russian cities: the role of spatial heterogeneity and background immunity levels

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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
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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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**Subject:** Modelling, bioinformatics and other biostatistical methods
**Keywords:** influenza, vaccination, adverse event, mathematical model, economic evaluation, public health
**ABSTRACT ID:** 431
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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 studies
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

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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%CI, 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%CI, 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
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8.5. ADVANCE system testing: benefit-risk analysis of a marketed vaccine using MCDA and cohort modelling

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8,12,13 Epidemiological Information for Clinical Research from an Italian
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 beNeft-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 (<6 years). 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 (RCP & 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

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References:
1 Erasmus University Medical Centre, Rotterdam, The Netherlands & VACCINE.GRID Foundation, Basel Switzerland
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3-5 GlaxoSmithKline Biologicals S.A., Rixensart, Belgium
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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 (IRR) 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 (IR), 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 hypertensive episode (HHE). IRs were similar across similar databases but differed based on where outcome is captured (primary or secondary care). The risk for febrile convulsions, fever, ISR, persistent crying, and somnolence was slightly higher for wP than aP during 1st dose 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.
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

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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.

9.2. Epidemiology of carbapenemase-producing bacteria in England, 2016–2018: results from the national enhanced surveillance system

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D. Ironmonger 1, K. Hopkins 1, R. Puleston 1, B. Muller-Pebody 1, R. Hope 1, S. Hopkins 1, A. Johnson 1, N. Woodford 1, I. Oliver 1

1 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 (1159, 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

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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. pneumonia 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. pneumonia 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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3 Department of Biomedical Sciences and Human Oncology - University of Foggia
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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. Pl 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: 547
PRESENTED BY: Daniela Loconsole / loconsole.daniela@libero.it

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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. 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 antifungal agents Fluconazole, 5-Flucytosine, Amphotericin, Voriconazole, Posaconazole, and the drug candidate Sertraline. Resistance to Fluconazole and 5-Flucytosine was defined at a minimal inhibitory concentration (MIC) >8 μg/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 within range with previous reports (MIC90 = 8 μg/ml).

5-Flucytosine was defined at a minimal inhibitory concentration (MIC) >32 μg/ml. Furthermore, 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 relapse. Sertraline shows promising in vitro activity.

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
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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
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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, 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.

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
Poster Abstracts

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, mosquito nets
ABSTRACT ID: 325
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10.2. Implementing WHO's Early Warning, Alert and Response System (EWARS) for outbreak detection during the Rohingya Crisis, Bangladesh 2017-2018
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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,

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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% (3/1139) in CS [OR=33.63, CI 95%, 22.29-50.76]. For LF, occupation, completeness was 89% (253/291) in SORMAS versus 19% (55/1139) in CS [OR=35.59 CI 95%, 23.94-52.92] for CSM, and 71% (171/242) 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 conventional surveillance in IDSR most likely due to improved user friendliness and early digitalization in SORMAS.

10.5. Descriptive epidemiology of a large outbreak of Diphtheria among Forcibly Displaced Myanmar Nationals, Bangladesh, 2017-2018

Jonathan Polonsky¹

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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 line-listed 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.
### 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 <15 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:**
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.

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**Keywords:** Diphtheria, Refugees, Disease Outbreaks, Bangladesh

**ABSTRACT ID:** 322
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Poster Abstracts

**11.2. Risk factors for autochthonous Hepatitis E in Germany**

**Mirko Faber**

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Robert Koch Institute, Department for Infectious Disease Epidemiology

**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. 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

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**11.3. Emergence of Hepatitis E virus in Belgium, 2010-2016**

**Lorenzo Subissi**


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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 phyloptype 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 phylootypes 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

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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 a 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

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.
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 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. 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 CEVS and EEVS; 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.
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
12.4. Multi-country outbreak of listeriosis due to Listeria monocytogenes, multi-focus sequence type 6, infections probably linked to frozen corn, European Union 2015–2018

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¹⁴

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 Baudh 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.
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 0.0001), and cases were older (mean age of 47 versus 42 years, p-value 0.0001) 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.
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
PRESENTED BY: Emmi Sarvikivi / emmi.sarvikivi@thl.fi

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

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**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. LDL 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 HAL.

**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.

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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) and HA-CDI cases (community onset) in Northern Ireland. We defined cases as possible matches when onset dates matched and as possible match if onset dates were less than 15 days apart.

**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.

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**Subject:** Surveillance  
**Keywords:** Clostridium difficile, community-associated infections, hospital-associated infections, enhanced surveillance  
**ABSTRACT ID:** 15  
**PRESENTED BY:** Anna Maisa / anna.maisa@gmail.com

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**European Scientific Conference on Applied Infectious Disease Epidemiology**
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 (SGA), but these differences are not considered in studies. We aim to describe the extent to which sex/gender based analysis (SGA) 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 SGSR-PT 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.

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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2 East of England Health Protection Team, Public Health 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 33% 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 at the meeting).
14.2. Laboratory results of HIV-syphilis co-infection in Bavaria 2010-2017

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4 Bavarian Health and Food Safety Authority

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 (2.78-14.2%). 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: 166
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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
PRESENTED BY: Lois O’Connor / lois_oconnor@hotmail.com
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 ≥18 years and attending specialist primary healthcare (HIV/infected 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 vaccinated 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.

Results:
There were 756 MSM in the cross-sectional survey, 52.6% (n=242) had complete and 34.8% (n=263) partial HAV vaccination. Complete HAV vaccination was less likely among foreign-born and 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.

Conclusions:
MSM who were provided with HAV vaccination may represent a higher risk population and it is essential 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
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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 140 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 classified as non-ASC, we compared baseline proportion of males 140 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 140 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
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 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%CI: -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: Hepatitis B, Refugees, Germany, Epidemiologic Surveillance

ABSTRACT ID: 231
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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. 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.
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: -32-84) and 66% (95% CI: -168-96) respectively. Among 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: -32-84) and 66% (95% CI: -168-96) respectively. Among 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: -32-84) and 66% (95% CI: -168-96) respectively.

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
Key words: influenza, vaccine effectiveness, prevention & control, surveillance
ABSTRACT ID: 408
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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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19 11 European countries

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.
Poster Abstracts

**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% (4-35) 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% (3-54) 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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28 11 European countries

**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).

**Conclusions:**
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 (21/35) 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 2645 B viruses systematically selected for lineage identification, 2605 (99%) belonged to the trivalent vaccine-matched 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: 12-33); 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 analyze 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
PRESENTED BY: Sabine Schroeder / Sabine.Schroeder@tlv.thueringen.de

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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4 Santé publique France, Saint-Maurice, France

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
PRESENTED BY: Anne Bernadou / anne.bernadou@santepubliquefrance.fr

16.3. Epidemiology of Invasive Meningococcal Disease (IMD) in Greece during 2006-2016

Anastasia Flountzi ¹
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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(90%) 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 the 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
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16.4. A measles outbreak in Ireland, 2017: Low vaccination coverage at subnational level challenges the elimination goal

Annalisa Quattrocchi

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2 Health Protection Surveillance Centre, Dublin, Ireland
3 Department of Public Health, HSE East, Dublin, Ireland
4 Department of Public Health, HSE North East, Meath, Ireland

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: 1-month-57years), and 45% were ≥16 years old.

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=10) 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 (eg. outbreak investigations)
Keywords: Measles-Mumps-Rubella vaccine, Immunisation, Measles elimination, Outbreak
ABSTRACT ID: 84
PRESENTED BY: Annalisa Quattrocchi
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### 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
Kassiani Melou ¹, Eirini Saranti-Papasaranti ¹, Georgia Mandilara ¹, Kyriaki Tryfinopoulou ¹, Theano Georgakopoulou ¹, Alkiviadis Vatopoulos ³

**Abstract**

In August 2017, an increase of human salmonellosis cases due to serotype Typhimurium 1,4 [5],12:i:- was observed in Magnisia and Pieria prefectures, Greece by the Reference Laboratory. An outbreak investigation was initiated to identify the source and implement control measures.

**Methods:**

The outbreak strain was defined as “Salmonella Typhimurium 1,4 [5],12:i:-” with AMR profile “ACSSuTTM” and PFGE profile “XbaI.GR01”. We defined outbreak cases as residents or visitors of Magnisia/Pieria, laboratory-confirmed with the outbreak strain from August 2017 onwards. We interviewed outbreak cases to identify exposures and carried out a retrospective case-case comparison study. We compared outbreak cases with sporadic Salmonella cases of other serotypes, matching on date of symptoms onset and age group. Adjusted odds ratios were calculated using logistic regression. We traced back the distribution chain of suspected food items and sampled them for microbiological analysis.

**Results:**

During August 2017, 40 outbreak cases were identified; 59% female with age-range 1-81 years (median 27). The food history of thirty outbreak cases was compared with 30 matched comparison cases. Outbreak cases were more likely to have consumed pork in the three days before symptoms onset (aOR 19, 95% CI 1.2-309). Trace-back investigations led to a common supplier for two restaurants; all food samples collected there were negative. Monitoring criteria for prevention of similar events were suggested.

**Conclusions:**

In the absence of microbiological evidence, epidemiological evidence from a case-case comparison study made it possible to identify pork as the most likely vehicle of this outbreak. This choice of study design should be considered more frequently in field investigations. The outbreak was first detected by the Reference Laboratory illustrating the importance of laboratory-based Salmonella spp. surveillance.

**Keywords:** Field epidemiology (e.g. outbreak investigations)

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

**ABSTRACT ID:** 3

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### 17.2. Freshly pressed grape must as a novel vehicle for infection with Francisella tularensis: an outbreak of oropharyngeal tularemia in autumn 2016, Germany

**Florian Burckhardt** ⁴
D. Hoffmann ², K. Jahn ³, K. Heuner ⁴, D. Jacob ², M. Vogt ⁴, R. Grunow ⁷, P. Zanger ⁸

**Abstract**

During the autumn of 2016, an outbreak of oropharyngeal tularemia occurred in the Federal State of Rhineland-Palatinate, Germany. The outbreak started with the consumption of freshly pressed grape must and affected 33 people, 29 of whom needed hospitalization. Francisella tularensis was identified by whole-genome sequencing of two isolates. Infection was not related to contact with infected animals or to consumption of other foods.

**Keywords:** Field epidemiology (e.g. outbreak investigations)

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

**ABSTRACT ID:** 4

**PRESENTED BY:** Florian Burckhardt / florian.burckhardt@robertkoch.de

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**References:**

1. Institute for Infectious Disease Prevention Landau, Federal State Agency for Consumer & Health Protection Rhineland-Palatinate, Germany
2. County Health Department Mainz-Bingen, Germany
3. Federal State Ministry for Social Affairs, Employment, Health, and Demographics Rhineland-Palatinate, Mainz, Germany
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5. Institute for Infectious Disease Prevention Landau, Federal State Agency for Consumer & Health Protection Rhineland-Palatinate, Germany
17.3. Investigation of a large hospital outbreak of Legionnaires’ disease in Lisbon, Portugal, October to November 2017

Alexis Sentís 1
P. Vasconcelos 1, G. Augusto 1, C. Abreu Santos 1, A. Silva Costa 1, P. Nogueira 1, R. Rodrigues 1, R. Gonçalves 1, M. Chasqueira 1, G. Freitas 1

1 Direção-Geral da Saúde, Lisboa. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden

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- ST) was detected. Among 77 samples taken in the water systems, 19 were positive for Lp, 10 of which were positive for STs, 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

PRESENTED BY: Alexis Sentís / alexissentis@gmail.com
ABSTRACT ID: 127

17.4. Investigating a cluster of Yersinia enterocolitica using Whole Genome Sequencing, United Kingdom, 2017

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1 National Infection Service, Public Health England, UK
2 2 North West Health Protection Team, Public Health England, UK
3 3 National Infection Service, Public Health England, UK
4 4 Royal Liverpool and Broadgreen University Hospitals NHS Trust, UK

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.

Subject: Field epidemiology (e.g. outbreak investigations)
Keywords: outbreak, oropharyngeal tularemia, grape must, Francisella tularensis, Germany

PRESENTED BY: Florian Burckhardt / florian.burckhardt@lua.rlp.de
ABSTRACT ID: 400

15.3. Investigation of a large hospital outbreak of Legionnaires’ disease in Lisbon, Portugal, October to November 2017

Alexis Sentís 1
P. Vasconcelos 1, G. Augusto 1, C. Abreu Santos 1, A. Silva Costa 1, P. Nogueira 1, R. Rodrigues 1, R. Gonçalves 1, M. Chasqueira 1, G. Freitas 1

1 Direção-Geral da Saúde, Lisboa. European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control, (ECDC), Stockholm, Sweden

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

PRESENTED BY: Florian Burckhardt / florian.burckhardt@lua.rlp.de
ABSTRACT ID: 400
17.5. Health risks associated with participating in mud and obstacle runs; a prospective cohort study between April and October 2017, the Netherlands

Elke den Boogert ¹

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² Department of Infectious Disease Control, Municipal Health Service Hart voor Brabant, s-Hertogenbosch, The Netherlands
³ Centre for Infectious Diseases, Epidemiology and Surveillance, National Institute for Public Health and the Environment (RIVM), Bilthoven, The Netherlands
⁴ Department of Infectious Disease Control, Public Health Service Rotterdam-Rijnmond, Rotterdam, The Netherlands
⁵ Department of Medical Microbiology and Infection Control, Jeroen Bosch Hospital, s-Hertogenbosch, The Netherlands
⁶ Department of Primary and Community Care, Radboud university medical centre, Nijmegen, The Netherlands

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:
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.

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.
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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¹ Field Epidemiology Training Programme, Public Health England
², ³, ⁴ Centre for Infectious Disease Surveillance and Control, Public Health England

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 prioritised.

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

18.2. Effect of culture-independent diagnostic tests on enteric disease surveillance, Wellington, New Zealand

Craig Thornley ¹
¹ Regional Public Health, Hutt Valley District Health Board, Lower Hutt, New Zealand

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, 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:
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:
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 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
Poster Abstracts

18.3. Description of the norovirus laboratory data to inform a surveillance system in Denmark

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5 6 Department of Infectious Disease Epidemiology and Prevention, Statens Serum Institut, Copenhagen, Denmark

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 15 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 (44 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.

18.4. Patient foreign travel information in the Danish National Microbiological Database (MiBa)

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1 Secretariat of Data Integration and Analysis (DIAS), Statens Serum Institut, Copenhagen, Denmark.
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3 Department of Infectious Disease Epidemiology and Prevention, Statens Serum Institut, Copenhagen, Denmark.
4 Department of Infectious Disease Epidemiology and Prevention, Statens Serum Institut, Copenhagen, Denmark.
5 Representatives from all clinical microbiology laboratories in Denmark.

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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⁶ Field Epidemiology Service North West, National Infection Service, Public Health England, United Kingdom
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⁸ Field Epidemiology Service North West, National Infection Service, Public Health England, United Kingdom

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 diarrhea 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=33), 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, ST19 (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

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 IP 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
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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

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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 in Staphylococcus 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:
Eighty isolates were ST101 and one was ST407. We detected two genetically 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 genetically 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
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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 55 hospitals. 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.

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
Poster Abstracts

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
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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 SSI 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
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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
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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 gonorrhoeae, Sexually transmitted infections (STIs), STI clinic, Bacterial load, Microbiology
ABSTRACT ID: 188
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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
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 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.
Poster Abstracts

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

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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:
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/NRTI 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
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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:
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

21.3. 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
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=2), 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

Prepared by: David Hendrickx / adonachie@hotmail.co.uk


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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 (38.4% of total deaths) followed by communicable diseases (12.8%) and injuries with 3.6%. 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 12,700 PYLL, the external causes 7,622 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: Mortality, underlying cause of death, potential years of life lost, epidemiological transition
ABSTRACT ID: 504
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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, 4,091 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 (525 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%; 2,372 of 4,091 cases) followed by 1 to 5 age group (874 cases).

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.
Poster Abstracts

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 (5+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

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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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¹ Epiconcept, France

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Poster Abstracts

N. Fry 15, E. Colzani 24, L. Pastore-Celentano 15, G. Hanquet 26, A. SpIDnet group 16
14 National Institute of Public Health, Prague, Czech Republic 3,14 Statens Serum Institut, Copenhagen, Denmark
1 ACTIV, Saint-Maur des Fossés, France
1 Health Protection Surveillance Centre, Dublin, Ireland
2 RIVM, Bilthoven, The Netherlands
3 Norwegian Institute of Public Health, Oslo, Norway
8 Public Health Agency of Catalonia, Barcelona, Spain
9 General Sub-directorate of Epidemiology - Madrid Region, Madrid, Spain
10-11 Public Health Institute of Navarra, Pamplona, Spain
11 Health Protection Scotland, Glasgow, United Kingdom
12-13 Public Health England, London, United Kingdom
14 European Hospital Georges - Pompidou, National Reference Centre for Pneumococci, Paris, France
15 Temple Street Children’s University Hospital, Irish Pneumococcal Reference Laboratory, Dublin, Ireland
16 Academic Medical Centre, National Reference Laboratory for Bacterial Meningitis, Amsterdam, The Netherlands
17 Hospital Sant Joan de Déu, Institute of Pediatric Research, Barcelona, Spain
18 General Sub-directorate of Epidemiology- Madrid Region, Madrid, Spain
19 Scottish Haemophilus- Legionella- Meningococcus and Pneumococcus Reference Laboratory, Glasgow, United Kingdom
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21 European Centre for Disease Prevention and Control, Stockholm, Sweden
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23 Epiconcept, France

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
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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 (6.6) 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=0.002). 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).
Poster Abstracts

Conclusions:
Surveillance data indicate evidence of serotype replacement. Surveillance evaluation should assess 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

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**Abstracts**

### 23.1. A review of evaluations of the Norwegian Surveillance System for Communicable Diseases: Need for a systematic approach

**Astrid Lovlie**

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7, S. Hauge, E. MacDonald

**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 Lovlie / astrid.louise.lovlie@fhi.no

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23.2. Primary diphtheria immunisation for adults using a low dose vaccine: a literature review

**Theresa Enkirch**

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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 1921-2017 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), vaccine dose (≤ 7.5 Lf, minimum of two doses) and 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

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**European Scientific Conference on Applied Infectious Disease Epidemiology**
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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³ Netherlands Reference Laboratory for Bacterial Meningitis (NRLBM), Academic Medical Center, Amsterdam, the Netherlands

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 underlying 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 56.5; 6.6%; 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
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 immunisation 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 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: Preparedness
Keywords: Measles, vaccination, health knowledge attitudes, practices, adolescent behaviours, school enrolment

ABSTRACT ID: 320
PRESENTED BY: Peter Kreidl / peter.kreidl@i-med.ac.at

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...
Poster Abstracts

Information to select locations for prospective observational studies assessing brand-specific vaccine effectiveness.


Subject: Preparedness
Keywords: immunization programs, influenza vaccines, influenza, equipment and supplies, Europe, vaccines
ABSTRACT ID: 200
PRESENTED BY: Anke L. Stuurman / anke.stuurman@p-95.com

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

Diogo F. P. Marques 1


1 Health Protection Scotland (HPS), Glasgow, United Kingdom
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3 Centers for Disease Control and Prevention (CDC), Atlanta, United States of America
4 415-2 Public Health England (PHE), London, United Kingdom
5 813 NHS Tayside, Dundee, United Kingdom
6 10,14 Scottish Microbiology Reference Laboratory, Glasgow, United Kingdom
11,12 NHS Western Isles, Stornoway, United Kingdom

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

Amrei Krings 1
T. Eckmanns 1, J. Hermes 3

1 Postgraduate Training for Applied Epidemiology (PAE), Robert Koch Institute, Germany; European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden; Department of Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany
3 Department of Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany

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.

Subject: Preparedness
Keywords: immunization programs, influenza vaccines, influenza, equipment and supplies, Europe, vaccines
ABSTRACT ID: 200
PRESENTED BY: Anke L. Stuurman / anke.stuurman@p-95.com

Track 24: Late breakers

Moderator:
Aftab Jasir

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Conclusions:
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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

Amrei Krings 1
T. Eckmanns 1, J. Hermes 3

1 Postgraduate Training for Applied Epidemiology (PAE), Robert Koch Institute, Germany; European Programme for Intervention Epidemiology Training (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden; Department of Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany
3 Department of Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany

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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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S. Márcio Crima ³, J. Péricio ³, M. Moulin Achcar ³, I. Andreatta Menegolla ³, P. Pauli Kist ³, J. dos Santos Ribeiro ³, C. Márcio Difante ³, L. Pacheco ³, R. Mauro Faria ³, É. Giotto ³, C. Mendes Cabral ³
1- Ministry of Health, Secretariat of Health Surveillance, Department of Surveillance of Communicable Diseases, General Coordination of Surveillance and Response to Emergencies in Public Health, Program of Training in Epidemiology Applied to Services of the Single Health System.
2-3 - Ministry of Health, Secretariat of Health Surveillance, Department of Surveillance of Communicable Diseases, General Coordination of Surveillance and Response to Emergencies in Public Health, Program of Training in Epidemiology Applied to Services of the Single Health System.
4 Ministry of Health, Secretariat of Health Surveillance, Department of Surveillance of Communicable Diseases.
5-6 State Department of Health of Rio Grande do Sul, State Center for Health Surveillance, Department of Epidemiological Surveillance.
7 4th Regional Health Coordination of Rio Grande do Sul, Department of Health Surveillance, Department of Water Quality Surveillance for Human Consumption.
8 Municipal Health Secretariat of Santa Maria-RS, Superintendent of Health Surveillance, Epidemiological Surveillance.
9 Federal University of Santa Maria, University Hospital of the Federal University of Santa Maria, Nucleus of Hospital Surveillance.
10 Federal University of Santa Maria, Department of Geosciences / Geography in Health.
11 Federal University of Santa Maria, Department of Agrarian Sciences, Geomatics Laboratory.
12 Ministry of Health, Secretariat of Health Surveillance, Department of Surveillance of Communicable Diseases, General Coordination of Emergency Surveillance and Response in Public Health, Program of Training in Epidemiology Applied to Services of the Unified Health System.
24.5. Nationwide outbreak of puerperal group A streptococcal infection in the Netherlands

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⁴ Center for Infectious Disease Control, National Institute for Public Health and the Environment, Bilthoven, The Netherlands

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 studyemm-types involved, in order to generate hypotheses about its cause.

Methods:
P GAS 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
ABSTRACT ID: 562
PRESENTED BY: Jossy van den Boogaard / jossyvandenboogaard@gmail.com

24.6. Implementation of influenza POCT and influenza ward to improve hospital capacity and to reduce costs

Suzanne Lutgens ¹

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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

**ABSTRACT ID:** 539

**PRESENTED BY:** Suzanne Lutgens / s.lutgens@jbz.nl
## Index by Subject

<table>
<thead>
<tr>
<th>PLENARY SESSION A</th>
<th>Antimicrobial resistance</th>
</tr>
</thead>
<tbody>
<tr>
<td>20</td>
<td>Keynote address: “New diseases in the Old World”: Perspectives on pathogen emergence and capacity to respond in Africa and beyond</td>
</tr>
<tr>
<td>20</td>
<td>“Sequencing for Public Health; the four S’s (sensing, surveillance, source attribution, and sharing)”</td>
</tr>
<tr>
<td>21</td>
<td>“What have we overlooked in the epidemiology of antimicrobial resistance (AMR) in Europe?”</td>
</tr>
<tr>
<td>22</td>
<td>“Respondent driven sampling for communicable disease control”</td>
</tr>
<tr>
<td>23</td>
<td>“Intercontinental response to emerging health threats: capacity and coordination”</td>
</tr>
</tbody>
</table>

### Plenary

| 29 | Factors associated with Methicillin-Resistant Staphylococcus aureus (MRSA) acquisition rates of wards in a Singapore tertiary hospital: An electronic medical records study |
| 49 | Concurrent outbreaks of extensively-resistant Shigella sonnei and Shigella flexneri in men who have sex with men, Melbourne Australia |
| 52 | Antimicrobial resistance |
| 52 | Antimicrobial resistance in Aspergillus fumigatus isolated February to September 2017 from clinical specimens in Lyon, France |
| 53 | OXA-48-producing Enterobacteriales detected in Irish seawater, 2017 |
| 53 | National surveillance of methicillin-resistant Staphylococcus aureus bacteraemia following the implementation of Whole-Genome Sequencing in England, April-December 2017 |
| 54 | Burden of infections caused by antibiotic-resistant bacteria in the European Union and the European Economic Area in 2015 using disability-adjusted life years |
| 76 | Antimicrobial resistance and healthcare-associated infections: intervention and assessment |
| 80 | Increased risk of invasive group A streptococcal disease in the household contacts of scarlet fever cases in England, 2011-2016 |
| 91 | The burden of resistant Neisseria gonorrhoeae in the EU/EEA |
## Index by Subject

<table>
<thead>
<tr>
<th>Page</th>
<th>Title</th>
<th>Type</th>
</tr>
</thead>
<tbody>
<tr>
<td>91</td>
<td>Enhanced surveillance of a long term outbreak of gonorrhoea with high-level resistance to azithromycin in England since 2014</td>
<td>Poster</td>
</tr>
<tr>
<td>99</td>
<td>Outbreak of a rare type of Methicillin-resistant Staphylococcus aureus (MRSA) among teenagers and their families in a small community in Norway, 2016-2017</td>
<td>Poster</td>
</tr>
<tr>
<td>99</td>
<td>Epidemiology of carbapenemase-producing bacteria in England, 2016–2018: results from the national enhanced surveillance system</td>
<td>Poster</td>
</tr>
<tr>
<td>100</td>
<td>First report of macrolide-resistant Mycoplasma pneumonie in adults with community-acquired pneumonia in Italy</td>
<td>Poster</td>
</tr>
<tr>
<td>111</td>
<td>Specific characteristics of healthcare-associated infection (HAI)-outbreaks - results from the national surveillance system in Germany, 2012-2017</td>
<td>Poster</td>
</tr>
<tr>
<td>78</td>
<td>Emerging and vector-borne diseases (1)</td>
<td>Poster</td>
</tr>
<tr>
<td><strong>Food- and waterborne diseases and zoonoses</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>32</td>
<td>Food- and waterborne diseases and zoonoses (1): microbiology and whole genome sequencing</td>
<td>Parallel</td>
</tr>
<tr>
<td>34</td>
<td>Impact of whole genome sequencing on food-borne outbreak detection and response in Canada</td>
<td>Parallel</td>
</tr>
<tr>
<td>34</td>
<td>Food- and waterborne diseases and zoonoses (2): epidemiology and surveillance 1</td>
<td>Parallel</td>
</tr>
<tr>
<td>42</td>
<td>Food- and waterborne diseases and zoonoses (3): outbreaks</td>
<td>Parallel</td>
</tr>
<tr>
<td>51</td>
<td>Food- and waterborne diseases and zoonoses (4): epidemiology and surveillance 2</td>
<td>Parallel</td>
</tr>
<tr>
<td>81</td>
<td>Food- and waterborne diseases and zoonoses (1): Epidemiology- Salmonellosis</td>
<td>Poster</td>
</tr>
<tr>
<td>83</td>
<td>A Salmonellosis outbreak caused by Italian truffle salami, Stockholm 2018</td>
<td>Poster</td>
</tr>
<tr>
<td>84</td>
<td>Food- and waterborne diseases and zoonoses (2): Surveillance</td>
<td>Poster</td>
</tr>
<tr>
<td>104</td>
<td>Food- and waterborne diseases and zoonoses (3): Hepatitis and viral infection</td>
<td>Poster</td>
</tr>
</tbody>
</table>
# Index by Subject

<table>
<thead>
<tr>
<th>Page</th>
<th>Title</th>
<th>Type</th>
</tr>
</thead>
<tbody>
<tr>
<td>106</td>
<td>Improving preparedness to respond to cross-border hepatitis A outbreaks in the European Union/European Economic Area: towards comparable sequencing of hepatitis A virus</td>
<td>Poster</td>
</tr>
<tr>
<td>122</td>
<td>Food- and waterborne diseases and zoonoses (5): Epidemiology and Outbreaks 2</td>
<td>Poster</td>
</tr>
<tr>
<td>125</td>
<td>Food- and waterborne diseases and zoonoses (6): Surveillance systems</td>
<td>Poster</td>
</tr>
<tr>
<td>111</td>
<td>Specific characteristics of healthcare-associated infection (HA)-outbreaks - results from the national surveillance system in Germany, 2012-2017</td>
<td>Poster</td>
</tr>
<tr>
<td>112</td>
<td>Possible underreporting and misclassification of healthcare-associated Legionnaires’ disease cases in the EU/EEA</td>
<td>Poster</td>
</tr>
<tr>
<td>145</td>
<td>Nationwide outbreak of puerperal group A streptococcal infection in the Netherlands</td>
<td>Poster</td>
</tr>
</tbody>
</table>

## Healthcare-associated infections

<table>
<thead>
<tr>
<th>Page</th>
<th>Title</th>
<th>Type</th>
</tr>
</thead>
<tbody>
<tr>
<td>27</td>
<td>Healthcare-associated infections</td>
<td>Parallel</td>
</tr>
<tr>
<td>27</td>
<td>Validation of an electronic nationwide surveillance system for periprosthetic joint infections following primary total knee replacement in Denmark</td>
<td>Parallel</td>
</tr>
<tr>
<td>28</td>
<td>Occupational exposure to percutaneous injuries and prevalence of HBV, HCV and HIV among hospital staff in Poland: a multicenter study</td>
<td>Parallel</td>
</tr>
<tr>
<td>28</td>
<td>Epidemiology and impact of norovirus outbreaks in Norwegian healthcare institutions, 2006-2018</td>
<td>Parallel</td>
</tr>
<tr>
<td>111</td>
<td>Specific characteristics of healthcare-associated infection (HA)-outbreaks - results from the national surveillance system in Germany, 2012-2017</td>
<td>Poster</td>
</tr>
<tr>
<td>112</td>
<td>Possible underreporting and misclassification of healthcare-associated Legionnaires’ disease cases in the EU/EEA</td>
<td>Poster</td>
</tr>
<tr>
<td>145</td>
<td>Nationwide outbreak of puerperal group A streptococcal infection in the Netherlands</td>
<td>Poster</td>
</tr>
</tbody>
</table>

## HIV, sexually transmitted infections and viral hepatitis

<table>
<thead>
<tr>
<th>Page</th>
<th>Title</th>
<th>Type</th>
</tr>
</thead>
<tbody>
<tr>
<td>49</td>
<td>HIV, sexually transmitted infections and viral hepatitis (1): epidemiology and surveillance</td>
<td>Parallel</td>
</tr>
<tr>
<td>113</td>
<td>Sexually transmitted infections (2), HIV and Viral Hepatitis: Surveillance</td>
<td>Poster</td>
</tr>
<tr>
<td>131</td>
<td>Post-exposure prophylaxis for HIV after sexual exposure is a marker of future risk of sexually transmitted infections among heterosexual STI clinic attendees</td>
<td>Poster</td>
</tr>
</tbody>
</table>

## Influenza and other respiratory viruses

<table>
<thead>
<tr>
<th>Page</th>
<th>Title</th>
<th>Type</th>
</tr>
</thead>
<tbody>
<tr>
<td>63</td>
<td>Influenza and other respiratory viruses(1): epidemiology and surveillance</td>
<td>Parallel</td>
</tr>
<tr>
<td>63</td>
<td>Whole genome analysis of influenza A(H3) viruses detected between 2016-2018 in the scope of EuroEVA/I-MOVE vaccine effectiveness study</td>
<td>Parallel</td>
</tr>
<tr>
<td>63</td>
<td>Predicting peak influenza activity in primary and secondary care in Scotland – is the Moving Epidemic Method the way forward?</td>
<td>Parallel</td>
</tr>
<tr>
<td>Page</td>
<td>Title</td>
<td>Type</td>
</tr>
<tr>
<td>------</td>
<td>----------------------------------------------------------------------</td>
<td>---------</td>
</tr>
<tr>
<td>70</td>
<td>Influenza and other respiratory viruses</td>
<td>Parallel</td>
</tr>
<tr>
<td>70</td>
<td>2017–18 Vaccine effectiveness against influenza A(H3N2) and lineage mismatched influenza B in older adults: Results from the I-MOVE+ hospital network</td>
<td>Parallel</td>
</tr>
<tr>
<td>71</td>
<td>High live-attenuated influenza vaccine effectiveness against influenza B in two-year-olds, 2017/18, Finland</td>
<td>Parallel</td>
</tr>
<tr>
<td>80</td>
<td>Six year experience of detection and investigation of possible MERS-CoV cases, England, 2012-2018</td>
<td>Poster</td>
</tr>
<tr>
<td>87</td>
<td>Influenza, TB and other respiratory viruses (1): Surveillance, Incidence and Burden</td>
<td>Poster</td>
</tr>
<tr>
<td>87</td>
<td>Evaluation of ECDC Influenza-like illness (ILI) case definition to detect respiratory syncytial virus (RSV) infection through the Influenza Surveillance System in Portugal</td>
<td>Poster</td>
</tr>
<tr>
<td>88</td>
<td>Performance of ECDC ILI case definition and ICPC R80 code for influenza surveillance based on the Portuguese Influenza Surveillance System</td>
<td>Poster</td>
</tr>
<tr>
<td>88</td>
<td>Burden of respiratory syncytial virus associated hospitalisation in the first year of life in a major urban city, Lyon, France 2010 to 2016</td>
<td>Poster</td>
</tr>
<tr>
<td>89</td>
<td>The incidence of symptomatic infection with influenza virus in the Netherlands 2011/2012 to 2016/2017, estimated using Bayesian evidence synthesis</td>
<td>Poster</td>
</tr>
<tr>
<td>89</td>
<td>Real-time mortality attributed to seasonal influenza in Spain, 2012-13 to 2017-18</td>
<td>Poster</td>
</tr>
<tr>
<td>90</td>
<td>Contrasting socioeconomic differences in acute infectious diseases in the Netherlands</td>
<td>Poster</td>
</tr>
<tr>
<td>116</td>
<td>Influenza, TB and other respiratory viruses (2): Vaccination and interventions</td>
<td>Poster</td>
</tr>
<tr>
<td>116</td>
<td>Previous vaccination and viral genetic variation effects over the 2016-17 influenza vaccine in Spain</td>
<td>Poster</td>
</tr>
<tr>
<td>117</td>
<td>Effectiveness of the 2017/18 trivalent and tetravalent influenza vaccines against influenza B in children and adolescents in Germany</td>
<td>Poster</td>
</tr>
<tr>
<td>117</td>
<td>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</td>
<td>Poster</td>
</tr>
</tbody>
</table>
### INDEX BY PRESENTING AUTHOR / MODERATOR

<table>
<thead>
<tr>
<th></th>
<th>Author</th>
<th>Title</th>
<th>Type</th>
</tr>
</thead>
<tbody>
<tr>
<td>38</td>
<td>Aaberge Ingeborg S.</td>
<td>Parallel</td>
<td></td>
</tr>
<tr>
<td>68</td>
<td>Alpers Katharina</td>
<td>Parallel</td>
<td></td>
</tr>
<tr>
<td>91</td>
<td>Amato-Gauci Andrew</td>
<td>Poster</td>
<td></td>
</tr>
<tr>
<td>131</td>
<td>Andreasen Aura</td>
<td>Poster</td>
<td></td>
</tr>
<tr>
<td>84</td>
<td>Barrasa Alicia</td>
<td>Poster</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Beaute Julien</td>
<td>Poster</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Bishop Louise</td>
<td>Poster</td>
<td></td>
</tr>
<tr>
<td>63, 112</td>
<td>Borges Vitor</td>
<td>Parallel</td>
<td></td>
</tr>
<tr>
<td>136</td>
<td>Bosman Arnold</td>
<td>Poster</td>
<td></td>
</tr>
<tr>
<td>90</td>
<td>Bremer Viviane</td>
<td>Poster</td>
<td></td>
</tr>
<tr>
<td>122, 123</td>
<td>Burkhardt Florian</td>
<td>Poster</td>
<td></td>
</tr>
<tr>
<td>60</td>
<td>Carvalho Carlos</td>
<td>Parallel</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Cotter Suzanne</td>
<td>Parallel</td>
<td></td>
</tr>
<tr>
<td>80</td>
<td>Dabrera Gavin</td>
<td>Poster</td>
<td></td>
</tr>
<tr>
<td>60</td>
<td>de Carvalho Gomes Helena</td>
<td>Parallel</td>
<td></td>
</tr>
<tr>
<td></td>
<td>de Valk Henriette</td>
<td>Parallel</td>
<td></td>
</tr>
<tr>
<td>115</td>
<td>Diercke Michaela</td>
<td>Poster</td>
<td></td>
</tr>
<tr>
<td>117</td>
<td>Dreesman Johannes</td>
<td>Poster</td>
<td></td>
</tr>
<tr>
<td>115</td>
<td>Dudareva Sandra</td>
<td>Poster</td>
<td></td>
</tr>
<tr>
<td>61</td>
<td>Edelstein Michael</td>
<td>Parallel</td>
<td></td>
</tr>
<tr>
<td>102</td>
<td>Fontaine Johann</td>
<td>Poster</td>
<td></td>
</tr>
<tr>
<td>140</td>
<td>Gauci Charmaine</td>
<td>Poster</td>
<td></td>
</tr>
<tr>
<td>27, 110</td>
<td>Gubbels Sophie</td>
<td>Parallel</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Hahne Susan</td>
<td>Parallel</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Hajdu Ágnes</td>
<td>Poster</td>
<td></td>
</tr>
<tr>
<td>125</td>
<td>Hansen Lisa</td>
<td>Poster</td>
<td></td>
</tr>
<tr>
<td>104</td>
<td>Hecht Jane</td>
<td>Poster</td>
<td></td>
</tr>
<tr>
<td>55</td>
<td>Ingrosso Loredana</td>
<td>Parallel</td>
<td></td>
</tr>
<tr>
<td>60, 62</td>
<td>Jansen Klaus</td>
<td>Parallel</td>
<td></td>
</tr>
<tr>
<td>143</td>
<td>Jasir Aftab</td>
<td>Poster</td>
<td></td>
</tr>
<tr>
<td>108</td>
<td>Jurke Annette</td>
<td>Poster</td>
<td></td>
</tr>
<tr>
<td>101</td>
<td>Karagiannis Ioannis</td>
<td>Poster</td>
<td></td>
</tr>
<tr>
<td>56</td>
<td>Kohlenberg Anke</td>
<td>Parallel</td>
<td></td>
</tr>
<tr>
<td>46, 137</td>
<td>Krizova Pavla</td>
<td>Parallel</td>
<td></td>
</tr>
<tr>
<td>52</td>
<td>Lina Bruno</td>
<td>Poster</td>
<td></td>
</tr>
<tr>
<td>46</td>
<td>Lopalco Pierluigi</td>
<td>Parallel</td>
<td></td>
</tr>
<tr>
<td>76, 100, 111, 129</td>
<td>Lytyikäinen Outi</td>
<td>Poster</td>
<td></td>
</tr>
<tr>
<td>83, 140</td>
<td>MacDonald Emily</td>
<td>Poster</td>
<td></td>
</tr>
<tr>
<td>32, 81</td>
<td>Manley Petra</td>
<td>Poster</td>
<td></td>
</tr>
<tr>
<td>60, 100</td>
<td>Martinelli Domenico</td>
<td>Parallel</td>
<td></td>
</tr>
<tr>
<td></td>
<td>McMenamin Jim</td>
<td>Poster</td>
<td></td>
</tr>
<tr>
<td>93, 96</td>
<td>Melillo Tanya</td>
<td>Poster</td>
<td></td>
</tr>
<tr>
<td>79, 99</td>
<td>Muller-Pebody Berit</td>
<td>Poster</td>
<td></td>
</tr>
<tr>
<td>123</td>
<td>Nogueira Paulo J</td>
<td>Poster</td>
<td></td>
</tr>
<tr>
<td>48, 64, 71, 97, 119</td>
<td>Nohyne Hanna</td>
<td>Poster</td>
<td></td>
</tr>
<tr>
<td>83, 84, 140</td>
<td>Nygård Karin</td>
<td>Poster</td>
<td></td>
</tr>
<tr>
<td>33, 99</td>
<td>Oliver Isabel</td>
<td>Poster</td>
<td></td>
</tr>
<tr>
<td>82</td>
<td>Orlikova Hana</td>
<td>Poster</td>
<td></td>
</tr>
<tr>
<td>117, 118</td>
<td>Penttinen Pasi</td>
<td>Poster</td>
<td></td>
</tr>
<tr>
<td>39, 135</td>
<td>Pfaff Guenter</td>
<td>Parallel</td>
<td></td>
</tr>
<tr>
<td>54, 112, 130</td>
<td>Plachouras Diamantis</td>
<td>Parallel</td>
<td></td>
</tr>
<tr>
<td>63, 143</td>
<td>Reynolds Arlene</td>
<td>Parallel</td>
<td></td>
</tr>
<tr>
<td>72, 144</td>
<td>Rezza Giovanni</td>
<td>Parallel</td>
<td></td>
</tr>
<tr>
<td>70, 71,</td>
<td>Rose Angela MC</td>
<td>Parallel</td>
<td></td>
</tr>
</tbody>
</table>
# INDEX BY PRESENTING AUTHOR / MODERATOR

<table>
<thead>
<tr>
<th>Page</th>
<th>Author</th>
<th>Name</th>
<th>Type</th>
</tr>
</thead>
<tbody>
<tr>
<td>86</td>
<td>Salmenlinna</td>
<td>Saara</td>
<td>Poster</td>
</tr>
<tr>
<td>56, 57</td>
<td>Sane</td>
<td>Jussi</td>
<td>Parallel</td>
</tr>
<tr>
<td>100, 119</td>
<td></td>
<td></td>
<td>Poster</td>
</tr>
<tr>
<td>106</td>
<td>Severi</td>
<td>Ettore</td>
<td>Poster</td>
</tr>
<tr>
<td>107</td>
<td>Shankar</td>
<td>Giri</td>
<td>Poster</td>
</tr>
<tr>
<td>44, 91</td>
<td>Spiteri</td>
<td>Gianfranco</td>
<td>Parallel</td>
</tr>
<tr>
<td>93, 113</td>
<td></td>
<td></td>
<td>Poster</td>
</tr>
<tr>
<td>29</td>
<td>Stefanoff</td>
<td>Pawel</td>
<td>Parallel</td>
</tr>
<tr>
<td>36</td>
<td>Steffens</td>
<td>Ines</td>
<td>Parallel</td>
</tr>
<tr>
<td>36, 37</td>
<td>Stoitsova</td>
<td>Savina</td>
<td>Parallel</td>
</tr>
<tr>
<td>34</td>
<td>Thomas</td>
<td>Daniel</td>
<td>Parallel</td>
</tr>
<tr>
<td>120</td>
<td>Tzanakaki</td>
<td>Georgina</td>
<td>Poster</td>
</tr>
<tr>
<td>92, 128</td>
<td>van Alphen</td>
<td>Lieke</td>
<td>Poster</td>
</tr>
<tr>
<td>39, 40</td>
<td>van der Sande</td>
<td>Marianne</td>
<td>Parallel</td>
</tr>
<tr>
<td>68</td>
<td></td>
<td></td>
<td>Poster</td>
</tr>
<tr>
<td>93</td>
<td>Varela Santos</td>
<td>Carmen</td>
<td>Poster</td>
</tr>
<tr>
<td>123</td>
<td>Vasconcelos</td>
<td>Paula</td>
<td>Poster</td>
</tr>
<tr>
<td>38, 45</td>
<td>Vestrheim</td>
<td>Didrik Frimann</td>
<td>Parallel</td>
</tr>
<tr>
<td>46, 137, 140</td>
<td></td>
<td></td>
<td>Poster</td>
</tr>
<tr>
<td>66</td>
<td>Wagner-Wiening</td>
<td>Christiane</td>
<td>Parallel</td>
</tr>
<tr>
<td>78</td>
<td>Winter</td>
<td>Christian</td>
<td>Poster</td>
</tr>
<tr>
<td>120</td>
<td>Xirogianni</td>
<td>Athanasia</td>
<td>Poster</td>
</tr>
<tr>
<td>117, 118, 140</td>
<td>Zakikhany</td>
<td>Katherina</td>
<td>Poster</td>
</tr>
</tbody>
</table>
## Index by Keyword

### A
- Acceptability, 30, 37, 114, 132-133
- Acetabular pertussis vaccines, 139
- Acinetobacter baumannii, 143
- Acute Watery Diarrhea, 42
- addictive behaviour, 50
- adenoviral keratoconjunctivitis, 110-111
- adenovirus, 81, 110-111
- Adolescent, 49, 60, 99, 117, 141
- adverse event, 42, 48, 96
- Africa, 2, 14, 20, 37, 52
- Agent-Based Modeling, 96
- Alaiski district, 35
- algorithm, 13, 27, 51, 78, 80, 101, 107-127
- all hazard, 103
- Animal bites, 95
- Anticorrelated consumption, 76
- Antibacterials for systemic use, 76
- Antibiotic resistance, 27-28, 54, 77, 92, 130
- antibiotics, 20, 27-28, 92, 104, 122
- Antifungal Agents, 101
- antifungals, 52-53, 101
- Antigens, 119, 141
- antimicrobial resistance, 2, 4-5, 16, 20-21, 25, 29, 49-50, 52-54, 75-76, 80, 91, 99, 101, 111
- Antimicrobial susceptibility testing, 49, 78
- Arboviruses, 30-31
- Ascaris suum, 30
- Asian tiger mosquito, 73
- asolescent behaviour, 142
- aspergillosis, 52-53
- Aspergillus fumigatus, 52
- asylum seekers, 104, 115
- asymptomatic infection, 74, 87
- automated data collection, 126-127
- automated incidence monitoring, 126
- Automated reporting, 64
- avian influenza, 13, 94
- azole resistance, 53

### B
- background immunity, 96
- Bacterial Endocarditis, 130
- bacterial gastroenteritis, 85
- Bacterial load, 131
- bacterial meningitis, 38, 47, 121, 134-135, 141
- Bangladesh, 47, 102-104, 122
- Bayesian, 89, 140
- benefit-risk assessment, 98
- bioinformatics, 7, 15, 29, 49-50, 63, 77, 89, 96-97, 140
- Bishkek city, 55-56
- Blastocystis spp., 86-87
- blood cultures, 77-78, 128
- blood-borne infections, 28
- bloodstream infection, 54, 78, 111
- Boil water advisories, 84
- Borna Disease, 66-67
- Brandenburg, 134
- Bronchiolitis, 89
- Brucellosis, 43-44, 94-95
- Burden of disease, 5, 30, 32, 38, 45, 52-54, 61, 63, 72-73, 75, 86, 89-91, 95, 110, 133-136
- Burden of Illness, 54
- Carbapenemase, 53, 99-100
- carbapenemase-producing Enterobacteriaceae, 53, 100
- cardiovascular diseases, 133, 136
- case definition, 41, 44, 67, 87-88, 106, 121, 123-124, 135-136
- case fatality rate, 38, 42, 121
- case-control, 42, 67, 71, 82, 105, 107-108, 116-117
- Case-control study, 42, 67, 82, 105, 107, 117
- Chemsex, 50-51, 93
- Chikungunya virus, 72-73
- Child health, Pacific, 74
- Chlamydia trachomatis, 60-63, 131
- Cholecystectomy, 130-131
- Cholera, 3, 13, 25, 39-42
- Cholera/epidemiology, 40
Index by Keyword

chronic hepatitis b, 36, 61-62
climate change, 52
clinical pathway, 145-146
Clostridium difficile, 76, 111-112, 128
Clostridium perfringens, 42-43, 107-108
cluster, 22, 31-34, 38, 41-42, 44, 47, 49-50, 55-57, 67, 72-73, 80, 82-83, 86-87, 93, 99-101, 107, 109, 120, 123-125, 128-129, 145
cluster detection, 34, 107
clustering, 22, 33, 56-57, 92, 124
co-infection, 65-66, 81, 93, 114, 143
cochrane, 113
colistin, 77-78
communicable disease, 2, 10, 17, 22-23, 34, 67, 83, 94, 108, 114, 136, 140, 144
Communicable Disease Control, 2, 17, 22, 67, 83, 94, 108
Communicable Diseases -Emerging, 67
communication, 6, 10, 36-37, 64, 82, 84, 93-94, 108
community-acquired pneumonia, 27, 100-101
community-associated infections, 112
comorbidity, 27, 104, 116-117
Complex Emergency, 41-42
compliance, 84
congenital rubella infection, 135
congenital rubella syndrome, 135
Congenital Zika syndrome, 73-74
Conjugate vaccines, 48, 138
consumer communication, 84
Contact Tracing, 22, 47, 55, 57, 61, 86, 143
cost, 73
Core genome MLST, 128
corn, 68, 86, 109
Coronary Artery Bypass, 130
cost of illness, 73, 135
cost-effectiveness, 36, 71
countrywide outbreak, 82
Coxiella burnetii, 93-94
CPE, 53, 100
Cryptococcosis, 101
Cryptococcus, 101
Cryptosporidium spp, 86-87
CSM, 103

D
Danish Microbiology Database, 27, 78, 126
data network, 70, 99
Data quality, 30, 37, 103, 114
Decision Making, 54-55, 113, 124, 142
Delay, 30, 57, 59, 78, 125-126
Delayed Diagnosis, 114
Democratic Republic of the Congo, 23, 39-40, 101-102
Denmark, 8, 27, 42, 45-46, 68-70, 78-79, 97-98, 126, 138, 142
diabetes mellitus, 117, 133, 137
digital reporting, 79
Diphtheria, 47-49, 60, 103-104, 122, 140-141
Diphtheria Antitoxin, 48-49
Diphtheria Toxoid, 47, 140-141
disease Notification, 39, 81, 125
disease outbreaks, 7, 11, 13, 23, 28, 40, 47, 50, 73, 81, 83, 93, 99, 104, 106, 108-109, 122-123, 125, 143-144
disease surveillance, 6, 11, 13, 23, 37, 102-103, 112, 125-126, 140
domestic, 42, 67-68, 100, 109-110
drug resistance, 55, 101
Drug Resistance Fungal, 101
Drug users, 132

E
E. coli, 21, 53, 81, 109, 125-126
Echo-6, 107
economic evaluation, 96
eggs, 44, 82
eHealth, 13, 37, 103
EIEC, 108-109, 125-126
elderly, 38, 45, 47-48, 54, 64, 71-72, 90, 116, 119, 140, 143
electronic health care databases, 99
emergency settings, 102
enhanced surveillance, 49, 54, 91-92, 99-100, 112, 114, 141
Enteric fever Salmonella, 86
Enteric infections, 125-126
Enterococcus sp., 78
Enterohemorrhagic Escherichia coli, 81
Entero virus, 31, 79-80, 107
environmental surveillance, 107
epidemic, 13-14, 37, 39, 44, 49, 51, 63-64, 67, 73, 80, 86, 96, 102, 106, 109, 120, 146
epidemic response, 13, 73
epidemics, 7, 13, 35, 40, 88-90, 145
Epidemics/history, 40
## Index by Keyword

<table>
<thead>
<tr>
<th>Epidemiologic Determinants, 77</th>
</tr>
</thead>
<tbody>
<tr>
<td>Epidemiologic Surveillance, 55, 116</td>
</tr>
<tr>
<td>epidemiological transition, 136</td>
</tr>
<tr>
<td>Epidemiology, 1-8, 10-12, 14, 16-18, 20-52, 54-58, 60-76, 78-130, 132, 134-138, 140-146</td>
</tr>
<tr>
<td>equipment and supplies, 143</td>
</tr>
<tr>
<td>ethnicity, 59, 86, 116, 132</td>
</tr>
<tr>
<td>EU, 1-2, 10-12, 15-18, 21, 31, 44-45, 54, 56, 67-68, 91, 106, 109, 112, 118, 125, 128-131, 135, 142-144</td>
</tr>
<tr>
<td>Europe, 2, 6, 10-12, 16, 21, 23, 29, 31, 48-49, 53, 56, 68, 71-73, 84, 88, 91-92, 98, 107, 112, 117, 123, 135, 139, 142-143</td>
</tr>
<tr>
<td>European Surveillance System (TESSy), 56</td>
</tr>
<tr>
<td>European Union, 10, 21, 54, 56, 71, 91, 106-107, 109, 112, 130, 142</td>
</tr>
<tr>
<td>EV-D68 outbreak, 80</td>
</tr>
<tr>
<td>Evaluation, 5, 15, 28, 30-31, 37, 46, 48, 55-60, 62-67, 71, 74, 76, 81-84, 86, 94, 97, 104-109, 120, 123-124, 131-133, 140, 144</td>
</tr>
<tr>
<td>Exposures, 28, 30, 32, 35, 43, 66-67, 74, 81-82, 84, 94, 105-106, 108, 123-124</td>
</tr>
<tr>
<td>F</td>
</tr>
<tr>
<td>farm outbreaks, 94</td>
</tr>
<tr>
<td>Finland, 8, 46-48, 64-65, 70-71, 76, 86, 97, 100, 109, 111, 119, 129, 142</td>
</tr>
<tr>
<td>flow-cytometry, 78</td>
</tr>
<tr>
<td>Follow-Up Studies, 137</td>
</tr>
<tr>
<td>food contamination, 34</td>
</tr>
<tr>
<td>food isolates, 85-86, 109, 128</td>
</tr>
<tr>
<td>food processing industry, 34</td>
</tr>
<tr>
<td>food safety, 15, 29-30, 33-34, 83, 86, 109, 114, 127, 137</td>
</tr>
<tr>
<td>foodborne disease, 34, 83, 107, 109</td>
</tr>
<tr>
<td>France/epidemiology, 81</td>
</tr>
<tr>
<td>Francisella tularensis, 35, 122-123</td>
</tr>
<tr>
<td>FRED, 96</td>
</tr>
<tr>
<td>fungal infections, 53</td>
</tr>
</tbody>
</table>

### G

gardening, 67
gastroenteric disease, 36
gastroenteritis, 32, 43, 52, 58, 85, 104, 108-109, 124-127, 144
gastrointestinal disease, 43
gender, 22, 55, 58, 81, 91, 95, 104, 110, 113, 127, 130, 132-133, 136
general practice, 90
genomics, 15-16, 50
genotype, 42, 50, 93, 100, 105-106
genotyping, 44, 85, 92-93, 105, 127

### H

H5N8, 94
Haiti, 41
harm reduction, 50-51, 132
HBV, 28, 36, 60-61, 115, 132
HCAI, surveillance, 128
HCV, 28, 36, 50
health care costs emergency department, 146
Health Facilities, 28, 37, 102
health impact, 58, 73
health inequalities, 90
health infections, 113
health status, 23, 95, 101
Health survey, 102
Healthcare Associated Infections, 4, 16, 54, 75, 128
Healthcare Cost-Analysis, 89
healthcare-associated infections, 3, 5, 25, 27, 75, 111-112
hepatitis, 4-5, 22, 25-26, 28, 36, 42, 49-50, 60-62, 75, 80, 104-107, 113-116, 132
Hepatitis A, 42, 106-107, 115
Hepatitis B, 28, 36, 60-62, 114-116, 132
Hepatitis C, 36, 50
<table>
<thead>
<tr>
<th>Keyword</th>
<th>Page(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>hepatitis E</td>
<td>104-105</td>
</tr>
<tr>
<td>Herd immunity</td>
<td>49, 58, 120</td>
</tr>
<tr>
<td>herpes zoster</td>
<td>134</td>
</tr>
<tr>
<td>Heterosexual</td>
<td>61, 91, 131-132</td>
</tr>
<tr>
<td>high-level azithromycin resistant</td>
<td>92</td>
</tr>
<tr>
<td>HIV</td>
<td>4-6, 14, 17, 22, 25-26, 28, 49-51, 60, 62-63, 75, 91, 93, 113-115, 131-133</td>
</tr>
<tr>
<td>HIV infections</td>
<td>132-133</td>
</tr>
<tr>
<td>HIV Pre-Exposure Prophylaxis</td>
<td>62-63</td>
</tr>
<tr>
<td>Homosexuality</td>
<td>106</td>
</tr>
<tr>
<td>Hospital Acquired Infections</td>
<td>27</td>
</tr>
<tr>
<td>hospital outbreak</td>
<td>123</td>
</tr>
<tr>
<td>hospital-acquired infections</td>
<td>7, 29</td>
</tr>
<tr>
<td>hospital-associated infections</td>
<td>112</td>
</tr>
<tr>
<td>household cluster</td>
<td>80</td>
</tr>
<tr>
<td>Human brucellosis</td>
<td>43-44, 94</td>
</tr>
<tr>
<td>human echinococcosis</td>
<td>35</td>
</tr>
<tr>
<td>I</td>
<td></td>
</tr>
<tr>
<td>immunization programs</td>
<td>48, 58, 143</td>
</tr>
<tr>
<td>impact daily life</td>
<td>77</td>
</tr>
<tr>
<td>Imported malaria</td>
<td>78-79</td>
</tr>
<tr>
<td>India</td>
<td>47, 103, 109-110, 122</td>
</tr>
<tr>
<td>Infant</td>
<td>44-45, 48, 54, 57-58, 60, 67-68, 73, 82-83, 112, 138, 145</td>
</tr>
<tr>
<td>infant formula</td>
<td>83</td>
</tr>
<tr>
<td>infection prevention</td>
<td>16, 27-28, 99, 111, 115, 128, 130</td>
</tr>
<tr>
<td>infectious disease</td>
<td>1-2, 4, 6-8, 10-12, 14-18, 20, 22, 24, 26-30, 32-34, 36-38, 40, 42, 44, 46, 48-50, 52, 54, 56-58, 60, 62-64, 66-68, 70, 72-74, 76, 78, 80, 82, 84, 86-88, 90, 92-94, 96, 98, 100-102, 104-108, 110-112, 114-118, 120, 122, 124-126, 128-130, 132-146</td>
</tr>
<tr>
<td>Infectious Encephalitis</td>
<td>67</td>
</tr>
<tr>
<td>Influenza</td>
<td>4-5, 7, 13, 24, 26, 59, 63-66, 68, 70-72, 75, 81, 87-90, 94, 96, 116-119, 136-137, 142-146</td>
</tr>
<tr>
<td>Influenza B</td>
<td>70-71, 117-119, 143</td>
</tr>
<tr>
<td>influenza hospitalizations</td>
<td>65-66</td>
</tr>
<tr>
<td>Influenza surveillance</td>
<td>65-66, 87-88, 90</td>
</tr>
<tr>
<td>Influenza vaccines</td>
<td>96, 117, 137</td>
</tr>
<tr>
<td>influenza virus</td>
<td>63, 71, 81, 89, 94, 118</td>
</tr>
<tr>
<td>influenza-like illness</td>
<td>87-90</td>
</tr>
<tr>
<td>information sharing</td>
<td>102-103</td>
</tr>
<tr>
<td>Intensive care</td>
<td>65, 79, 111-112</td>
</tr>
<tr>
<td>Internally Displaced Person</td>
<td>42</td>
</tr>
<tr>
<td>international cooperation</td>
<td>143-144</td>
</tr>
<tr>
<td>Interrupted Time Series</td>
<td>137</td>
</tr>
<tr>
<td>invasive group A streptococcal infection</td>
<td>80</td>
</tr>
<tr>
<td>invasive listeriosis</td>
<td>33, 127-128</td>
</tr>
<tr>
<td>invasive pneumococcal disease</td>
<td>38, 45-46, 48, 137-139</td>
</tr>
<tr>
<td>Isoniazid mono-resistance</td>
<td>56</td>
</tr>
<tr>
<td>Italy</td>
<td>8, 44, 46, 54, 56, 58, 60, 67-70, 72, 76, 79-80, 98, 100-101, 108-109, 117-118, 142, 144</td>
</tr>
<tr>
<td>J</td>
<td>27, 129</td>
</tr>
<tr>
<td>Jordan</td>
<td>7, 9, 95</td>
</tr>
<tr>
<td>K</td>
<td></td>
</tr>
<tr>
<td>Kaplan-Meier Estimates</td>
<td>132</td>
</tr>
<tr>
<td>Klebsiella pneumoniae</td>
<td>21, 53, 100, 111</td>
</tr>
<tr>
<td>Kyrgyzstan</td>
<td>35, 56</td>
</tr>
<tr>
<td>L</td>
<td></td>
</tr>
<tr>
<td>laboratory detection</td>
<td>31</td>
</tr>
<tr>
<td>Lassa fever</td>
<td>13, 103</td>
</tr>
<tr>
<td>Legionella non-pneumophila</td>
<td>67</td>
</tr>
<tr>
<td>Legionella pneumonia</td>
<td>123</td>
</tr>
<tr>
<td>Legionnaires’ disease</td>
<td>112, 123</td>
</tr>
<tr>
<td>lemming</td>
<td>34-35</td>
</tr>
<tr>
<td>life expectancy</td>
<td>133, 135</td>
</tr>
<tr>
<td>Listeria monocytogenes</td>
<td>33-34, 68, 86, 109, 127-128</td>
</tr>
<tr>
<td>Listeriosis</td>
<td>33-34, 68, 109, 127-128</td>
</tr>
<tr>
<td>literature review</td>
<td>54, 133, 135, 140</td>
</tr>
<tr>
<td>logistic models</td>
<td>117</td>
</tr>
<tr>
<td>longbeachae, outbreak</td>
<td>67</td>
</tr>
<tr>
<td>Lyme borreliosis</td>
<td>29</td>
</tr>
<tr>
<td>Lymphogranuloma venereum</td>
<td>93</td>
</tr>
<tr>
<td>M</td>
<td></td>
</tr>
<tr>
<td>Macrolide-resistant Mycoplasma pneumoniae</td>
<td>100</td>
</tr>
</tbody>
</table>
Index by Keyword

Mandatory Programs, 58
Mandatory vaccination, 58-60, 67-68
mapping, 18, 40, 69, 102, 128
Markov Chains, 22
mathematical model, 6, 72, 77, 96
MDR microorganisms, 78
measles, 13, 37, 60, 67-69, 102, 119-121, 133-134, 141-142
Measles elimination, 121
measles mumps rubella immunization programme, 134
medical devices, 69, 98, 113
medical personnel, 28
Men who have sex with men (MSM), 50, 61-62, 106, 131-132
Meningococcal ACWY vaccine, 120
Meningococcal infections, 39
MERS-CoV, 7, 80-81
meta-analysis, 47, 95, 98, 138
meteorological data, 123
Methicillin-Resistant Staphylococcus aureus (MRSA), 76, 99
methodological study, 98
MHealth, 37, 103
MiBa, 78-79, 126-127
microbiology database, 27, 78, 126
Middle East Respiratory Syndrome, 7, 80-81
migrants, 17, 22-23, 36-37
Mixed-effects Poisson Model, 139-140
Molecular epidemiology, 7, 73, 92, 101
Molecular testing, 32
molecular typing, 34, 43, 82, 101, 107
Monoclonal Antibodies, 48-49
morbidity, 27, 57, 78, 94-95, 101-102, 113, 133, 135
Mortality, 33, 54, 64, 72, 78, 89-90, 95, 101-102, 110, 112-113, 121-122, 130-131, 133, 135-136, 141
mosquitoe nets, 102
mortality, 136
mothers, 59, 61, 73-74
multi-center observational studies, 99
multicentre studies, 119
Multilocus Sequence Typing, 33, 101
Mumps, 24, 60, 69, 119, 121, 133-134, 136, 141
Mycobacterium Infections, 30
Mycoplasma pneumoniae, 100-101

N
National health examination survey, 61
Neisseria, 4, 38-39, 49, 61, 63, 75, 90-93, 131
Neisseria gonorrhoeae, 4, 61, 75, 90-92, 131
Neisseria meningitidis, 39, 49
neonatal sepsis, 135
NITAG, 142
Norovirus, 28, 108, 124-126
Norwalk Virus, 108
nosocomial, 58, 111

O
occupational exposure, 28, 30
Odisha, 109-110
One-health, 103
open source, 13, 37, 102-103
open source information, 102-103
Oral Cholera Vaccine, 41-42
Oropharyngeal, 61, 122-123, 131
oropharyngeal tularemia, 122-123
outbreak detection, 13, 23, 51, 102, 106, 127
outbreak response, 7, 13, 34, 37, 41, 49, 103

P
Pandemic influenza, 64, 68, 96
parechovirus, 31
parental, 59
Patient Registry, 27
Patient travel, 126-127
PCR, 42, 45, 47, 60, 63, 71, 79-80, 87, 92-93, 100, 104-105, 108, 110, 117, 125-126, 131, 145-146
percutaneous injuries, 28
perinatal care, 145
pertussis, 39, 44-45, 60, 69-70, 96-98, 139, 141
Pertussis vaccine, 44-45, 97-98, 139
PFGE, 33-34, 82
Phylogeny, 33, 72, 107
Pigs, 30, 105
Pneumococcal carriage, 38
Pneumococcal Conjugate Vaccine (PCV), 139
Index by Keyword

Pneumococcal Infections, 46, 48, 137-138
Pneumococcal Meningitis, 137-140
pneumococcal serotypes, 47
Pneumococcal Vaccines, 46, 133, 138
point-of-care testing, 146
Poisson regression, 51, 58, 65-66, 115
Policy Making, 48, 141
polimyxin, 78
Population Surveillance, 46, 138
portable surveillance system, 102
Post-Exposure Prophylaxis, 131-132
Post-licensure vaccine safety, 99
potential years of life lost, 135-136
Pre-Exposure Prophylaxis (PrEP), 51, 62, 132
pregnancy, 51, 73-74, 97, 135
preparedness, 4, 14, 24, 26, 31, 40-41, 64, 67-70, 73, 84, 94, 96, 98-99, 106-107, 126, 142-143
prescribing, 21, 27-28
prevention & control, 16, 119
preventive measures, 29, 33, 91, 93, 124
previous vaccination, 116, 118
program evaluation, 58
Proportional Hazards Models, 132
prospective, 34, 55, 94, 97, 124, 129, 135, 142-143
Public health surveillance, 13, 28, 30-32, 88, 90, 129-130, 140, 145
public perceptions, 66, 93
Public-private collaboration, 68-69
puerperal infection, 145
Q
Q fever, 93-95
R
Rabies, 95
Randomised controlled trial, 62
record linkage, 57
recreational water, 53
Refugees, 23, 102-104, 116, 122
Regression Analysis, 52, 61-62, 65, 82, 132
reinfections, HIV, 91
Republic of Macedonia, 94-95
Respiratory Syncytial Virus, 87-89
retrospective studies, 135
reverse transcriptase inhibitors, 133
risk areas, 29, 40
Risk Assessment, 24, 33, 79, 85, 96, 98, 102, 129-130, 143
risk populations, 29
rodent, 34-35
Rohingya Crisis, 102
rotavirus, 57-58, 104
Rubella, 60, 69, 119, 121, 133-135, 141
running, 52, 124
S
salami, 83-84
Salmonella, 32-35, 44, 51, 81-84, 86, 109, 122, 125-127
Salmonella Enteritidis, 44, 125
Salmonella infections, 83
Salmonella serovar Bareilly, 82
Salmonella Typhimurium, 33, 82-84, 122
scarlet fever, 80
school enrollment, 142
schools, 59, 87, 99, 141-142, 144
Screening recommendations, 60-61
secondary care, 27-28, 63-64, 98
Sequence Analysis, 63, 72, 85, 107
Seroepidemiologic Studies, 39, 67, 97
Serogroup, 38-39, 81, 84-86, 120-123, 141
serogroup W, 38, 121-122
Serology, 52, 62, 105, 123
serotype replacement, 139
Severe Dehydration, 40, 42
Severity assessment, 64
Sex Ratio, 106
Sexual Health, 6, 50, 62, 91-93, 113-114, 132
Sexually Transmitted Diseases, 63, 92, 114
Sexually transmitted infections (STIs), 131
Shiga-Toxigenic Escherichia coli, 81, 85
# Index by Keyword

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Page Range</th>
</tr>
</thead>
<tbody>
<tr>
<td>Shiga-Toxigenic Escherichia coli/epidemiology</td>
<td>81</td>
</tr>
<tr>
<td>Shigellosis, 35-36, 49-50, 109, 126</td>
<td></td>
</tr>
<tr>
<td>shingles</td>
<td>134</td>
</tr>
<tr>
<td>Singapore, 29, 63, 118</td>
<td></td>
</tr>
<tr>
<td>Single-Chain Antibodies</td>
<td>49</td>
</tr>
<tr>
<td>Slovenia, 7, 9, 21, 59, 110-111, 142</td>
<td></td>
</tr>
<tr>
<td>social network analysis</td>
<td>29</td>
</tr>
<tr>
<td>soil</td>
<td>67</td>
</tr>
<tr>
<td>SORMAS, 13, 37, 103</td>
<td></td>
</tr>
<tr>
<td>South Morocco, 43-44</td>
<td></td>
</tr>
<tr>
<td>spatial analysis</td>
<td>144-145</td>
</tr>
<tr>
<td>spatial cluster</td>
<td>41, 145</td>
</tr>
<tr>
<td>Staphylococcus aureus, 21, 76-77, 99, 111, 129</td>
<td></td>
</tr>
<tr>
<td>statistics &amp; numerical data</td>
<td>81</td>
</tr>
<tr>
<td>statutory surveillance</td>
<td>134</td>
</tr>
<tr>
<td>STEC, 81, 85, 126</td>
<td></td>
</tr>
<tr>
<td>STI clinic, 50, 61, 131</td>
<td></td>
</tr>
<tr>
<td>streptococcal infections</td>
<td>143-144</td>
</tr>
<tr>
<td>Streptococcus agalactiae</td>
<td>135</td>
</tr>
<tr>
<td>Streptococcus pneumoniae</td>
<td>46, 48, 138</td>
</tr>
<tr>
<td>Streptococcus pyogenes</td>
<td>128-129</td>
</tr>
<tr>
<td>Students, 108, 120, 144</td>
<td></td>
</tr>
<tr>
<td>Surgical site infections</td>
<td>129-130</td>
</tr>
<tr>
<td>Surgical Wound Infection</td>
<td>131</td>
</tr>
<tr>
<td>surveillance, 3-6, 10-11, 13, 15, 18, 20, 23-40, 44-47, 49-51, 53-58, 60-61, 63-68, 70-72, 75-76, 78-81, 84-85, 87-93, 95, 99-103, 105-107, 109-121, 123-132, 134-141, 144-145</td>
<td></td>
</tr>
<tr>
<td>Surveys and Questionnaires</td>
<td>94, 99, 107</td>
</tr>
<tr>
<td>Swine, 30, 104-105</td>
<td></td>
</tr>
<tr>
<td>syndromic surveillance</td>
<td>31-32, 40, 89, 127</td>
</tr>
<tr>
<td>synthetic populations</td>
<td>96</td>
</tr>
<tr>
<td>Syphilis, 4, 75, 90-91, 114, 132</td>
<td></td>
</tr>
<tr>
<td>Systematic evaluation</td>
<td>37, 103</td>
</tr>
<tr>
<td><strong>T</strong></td>
<td></td>
</tr>
<tr>
<td>targeting resources</td>
<td>69</td>
</tr>
<tr>
<td>Therapeutics</td>
<td>49</td>
</tr>
<tr>
<td>Tick-Borne Encephalitis</td>
<td>31-32, 141</td>
</tr>
<tr>
<td>Time series, 35, 85, 90, 110, 137</td>
<td></td>
</tr>
<tr>
<td>time series analysis</td>
<td>35, 85, 110, 137</td>
</tr>
<tr>
<td>time-to-event</td>
<td>57</td>
</tr>
<tr>
<td><strong>Toxoplasma gondii</strong>, 52</td>
<td></td>
</tr>
<tr>
<td><strong>Toxoplasmosis</strong>, 51-52, 144-145</td>
<td></td>
</tr>
<tr>
<td>treatment none-adherence</td>
<td>56</td>
</tr>
<tr>
<td>Treatment outcome</td>
<td>56</td>
</tr>
<tr>
<td>Tuberculosis, 4, 25, 55-57, 113, 116-117</td>
<td></td>
</tr>
<tr>
<td>tularemia</td>
<td>34-35, 122-123</td>
</tr>
<tr>
<td>typing, 7, 31, 33-34, 38, 42-43, 51, 82-83, 92-93, 100-101, 106-107, 109, 120, 123, 125, 127-129, 143, 145</td>
<td></td>
</tr>
<tr>
<td><strong>U</strong></td>
<td></td>
</tr>
<tr>
<td>underlying cause of death</td>
<td>135-136</td>
</tr>
<tr>
<td>underreporting</td>
<td>46, 79, 112, 114, 135</td>
</tr>
<tr>
<td>Uptake, 4, 25, 36, 45, 48-49, 57-61, 69, 72, 114, 121, 132-133</td>
<td></td>
</tr>
<tr>
<td>Urban flooding</td>
<td>52</td>
</tr>
<tr>
<td><strong>V</strong></td>
<td></td>
</tr>
<tr>
<td>vaccination campaign</td>
<td>47, 96, 120, 122, 142</td>
</tr>
<tr>
<td>vaccination coverage</td>
<td>39, 41, 47, 58-60, 67, 102, 104, 121, 134, 140</td>
</tr>
<tr>
<td>vaccination refusal</td>
<td>37</td>
</tr>
<tr>
<td>vaccination uptake</td>
<td>69</td>
</tr>
<tr>
<td>vaccine effectiveness</td>
<td>3, 5, 25, 44-46, 63, 65, 70-71, 75, 116-118, 136, 138, 142-143</td>
</tr>
<tr>
<td>vaccine failure</td>
<td>63</td>
</tr>
<tr>
<td>vaccine hesitancy</td>
<td>59</td>
</tr>
<tr>
<td>vaccine impact</td>
<td>47</td>
</tr>
<tr>
<td>Vaccine post-marketing setting</td>
<td>68</td>
</tr>
<tr>
<td>vaccine preventable diseases</td>
<td>46, 59, 141</td>
</tr>
<tr>
<td>Vaccines, 20, 41, 45-46, 48, 58-60, 62, 68, 71-72, 96-98, 117, 120, 132-134, 137-139, 142-143</td>
<td></td>
</tr>
<tr>
<td>Varicella, 60, 104, 134</td>
<td></td>
</tr>
<tr>
<td>varicella vaccination</td>
<td>134</td>
</tr>
<tr>
<td>vascular line</td>
<td>111</td>
</tr>
<tr>
<td>Veterinarians, 30, 66</td>
<td></td>
</tr>
<tr>
<td>Vibrio cholera</td>
<td>40</td>
</tr>
<tr>
<td>Viral Diseases</td>
<td>67</td>
</tr>
<tr>
<td>viral mutations</td>
<td>116</td>
</tr>
<tr>
<td>Virulence</td>
<td>53, 85</td>
</tr>
<tr>
<td>VZV, 134</td>
<td></td>
</tr>
</tbody>
</table>
Index by Keyword

W
Wales, 12, 80, 85, 128, 132-133
water outages, 84
water supply, 84
West Nile fever, 31
West Nile Virus, 24, 30-31
Whole Genome Sequencing, 3, 25, 32-34, 44, 53-55, 67-68, 82-83, 85-86, 92, 99-100, 109, 125, 128-129
Whooping cough, 45, 97

XYZ
Yersinia, 123-125
Zika virus infection, 74
Zoonoses, 3-5, 25, 32, 34, 42, 51, 75, 81, 84, 94-95, 104-105, 107, 122, 125