

ESCAIDE

European Scientific Conference on
Applied Infectious Disease Epidemiology

19-21 November 2025

HYBRID Warsaw and online



ABSTRACT BOOK



ABOUT ESCAIDE

The European Scientific Conference on Applied Infectious Disease Epidemiology (ESCAIDE) is Europe's leading public health conference dedicated to sharing knowledge on infectious disease epidemiology, public health microbiology, and related scientific fields.

Since 2007, it has been organised annually by the European Centre for Disease Prevention and Control (ECDC), bringing together experts, professionals, and students from diverse backgrounds.

The scientific content of the conference primarily consists of plenary sessions, oral and poster abstract presentations, and other side events, which provide a platform to share research, discuss scientific advances, and form lasting professional networks.

FOREWORD



Witamy na ESCAIDE 2025! I am delighted to welcome you to this year's edition of ESCAIDE, hosted online and in my home country, Poland. By bringing the conference to such a vibrant and well-connected city in Central Europe, we have sought to make it more accessible to participants from Poland's neighbouring countries, while still allowing thousands of people to attend online. ESCAIDE is a uniquely exciting opportunity to learn and connect to colleagues from across Europe and the world; I hope we will all come away from the conference with renewed inspiration, knowledge and networks that will enhance our work in public health.

As a scientific conference, ESCAIDE aims to showcase the work carried out by researchers and public health professionals working in a variety of fields related to infectious disease prevention and control. This year's call for abstracts attracted scores of high-quality submissions; thank you to each of the authors, co-authors and presenters, who have taken the time to submit and share their work at the Conference. My gratitude also goes to all the experts who acted as reviewers of abstracts during the selection process, and to those who will act as moderators during abstract-led sessions.

This year's plenary sessions aim to guide the audience through three critical issues in public health: the challenges of evidence-based decision-making, the need for better collaboration in a One Health framework, and the importance of placing health equity and inclusion at the centre of our work. I am very grateful to the experts who will take part in these panel discussions and hope we can all learn from the insights they will share with us.

As Chair of the ESCAIDE Scientific Committee, with great support from the ECDC ESCAIDE Team, it has been a pleasure to work alongside both new and returning members of the Committee this year. In this year's scientific programme, we have endeavoured to place cutting-edge knowledge and research in the wider context, bringing together novel advances in public health with essential social and methodological challenges. The members' commitment to the conference, both behind the scenes and on stage, is commendable.

Since 2022, ESCAIDE has been held as a hybrid event, allowing thousands of attendees to access sessions remotely and connect with one another through the online platform. I am pleased that the invaluable content of the conference can reach so many participants across the world, including through YouTube and modules on the ECDC Learning Portal. As we aim to keep improving the accessibility and sustainability of the conference, we have also reflected this year on our commitment and contributions to the Sustainable Development Goals, which you can read more about on the [ESCAIDE website](#).

Finally, I would like to express my appreciation for my colleagues at the Polish Ministry of Health and the National Institute of Public Health, whose support has been invaluable in making ESCAIDE feel at home in Poland. To them, and to everyone else who makes ESCAIDE possible, *bardzo dziękuję!*

Piotr Kramarz

Chair, ESCAIDE Scientific
Committee

A handwritten signature in blue ink, reading 'Piotr Kramarz'. The signature is stylized, with a large, flowing 'P' and 'K'.

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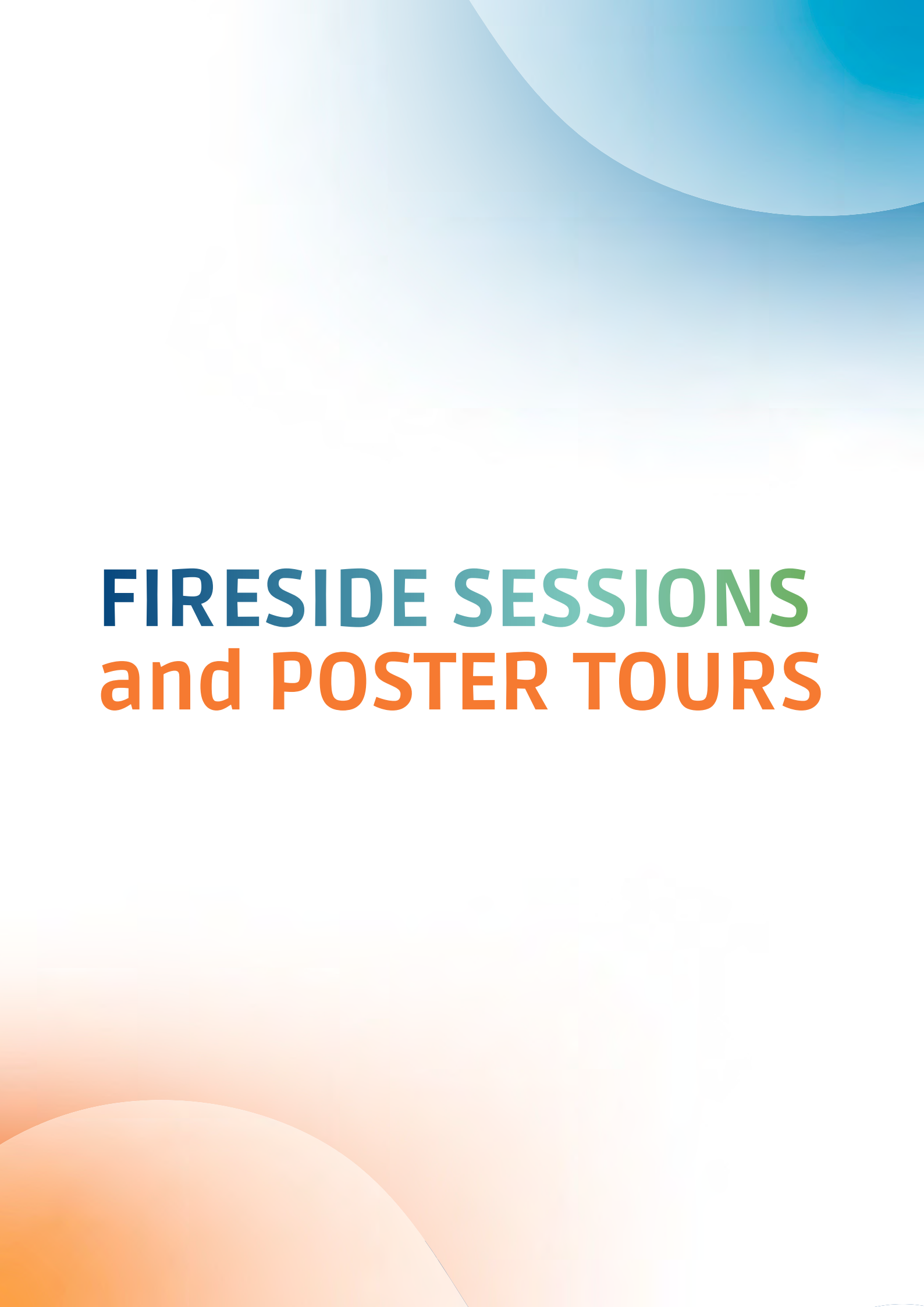
08.00-09.00	Registration and welcome coffee		
09.00-09.25	Opening ceremony AUDITORIUM 1		
09.25-10.25	PLENARY SESSION A: HIGH STAKES, LOW CERTAINTY: POST-NORMAL SCIENCE IN PUBLIC HEALTH GOVERNANCE Chaired by the ESCAIDE Scientific Committee members Agnes Hajdu (National Center for Public Health and Pharmacy, Hungary) and Henriette de Valk (Santé Publique, France) Speaker: <i>Silvio Funtowicz (University of Bergen, Norway)</i> AUDITORIUM 1		
10.25-10.30	SPOTLIGHT ON THE NEW EU REFERENCE LABS FOR PUBLIC HEALTH AUDITORIUM 1		
10.30-11.00	Coffee break		
11.00-12.30	FIRESIDE SESSION 1 Preparedness AUDITORIUM 1	FIRESIDE SESSION 2 COVID-19 vaccination AUDITORIUM 2	FIRESIDE SESSION 3 Quantitative methods AUDITORIUM 3
12.30-14.00	Lunch break	12.35-13.35 Thematic session 1: Artificial intelligence in public health: hype or help? Moderated by: <i>Laura Espinosa (ECDC) and Katja Siling (ECDC)</i> Speakers: <i>Sergio Consoli (Joint Research Centre, Italy), Yannis Paschalidis (Boston University, United States), and Annie Hartley (EPFL, Switzerland)</i> AUDITORIUM 1 12.35-13.55 Career compass <i>Organised by EPIET Alumni Network (EAN)</i> Moderated by <i>Ioannis Karagiannis (EAN) and Liza Coyer (EAN)</i> Speakers: <i>Ewout Fanoy (GGD regio Utrecht, Netherlands), Justine Schaeffer (Agence régionale de santé, France), Louise Coole (UK FETP), Steen Ethelberg (SSI, Denmark), and Kassiani Mellou (EODY, Greece)</i> AUDITORIUM 2	
14.00-15.30	FIRESIDE SESSION 4 Respiratory infections: evidence to practice AUDITORIUM 1	FIRESIDE SESSION 5 Vaccine research and immunisation programmes AUDITORIUM 2	
15.40-16.40	Poster tour 1: Sexually transmitted infections Poster tour 2: Respiratory infections: evidence to practice Poster tour 3: Outbreaks of food-borne diseases Poster tour 4: Surveillance of antimicrobial resistance Poster tour 5: Preparedness Poster tour 6: Surveillance of infectious diseases Poster tour 7: Late breakers (1) Poster tour 8: Late breakers (2) Vaccine preventable diseases FLOOR 3	Thematic session 2: Global Epidemic Intelligence: strengthening early detection and assessments of public health events Moderated by: <i>Merawi Aragaw (Africa CDC) and Vicky Lefevre (ECDC)</i> Speakers: <i>Gianfranco Spiteri (ECDC), Kyeng Mercy (Africa CDC)</i> AUDITORIUM 1	
16.40-17.00	Coffee break		
17.00-18.30	PLENARY SESSION B: SCIENCE-BASED LEADERSHIP IN PUBLIC HEALTH: DECISIONS UNDER PRESSURE Chaired by the ESCAIDE Scientific Committee members Bruno Ciancio (ECDC, Sweden) and Jacobo Mendioroz Peña (Public Health Agency of Catalonia, Spain) Speakers: <i>Alemka Markotić (University Hospital for Infectious Diseases, Croatia), Tanja Kuchenmüller (WHO, Switzerland), Eirini Agapadaki (Ministry of Health, Greece), and Karin Maria Nygård (Norwegian Institute of Public Health, Norway)</i> AUDITORIUM 1		
19.00-21.00	Networking event KINOGRAM FABRYKA NORBLINA		

DAY 2 – Thursday 20 November

08.00-09.00	Registration and welcome coffee		
09.00-10.30	Plenary session C: THE THIRD PILLAR OF ONE HEALTH: WHY ENVIRONMENT CAN'T BE AN AFTERTHOUGHT Chaired by the ESCAIDE Scientific Committee members Carlos das Neves (EFSA, Italy) and Tyra Grove Krause (Statens Serum Institut, Denmark) Speakers: Jan Semenza (Umeå University, Sweden), Gerardo Sanchez Martinez (European Environment Agency, Denmark), Frank Möller Aarestrup (Danish Technical University, Denmark) and Boudewijn Catry (Sciensano, Belgium) AUDITORIUM 1		
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12.30-14.00	Lunch break	12.35-13.35 Thematic session 3: Impact of the use of conjugate pneumococcal vaccines on invasive pneumococcal disease: current status of evidence Moderated by Piotr Kramarz (ECDC) Speakers: Sabrina Bacci (ECDC) and Nathalie Nicolay (ECDC) AUDITORIUM 1 12.35-13.55 EAN General Assembly AUDITORIUM 2	
14.00-15.30	FIRESIDE SESSION 9 One Health AUDITORIUM 1	Eurosurveillance seminar: Vaccines and the future of public health Moderated by Susana Monge (Instituto de Salud Carlos III, Spain) Speakers: Mateusz Hasso-Agopsowicz, (WHO, Switzerland), Gerald McInerney (Karolinska Institute, Sweden), and Fernanda Boulos (Instituto Butantan, Brazil). AUDITORIUM 2	
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16.40-17.00	Coffee break		
17.00-18.30	PLENARY SESSION D: ONE BIRD, TWO STONES: VETERINARY AND HUMAN HEALTH COLLABORATION IN ACTION Chaired by the ESCAIDE Scientific Committee members Angeliki Melidou (ECDC, Sweden) and Carlos das Neves (EFSA, Italy) Speakers: Richard Webby (St. Jude Children's Research Hospital, United States), Andrea Gervelmeyer (EFSA, Italy), Alice Fusaro (European Union Reference Laboratory for Avian Influenza and Newcastle Disease, Italy), and Ramona Trebbien (Statens Serum Institut, Denmark) AUDITORIUM 1		
18.45-20.15	BarCamp AUDITORIUM 2		

DAY 3 – Friday 21 November

08.00-08.30	Registration and welcome coffee		
08.30-09.15	Poster tour 17: Vaccination acceptance and uptake Poster tour 18: Childhood and maternal immunisation Poster tour 19: Social and behavioural perspectives Poster tour 20: Prevention of respiratory diseases Poster tour 21: International health Poster tour 22: Health equity and disease outbreaks Poster tour 23: Tools for advances in public health FLOOR 3		
09.20-10.45	PLENARY SESSION E: HEALTH FOR ALL: EQUITY CHALLENGES IN ACCESSING ESSENTIAL HEALTH SERVICES Chaired by the ESCAIDE Scientific Committee members Miłosz Parczewski (Pomeranian Medical University, Poland) and Nadine Zeitlmann (Robert Koch Institute, Germany) Speakers: Viviane Bremer (Robert Koch Institute, Germany), Susan Hahné (National Institute for Public Health and the Environment, Netherlands), and Adrian Stoica (Arges County Directorate of Public Health, Romania) AUDITORIUM 1		
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11.00-12.30	FIRESIDE SESSION 10 Strengthening epidemic intelligence and surveillance AUDITORIUM 1	FIRESIDE SESSION 11 Blood-borne and sexually transmitted infections AUDITORIUM 2	FIRESIDE SESSION 12 Healthcare-associated infections AUDITORIUM 3
12.30-14.00	Lunch break	12.35-13.35 Thematic session 5: Diagnosing barriers to vaccination Moderated by Sarah Earnshaw Blomquist (ECDC) and Andrea Würz (ECDC) Speakers: Bolette Soberg (Danish Health Authority), Agnieszka Sochoń-Latuszek (UNICEF Refugee Response Office, Poland) 12.35-13.35 Meet Public Health podcasters AUDITORIUM 1	
14.00-15.30	FIRESIDE SESSION 13 Health inequalities and key populations AUDITORIUM 1	FIRESIDE SESSION 14 Late breakers AUDITORIUM 2	
15.30-15.45	Coffee break		
15.45-16.30	PLENARY SESSION F: BEYOND NUMBERS: HUMANISING PUBLIC HEALTH TO ADDRESS HEALTH INEQUITIES Chaired by the ESCAIDE Scientific Committee members Alicia Barrasa (EAN Network and UK Health Security Agency, United Kingdom) and Piotr Kramarz (ECDC, Sweden) Speakers: Grazia Caleo (Independent public health consultant, United Kingdom) and Elburg van Boetzelaer (Médecins Sans Frontières, Netherlands) AUDITORIUM 1		
16.30-16.45	Closing ceremony AUDITORIUM 1		



FIRESIDE SESSIONS and POSTER TOURS

FIRESIDE SESSIONS

DAY 1 – 19 November

11.00-12.30

FIRESIDE SESSION 1

Preparedness

- The first 1000 days of the EU Health Task Force: Supporting stronger preparedness and response through partnership within the EU/EEA and globally, **Orla Condell**
- Efficacy and safety of Ebola vaccines in children: a systematic review and meta-analysis, **Marianna Zarro**
- Evaluating the implementation of a digital Surveillance Outbreak Response Management and Analysis System in Germany during the COVID-19 pandemic: Results and lessons learned, **Christin Walter**
- Barriers and enablers to the timely activation and effectiveness of provincial rapid response teams in responding to public health alerts across Papua New Guinea (2024), **Celeste Marsh**
- A cross-border large-scale pandemic simulation exercise in two European public health emergency operations centres using an innovative pandemic management dashboard, **Jessica Hayes**
- Building modelling capacity in Germany: An interdisciplinary infectious diseases modelling network supporting pandemic preparedness, **Beryl Onyuma**

FIRESIDE SESSION 3

Quantitative methods

- Estimating measles immunity gaps and transmission risks in Italy: regional heterogeneities and the role of unvaccinated adults, **Valentina Marziano**
- Identifying key target populations and screening intensity for gonorrhoea and chlamydia - a modelling study of MSM in Belgium, **Achilleas Tsoumanis**
- A modelling approach for correcting reporting delays in Polish health care system: nowcasting hospital admissions for respiratory infectious disease real-time surveillance, **Jakub Michalowski**
- Modelling the interplay between disease spread, behaviours, and disease perception with a data-driven approach, **Daniela Paolotti**
- Modelling the risk of mpox Clade Ib outbreaks among MSM in the EU/EEA and the impact of targeted vaccination, **Bastian Prasse**
- Predicting hospital admissions due to COVID-19 in Denmark using wastewater-based surveillance, **Steen Ethelberg**

FIRESIDE SESSION 2

COVID-19 vaccination

- Estimating effectiveness of monovalent JN.1 COVID-19 vaccination in EU/EEA countries between October 2024 and January 2025, a period of low SARS-CoV-2 circulation, as part of the VEBIS electronic heal, **James Humphreys**
- COVID-19 vaccine effectiveness against hospitalisation in older adults, VEBIS hospital network, Europe, September 2024–March 2025, **Madelyn Yiseth Rojas Castro**
- Effectiveness of the Autumnal COVID-19 Vaccine Dose During the Winter and Summer Waves of the 2023/24 Season in Spain, **Ayelén Rojas-Benedicto**
- Do COVID-19 and Influenza vaccines influence susceptibility to other respiratory viruses? A population-based study, **Joao Almeida Santos**
- Effectiveness of 2024/25 COVID-19 vaccines against laboratory-confirmed symptomatic SARS-CoV-2 infection in adults aged ≥ 65 years, European VEBIS primary care multicentre study, autumn/winter 2024/25, **Esther Kissling**
- Why studies reporting waning vaccine effectiveness against severe outcomes should be interpreted with caution, **Christian Hansen**

FIRESIDE SESSIONS

DAY 1 – 19 November

14.00-15.30

FIRESIDE SESSION 4

Respiratory infections: evidence to practice

- Post COVID-19 condition among older people: results from Swedish national data, **Zhongsong Zhang**
- The predictive value of socioeconomic status and migration background for a complicated course of lower respiratory tract infections in primary care, **Ernst van Dokkum**
- Estimating the influenza disease burden averted through vaccination for children and elderly – Lebanon, 2016-2020, **Zeina Farah**
- Monitoring nirsevimab effectiveness using surveillance data: a test-negative case-control study, Spain, October 2024-March 2025, **Sandra Campos Mena**
- Subtyping of seasonal Influenza A: Assessing Wastewater for Enhanced Detection Methods and Surveillance in Sweden, **Fredrik Oscarson**
- Nirsevimab effectiveness against hospitalised Respiratory Syncytial Virus infection in Portugal, 2024/25 season, **Vânia Gaio**

FIRESIDE SESSION 5

Vaccine research and immunisation programmes

- Brand-specific influenza vaccine effectiveness in three Nordic countries: estimates for the 2024-2025 season, **Kristyna Faksova**
- Childhood vaccination coverage and completion in children born in Regensburg, Germany, between 2015 and 2019: Insights from a longitudinal cohort study, **Margarida Arede**
- Effectiveness of infant vaccination against pertussis in 1- and 2-year-olds, the Netherlands, 2013-2022, **Dimphey van Meijeren**
- Immunity gaps despite high vaccination coverage: a mumps seroprevalence study in The Netherlands, **Kevin Wassing**
- Psychological antecedents of vaccination: mapping social and demographic heterogeneity in six European countries, **Chiara Chiavenna**
- Impact of COVID-19 restrictions on invasive meningococcal disease notification in the European Union /European Economic Area: an interrupted time series analysis of surveillance data, 2013-2023, **Joana Gomes Dias**

FIRESIDE SESSIONS

DAY 2 – 20 November

11.00-12.30

FIRESIDE SESSION 6

Antimicrobial resistance

- Difficult-to-treat and pandrug resistance among carbapenem-resistant Enterobacterales and Acinetobacter spp. notifications in Germany, 2017–2024, **Teresa Marie Nygren**
- Describing the establishment of a multi antimicrobial resistant strain of Escherichia coli in a hospital setting in North Wales; trends over time and patient outcomes, **Craig Hogg**
- Is mandatory surveillance of carbapenemase-producing Gram-negative organisms (CPOs) working? A surveillance evaluation, England, 2023, **Lucy Findlater**
- Transmission of NDM-4-producing Enterobacterales across multiple hospitals and states – Insights from an outbreak investigation and surveillance in Germany between July 2023 and February 2025, **Mirco Sandfort**
- Trends in Extended-Spectrum β -Lactamase and Carbapenem Resistance in Enterobacterales in the Paediatric patient population, Germany, 2018–2023: Findings from National Surveillance, **Imme Roewer De Porto**

FIRESIDE SESSION 8

Food- and water-borne diseases

- A foodborne outbreak of Salmonella Enteritidis in an institution – Honaz district, Denizli province, Turkiye, July 2024, **Fatma Durmus**
- Multi-country outbreak of Salmonella Blockley, associated with tomato consumption in the United Kingdom, July to October 2024, **Ann Hoban**
- Rapid genotyping of Salmonella using nanopore-only sequencing for outbreak investigation, **Celia Souque**
- A comparison of using online market panel members and traditional epidemiological methods in control recruitment for a case-control study during a national outbreak of STEC O145, United Kingdom, **Grace King**
- Salmonella Infantis outbreak in young children caused by cashew butter with raspberry, Germany 2025, **Anika Meinen**
- Disentangling two large hepatitis A outbreaks in a very low endemicity country: Portugal, Oct 2023-Aug 2025, **Joana Vidal-Castro**

FIRESIDE SESSION 7

Emerging and vector-borne diseases

- How has the spatial distribution of malaria changed in the past 20 years in Kenya?, **Justine Blanford**
- Risk factors for rodent-borne diseases: A cross-sectional study in rural Madagascar, **Niamh McAuley**
- Serological evidence supports the transmission of clade Ib mpox virus by professional sex workers and spread within households in South Kivu, DRC, **Luca M. Zaeck**
- A decade-long molecular epidemiological study of Enterovirus-C105 (2013–2023): Tracing its shift from rare detection to an outbreak in 2023 in Europe, **Laura Bubba**
- Characteristics of travellers who received post-exposure prophylaxis in a tertiary hospital in Barcelona after an animal-associated injury abroad, **Luis Alberto Benegas Rodriguez**
- National outbreak of iatrogenic botulism associated with cosmetic injections of botulinum neurotoxin-containing products in England, 2025, **Katie Wrenn**

FIRESIDE SESSIONS

DAY 2 – 20 November

14.00-15.30

FIRESIDE SESSION 9

One Health

- Seasonal trends of sand fly abundance and Leishmania infection: The case of Bologna province, Italy (2016–2023), **Juthathip Khongpetch**
- Swimmer's itch: a One Health approach to assess an emerging zoonosis at a reservoir in Wales, **Ameze Simbo**
- Rising scabies incidence in Spain, 2011–2023: a retrospective observational analysis of four national data sources, **Allegra Chatterjee**
- Seasonality and effects of climatic exposures on community-acquired Legionnaires' Disease incidence: an evaluation of the Italian surveillance data, 2005-2022, **Antonio Sciurti**
- Effectiveness of community trainings for population-based control of Aedes albopictus: Results of a pilot project in a town in Baden-Wuerttemberg, Germany in 2024, **Bernadette Walter**
- Assessing the timeliness of the seasonal surveillance system for imported cases of dengue, chikungunya, and Zika in mainland France (2019–2024) at the national and regional level, **Yasemin Inaç**

FIRESIDE SESSIONS

DAY 3 – 21 November

11.00-12.30

FIRESIDE SESSION 10

Strengthening epidemic intelligence and surveillance

- Building resilient intelligence networks for Europe: strengthening governance of evidence for pandemic preparedness, **Miriam Saso**
- Finding the needle in the haystack: using machine learning to detect signals of public health threats in the Epidemic Intelligence from Open Sources, **Laura Espinosa**
- Community stool survey following detection of poliovirus in the environment in London, United Kingdom, October 2022 to April 2023, **Thomas Rowland**
- Paper-based surveillance for infectious diseases in Dutch childcare: added value or added burden?, **Rosaline van den Berg**
- Harmonising the surveillance of respiratory viruses to monitor activity levels, **Beth Savagar**
- The OECD PaRIS survey in 18 countries estimates that 7.2% of primary care patients aged 45 and older have experienced Long COVID as of 2024, **David Kelly**

FIRESIDE SESSION 12

Healthcare-associated infections

- Identifying the optimal timeframe of potential *Clostridioides difficile* transmission events for genomically linked patients, **Phillip Butterick**
- Infant Gram-negative bloodstream infections in England, 2011-2019: A population-based study of case characteristics and risk factors for mortality, **Maria Suau Sans**
- Respiratory Syncytial Virus-associated hospitalizations in children younger than 5 years in Brazil using National Severe Acute Respiratory Infections Surveillance, 2013 – 2022, **Felipe Teixeira De Mello Freitas**
- Prospective enhanced surveillance study of respiratory syncytial virus (RSV) outbreaks in care homes in England during winter 2024-25, **Luke McGeoch**
- Gastrointestinal infections outbreak in a care home involving *C. perfringens* from an environmental source in Wales, UK, **Dominic Power**
- Investigation of a multi cluster outbreak of emm-type 80.0 Group A *Streptococcus* in the West Midlands, England, **Anna Gavan**

FIRESIDE SESSION 11

Blood-borne and sexually transmitted infections

- New nationwide surveillance of chlamydia-related long-term complications using hospitalization data, The Netherlands, 2015-2022, **Marta Bertran**
- Targeting risk by connecting the dots: Molecular HIV transmission clusters enriched with people who use crystal meth in Mexico City (2022–2024) reveal behavioural and structural risk patterns, **Samuel E. Schulz-Medina**
- Evaluating syphilis surveillance in Finland 2020-2024: identifying missed reinfections, **Jakub Czarnecki**
- Introducing late HIV diagnosis cohort reviews in Wales: Exploring missed opportunities for testing, **Sophie Harker**
- Is the congenital syphilis (CS) elimination target fit for purpose? Insights from Polish neonates cohort (2017-2023) exposed to maternal *Treponema pallidum* seropositivity, **Karolina Zakrzewska**
- Determinants of interruption in treatment among people living with HIV in Murang'a County, Kenya: a sequential explanatory mixed-method study, **Moses Njiru**

FIRESIDE SESSIONS

DAY 3 – 21 November

14.00-15.30

FIRESIDE SESSION 13

Health inequalities and key populations

- Health disparities in complicated lower respiratory tract infections: the role of socioeconomic status, **Ernst Van Dokkum**
- Decline in incidence and prevalence of hepatitis C virus infection among drug users in France, 2004-2023, **Chiara Elisa Sabbatini**
- Inequalities in a measles outbreak in the South West region of England, 2024-2025, **Fariya Abdullahi**
- Ongoing outbreak of invasive *Haemophilus influenzae* type b in people using substances and experiencing homelessness in Northern Germany since September 2024, **Vanessa Piechotta**
- Zooming in on Genomics to See the Bigger Picture: Suspected Autochthonous Transmission of an Imported Tuberculosis Strain Affecting Migrants in Austria, **Fiona Alma Költringer**
- Largest European *Corynebacterium diphtheriae* outbreak in 50 years leading to secondary cases in general population, **Andreas Hoefler**

FIRESIDE SESSION 14

Late breakers

- Ongoing large STEC/HUS outbreak centred on North-East-Germany (STEC O45:H2), **Christina Frank**
- Influenza vaccination attenuates acute myocardial infarction and stroke risk following influenza infection: a registry-based, self-controlled case series study, Denmark, 2014- 2025, **Roberto Croci**
- Effectiveness of long-acting monoclonal antibodies against respiratory syncytial virus infection in hospitalised children <24 months from three European countries, winter season 2024-2025, **Camelia Savulescu**
- Out-of-season influenza A(H1N1)pdm09 outbreak among >50,000 attendees of an open-air music festival in Denmark, August 2025, **Hanne-Dorthe Emborg**
- Protecting infants from respiratory syncytial virus (RSV) in Ireland: High impact of a novel infant immunisation with nirsevimab, 2024/2025, **Laura Paris**

POSTER TOURS

DAY 1 – 19 November 15:40-16:40

POSTER TOUR 1

Sexually transmitted infections

- Hepatitis B and C Prevalence Among Transgender Individuals and Men Who Have Sex with Men in Pakistan, **Hassan Mahmood**
- Fitting beta distributions for the analysis of minimum inhibitory concentrations in *Neisseria gonorrhoeae*: insights from Germany's antimicrobial resistance surveillance, 2014–2023, **Lena Böff**
- HPV35 dominance in high-grade cervical lesions in Eswatini: are the currently available vaccines enough?, **Clara Fappani**
- Diagnostic confirmation, clinical characteristics and surveillance classification of suspected congenital syphilis in Poland, 2017–2024, **Karolina Zakrzewska**
- Chlamydia in Poland, 2020–2024: emerging trends in incidence and national screening programme needs, **Marta Niedzwiedzka-Stadnik**

POSTER TOUR 3

Outbreaks of food-borne diseases

- Outbreak of *Salmonella* Agona linked to cross-contamination via doner kebab and electric knives in Hesse and Baden-Wuerttemberg, Germany, January 2022 - December 2024, **Syamend Saeed**
- A large outbreak of multiple *Salmonella* serovars linked to alfalfa sprouts in Norway, October to December 2024, **Arthur Rakover**
- Foodborne outbreak in 12 construction sites in Ankara province-Türkiye, August 2023, **Gülşen Barlas**
- Multi-cluster outbreak of *Salmonella* Typhimurium sequence type 36 linked to alfalfa sprouts, Sweden, August – November 2024, **Kate Lillepold**
- *Listeria monocytogenes* (L. monocytogenes) CC217 outbreak linked to ready-to-eat smoked fish products in Great Britain, 2020–2025, **Thomas Thackray**
- Outbreak of *Salmonella* Saintpaul in the UK likely associated with watermelon consumption, **Ella Rodwell**

POSTER TOUR 2

Respiratory infections: evidence to practice

- Risk factors associated with laboratory-confirmed SARS-CoV-2 infection among healthcare workers: a European prospective multicentre cohort study, May 2021 - April 2024, **Iris Ganser**
- Individual and seasonal determinants of death among influenza patients admitted to intensive care units, Portugal 2012–2024, **Sebastian von Schreeb**
- Impact of RSV Vaccination in Wales – Maternal programme to protect infants, **Malorie Perry**
- Seasonal influenza vaccine effectiveness estimates in primary care, 2024/25 season, Europe, **Héloïse Lucaccioni**
- Association of nirmatrelvir/ritonavir and molnupiravir with long COVID in patients with chronic liver disease: cohort study, **Ka Chun Chong**
- Two-season effectiveness of a single nirsevimab dose against RSV hospitalisation in healthy term-born infants: a population-based case-control study in Spain, October 2023 – March 2025, **Susana Monge**

POSTER TOUR 4

Surveillance of antimicrobial resistance

- Endemic IncN plasmid caused the majority of blaKPC-2 Enterobacterales cases in Lithuania since 2019, **Paulius Greicius**
- An update on a regional AMR surveillance network in the Netherlands: challenges and opportunities, **Carsten Van Rossum**
- Nationwide Retrospective Study on the Performance of the WHO Mutation Catalogue for Genomic Prediction of Antibiotic Resistance in the *Mycobacterium tuberculosis* Complex in Spain, 2022–2025, **Jasmin S. Kutter**
- The epidemiology of sterile site acquired carbapenemase-producing Gram-negative organisms in England, October 2020 – September 2024, **Jacquelyn McCormick**
- Majority of cases with carbapenemase-producing *Klebsiella pneumoniae* are part of genomic clusters deriving from either regional, national, or international spread in Germany, 2022–2023, **Sebastian Haller**

POSTER TOURS

DAY 1 – 19 November 15:40-16:40

POSTER TOUR 5

Preparedness

- Intra-Action Review IAR of Cholera emergency response in Malawi: Country experience, **Motuma Guyassa**
- Advancing integrated scientific advice in pandemic preparedness, **Femke Overbosch**
- Prioritisation of epidemic-prone diseases for emergency preparedness and response in Southern Africa, 2024, **Neema Kamara**
- From influenza to COVID-19 to future pandemic threats: Revising the Swiss national pandemic plan, **Maude Montani**
- Infodemic preparedness through social listening: Generating insights into (mis)information about measles vaccination in Amsterdam, August-September 2024, **Kirsten Bisschops**

POSTER TOUR 7

Late breakers (1)

- Outbreak investigation of visceral leishmaniasis in Sanaag Region, Somaliland, December 2024-August 2025, **Umalkhair Jama Mohamoud**
- Local multistrain outbreak of Shiga toxin-producing *Escherichia coli* (STEC) linked to the consumption of meat from butcher shops, France, June to July 2025, **Fanny Chereau**
- Large outbreak of severe Shiga toxin-producing *E. coli* O157:H7 infections in multiple nursing homes in Belgium, August 2025, **Clara Mazagatos**
- Epidemiology and Characteristics of Mpox virus Clade I Importations and Onward Transmission in the WHO European Region, 2024-2025, **Ioannis Karagiannis**
- Descriptive analysis of invasive Group A streptococcal infection outbreaks and their management in London and the South East Region, UK, April 2024-July 2025, **Maria Saavedra-Campos**
- An outbreak of impetigo during June -July 2025 in a semi-urban setting in Portugal: the putative role of insect bites, **Raquel Mulongeni**

POSTER TOUR 6

Surveillance of infectious diseases

- Human Q fever cases in Germany (2001-2023): A 23-year descriptive overview of national surveillance data, **Antonia Genath**
- 20 years of hepatitis C surveillance in correctional facilities in Lower Saxony, Germany – A surveillance system evaluation, **Lilas Mercuriali**
- Invasive pneumococcal disease in Latvia and factors associated with fatal disease outcome, 2012-2022, **Larisa Savrasova**
- Integrated genomic surveillance of pregnancy-associated *Listeria monocytogenes* infections in northern Italy, 2021–2024, **Maria Gori**
- Changing epidemiology of invasive meningococcal disease in France, 2023 - 2025, **Anne-Sophie Barret**
- Age-standardised mortality rates related to viral hepatitis B and C in Belgium, **Laure Mortgat**

POSTER TOUR 8

Late breakers (2):

Vaccine preventable diseases

- Carriage of *Corynebacterium diphtheriae* in people experiencing homelessness in London, England - interim findings from a rapid prevalence study in spring/summer 2025, **Jin-Min Yuan**
- Out-of-Season Surges: Unprecedented Summer Peaks of Influenza in Malta, 2024-2025, **Norman Galea**
- Containing Measles: Outbreak Dynamics and Control in the Charedi Jewish Community, England, 1st April 2025 to 31st August 2025, **Erjola Hani**
- Effectiveness of Nirsevimab against RSV infection in primary and secondary care: a test-negative case-control study in infants in Germany, November 2024 - May 2025, **Annika Erdwiens**
- Wastewater surveillance as a public health tool for measles monitoring in Belgium, **Anke Meyers**
- Herpes Zoster Vaccination and Risk of Dementia - Updated Evidence from a Systematic Review and Meta-Analysis, **Hendrik Sauskojus**

POSTER TOURS

DAY 2 – 20 November 15:40-16:40

POSTER TOUR 9

Emerging and vector-borne diseases

- High epilepsy prevalence and excess mortality in onchocerciasis-endemic counties of South Sudan: A call for integrated interventions, **Luís-Jorge Amaral**
- Risk assessment and perspectives of local transmission of chikungunya and dengue in Italy, a European forerunner, **Francesco Menegale**
- Emergence and epidemiology of Trichophyton indotineae in the United Kingdom and Republic of Ireland, 2017–2025, **Alexandra Czerniewska**
- Occult Transmission of Crimean-Congo Hemorrhagic Fever Virus among Farm Animal Owners in Rural Villages, Georgia, 2024, **Nadezhda Zhgenti**
- Tularaemia as a persistent problem: a study of the prevalence of tularaemia in Armenia, **Ofelya Harutyunyan**
- Development of a WHO Global Arbovirus Surveillance System in Response to an Increasing Global Threat, **Martina McMenamin**

POSTER TOUR 11

Social determinants of infectious diseases

- Factors associated with lack of evidence of successful tuberculosis treatment in regional surveillance data, Saxony, Germany, 2012–2023, **Pontus Christopher Hedberg Wang**
- Predictors of poor outcome in people with tuberculosis disease, Wales 2012–2022, **George Ahern**
- Predictors of mortality among adult PLHIV receiving antiretroviral therapy in AIDS centers in Sughd Province, Tajikistan: a retrospective cohort study, **Emomali Kurbonov**
- The multidrug-resistance characteristics of extrapulmonary tuberculosis, Tajikistan, 2017–2022, **Zulfiya Tilloeva**
- Tuberculosis in Greek correctional facilities: A nationwide mapping of epidemiological burden and system responses, **Maria Tseroni**
- Pharmacies supply needles and syringes for safer injecting drug use: a cross-sectional study in Germany, 2024, **Teresa Marie Nygren**
- Access to sexual health services among ethnic minorities under the age of 25 years in the Netherlands, **Rianne Reijs**

POSTER TOUR 10

Research to policy and practice

- Urinary tract infections and antibiotic overuse in a long-term care facility, The Netherlands, May 2024–March 2025, **Ilse Hazelhorst**
- Linkage to care and health education for promoting water, sanitation, and hygiene (WASH) and primary healthcare services in underserved communities of Islamabad, Pakistan, **Hassan Mahmood**
- Lessons learned from a cluster of invasive group A streptococcal infections related to an elementary school in the Netherlands, June 2024, **Nienke Van Schaik**
- Hospital admissions for respiratory infections in those with lived experience of homelessness, evidence for vaccine policy from Wales; UK, **Malorie Perry**
- Evaluation of the measles surveillance system in the Kyrgyz Republic, 2024, **Aigul Mamatova**
- First evaluation of Somaliland's national HIV surveillance system, **Yingshih Su**

POSTER TOUR 12

Surveillance of respiratory infections

- Assessment of the timeliness of reporting severe acute respiratory infections in five European Union countries, 2024–2025: an electronic health record-based surveillance study, **Miguel Angel Sanchez Ruiz**
- Pre-Event Social Dynamics Dominate Potentially Infectious Contacts at Mass Gatherings: Insights from UEFA EURO 2024, **Andrzej Jarynowski**
- Vaccine effectiveness against influenza infection and hospitalization in older adults in Spain: Analysis of surveillance data from 2022/23 to 2024/25 seasons, **Gloria Pérez Gimeno**
- Qualitative evaluation and SWOT analysis of the Spanish SARI surveillance system, **Elsa Negro Calduch**
- Assessing children's RSV clinical presentation across 5 seasons in primary care setting in Italy, **Francesco Baglivo**
- Quantifying the Underestimation of RSV-Associated Respiratory Hospitalisations in Older Adults: A Time Series Modelling Study in the Veneto Region, Italy, **Claudia Cozzolino**
- Combined monitoring of individuals and wastewater for a strategic genomic surveillance of SARS-CoV-2 in Sweden 2025, **Elin Møvert**

POSTER TOURS

DAY 2 – 20 November 15:40-16:40

POSTER TOUR 13

Surveillance of healthcare-associated infections

- Investigating the source of 12-year long outbreak of a unique genotypic strain of Salmonella Montevideo in a hospital in England, **Sooria Balasegaram**
- Recent trends and current situation of invasive Methicillin-resistant Staphylococcus aureus (MRSA) infections in Germany: An epidemiological description for the years 2015–2024, **Dunja Said**
- Ethnicity and Deprivation: Association with Escherichia coli Bloodstream and Antimicrobial-Resistant Infection Burden in England, **Zahin Amin-Chowdhury**
- Genomic and epidemiological patterns in Staphylococcus aureus bacteraemia: A national surveillance study, England, 2017-2024, **Aishwarya Krishna**
- Higher burden of co-morbidities increases Clostridioides difficile cause-specific mortality in under 80 but not in the very elderly: Findings from mandatory surveillance in Wales, 2020-2024, **Phillip Butterick**
- Active surveillance of healthcare-associated infections in Pediatric Intensive Care Unit: a two-year study period (January–March), 2023-2024, **Lara Ricotta**

POSTER TOUR 15

Antimicrobial resistance

- Genomic surveillance of vancomycin-resistant Enterococcus faecium reveals shift of dominant clones between ST80 and ST117, and from vanB to vanA in Stockholm, Sweden, 2018-2024, **Hong Fang**
- A nationwide study of antimicrobial stewardship tools and activities coordinated by Infection Control and Antibiotic Committees in Hungarian hospitals, 2023, **Márton Falus**
- Clonal structure and mechanisms of resistance of carbapenemase-producing Enterobacterales from two regions in Slovenia, **Tjaša Žohar Cretnik**
- Epidemiology of extensively-drug resistant Shigella in England: 2017 to 2024, **Hannah Charles**
- Characterization of azole resistance in Portuguese Candida parapsilosis isolates, **Veronica Mixao**

POSTER TOUR 14

One Health

- Pilot Assessment of Antimicrobial Resistance Gene Detection in Hospital & Urban Wastewater to compare AMR Ecology using Molecular Methods, **Paul Reidy**
- Seasonal Variations and reported rates of Human Brucellosis in Egypt: A Three-Year Study (2021-2023), **Salma Mohasseb**
- Floodborne Infections and One Health Responses: Lessons from Poland's 2024 Disaster, **Stanislaw Maksymowicz**
- Winter wonderland in Austria - an outbreak of Legionnaires' disease due to a cooling tower in Vorarlberg, 2024/2025, **Miriam Van den Nest**
- Mortality risk attributable to high temperatures from 2021 to 2024 in Spain: the effect of heat waves, **Raquel Barba Sanchez**
- Guts of healthy humans, livestock and pets harbor critical priority and pandemic Escherichia coli clones, **Idris Nasir Abdullahi**
- Genomic overlap and antimicrobial resistance of Campylobacter jejuni in poultry and wild birds around organic farms in Sweden, **Evangelos Mourkas**

POSTER TOUR 16

Food- and water-borne diseases

- Factors associated with the presence of anti-hepatitis A virus antibodies in Poland's population- results from a 2023 cross-sectional study, **Piotr Polanski**
- Detection of non-tuberculous mycobacteria and other bacterial pathogens in dental unit waterlines, 2024, Germany: a microbiological single-centre study, **Lea-Elisa Heinz**
- An outbreak of waterborne tularemia in 6 districts in Sivas province, Türkiye, case-control study, January 2024, **Gulsum Zoroglu**
- Survey on the impact of the increased use of multiplex PCR on the surveillance and control of foodborne pathogens in Germany, **Laura Giese**
- Nationwide outbreak of haemolytic uraemic syndrome in adults linked to an atypical strain of Shiga toxin-producing Escherichia coli, France, December 2024-January 2025, **Fanny Chereau**
- Estimating under-diagnosis of Hemolytic Uremic Syndrome attributable to Shiga toxin-producing Escherichia coli infections in England, **Yanshi Yanshi**

POSTER TOURS

DAY 3 – 21 November 08:30-09:15

POSTER TOUR 17

Vaccination acceptance and uptake

- Estimation of vaccination coverage from mandatory notification data using a reversed Farrington screening method, exemplified by Mpox data from Berlin, Germany, in 2023, **Francisco Rios**
- A large data linkage study to quantify waning of MMR vaccine against mumps, Wales, UK, **Malorie Perry**
- First school-based HPV vaccination campaign in France: at last some progress!, **Laure Fonteneau**
- Algorithm-based identification of high-risk patients requiring meningococcal vaccination: coverage assessment and implications for catch-up programmes, **Álvaro Serrano-Ortiz**
- Factors associated with influenza vaccination among healthcare workers in three hospitals in Albania, September 2023- March 2024, **Arlinda Ramaj**

POSTER TOUR 19

Social and behavioural perspectives

- Co-creation of a toolbox to improve infection prevention and control behaviour in general practice care: a qualitative study, **Jorg Van Beek**
- Integrating epidemic modelling with human behaviour: An interdisciplinary framework for the collection of empirical data, **Vittoria Offeddu**
- Enhancing Vaccine Uptake: A Randomized Trial of Active Invitation, Motivational Interviewing, and On-Site Vaccination Among Hesitant Parents – The MICK Study, **Veja Widdershoven**
- Factors associated with intention to be vaccinated against seasonal influenza in healthcare workers: a cross-sectional study assessing Health Belief Model constructs in Serbia, **Larisa Vujnovic**
- Contesting global health governance: Opposition to the WHO pandemic agreement in online media, **Noé Hernández Valdivia**

POSTER TOUR 18

Childhood and maternal immunisation

- Measles – analysis of data reported in the national surveillance system, Czech Republic, 2018–2024, **Monika Liptáková**
- Establishing Timely Surveillance of Maternal Pertussis Vaccine Uptake, **Margrethe Greve-Isdahl**
- One year of maternal pertussis vaccination in Stockholm region- a success with challenges, **Katarina Widgren**
- Estimating age-specific seroprevalence of measles IgG antibodies among adult blood donors in Wales, January – July 2024, **Ameze Simbo**
- Assessment of population immunity to measles in Canada, 2023: a Canadian Immunization Research Network study, **Heili Poolsaar**
- Measles clinical presentation by vaccination status in Portugal, 2015-2025: implications for case definition in elimination settings, **Raquel Eusébio**

POSTER TOUR 20

Prevention of respiratory diseases

- Effectiveness of COVID-19 vaccine in preventing SARS-CoV-2 severe outcomes 2021-2023, **Ahlem Fourati**
- Effectiveness of vaccination programmes against serotype B invasive meningococcal disease using the screening method on surveillance data from countries in Europe, **Nathalie Nicolay**
- Interim 2024/25 season RSV vaccine effectiveness against hospitalisation in older adults in Northern Ireland, **Magda Bucholtz**
- Invasive pneumococcal disease caused by serotype 4 in Andalusia (Spain), 2022 to 2024, **Elvira Marín Caba**
- Impact of Nirsevimab on the epidemiology of pediatric RSV in Belgium in season 2024-2025, **Laurane De Mot**

POSTER TOURS

DAY 3 – 21 November 08:30-09:15

POSTER TOUR 21

International health

- Patient Rights and Safety as Instruments of Health Diplomacy in Infectious Disease Preparedness and Response, **Jasna Karacic Zanetti**
- Crossing Borders: Findings from a Multinational, Foodborne Shigella sonnei Outbreak with an International Travel Signal, **Rosie Collins**
- Characteristics of rabies exposure incidents in travellers consulting a Dutch regional health service (2014-2024) **Hanna Verweij**
- No vacation from risk: Investigating a Salmonella Enteritidis outbreak linked to poultry and international travel, **Vanessa Morton**
- Malaria cluster near Benina international airport, Libya: a re-emerging threat in a malaria-free country, **Ahmed M Alarbi**

POSTER TOUR 23

Tools for advances in public health

- Who Sets the Rules? Generative AI Policies in Leading Medical Journals, **Pinar Dilbaz**
- Calibration of an epidemiological model with intermittent sentinel hospital surveillance and wastewater data, **Esteban Foncoux**
- Pandemic preparedness: potential of routine general practice data for infectious disease surveillance and early warning, **Jessica Aguilar Diaz**
- Strengthening epidemiological capacities in municipal public health services: findings and perspectives from the FETP4ÖGD project, **Katja Kajikhina**
- Noise classification in Epidemic Intelligence from Open Sources articles using natural language processing: A random forest approach, **Hwaraa Sweidan**
- Developing a European bloodstream infection surveillance system using data from electronic health records, **Alexis Sentis**

POSTER TOUR 22

Health equity and disease outbreaks

- Waterborne diarrheal Outbreak in a Migrant Residence Center - Tripoli, Libya, 2024, **Zakaria Elboukhari**
- Health Equity Evaluation of Public Health Interventions during Outbreak Response: The Scoping, Execution and Action (SEA) Framework, **Aswathikuty Gireesh**
- Adapting Wastewater-Based Epidemiology for Infectious Disease Surveillance in Remote Arctic Communities: Insights from Nunavik, Canada, **Caroline Russo**
- Water Monitoring in Lebanon: Addressing Hepatitis A and Cholera through Bacteriological Testing, **Zeina Farah**

PLENARY SESSIONS

Plenary sessions at **ESCAIDE** aim to provide an opportunity to discuss public health challenges and scientific advances. By bringing together experts across different fields, these sessions seek to translate evidence from infectious disease research and epidemiology into improvements in public health. The content of plenaries is proposed by the ESCAIDE Scientific Committee, composed of 11 members from different disciplines, who invite high level speakers to discuss and tackle topics of current importance in infectious disease and public health, offering inspiring presentations and addressing questions from the audience.

ESCAIDE 2025 will feature six plenary sessions, chaired by the ESCAIDE Scientific Committee.

Scientific Committee



PIOTR KRAMARZ

SWEDEN

Head of Unit & Chief Scientist | Chair of ESCAIDE Scientific Committee | ECDC

Piotr Kramarz is a physician, with a PhD in immunology of viral infections, and eight years of clinical practice at a teaching hospital in the field of infectious diseases. During the period 1997–2000, he worked at the US Centers for Disease Control and Prevention (CDC), first in the Epidemic Intelligence Service (EIS) and then as a medical epidemiologist. Since 2007, he has worked at ECDC as a Deputy Head of the Unit and, since 2024, as the Chief Scientist. His research interests include burden of communicable diseases and vaccine-preventable diseases.



JET (HENRIETTE) DE VALK

FRANCE

Head of Unit | Foodborne, Vectorborne and Zoonotic Infections Unit | Santé Publique France

Jet (Henriette) de Valk is a medical doctor and infectious disease epidemiologist at the French national public health agency (Santé Publique France). As head of the Food-borne, Vector-borne and Zoonotic Infections Unit she is in charge of surveillance, outbreak investigations and applied research. She is actively involved in European networking activities for surveillance of infectious diseases, as a national representative in supranational surveillance networks, as a member of the coordination group of the Vector-borne and Emerging Diseases network of the European Centre for Disease Prevention and Control (ECDC) and as a supervisor in the European Programme for Intervention Epidemiology Training. She has recently been working on guidelines for surveillance of emerging arboviruses, on the disease burden of food-borne intestinal infectious diseases and on whole genome sequencing for surveillance. She serves on the national committee nominating the National Reference Centres (laboratories) for infectious agents in France and Belgium. Jet is a graduate of the University of Leyden in the Netherlands, the London School of Hygiene and Tropical Medicine in the United Kingdom and the Institute for Tropical Medicine in Antwerp, Belgium. She is also an alumnus of The European Programme for Intervention Epidemiology Training. Before working at Santé Publique France she worked for the NGO Médecins Sans Frontières (Doctors Without Borders) on emergency relief programmes in Sudan, Uganda and Mali, for the German Technical Cooperation (GTZ) in Cameroon and for the World Health Organization in Indonesia, where her focus was on control programmes for diarrhoeal and respiratory infections.

Scientific Committee



JACOBO MENDIOROZ PEÑA

SPAIN

Sub-director General | Surveillance and Response to Public Health Emergencies | Public Health Agency of Catalonia

Jacobo Mendioroz is a medical doctor (MD) specialising in preventive medicine and public health, with a masters in public health from Pompeu Fabra University. In 2020, he was designated by the Catalan government as director of the COVID-19 Response Unit for the Health Department of Catalonia. He is currently the Sub-Director for Surveillance and Response to Public Health Emergencies at the Public Health Agency of Catalonia. He began his career as a researcher in the epidemiology of congenital diseases for the Carlos III Health Institute (ISCIII) in Madrid. He also worked as field epidemiologist and researcher of tropical diseases in Angola as part of the International Health Programme (PROSICS) of the Catalan Health Institute (ICS). Working for the same institution, he also held positions at the Health Territorial Management Unit of Central Catalonia as head of Health Data Systems and as scientific coordinator of the Research Support Unit for primary healthcare professionals. As a researcher, he has studied the epidemiology of both transmissible and non-transmissible diseases and, in recent years, has focussed on medical information systems and the delivery of healthcare. During this time, he combined his research interests with providing technical support to health managers and working as an emergency room MD at hospitals and primary healthcare centres in Catalonia.



ÁGNES HAJDU

HUNGARY

Senior Advisor | Unit of Infection Control and Hospital Epidemiology | National Center for Public Health and Pharmacy, Hungary

Ágnes Hajdu is a medical doctor, specialising in preventive medicine and public health, and an EPIET alumna. For more than 15 years she has worked in the field of healthcare epidemiology and antimicrobial resistance (AMR). As a senior advisor in the Unit of Infection Control and Hospital Epidemiology at the National Public Health Center in Hungary, she has contributed to the development of national methodological guidance in infection prevention and control (IPC), coordination of surveillance modules on healthcare-associated infections, multidisciplinary investigations of nosocomial outbreaks, policy initiatives on IPC and AMR, and behavioural research on antimicrobial prescription in primary care. She is a member of the Hungarian National Infection Control and Antibiotic Committee. She has a longstanding collaboration with the European Centre for Disease Prevention and Control (ECDC) and the World Health Organization's Regional Office for Europe (WHO/Europe) through various national functions.

Scientific Committee



ANGELIKI MELIDOU

SWEDEN

Principal Expert Respiratory Viruses | ECDC

Angeliki Melidou is a virologist and has been an associate professor of molecular microbiology and virology at the Microbiology Department of the Aristotle University of Thessaloniki Medical School in Greece since 2012. She has been working at the European Centre for Disease Prevention and Control (ECDC) since 2016, and is currently a Principal Expert in Respiratory Viruses. Her expertise lies in the areas of microbiology, disease surveillance, and scientific advice related to respiratory viruses.



ALICIA BARRASA

SPAIN

EAN Network

Alicia Barrasa is part of the EPIET Alumni Network which brings together more than 600 European field epidemiologists and public health microbiologists. She has a PhD and an MSc in public health and epidemiology. She has worked in the area of HIV, focussing on factors associated with disease progression, and as Scientific Coordinator for the Spanish field epidemiology training programme (2004–2008), and EPIET (2008–2020). She is currently working for the UK field epidemiology training programme. She was also a member of the TEPHINET Accreditation Working Group from 2019 to 2023.

Scientific Committee



NADINE ZEITLMANN

GERMANY

Senior epidemiologist | Robert Koch Institute

Nadine Zeitlmann is a senior epidemiologist at the Robert Koch Institute (RKI) in Berlin, Germany and a part-time scientific coordinator for ECDC's European Programme for Intervention Epidemiology Training (EPIET). She has a Masters in Public Health from the University of Munich and in Applied Epidemiology from the Berlin Charité. Between 2011 and 2013, she worked in the field of public health and infectious disease epidemiology in Denmark before completing her EPIET/PAE fellowship at the Bavarian Health and Food Safety Authority in Munich, Germany, 2013–2015. She then worked as an epidemiologist in different international programmes at the RKI for eight years where she supported partner countries in North Africa and the Balkan peninsula in building up surveillance, outbreak investigation and crisis management structures and implementing International Health Regulations (IHR). During this time, she was also deployed as an epidemiologist for various international assignments on the African and Asian continents. She also worked as a field epidemiologist in various COVID-19 outbreak investigations in Germany during the pandemic. In addition to her role as an EPIET Coordinator, she currently works as a coordinator in the field of epidemic intelligence, early warning and outbreak coordination in RKI's 'Unit for crisis management, outbreak investigation and training programmes'.



MIŁOSZ PARCZEWSKI

POLAND

Head of Department | Infectious and Tropical Diseases and Acquired Immunodeficiency | Pomeranian Medical University

Miłosz Parczewski graduated as an MD from the Pomeranian Medical University, Szczecin, Poland in 2002 and gained a PhD in the molecular epidemiology of HIV in 2007. In 2016, he became a professor of medicine based on his scientific publications on HIV resistance and transmission networks. Between 2017 and 2024, Miłosz was the President of the Polish Scientific AIDS Society, and is currently also a council member of the European Society on Antiviral Resistance and associate editor of the BMJ journal 'Sexually Transmitted Infections (STI)' and 'HIV Medicine' journal. He is currently Head of Department for Infectious, Tropical Diseases and Acquired Immunodeficiency at the Pomeranian Medical University, Szczecin, Poland and President of the European AIDS Clinical Society for the term 2025–2027 and the Polish National Consultant for Infectious Diseases, appointed in 2023. His research focuses on the molecular epidemiology of HIV infection and hepatitis C co-infection. He is author of multiple scientific publications in the field of HIV/AIDS, and an investigator in a number of clinical trials and cohorts, including EUROSIDA.

Scientific Committee



CARLOS DAS NEVES

ITALY

Chief Scientist | Executive Director Office | EFSA

Carlos das Neves has been EFSA's Chief Scientist since 2022. Before joining EFSA, he was the Director of Research and Internationalisation at the Norwegian Veterinary Institute (NVI) and served as Head of Virology and Head of Food Safety & Emerging Threats at the NVI. Carlos is a veterinarian (DVM – Technical University of Lisbon) and holds a PhD in veterinary sciences (Norwegian School of Veterinary Sciences). He also has Postgraduate Certificates in Public Health from the London School of Hygiene and Tropical Medicine, and Public Policy Analysis from the London School of Economics and Political Science. In April 2024, he was appointed as a member and co-chair of the One Health High-Level Expert Panel (OHHLEP), the scientific and strategic advisory group to the Quadripartite organisations – Food and Agriculture Organisation, UN Environment Programme, World Health Organization and World Organisation for Animal Health.



TYRA GROVE KRAUSE

DENMARK

Head of Department | Infectious Disease Epidemiology and Prevention | Statens Serum Institut

Tyra Grove Krause is the Executive Vice President for Epidemiological Infectious Disease Preparedness at Statens Serum Institut, Denmark, and a Professor of Infectious Disease Epidemiology at the University of Copenhagen. She is a specialist in public health medicine with a PhD in epidemiology. Her primary areas of expertise include infectious disease surveillance, epidemiological methods, outbreak investigation and control, and One Health implementation. For several years, she led the surveillance of influenza and other respiratory infections and played a key role in Denmark's response to the COVID-19 pandemic, advising the Ministry of Health. She has been instrumental in developing and implementing the Danish Immunisation Information System and strengthening Denmark's digital data infrastructure for infectious disease surveillance and research, leveraging the country's unique e-health registries.

Tyra Grove Krause is also a member of the Advisory Forum for the European Centre for Disease Prevention and Control (ECDC) and the Health Emergency Preparedness and Response Authority

Scientific Committee

(HERA).

BRUNO CIANCIO

SWEDEN

Head of Unit | Directly Transmitted and Vaccine-preventable Diseases | ECDC



Bruno Ciano is a medical epidemiologist and infectious disease specialist. After working as clinical researcher in Italy and completing his EPIET training in the UK, he joined the European Centre for Disease Prevention and Control (ECDC) in 2006. At ECDC he focused on implementing EU strategies for increasing influenza vaccination coverage, including defining the scientific basis for vaccination strategies, the setting up of the I-MOVE network for monitoring vaccine effectiveness, and the strengthening of surveillance. Between 2011 and 2020 he focussed on establishing the mathematical modelling, GIS, and biostatistical functions of the Centre, supporting the issuing of more impactful scientific outputs, and coordinated the development of EpiPulse, the Atlas of Infectious Diseases, and the ECDC map maker tool (EMMa). Since 2020 he coordinates ECDC surveillance activities, including the implementation of strategies for harnessing new technologies, such as eHealth, molecular typing, and artificial intelligence, and the implementation of the new ECDC mandate. During the COVID-19 pandemic he worked as incident manager and coordinator of the surveillance team. Bruno Ciano has authored about fifty scientific articles in peer-reviewed journals and a book chapter on influenza surveillance.

Plenary speakers

PLENARY A

High stakes, low certainty: Post-Normal Science in public health governance



SILVIO FUNTOWICZ
NORWAY

Guest Researcher | University of Bergen

Silvio Funtowicz began his career teaching mathematics, logic and research methodology in Buenos Aires, Argentina. During the 1980s, he was a Research Fellow at the University of Leeds, England. He was a scientific officer at the Joint Research Centre of the European Commission (EC-JRC) until his retirement in 2011. From February 2012 until April 2021, he was an Adjunct Professor at the Centre for the Study of the Sciences and the Humanities (SVT) at the University of Bergen, Norway, where he is now a guest researcher. He is also co-Director of the European Centre for Governance in Complexity (ECGC), a non-profit organisation that promotes academic research and public debate on issues and institutions of public governance and how they perform in conditions of complexity.

PLENARY B

Science-based leadership in public health: decisions under pressure



ALEMKA MARKOTIĆ
CROATIA

Head of Unit | Department of Urogenital Infections | University Hospital for Infectious Diseases

Alemka Markotić is a Croatian physician, scientist, professor at the Faculty of Medicine at the University of Rijeka. She is also director of the Clinic for Infectious Diseases "Dr. Fran Mihaljević" in Zagreb, where she founded the Centre for Emergent and Re-Emerging Infectious Diseases. Throughout her career she has worked at the Institute of Immunology in Zagreb, has founded the Croatian Society for Biosafety and Bioprotection at the Croatian Medical Association, and has been an associate member of the Croatian Academy of Sciences and Arts since 2012. She has received a total of seven national and nine international awards for her research so far. Since 2020, she has been a member of the Civil Protection Headquarters of the Republic of Croatia, with a significant role in containing the coronavirus epidemic.

Plenary speakers - Plenary B



EIRINI AGAPIDAKI

GREECE

Deputy Minister of Health | Ministry of Health

Eirini Agapidaki is a Psychologist, with an MSc in Health Promotion and Education from the Medical School of the National and Kapodistrian University of Athens; and a PhD in Health Psychology from the same university. She has also specialised in matters of prevention of mental disorders and promotion of mental health.

In addition, she has many years of teaching and research experience in the fields of public health policy, public health research methodology and mental health promotion – in the context of national, European and international research programs. She has worked for many years as a research associate at the Department of Hygiene, Epidemiology and Medical Statistics, of the Medical School of the National and Kapodistrian University of Athens. In recent years she was elected and served as a Lecturer in Public Health at the Medical School of the European University of Cyprus.

In 2019, she resigned from her academic role to take up her duties as the Special Secretary for the Protection of Unaccompanied Minors (at the Ministry of Migration and Asylum). At the end of December 2022, she assumed the duties of Secretary General of Public Health, and since July 2023 she serves as the Alternate Minister of Health and as a member of the Greek Parliament.

She has written and published research papers in peer-reviewed scientific journals, while she has presented the results of her research papers at many national and international conferences.



KARIN MARIA NYGÅRDI

NORWAY

Senior advisor | Norwegian Institute of Public Health

Karin Nygård, DVM, PhD, is a special adviser at the Norwegian Institute of Public Health (NIPH). She joined the EPIET programme in 2000 and has extended experience from her work at the Norwegian Institute of Public health with epidemic intelligence activities, outbreak investigations, One Health collaboration and general work to strengthen public health preparedness, both at national and global level. She has authored several scientific publications in this area.

During the pandemic, she was in the outbreak team lead in the NPHI responsible for coordinating surveillance and knowledge production for evidence-based pandemic management.

After the covid-19 pandemic she worked in the MOH with public health and preparedness, including contributing to the first white paper on health preparedness in Norway.

Currently she is working as a preparedness coordinator at the NIPH and is involved in preparedness and response activities both at national and international level, including as ECDC National focal point for preparedness and response and as expert in the technical working group on preparedness under the Health Security Committee.

Plenary speakers - Plenary B



TANJA KUCHENMÜLLER
SWITZERLAND

Head of Unit for Policy | Evidence to Policy and Impact | World Health Organization

Tanja Kuchenmüller, PhD, M.A., MSc, heads the Evidence to Policy and Impact unit in the Research for Health Department/Science Division at WHO. Her unit has a dual mandate: (1) to build country capacity in generating, translating, and applying research evidence in policies and practices, and (2) to provide strategic leadership on research policies that promote access and support scale-up.

Previously, she led knowledge translation work at the WHO Regional Office for Europe and coordinated a unit on Knowledge Management, Evidence and Research for Policy-Making. Before joining WHO, she worked in the HIV/AIDS field for the United Nations Development Programme and the German Development Service.

PLENARY C:

The third pillar of One Health: why environment can't be an afterthought



JAN SEMENZA
SWEDEN

Umeå University

Jan C. Semenza is an environmental epidemiologist renowned for his pioneering work at the nexus of climate change and public health. Early in his career, as an Epidemic Intelligence Service Officer at the U.S. Centers for Disease Control and Prevention (CDC), he led the CDC response to the devastating 1995 Chicago heat wave—an event that claimed over 700 lives—where he investigated the medical, environmental, societal, and behavioural factors driving heat-related mortality and morbidity. As part of his work with the regional offices of World Health Organization (WHO) including EURO, PAHO, and EMRO, he provided technical and scientific advice to the countries within their region. He conducted public health projects in Uzbekistan, Sudan, Egypt, Denmark, Brazil, and Haiti through CDC, WHO, US Agency for International Development (USAID), and non-governmental organizations. More recently, Semenza served as the Head of the Health Determinants Section at the European Centre for Disease Prevention and Control (ECDC), where he led efforts integrating climate change insights into infectious disease surveillance and risk assessment. Semenza is a lead author on the IPCC Sixth Assessment Report (AR6) and co-leads Working Groups 1 and 2 of the Lancet Countdown in Europe that aims to develop indicators for climate change impacts as well as indicators for adaptation, planning, and resilience for health. In addition, he holds affiliations with Umeå and Heidelberg Universities.



FRANK MØLLER AARESTRUP
DENMARK

Group Head | Research Group for Genomic Epidemiology | Danish Technical University

Since 1995, Frank Møller Aarestrup has led the antibiotic resistance group at the DTU Food Institute. Following the completion of his veterinary degree, he has worked extensively across various domains of microbiology and epidemiology, with a focus on both animal and human pathogenic bacteria.

Over the past 13 years, his research has primarily centred on the surveillance and dissemination of antibiotic resistance, the characterisation of resistant bacteria and resistance genes, and the optimisation of antibiotic use. While his work has largely concentrated on foodborne pathogens from a global perspective, his scope has broadened in recent years to encompass additional areas of concern.

He is responsible for resistance determinations related to the national monitoring of antibiotic resistance in animals. He has served as project manager for several national initiatives involving multiple institutions and has coordinated an EU-funded concerted action comprising 19 laboratories across 18 European countries.

Since 2006, Professor Aarestrup has headed both the WHO Collaborating Centre for Antimicrobial Resistance among Foodborne Pathogens and the Community Reference Laboratory for Antimicrobial Resistance in bacteria from animals and food.

Plenary speakers - Plenary C



GERARDO SANCHEZ MARTINEZ
DENMARK

European Environment Agency

Gerardo Sanchez is an Environment and Health Expert at the European Environment Agency in Copenhagen. His work focuses on the impacts of environmental and social determinants on health, the environmental burden of disease and prevention policies. Prior to joining the EEA, he worked for the UNEP DTU Partnership, the World Health Organization, the World Bank and the Massachusetts Department of Public Health, and has been stationed in the USA, Japan, Peru and Germany.



BOUDEWIJN CATRY
BELGIUM

Head of Healthcare-associated infections and Antimicrobial resistance | Sciensano

Boudewijn Catry specialises in antimicrobial resistance in human medicine, with a particular focus on antimicrobial stewardship and the transmission from the animal sector and vice versa. He began his career as a veterinary surgeon and researcher (~2005 PhD) at Ghent University before joining Sciensano in 2007 where he has been the head of Healthcare-associated Infections & Antimicrobial Resistance since 2009, playing an active role in national and international infection prevention and control initiatives. Catry, a co-founder of hospital outbreak control teams, has also been teaching different public health classes at Université libre de Brussels since 2018.

Plenary speakers - Plenary D

PLENARY D:

One bird, two stones: veterinary and human health collaboration in action



RICHARD WEBBY
UNITED STATES

Professor | St Jude Children's Research Hospital

Richard Webby completed his PhD from the University of Otago, New Zealand, before joining St Jude Children's Research Hospital, Memphis, US. He is currently a Member of the Department of Host Microbe Interactions at St Jude where he has a research programme focused on influenza at the human animal interface. He is the Director of the WHO Collaborating Center for Studies on the Ecology of Influenza in animals and the St Jude Center of Excellence for Influenza Research and Response. In these roles he participates in One Health responses and preparedness for influenza virus threats.



ANDREA GERVELMEYER
ITALY

Senior Scientific Officer | European Food Safety Authority

Andrea is a German veterinary doctor and infectious disease epidemiologist. She worked in national public health and food safety authorities before joining EFSA in 2009, where she has been responsible for emerging risk identification, crisis preparedness and animal health. Her special interests are zoonotic diseases and One Health, and she currently leads a large network of European countries carrying out surveillance in animals and the environment for zoonotic pathogens that threaten public health. Andrea is an EPIET alumnus (cohort 8).

Plenary speakers - Plenary D



ALICE FUSARO
ITALY

Biologist | European Union Reference Laboratory for Avian Influenza and Newcastle Disease

Alice Fusaro is a computational biologist at the Viral Genomics and Transcriptomics Laboratory at the IZSve in Padua, Italy. She coordinates sequencing and genetic analyses of emerging and zoonotic RNA viruses responsible for the major diseases of animals. Her current research focuses on evolutionary genetics, with special emphasis on the major mechanisms of virus evolution, the molecular epidemiology of important emerging pathogens and the roles played by mutations, natural selection, recombination, and gene flow in shaping patterns of genetic diversity on RNA viruses. She actively participates in various national and international research projects and collaborates with international and European organisations such as FAO, EFSA, and ECDC. She has authored or co-authored over 130 articles published in national and international journals.



RAMONA TREBBIEN
DENMARK

Senior Scientist and Head of Section | Influenza Laboratory | Statens Serum Institut

Doctor of Veterinary Medicine (DVM), PhD, Senior Scientist. Head of Section for Influenza and respiratory viruses at Statens Serum Institut, Denmark which is the National Influenza Center for WHO and National Reference Laboratory for human and animal influenza viruses as well as respiratory syncytial virus (RSV).

Ramona Trebbien has been working in the field of virology since 2003, and started at The National Food Institute working with foodborne viruses, before entering into the world of Influenza at the National Veterinary Institute in 2006. In 2013 she expanded her expertise to influenza in humans at Statens Serum Institut, and is now in charge of the One Health influenza laboratory at Statens Serum Institut, where the animal and public health virology was merged in 2020.

Her research is especially focused on the zoonotic aspects of influenza A virus, and the evolutionary dynamics of influenza virus and RSV. A key component of this work is the investigation of viral genetics, phenotypic characteristics and antigenic drift, due to its role in host specificity, viral immune escape and antiviral resistance.

PLENARY E:

Health for all: equity challenges in accessing essential health services



VIVIANE BREMER
GERMANY

Head of Division | HIV/AIDS, STI and Blood-borne Infections | Robert Koch Institute

Dr. Viviane Bremer is a medical epidemiologist. Originally from Luxemburg and alumnus of the German FETP programme, she has been working in surveillance of sexually transmitted infections and HIV since 2001 at the Robert Koch-Institute (RKI). Between 2008 and 2012 she was the head of the EPIET programme at ECDC. After returning to RKI in 2014, she was appointed the head of the Unit for HIV/AIDS, STI and Bloodborne Infections, and in 2023 as the Deputy Head of Department for Infectious Disease Epidemiology. She has authored numerous articles in the field of infectious disease epidemiology. She is head of the WHO European Region Collaborating Center for Viral Hepatitis and HIV at RKI that is supporting WHO in reaching the elimination and control targets for HIV, STI and hepatitis.



SUSAN HAHNÉ
NETHERLANDS

Senior Epidemiologist | National Institute for Public Health and the Environment (RIVM)

Susan Hahné is an infectious disease epidemiologist, public health specialist and medical doctor. Her passion for infectious disease epidemiology started when she did an EPIET fellowship and during her subsequent training with the UK Faculty of Public Health. Her work has been mostly focused on surveillance, outbreak investigation, research and teaching focused on the epidemiology and control of vaccine preventable diseases. Equity of vaccination programmes is one of her special interests. She has published over 150 peer-reviewed papers, contributed to a number of book chapters and supervised several PhD students. She is currently senior medical epidemiologist at the RIVM's Centre for Infectious Disease Epidemiology and Surveillance, in the Netherlands. In addition, since 2024, she is Editor-in-Chief of Epidemiology & Infection.

Plenary speakers - Plenary E



ADRIAN STOICA
ROMANIA

Senior Medical Epidemiologist | Arges County Directorate of Public Health

Adrian Stoica from Romania is a medical epidemiologist trained in epidemiology applied to public health with over 30 years of experience working mainly on surveillance and control of vaccine preventable diseases at national and international levels.

Currently serving as senior medical epidemiologist on the surveillance and control of vaccine preventable diseases in Romania, he coordinated the WHO-led immunization activities of the EU-funded project 'Strengthening health systems resilience in the Western Balkans' during September 2022 – June 2025. Prior to this WHO position, he had been working mostly on surveillance and control of vaccine preventable diseases in Romania while also serving as a WHO consultant for the surveillance and control of vaccine preventable diseases in various countries of South-East Asia and the European region since 2003.

During 2000 – 2002 he served in the US Centers for Disease Control and Prevention 'Epidemic Intelligence Service' supporting South Carolina State Department of Health and Environmental Control in the prevention and control of infectious diseases. The included the epidemiological investigation of a gastroenteritis outbreak in four South Carolina prisons affecting 688 inmates in 2001 which was reported in US CDC's MMWR 2002, 51⁵¹:1149-1152 and the active surveillance designed in the investigation of the inhalational anthrax case in CT was described in Emerging Infectious Diseases 2002; 8¹⁰:1078-1082.

PLENARY F:

Beyond numbers: humanising public health to address health inequities



GRAZIA CALEO
UNITED KINGDOM

Independent public health consultant

Dr. Grazia Caleo, is a Medical Doctor and Public Health Specialist with over 15 years of experience in humanitarian and Global Health. She previously led the Social Science Team at Médecins Sans Frontières (MSF), where she coordinated a multidisciplinary group of anthropologists, child protection specialists, mental health professionals, and community engagement advisors. Dr. Caleo has designed and led public health and research initiatives across diverse settings, including Haiti, the Democratic Republic of Congo (DRC), the Central African Republic (CAR), Guinea, Zambia, Niger, Bangladesh, and Sierra Leone. Her work has focused on outbreak response, immunization, maternal and child health, occupational health, child labour, and health systems strengthening in complex emergencies.

She holds a Master's in Epidemiology and a PhD from the London School of Hygiene and Tropical Medicine, as well as a specialization in public health. A former EPIET fellow, Dr. Caleo has collaborated with the World Health Organization (WHO) and CDC/Stop Polio, contributing to emergency responses in Haiti and Chad.

In addition to her public health work, she is the author of *The Secret of the Bush*, a children's book that has been included in UK school reading lists. She is currently completing a Master's in Child Rights at King's College London, further deepening her focus on child protection in humanitarian settings.



ELBURG VAN BOETZELAER
NETHERLANDS

Epidemiology Advisor | Médecins Sans Frontières

Elburg is a public health professional specialised in humanitarian health emergencies with over a decade experience working in humanitarian crises across the world including in DRC, South Sudan, Iraq and Bangladesh. She has worked as an epidemiologist with the International Rescue Committee, Save the Children, WHO and Medecins sans Frontieres. Elburg holds an MPH from Columbia University and a PhD from Utrecht University focusing on the healthcare rights and needs of older people in humanitarian crises. She currently works as an Epidemiology Advisor with Medecins sans Frontieres.

Plenary summaries

PLENARY A

High stakes, low certainty: Post-Normal Science in public health governance

Day 1 - Wednesday 19 November, 9:25-10:25

Traditional science-based policy approaches often prove inadequate during health emergencies, when facts are uncertain, values are plural, stakes are high, and decisions are urgent. In such situations, the usual separation of facts from values becomes untenable.

This session features philosopher of science Silvio Funtowicz, who will explore Post-Normal Science perspectives on decision-making when conventional scientific approaches reach their limits. He will illustrate how in real-life scenarios, the pursuit of absolute truth gives way to the notion as fitness for purpose, fostered through dialogue between experts and extended peer communities. Funtowicz will argue that in high-stakes public crises and emergencies—marked by complexity, uncertainty, and value conflicts—science should help create just, responsible, and anticipatory knowledge, rather than strive for perfect predictions and impossible total control over policy actions.

PLENARY B

Science-based leadership in public health: decisions under pressure

Day 1 - Wednesday 19 November 17:00-18:30

Science-based public health leadership during infectious disease emergencies involves complex decision-making where scientific knowledge provides important but incomplete answers. Leaders must make urgent decisions to protect population health when evidence is emerging, uncertain, or disputed, while managing competing demands, cultural values, and limited resources. In an era of populism and misinformation, promoting evidence-based policy requires balancing scientific accuracy with governance realities.

This session features a moderated debate with panellists from healthcare, policymaking, and public health backgrounds. Following brief opening reflections based on personal experiences, the discussion will explore key challenges at the intersection of science, policy, and leadership. The debate will address decision-making during health emergencies, including setting priorities under pressure and maintaining evidence-based approaches when scientific facts compete with political and social pressures for public attention and trust.

Plenary summaries

PLENARY C:

The third pillar of One Health: why environment can't be an afterthought

Day 2 - Thursday 20 November 9:00-10:30

The One Health approach recognises the interconnectedness of human, animal, and environmental health, yet the environmental dimension is frequently overlooked in public health planning. This represents a missed opportunity as environmental systems crucially influence health risks and disease emergence, particularly for threats like climate change and antimicrobial resistance.

Drawing on EU Member States' experiences, speakers will explore how environmental systems influence health risks and examine the potential of environmental surveillance, including wastewater monitoring, for early warning. Through case studies and practical examples, the discussion will address how integrated surveillance and preparedness planning can be strengthened, offering policy recommendations and lessons learned to guide further action.

PLENARY D:

One bird, two stones: veterinary and human health collaboration in action

Day 2 - Thursday 20 November 17:00-18:30

Effective outbreak response to zoonoses depends on close coordination between veterinary and human health sectors, yet achieving seamless collaboration between these traditionally separate domains remains a significant operational challenge. Recent outbreaks, particularly of avian influenza, have highlighted both the potential for successful cross-sector collaboration and persistent gaps in communication, surveillance systems, and response protocols.

Through real-world case studies from recent outbreaks, speakers will share examples of cross-sector collaboration, highlighting successes and challenges in surveillance and response. The discussion will focus on practical lessons for strengthening operational collaboration, presenting recommendations for joint surveillance systems, outbreak investigation protocols, and integrated risk assessment approaches.

PLENARY E:

Health for all: equity challenges in accessing essential health services

Day 3 - Friday 21 November 9:20-10:45

Access to preventive and essential healthcare remains unequal across Europe, with some populations facing persistent barriers due to stigma, policy inconsistencies, financial constraints, and structural obstacles. These disparities are particularly visible in key public health areas where certain communities experience systematic exclusion from services.

This session features presentations from panellists who will examine how health inequities manifest, and explore how data, research, and practice can address them. The discussion will focus on three areas: combination prevention and PrEP access, vaccination inequities, and healthcare for migrant and displaced populations affected by re-emerging infectious diseases like tuberculosis and diphtheria. Speakers will present practical examples of inclusive approaches, targeted services, and people-centred systems that support health for everyone.

PLENARY F:

Beyond numbers: humanising public health to address health inequities

Day 3 - Friday 21 November 15:45-16:30

Moving beyond traditional approaches, public health systems need to become more resilient and inclusive by recognising that meaningful evidence extends beyond statistics to include lived experiences and community voices.

This session features Grazia Caleo and Elburg van Boetzelaer, bringing together experiences from EU and humanitarian settings. The discussion will explore how evidence can be communicated in accessible and humanising ways, demonstrating how data can be transformed into storytelling and art. Focusing on vulnerable populations such as children and the elderly, speakers will address how data-driven, inclusive strategies can help close healthcare access gaps and empower communities to co-create solutions.

ABSTRACT PRESENTATIONS

Abstract presentations are a key part of the ESCAIDE scientific programme. This year, we received a remarkable number of nearly 900 abstract submissions, encompassing both standard call and late breaker abstracts. Out of these, around 227 were selected for inclusion in the programme, spanning a wide array of topics in applied infectious disease research and epidemiology, thereby enhancing the diversity and richness of the conference content. These accepted abstracts have been allocated to poster sessions and oral presentations, ensuring a comprehensive distribution across different conference themes.

This abstract book has been produced based on the copy provided by the authors. The abstracts published in this book reflect the research and viewpoints of the individual authors. ECDC and the ESCAIDE Scientific Committee do not guarantee the accuracy or endorse the findings and recommendations. The responsibility for the content lies entirely with the author(s).

Oral presentations – fireside sessions

A fireside session is a moderated discussion where the presenters are given the opportunity to present their work and answer questions from the audience. During the session, each presenter has 15 minutes to discuss their work, which includes a short presentation by the speaker (~7 min), a moderator-led discussion (~5 min) and questions from the audience (~2 min).

Poster presentations – poster tours

Poster tours provide a platform to highlight recent research and developments across various fields. These sessions foster networking and potential collaborations between researchers, organisations, and interested attendees. Given the limited time, the primary objective is to facilitate initial connections, encouraging follow-up discussions and deeper engagement with the authors post-session. During a poster tour session, each presenter has 6 minutes to discuss their work, which includes a short presentation by the speaker (~3 min), a moderator-led discussion with the audience (~3 min).

Abstract reviewers

The Scientific Committee warmly thanks the reviewers of the abstracts submitted for **ESCAIDE 2025**.

Albania

Silvia Bino
Kujtim Mersini

Armenia

Lusine Paronyan

Australia

Alastair Donachie

Austria

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Dirk Werber
Adriana Cabal Rosel

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Bulgaria

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Croatia

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Czechia

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Lasse dam Rasmussen
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ECDC

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Kate Olsson
Katie Palmer
Katja Siling
Leah Martin
Luis Alves de Sousa
Luisa Hallmaier Wacker
Maike Winters
Maria Keramarou
Marieke Van der Werf
Maximilian Riess
Nathalie Nicolay
Eeva Broberg
Emmanuel Robesyn
Esther Kukiella
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Irina Ljungqvist
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Adam Roth
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Anke Kohlenberg
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Diamantis Plachouras
Bastian Prasse
Tanja Charles
Bruno Christian Ciano

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Finland

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Miriam Wiese-Posselt
Gerhard Falkenhorst
Julia Fitzner
Thomas Harder
Hofmann Alexandra
Ivo Foppa
Johann Fontaine
Gamze Aktuna
Maria An der Heiden
Andreas Sing
Jurke Annette
Michael Brandl
Viviane Bremer
Christiane Wagner-Wiening
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Michaela Diercke
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Florian Burckhardt

Greece

Vana Sypsa
Rengina Vorou
Theologia Sideroglou
Sotirios Tsiodras
Kassiani Mellou
Loukia Zerva
Dimitrios Paraskevis
Anastasia (Nancy) Flountzi
Georgina Tzanakaki
Andreas Mentis

Abstract reviewers

The Scientific Committee warmly thanks the reviewers of the abstracts submitted for **ESCAIDE 2025**.

Hungary

Agnes Galgoczi
Agnes Hajdu
Ida Prantner

Ireland

Patricia Garvey
Lisa Domegan
Lois O'Connor
Eve Robinson
Anne Carroll

Italy

Patrizio Pezzotti
Biagio Pedalino
Pier Luigi Lopalco
Saverio Caini
Lara Ricotta
Loredana Ingrosso
Domenico Martinelli
Enrico Girardi
Francesca Latronico
Claudia Lucarelli
Stef Bronzwaer
Carlos Das Neves

Latvia

Dzintars Mozgis

Lebanon

Zeina Farah

Luxembourg

Joël Mossong
Cinthia Menel Lemos

Malta

Tanya Melillo

Moldova

Alina Druc

Namibia

Hannah Lewis
Christian Winter

Netherlands

Alma Tostmann
Zsofia Igloi
Sonia Boender
Susan Hahné
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Jorrit Hofstra
Kim Benschop
Margreet Te Wierik
Mirjam Knol
Ingrid Friesema
John Rossen

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Preben Aavitsland
Lamprini Veneti
Umaer Naseer

Pakistan

Imran Nisar

Palestine

Diaa Hjaija

Poland

Karolina Zakrzewska
Magdalena Ankiersztejn-Bartczak
Marta Niedźwiedzka-Stadnik
Magdalena Rosinska
Malgorzata Sadkowska-Todys
Maria Ganczak
Justyna Kowalska
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Nils Anders Tegnell
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Cyril Barbezange

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Levent Akin
Fehminaz Temel

Ukraine

Olena Nesterova

United Kingdom

Giuseppina Ortu
Petra Manley
Ranya Mulchandani
Sooria Balasegaram
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Louise Coole
Malorie Perry
Mari Morgan
Gavin Dabrera
Giri Shankar
Alicia Barrasa
Androulla Efstratiou
Aoife Doyle
Aura Aguirre-Beltran
Caoimhe Mckerr
Daniel Thomas
Hikaru Bolt

United States

Peter Gerner-Smidt
Richard Goering

FIRESIDE SESSIONS

FIRESIDE SESSION 1

Day 1 | Wednesday 19 November | 11:00-12:30

Preparedness

PRESENTER

Orla Condell

ABSTRACT

The first 1000 days of the EU Health Task Force: Supporting stronger preparedness and response through partnership within the EU/EEA and globally

O. Condell¹

D. Pampaka², E. Lof³, A. Romani⁴, D. Cauchi⁵, D. Obach⁶, S. De Angelis⁷, E. Severi⁸, T. Hofmann⁹, V. Lefevre¹⁰

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BACKGROUND

The EU Health Task Force (EUHTF) was established by the EU regulation on serious cross-border threats to health (2022/2371) and ECDC's enhanced mandate, to overcome weaknesses highlighted by the COVID-19 pandemic. The EUHTF is a deployable public health workforce providing emergency response and preparedness support globally, upon request. We report on the first 1000 days of the EUHTF; its establishment, operations and support it has provided.

METHODS

ECDC designated a Coordination Team to develop working modalities, objectives and procedures of the EUHTF and to support its routine operations. Guidance was provided by an advisory group, including representatives from Member States, the European Commission (EC), GOARN, and other stakeholders. Three pools were created to provide expertise for EUHTF assignments: the ECDC Expert Pool, the ECDC Fellowship Pool, and the EUHTF External Expert Pool. Mechanisms were developed to directly manage assignment logistics within the EU/EEA. Partnerships were formalised with the EC, WHO and GOARN to facilitate EUHTF operations beyond the EU/EEA and large mobilisation efforts for EU-declared public health emergencies.

RESULTS

From its operationalisation in May 2023 until April 2025 the EUHTF received 26 requests and accepted 23; two of which were later discontinued. Of the 21 assignments, 15 originated from 10 EU/EEA countries, including 12 related to preparedness and three related to ongoing outbreaks. Six emergency response assignments were completed in countries outside of the EU/EEA, five of which were operationalised in collaboration with EU or UN partners, including GOARN. To complete all EUHTF assignments 15 experts were deployed and 30 supported remotely or through short missions.

CONCLUSIONS

The EUHTF facilitates stronger Union-level support for disease-outbreaks inside and outside the EU/EEA. The EUHTF enhances ECDC's capacity to mobilise EU expertise tailored to the specific needs of the requesting country and collaborate with global partners to ensure coordination and efficient use of resources.

KEYWORDS European Union; Public Health Emergencies; Preparedness; Outbreaks and crises

ABSTRACT ID: 275

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FIRESIDE SESSION 1

Day 1 | Wednesday 19 November | 11:00-12:30

Preparedness

PRESENTER

Marianna Zarro

ABSTRACT

Efficacy and safety of Ebola vaccines in children: a systematic review and meta-analysis

M. Zarro¹

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BACKGROUND

Ebola virus disease is an illness with high mortality and a disproportionate impact on children. Ebola vaccines have demonstrated efficacy in adults, data in pediatric populations remain limited. This meta-analysis evaluates the efficacy and safety of Ebola vaccines in children to support immunization strategies and outbreak preparedness.

METHODS

Following PRISMA statement, we included Phase IIb–IV trials and post-marketing studies identified through PubMed, SCOPUS, Web of Science, ClinicalTrials.gov, ISRCTN, EUCTR, CTIS, and PACTR. Eligible studies evaluated any Ebola vaccine (Ad26.ZEBOV and MVA-BN-Filo, rVSV-ΔG-ZEBOV, ChAd3 EBO-Z) in children (<18 years), comparing vaccinated groups to either unvaccinated controls or those receiving alternative vaccines. The outcomes were immunogenicity (seroconversion) and safety (serious adverse events, SAEs). We conducted proportion and head-to-head meta-analyses, including subgroup analyses by vaccine type.

RESULTS

Seven datasets (110,258 participants) were included. Following the first dose, the pooled seroconversion rate was 89%: 92% for rVSV, 82% for Ad26/MVA, and 99% for ChAd. After the full vaccination schedule, seroconversion increased to 96% overall: 92% and 96% for one versus two doses of rVSV, 98% for Ad26/MVA, and 99% for ChAd. At one year, seroconversion slightly declined to 91%. Head-to-head meta-analyses showed a risk ratio (RR) of 15.06 ($p<0.001$) after the first dose, 16.88 ($p<0.001$) post full vaccination, and 7.7 ($p=0.005$) at one year. No significant differences emerged between one and two doses of rVSV (RR 8.24 vs. 8.47, $p=0.05$). Both rVSV and Ad26/MVA maintained strong immunogenicity over time. The incidence of serious adverse events (SAEs) was 1% (RR=0.86, $p=0.834$), with most events deemed unrelated to vaccination.

CONCLUSIONS

Ebola vaccines are immunogenic and well-tolerated in children, supporting their inclusion in vaccination strategies. Protocols should be tailored to vaccine characteristics and outbreak context.

KEYWORDS: Ebola vaccine, Ebola virus disease, Hemorrhagic fever, Children

ABSTRACT ID: 294

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FIRESIDE SESSION 1

Day 1 | Wednesday 19 November | 11:00-12:30

Preparedness

PRESENTER

Christin Walter

ABSTRACT

Evaluating the implementation of a digital Surveillance Outbreak Response Management and Analysis System in Germany during the COVID-19 pandemic: Results and lessons learned

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BACKGROUND

During the COVID-19 pandemic, the German Federal Ministry of Health launched the rollout of the open-source Surveillance Outbreak Response Management and Analysis System (SORMAS) in 2020 to support overburdened local health departments (LHDs). We aimed to identify facilitators and barriers to support strategies for future implementations of digital tools.

METHODS

We used a mixed-method approach for this implementation research. Between 12/2020 and 12/2021, we conducted 12 Focus Group Discussions (FGD) with LHD staff and (political) decision makers, divided into four groups based on background and duration of SORMAS use and analyzed them via adapted content analysis using a deductive approach based on the Unified Theory of Acceptance and Use of Technology. An online survey was conducted within all 375 LHD in Germany in May 2022 and used lasso regression in R to identify characteristics associated with user and non-user satisfaction.

RESULTS

In 12 FGD with 70 participants from 42 districts, we identified 27 key categories of facilitators and barriers to the implementation such as political pressure, individual software development and age of personnel. However, the survey analysis showed no significant influence of user age on satisfaction, but longer LHD tenure was linked to dissatisfaction with the system. Political support and central software development was cited as facilitating and hindering.

CONCLUSIONS

The mixed-methods approach enabled a comprehensive understanding. While some findings converged, others diverged - highlighting the value of methodological triangulation in this context. Factors influencing tool acceptance are related to the tool itself, or to circumstantial conditions. The tension between LHD autonomy and standardized preparedness shows the need for a pre-pandemic strategy. Findings support recommendations to strengthen enablers and reduce barriers to digital tool implementation in public health. Political pressure due to the acute need during the COVID-19 pandemic seemed to facilitate and hinder the implementation of new digital tools in LHD.

KEYWORDS: Public Health Surveillance, Implementation Science, Pandemic Response, Preparedness, Digital Epidemiology

ABSTRACT ID: 416

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FIRESIDE SESSION 1

Day 1 | Wednesday 19 November | 11:00-12:30

Preparedness

PRESENTER

Celeste Marsh

ABSTRACT

Barriers and enablers to the timely activation and effectiveness of provincial rapid response teams in responding to public health alerts across Papua New Guinea ²⁰²⁴

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BACKGROUND:

The International Health Regulations ²⁰⁰⁵ require member states to demonstrate the ability to detect and respond to public health threats; crucial to this function are multidisciplinary rapid response teams (RRTs). Papua New Guinea's (PNG) provincial RRT training programme's reviews have highlighted factors that challenge RRT timeliness and effectiveness. This study aimed to further explore barriers and enablers to optimal provincial RRT function.

METHODS

This cross-sectional, explanatory-sequential mixed methods study included an online survey targeting all RRT members and relevant provincial management in 22 provinces. Maximum variability sampling was used to select provinces for focus group discussions (FGDs) and semi-structured interviews. Proportions of survey participants identifying each barrier/enabler were estimated using generalised estimating equations to account for clustering by province. Qualitative data, coded using the Framework Method were triangulated with quantitative findings.

RESULTS

The 145 respondents to the survey (63%) represented 21/22 provinces and all core RRT roles. The most commonly reported barriers to optimal RRT operation related to financial and logistical factors, particularly the lack of timely access to funds (69%) and logistics support (63%). Key enablers included the proper allocation of skilled staff to RRT roles (64%), and their knowledge of responsibilities (57%). Qualitative data (7 FGDs, 5 interviews) suggested challenges stemmed from the under-integration of RRT activities into governance architecture and systems. Solutions to identified challenges included pre-agreements with service-providers, incorporating RRT activities in provincial budgets, formalising processes through standard operating procedures and further technical training including simulation exercises.

CONCLUSIONS

Findings of this study, a first in the Pacific region, will inform advocacy efforts for essential policy and system change to improve RRT function and further adaption of RRT training in PNG. Results contribute to the limited existing empirical knowledge on the topic and could help inform regional and potentially global efforts to strengthen localised rapid response capacity and capability.

KEYWORDS: Rapid Response Teams, Papua New Guinea, Public Health, International Health Regulations

ABSTRACT ID: 428

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FIRESIDE SESSION 1

Day 1 | Wednesday 19 November | 11:00-12:30

Preparedness

PRESENTER

Jessica Hayes

ABSTRACT

A cross-border large-scale pandemic simulation exercise in two European public health emergency operations centres using an innovative pandemic management dashboard

J. Hayes¹

(GROUP) PANDEM-2 consortium

¹University of Galway

BACKGROUND

Cross-border health emergencies are a major threat to health security. In collaboration with six EU Public Health Agencies, the Horizon 2020 project PANDEM-2 (Pandemic Preparedness and Response, 883285) project developed a prototype online dashboard, incorporating harmonised pandemic-related data and a suite of readiness assessment tools to enhance planning, situational awareness, and decision support capabilities for pandemic management within the EU. The outputs were validated in a two-day functional exercise to assess the coordinated response to a large-scale pandemic.

METHODS

User requirements were gathered through consultations with public health experts in 13 European Union countries. Variables and indicators were refined and end-users provided iterative feedback on the prototype. Using the European Centre for Disease Prevention and Control (ECDC) simulation exercise cycle for public health settings, a two-day cross-border functional exercise enacting the emergence of an influenza pandemic from a novel avian H5N1 pathogen was conducted in the Public Health Emergency Operations Centres in the national public health agencies of Germany and the Netherlands. Several EU public health agencies, including ECDC, the Health Emergency Preparedness & Response Authority and the Directorate-General for Health and Food Safety's Early Warning and Response System simulation platform, were involved in supporting roles. The evaluation comprised both qualitative (hot-wash group interviews and after-action interviews) and quantitative (questionnaires and interviews) key performance indicators.

RESULTS

Participant feedback indicated that the PANDEM-2 dashboard met or exceeded their technical requirements in terms of user experience. Moreover, participants indicated that the dashboard addresses a current gap in national and cross-border training capacity for pandemic preparedness and response.

CONCLUSIONS

The PANDEM-2 system holds potential to become a robust training hub for pandemic management, serving as a valuable resource to support the implementation Article 5 of Regulation 2022/2730 on serious cross-border threats to promote effective and coordinated response to cross-border health threats at Union level.

KEYWORDS: preparedness; cross-border; simulation; communicable disease.

ABSTRACT ID: 433

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FIRESIDE SESSION 1

Day 1 | Wednesday 19 November | 11:00-12:30

Preparedness

PRESENTER

Beryl Onyuma

ABSTRACT

Building modelling capacity in Germany: An interdisciplinary infectious diseases modelling network supporting pandemic preparedness

B. Musundi¹

(GROUP) MONID

¹Martin Luther University Halle-Wittenberg (MLU)

BACKGROUND

The COVID 19 pandemic exposed the lack of capacity and coordination in infectious disease modelling efforts in Germany. Although several modelling groups contributed significantly to modelling the pandemic and its impact, there was lack of communication between the groups and with decision makers resulting in inadequate contribution of the modelling efforts to public health policy. To address these challenges, the Modelling Network for Severe Infectious Diseases (MONID) was established in 2022 with funding from the German Federal Ministry of Education and Research. The aim of MONID is to strengthen scientific expertise, advise the government, promote exchange in the scientific community and communicate modelling results to the public and decision makers.

METHODS

MONID is comprised of ten interdisciplinary research consortia, based in both university and non-university institutions, and a coordination office. The research consortia develop innovative modelling approaches using agent-based, compartmental and statistical models to study the dynamics of infectious diseases, mainly respiratory infections. On the other hand, the coordination office organizes training, conferences and capacity building programs and ensures communication and sustainability of the network.

RESULTS

Since its inception, MONID has contributed to three scenario-modelling rounds predicting the burden of respiratory infectious diseases every autumn, organized three conferences with increasing numbers of participants and abstract submissions each year, as well as three summer schools. It has established links with various public health and epidemiological networks with its members having leading roles in the German Society of Epidemiology and the Federal Standing Committee on Vaccination (RKI-STIKO) among others. Furthermore, it has established links with the European respiratory modeling Hub (ECDC - RespiCompass) and the EUVaccineHub. MONID has been awarded funding for the second phase.

CONCLUSIONS

The coordinated, sustainable and collaborative network has bridged relevant (inter-) national public health institutes with the university medicine infrastructure strengthening expertise and supporting national pandemic preparedness and response efforts.

KEYWORDS. Communicable diseases, Design support techniques, Mathematical concepts, Prevention and control, Models

ABSTRACT ID: 666

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FIRESIDE SESSION 2

Day 1 | Wednesday 19 November | 11:00-12:30

COVID-19 vaccination

PRESENTER

James Humphreys

ABSTRACT

Estimating effectiveness of monovalent JN.1 COVID-19 vaccination in EU/EEA countries between October 2024 and January 2025, a period of low SARS-CoV-2 circulation, as part of the VEBIS electronic heal

J. Humphreys¹,

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BACKGROUND

In autumn 2024, monovalent COVID-19 vaccines adapted for the Omicron sublineages JN.1 and KP.2 were administered to individuals aged ≥ 65 years in most EU/EEA countries to protect against severe COVID-19 outcomes. We evaluated the effectiveness (VE) of this dose against COVID-19-related hospitalisations and deaths during a period of low SARS-CoV-2 activity, in which BA.2.86, KP.3 and XEC were three of the main circulating Omicron sublineages.

METHODS

We conducted a historical cohort study by linking electronic health records in Denmark, Spain (Navarre), Portugal, Italy, and Sweden. Events between October 2024 and January 2025 were extracted between February-March 2025. At each site, we included individuals aged ≥ 65 years eligible for autumn 2024 COVID-19 vaccination, comparing risk of COVID-19 hospitalisation and death between those vaccinated at least 14 days ago versus those unvaccinated. Confounder-adjusted hazard ratios (aHRs) were calculated, controlling for age, sex, comorbidities, and previous booster doses in all study sites and in addition socioeconomic status and region in several study sites with access to these data. Pooled VE was estimated as $(1 - \text{pooled aHR}) \times 100$ using a two-stage random-effects model.

RESULTS

The unvaccinated and vaccinated cohorts accrued, respectively, 57,946,143 and 9,809,086 person-months at risk, 7,863 and 1,041 hospitalisations, and 1,008 and 144 deaths. Among individuals aged 65-79 years, VE against hospitalisation was 60% (95% CI: 48-70, Median Time Since Vaccination (TSV): 98 days) and 78% (95% CI: 64-87, Median TSV: 98 days) against death. In those ≥ 80 years old, VE was 58% (95% CI: 48-66 Median TSV: 100 days) against hospitalisation and 62% (95% CI: 32-79, Median TSV: 100 days) against death.

CONCLUSIONS:

Our findings indicate that the autumn 2024/25 dose conferred moderate-to-high protection against hospitalisation and death by January 2025, underscoring the benefits of COVID-19 vaccination in those aged ≥ 65 years.

KEYWORDS: COVID-19, SARS-CoV-2, vaccine effectiveness, hospitalisation, cohort design, electronic health records, multi-country study

ABSTRACT ID: 220

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FIRESIDE SESSION 2

Day 1 | Wednesday 19 November | 11:00-12:30

COVID-19 vaccination

PRESENTER

Madelyn Yiseth Rojas Castro

ABSTRACT

COVID-19 vaccine effectiveness against hospitalisation in older adults, VEBIS hospital network, Europe, September 2024–March 2025

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BACKGROUND

The autumn/winter 2024/25 COVID-19 vaccination campaigns in Europe targeted mainly adults ≥ 60 years and medically high-risk individuals, using primarily Omicron JN.1- and KP.2-adapted vaccines. September 2024–March 2025 was characterised by co-circulation of Omicron BA.2.86 sublineages (KP.3 and LP.8.1) and recombinant XEC lineage, with lower COVID-19 incidence than in summer 2024. We estimated vaccine effectiveness (VE) against COVID-19 hospitalisation in patients ≥ 60 years with severe acute respiratory infection (SARI) during autumn/winter 2024/25, through the multicentre VEBIS (Vaccine Effectiveness, Burden and Impact Studies) hospital network.

METHODS

We included data from 71 hospitals across six countries using a test-negative case-control design. We defined cases as SARI patients testing PCR-positive for SARS-CoV-2; controls were PCR-negative. We considered patients with symptom onset ≥ 14 days after vaccination as vaccinated. We estimated the confounding-adjusted odds ratio (aOR) of vaccination between cases and controls using logistic regression, adjusting for study site, date of symptom onset, sex, age, and chronic conditions. We calculated VE as $(1 - \text{aOR}) \times 100\%$, and estimated VE by time since vaccination (14–59, 60–119 and 120–168 days).

RESULTS

We included 291 cases (84 vaccinated; 29%) and 8011 controls (3930 vaccinated; 49%). Fifty-two percent of cases and 48% of controls were ≥ 80 years, 57% of cases and 56% of controls had two or more chronic conditions. Among the vaccinated, 69% received JN.1 vaccine, 7% KP.2, 1% XBB.1.5, and 23% vaccine of unknown type. The VE was 42% (95%CI: 13;62) 14–59 days post-vaccination, 38% (95%CI: 6;60) at 60–119 days, and 14% (95%CI: -59;54) at 120–168 days.

CONCLUSIONS

Our results indicate that, during autumn/winter 2024/25, two in five vaccinated older adults were protected from hospitalisation for up to 4 months. These results contribute to decision-making around vaccination campaigns and underline the importance of vaccination campaign timing.

KEYWORDS: Case-Control study, SARS-CoV-2, COVID-19 Vaccines, Immunisation Programs, Hospitalisation

ABSTRACT ID: 409

PRESENTED BY: Madelyn Yiseth Rojas Castro - France - m.rojas@epiconcept.fr

FIRESIDE SESSION 2

Day 1 | Wednesday 19 November | 11:00-12:30

COVID-19 vaccination

PRESENTER

Ayelen Rojas-Benedicto

ABSTRACT

Effectiveness of the Autumnal COVID-19 Vaccine Dose During the Winter and Summer Waves of the 2023/24 Season in Spain

A. Rojas-Benedicto¹

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BACKGROUND

In October 2023, a COVID-19 vaccine booster (monovalent XBB.1.5) was recommended in Spain for ≥60-year-olds. That season, there was a winter wave with SARS-CoV-2 variants substitution from XBB.1.5 to BA.2.86, and a summer wave due to BA.2.86 and later KP.3. We aimed to estimate vaccine effectiveness (VE) of the autumnal dose against COVID-19 infection and hospitalization during both waves.

METHODS

Using a test-negative design, within the Spanish Acute Respiratory Infections (ARI) Surveillance System, ARI patients ≥60 years-old consulting in primary-care or who required hospitalization were systematically RT-PCR tested for SARS-CoV-2. Patients swabbed between 1 October 2023 and 30 September 2024 within 10 days of symptoms onset were classified as cases if PCR-positive or as controls if PCR-negative. The odds of autumnal vaccination ≥14 days before onset was compared using logistic regression adjusted for sex, age, chronic conditions and week, separately for infection and hospitalization, winter (weeks 40/2023-05/2024) and summer (weeks 19-35/2024) waves, and by SARS-CoV-2 variants dominance; $VE = (1 - \text{Odds Ratio}) \times 100$.

RESULTS

We included 1,124/4,235 and 1,333/6,351 cases/controls in primary-care and hospitals, respectively. During the winter wave, VE (95% Confidence Interval) was 27% (4;45%) against COVID-19 infection [45% (-48;84%) during XBB.1.5 dominance; 26% (0;45%) during BA.2.86] and 41% (26;52%) against hospitalization [74% (38;91%) during XBB.1.5; 38% (22;51%) during BA.2.86]. During the summer wave, VE decreased to -3% (-26;17%) against infection [22% (-4;42%) during BA.2.86; -42% (-93;-5%) during KP.3] and to 8% (-11;23%) against hospitalization [4% (-24;25%) during BA.2.86; and 11% (-16;31%) during KP.3].

CONCLUSIONS

COVID-19 VE was moderate during the 2023/2024 winter wave, slightly higher for XBB.1.5 and against hospitalization. No protection was found during the 2024 summer wave, possibly due to waning immunity and SARS-CoV-2 variant substitution. Results support the need of spring COVID-19 vaccine boosters, but the decision should account for the changing COVID-19 epidemiology and expected vaccine acceptability.

KEYWORDS: COVID-19, Vaccine Efficacy, Test-Negative Design, Case-Control Studies, Sentinel Surveillance

ABSTRACT ID: 442

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FIRESIDE SESSION 2

Day 1 | Wednesday 19 November | 11:00-12:30

COVID-19 vaccination

PRESENTER

Joao Almeida Santos

ABSTRACT

Do COVID-19 and Influenza vaccines influence susceptibility to other respiratory viruses? A population-based study

J. Almeida Santos¹

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BACKGROUND

Studies have raised concerns that Influenza and COVID-19 vaccination may influence susceptibility to other respiratory viruses (ORV), potentially increasing the risk of non-target infections. This challenges a key assumption of test-negative design studies—that vaccines do not affect the risk of other infections within the same clinical syndrome. Nevertheless, current evidence remains inconclusive. This study aimed to evaluate the association between COVID-19 and influenza vaccination and the risk of non-influenza/COVID-19 respiratory virus infections.

METHODS

Test-negative design (TND) study using Portuguese data from a primary care vaccine effectiveness study (VEBIS Primary Care study) between October/2022-April/2025. Data on influenza/COVID-19 vaccination status, age, sex and chronic conditions were collected. Samples were tested by RT-PCR for influenza, SARS-CoV-2 and ORV. Patients with laboratory-confirmed influenza/COVID-19 infection were excluded. Logistic regression estimated adjusted odds ratios (aOR) of being vaccinated among cases (ORV positive) and controls (pan-negative).

RESULTS

Of the 1096 patients included, 4.5% received the COVID-19 vaccine, 5.9% the influenza vaccine, 13.3% both, and 76% neither. Human Rhinovirus (27.8%), Human Coronavirus (9.1%) and Respiratory Syncytial Virus (8.8%) were the viruses more frequently identified. Individuals 65+ exhibited significant lower odds of infection with ORV (OR=0.45, 95%CI:0.25-0.81) compared to younger age group (<18yo). Vaccination status, including influenza only (aOR=1.01, 95%CI:0.59?1.72, COVID only (aOR=0.87, 95%CI:0.48?1.56), and both vaccines (aOR=1.37, 95%CI:0.919?2.045), were not associated to ORV infection risk.

CONCLUSIONS

Our results suggest that vaccination status—whether for influenza, COVID-19, or both—was not significantly associated with the risk of ORV infections. This supports the use of test-negative controls for influenza/COVID-19 within the same clinical syndrome, as it upholds a key TND assumption of no association between vaccination and risk of non-target infections. While mechanisms such as reduced cross-protection from natural infection or potential vaccine-induced cross-immunity have been proposed, our findings reinforce the validity of the primary methodological assumption rather than suggesting evidence for these alternative effects.

KEYWORDS: COVID-19 Vaccine, Influenza Vaccine, Respiratory Tract Infections, Case-Control Studies, Primary Health Care, Population Surveillance

ABSTRACT ID: 472

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FIRESIDE SESSION 2

Day 1 | Wednesday 19 November | 11:00-12:30

COVID-19 vaccination

PRESENTER

Esther Kissling

ABSTRACT

Effectiveness of 2024/25 COVID-19 vaccines against laboratory-confirmed symptomatic SARS-CoV-2 infection in adults aged ≥ 65 years, European VEBIS primary care multicentre study, autumn/winter 2024/25

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BACKGROUND

In Europe, after a wave of SARS-CoV-2 infection in summer 2024, virus activity decreased during autumn/winter 2024/25. Omicron BA.2.86 lineages and sublineages (KP.3, XEC) were predominantly circulating during this time. Many European countries launched 2024/25 COVID-19 seasonal vaccination campaigns (using JN.1 and/or KP.2 vaccines) in autumn 2024, with older adults as a key target group. We conducted a European multicentre test-negative case-control study at primary care level to estimate 2024/25 COVID-19 vaccine effectiveness (VE) against laboratory-confirmed symptomatic SARS-CoV-2 infection in the 2024/25 autumn/winter season.

METHODS

Physicians swabbed patients aged ≥ 65 years presenting with acute respiratory infection at primary care and collected demographic, clinical and vaccination information. Those testing RT-PCR positive were cases; those testing negative were controls. A person was defined as vaccinated if symptom onset was ≥ 14 days post-vaccination; if onset was 1–13 days post-vaccination they were excluded. We estimated VE in adults aged ≥ 65 years overall and by time since vaccination using logistic regression adjusted for study site, age, sex, and onset date.

RESULTS

We included 105 cases and 2527 controls from 14 October 2024–12 March 2025 in four European countries (Germany, Spain, France, Ireland). Median age was 74 years among cases and controls. Among cases 13% (14/105) and among controls 32% (806/2527) were vaccinated with the 2024/25 COVID-19 vaccines. Overall, VE was 58% (95%CI: 27–78%) and 78% (95% CI: 45–93) at 14–59 days and 30% (95%CI: -43–69%) at 60–119 days since vaccination.

CONCLUSIONS

During a period of low SARS-CoV-2 circulation, VE against symptomatic infection at primary care was high at 78% within 2 months from vaccination among older adults in Europe. A relatively low vaccination rate among controls (32%) suggests missed opportunities for protection. Lineage-specific VE will help clarify the relative contributions of waning immunity and immune escape of circulating viruses to the lower VE (30%) 3–4 months after vaccination.

KEYWORDS: COVID-19,vaccine effectiveness,COVID-19 vaccine, multicentre study,case control studies, test-negative design,SARS-CoV-2

ABSTRACT ID: 515

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FIRESIDE SESSION 2

Day 1 | Wednesday 19 November | 11:00-12:30

COVID-19 vaccination

PRESENTER

Christian Hansen

ABSTRACT

Why studies reporting waning vaccine effectiveness against severe outcomes should be interpreted with caution

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BACKGROUND

The COVID-19 pandemic underscored the need for ongoing monitoring of vaccine effectiveness (VE), particularly as vaccines are updated to match emerging variants. A key concern guiding booster policy is the durability of protection; however, unrecorded infections may bias results and exaggerate signals of waning. We conducted a simulation study to quantify this effect on VE estimates for hospitalisation.

METHODS

We simulated a COVID-19 winter season (October–April) with most infections peaking mid-season and ~33% of adults aged ≥65 infected by April. Vaccine coverage was 65%, with fixed VE of 60% against infection and 70% against hospitalisation, with no waning modelled. Among unvaccinated individuals, 2% of infections resulted in COVID-19-related hospitalisation. Infected individuals were removed from risk, but only hospitalised infections were considered observed. Using a cohort design and Cox regression, we estimated VE against hospitalisation as 1 minus the hazard ratio. VE was estimated separately within consecutive 4-week periods. We repeated simulations under varying assumptions (e.g. vaccine uptake, attack rate), pooling results over 100 runs.

RESULTS

In the main simulation scenario, estimated VE against hospitalisation declined from 69% in the first month after vaccination to 45% by the seventh month. In alternative scenarios, the extent of this bias varied. Greater apparent waning was observed when the vaccine offered high protection against infection, amplifying differential depletion. Conversely, slower vaccination uptake and lower overall attack rates led to more stable VE estimates over time.

CONCLUSIONS

Unrecorded infections accumulated faster among unvaccinated than among vaccinated individuals resulting in differential depletion of susceptibles and apparent waning vaccine effectiveness against hospitalisation over seven months even when there truly was no waning. In the presence of large-scale unrecorded infections, vaccine effectiveness evaluations that demonstrate rapid waning over time may be largely due to bias. Caution is needed when interpreting waning in VE studies, especially for informing vaccination policy.

KEYWORDS: Vaccine effectiveness; ,Simulation,Bias (Epidemiology),COVID-19

ABSTRACT ID: 771

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FIRESIDE SESSION 3

Day 1 | Wednesday 19 November | 11:00-12:30

Quantitative methods

PRESENTER

Valentina Marziano

ABSTRACT

Estimating measles immunity gaps and transmission risks in Italy: regional heterogeneities and the role of unvaccinated adults

V. Marziano¹

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BACKGROUND:

The recent resurgence of measles outbreaks in several European countries highlights the importance of ensuring updated assessments of disease circulation and residual susceptibility in the population. We provide an overview of recent measles epidemiology in Italy, by quantifying key metrics to anticipate transmission risks and inform public health interventions.

METHODS

We analysed measles epidemiological data in Italy (2013-2022) to estimate the generation time and the proportion of transmission by age and vaccination status. Using a catalytic model, we estimated national and regional immunity profiles, and the effective reproduction number (R_e) for 2025, identifying high-risk age groups and regional disparities.

RESULTS

Estimated mean generation time was 11.7 days (95% CrI: 11.3-12.0). We estimated that 88.9% (95% CI: 86.8–91.1%) of infection episodes originated from unvaccinated individuals, and one third involved individuals aged 20 to 39 years. Among transmission episodes with a known setting, only 8.5% (95% CI: 4.3–13.5%) were linked to school contacts. We estimated that, in 2025, 88.2% (95% PI: 88.2-88.2%) of individuals under 20 years were immune to measles nationwide. Despite marked geographical heterogeneities, immunity gaps among individuals born in the 1980s-1990s were consistently observed across all regions. The average regional R_e estimated for 2025 ranged from 1.31 to 1.78, with higher values in regions with higher susceptibility levels among adults (e.g., Emilia-Romagna) or more than 15% susceptible individuals under 20 years (e.g., South Tyrol).

CONCLUSIONS

This study suggests that unvaccinated adults significantly contribute to measles transmission in Italy. Immunity gaps are heterogeneous across regions, with some showing persistently low vaccine uptake in children and others a high proportion of susceptible adults. National and regional R_e estimates above 1 highlight the ongoing risk of measles transmission in the country. Vaccination campaigns tailored to regional needs, including integration of adult vaccination into existing programmes should be considered, to achieve higher population immunity against measles.

KEYWORDS: measles, epidemiology, vaccination, immunity

ABSTRACT ID: 184

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FIRESIDE SESSION 3

Day 1 | Wednesday 19 November | 11:00-12:30

Quantitative methods

PRESENTER

Achilleas Tsoumanis

ABSTRACT

Identifying key target populations and screening intensity for gonorrhoea and chlamydia - a modelling study of MSM in Belgium

A. Tsoumanis¹,

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BACKGROUND

Chlamydia trachomatis (CT) and Neisseria gonorrhoeae (NG) are two of the most prevalent bacterial sexually transmitted infections among men who have sex with men (MSM). Screening for CT and NG has been promoted as a strategy to reduce the prevalence of these infections. This study aimed to assess how varying screening intensities affect the prevalence of CT, NG, and the emergence of azithromycin-resistant NG (AR-NG) in an MSM population.

METHODS

We developed a network-based model for CT and NG transmission among MSM in Belgium to estimate the prevalence of CT, NG, and AR-NG in the population. The model simulates transmission of CT/NG among three anatomical sites in a population of 10,000 MSM, divided into high- and low-activity groups, over a 10-year period. We evaluated the impact of different screening coverage and frequency levels on the prevalence of CT, NG, and AR-NG.

RESULTS

Increasing screening coverage from 0% to 80% in both groups, resulted in a 4% decrease in NG prevalence (from 16% to 12%). Screening among the low-activity MSM group had little effect on NG prevalence but increased the risk of AR-NG. The greatest risk of resistance occurred with infrequent screening (less than every 180 days) combined with high coverage (>40%). Screening up to 40% of HA-MSM every 90 days, and 20% of LA-MSM, reduced NG prevalence to 14% without promoting antimicrobial resistance. Screening coverage and frequency had little impact on CT prevalence in all scenarios.

CONCLUSION

Our model suggests that NG/CT screening has a modest effect in reducing the prevalence of these infections among MSM in Belgium. Screening should prioritize high-activity MSM, as targeting the low-activity group offers little benefit and may increase resistance. Screening alone would not be sufficient to control the CT/NG epidemic and future models should incorporate complementary interventions such as vaccination and doxycycline post-exposure prophylaxis.

KEYWORDS: Neisseria gonorrhoeae, Chlamydia trachomatis, antimicrobial resistance, men who have sex with men, mathematical model

ABSTRACT ID: 230

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FIRESIDE SESSION 3

Day 1 | Wednesday 19 November | 11:00-12:30

Quantitative methods

PRESENTER

Jakub Michalowski

ABSTRACT

A modelling approach for correcting reporting delays in Polish health care system: nowcasting hospital admissions for respiratory infectious disease real-time surveillance

J. Michalowski¹

¹Ministry of Health of the Republic of Poland

BACKGROUND

Population-based medical registries often exhibit reporting delays that hinder real-time surveillance of infectious disease burden on hospitals. In Poland, health care providers must report hospital admissions within 48 hours into the nationwide Medical Records registry - continuously sourced, yet not instantly providing interpretable outputs within surveillance system due to a two-step process. Provider-side reporting and central data processing. Although 90% of admissions are registered within 21 days, delays can vary with healthcare system load and awareness levels. This study evaluates a nowcasting model designed to account for such delays, improving interpretability of near real-time hospital admission trends.

METHODS

Registry data include both admission and reporting dates, allowing precise calculation of reporting delays. We assumed a maximum delay of 28 days, as records beyond this threshold fall outside regular processing and were excluded. For each day from 2021–2025, we computed the cumulative reporting proportion for delay d as the number of records reported with delay d divided by the number ultimately reported by day 28. These proportions were modeled using beta distributions to capture uncertainty and produce predictive delay-adjusted admission estimates. The nowcasting model integrates these distributions to correct incomplete data in real time.

RESULTS

The model was validated using a recent influenza-like illness season. When nowcasting the most recent 28 days, it achieved a mean absolute error (MAE) of 14.62 admissions. The average prediction interval coverage probabilities (PICP) were 66.6% for the 95% interval and 81.5% for the 99% interval. For the 14 most recent days—critical for surveillance—PICP improved to 85.7% for both intervals, indicating well-calibrated estimates with appropriate uncertainty.

CONCLUSIONS

The proposed nowcasting model effectively addresses reporting delays in hospital admissions due to vaccine-preventable respiratory infections. By providing timely and accurate estimates, it enables real-time tracking of seasonal trajectories, offering valuable support for decision-making in optimizing response strategies.

KEYWORDS: respiratory infections, hospital burden of infectious diseases, vaccine preventable diseases, surveillance, reporting delay, nowcasting

ABSTRACT ID: 618

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FIRESIDE SESSION 3

Day 1 | Wednesday 19 November | 11:00-12:30

Quantitative methods

PRESENTER

Daniela Paolotti

ABSTRACT

Modeling the interplay between disease spread, behaviors, and disease perception with a data-driven approach

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BACKGROUND

The dynamics of infectious disease spread are significantly influenced by human behaviors, particularly those shaped by individuals' perceptions of disease severity whose impact can be studied through integration in epidemiological models of real-world data on disease perception.

METHODS

In this work, we developed a deterministic, compartmental SLIR-type model that incorporates age and perceived severity stratification, vaccination, and behavior dynamics. Using data from the CoMix survey in Italy (2020–2021), we constructed age- and perception-stratified contact matrices to model compliant (protective) and non-compliant behaviors. Perceived severity was treated as a key determinant of behavioral transitions, modulated by different logistic functions depending on vaccination rates and ICU occupancy. Sensitivity analyses were conducted, and simplified models were also analyzed to audit the importance of behavioral feedback and data assumptions.

RESULTS

The model revealed that heterogeneity in perceived severity significantly affects epidemic outcomes. Groups with higher perceived severity maintained compliant behavior longer, offering protection especially to vulnerable populations. In contrast, early relaxation by low-perceived severity groups led to earlier and higher infection peaks, increasing deaths and ICU occupancy. These competing dynamics produced either a double-peak or single-peak epidemic curve depending on the average and variance in perceived severity. The specific form of the relationship between perception and behavior did not qualitatively alter outcomes. Simplified models confirmed that contact heterogeneity and feedback mechanisms are essential for capturing realistic dynamics.

CONCLUSIONS

Integrating disease perception into data-informed epidemiological models reveals complex feedback between behavior and spread that can significantly shift epidemic outcomes. Behavioral heterogeneity—driven by perceived severity—can both mitigate and exacerbate disease impacts depending on its distribution in the population. These findings stress the need for more granular behavioral data and support the development of public health strategies including specific drivers of individual actions. Even limited or approximate data on risk perception can enhance the realism and utility of transmission models.

KEYWORDS: Epidemic modeling, perceived severity, behavioral heterogeneities, contact matrices

ABSTRACT ID: 422

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FIRESIDE SESSION 3

Day 1 | Wednesday 19 November | 11:00-12:30

Quantitative methods

PRESENTER

Bastian Prasse

ABSTRACT

Modelling the risk of mpox Clade Ib outbreaks among MSM in the EU/EEA and the impact of targeted vaccination

B. Prasse¹

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BACKGROUND

Following a rise in mpox clade Ib cases in the Democratic Republic of the Congo and neighbouring countries, several importations have been reported in the EU/EEA since August 2024. While containment has been successful to date and largely restricted to returned travellers and subsequent household transmission without spreading to sexual networks, further undetected importations could trigger outbreaks in Europe, particularly among men who have sex with men (MSM), a population previously disproportionately affected by mpox clade II.

METHODS

We used an individual-based stochastic model to estimate the probability of clade Ib outbreaks among MSM in a typical EU/EEA urban setting, given the importation of a single undetected infectious individual. The model was built on a two-layer sexual contact network (steady and non-steady partnerships) with 10,000 individuals, incorporating disease progression, vaccination status, and contact tracing. Parameters were informed by the European MSM Internet Survey 2017 and by calibration to prior clade II outbreaks. The model accounted for historical smallpox vaccine uptake among older individuals, mpox-specific vaccination, and prior clade II exposure. Simulations explored different transmissibility scenarios for clade Ib relative to clade II, as well as the impact of increasing vaccine uptake.

RESULTS

We found a 22% (90% uncertainty interval (UI): 17.5–27.4%) probability of an outbreak exceeding 10 cases, and a 2.4% (90% UI: 0.6–5.6%) probability of an outbreak exceeding 100 cases, conditional on the introduction of an undetected infectious individual. Increasing vaccine uptake among MSM by 2.5 and 5 percentage points reduced the probability of an outbreak over 100 cases to 0.7% (90% UI: 0.1–2.8%) and 0.1% (90% UI: 0.0–1.3%), respectively.

CONCLUSIONS

Our results suggest that clade Ib outbreaks among MSM in the EU/EEA are plausible but likely to remain small. These findings provide enhanced situational awareness and actionable insights to support effective and proportionate public health interventions.

KEYWORDS: Disease Outbreaks, Mathematical Model, Men Who Have Sex With Men, Mpox, SIR Models

ABSTRACT ID: 529

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FIRESIDE SESSION 3

Day 1 | Wednesday 19 November | 11:00-12:30

Quantitative methods

PRESENTER

Steen Ethelberg

ABSTRACT

Predicting hospital admissions due to COVID-19 in Denmark using wastewater-based surveillance

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BACKGROUND

Wastewater-based surveillance (WBS) has been established as a valuable tool for infection monitoring, including for predicting infection rates. However, there is potential for further integration of WBS with other surveillance systems. We aimed to develop models that combine hospital admission and wastewater data to predict the weekly number of new hospital admissions due to COVID-19.

METHODS

We developed three state space models to predict hospital admissions in Denmark: one model without WBS data (MWO), one model including WBS data (MW) and one model including WBS data with a one-week time lag (MWlag). The models predicted hospital admissions across five forward horizons, which due to a three-week classification delay in the assessment of hospital admission cause resulted in two hindcasts, one nowcast and two forecasts. The models were compared using log likelihoods for the observed hospital admissions across a test period of 36 weeks.

RESULTS

The log likelihoods decreased across the horizons for each model, ranging from 54.15 for the first hindcast to -6.89 for the last forecast for MW (MWO: [53.84, -10.39], MWlag: [53.94, -7.75]), reflecting larger uncertainty for predictions further ahead. MWlag had the highest log likelihood values for the nowcast, whereas MW performed better for the hindcasts and the forecasts as well as across the horizons (MWO: 100.40, MW: 126.02, MWlag: 123.14). Based on the overall performance, MW was identified as the best model for predicting hospital admissions.

CONCLUSIONS

Integrating WBS data with hospital surveillance data improved predictions of hospital admissions. Furthermore, as hospital admission cause was subject to a three-week classification delay, the model also provided a nowcast of current hospital burden, allowing for more timely public health decision making. This highlights that utilizing WBS significantly improves overall surveillance efforts and robustness by effectively complementing existing systems.

KEYWORDS: Wastewater-Based Epidemiological Monitoring, COVID-19, Denmark, Models, Statistical

ABSTRACT ID: 632

PRESENTED BY: Steen Ethelberg - Denmark - set@ssi.dk

FIRESIDE SESSION 4

Day 1 | Wednesday 19 November | 14:00-15:30

Respiratory infections: evidence to practice

PRESENTER

Zhongsong Zhang

ABSTRACT

Post COVID-19 condition among older people: results from Swedish national data

Z. Zhang¹

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BACKGROUND

Post COVID-19 condition (PCC) poses huge disease burden globally. The prevalence and risk factors of PCC among older people in Sweden are insufficiently studied. This study aimed to explore the epidemiological characteristics of PCC among older people in Sweden and establish a machine learning tool to predict the risk of PCC.

METHODS

The study employed a cross-sectional design. It was conducted using Swedish nationwide registers. The population included people aged ≥ 65 years at the time of their first COVID-19 infection from 2020 to 2022. Logistic regression models were employed to assess the associations between various factors and the risk of PCC. Prediction model based on extreme gradient boosting was constructed based on selected features.

RESULTS

Of 236,943 older people having COVID-19, 2.5% of these people were diagnosed with PCC. The odds of PCC in women were significantly lower (OR=0.77, 95% CI: 0.72-0.81). The odds decreased by 3.0% for every year increase in age (OR=0.97, 95% CI: 0.97-0.97). Higher education level was associated with reduced odds of PCC. The odds increased by 7.0% for every unit increase in the Charlson Comorbidity Index (OR=1.07, 95% CI: 1.06-1.08). More types of medication were associated with increased odds of PCC. The highest predicted risk was observed among male individuals aged 65-74 with pre-secondary education, Charlson Comorbidity Index ≥ 5 , and ≥ 10 drug types, with a predicted risk of 7.8%.

CONCLUSIONS

We found that a higher burden of comorbidities and more types of medication use were associated with increased odds of PCC, while female sex, older age, higher education level, and higher income were associated with decreased odds of PCC. In addition, we established a machine learning tool to predict the risk of PCC based on individual-specific features and it may aid in early risk stratification for PCC. This study provides a reference for future health policies for PCC.

KEYWORDS: Post-COVID Conditions; Long COVID; Aged; Risk factors

ABSTRACT ID: 252

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FIRESIDE SESSION 4

Day 1 | Wednesday 19 November | 14:00-15:30

Respiratory infections: evidence to practice

PRESENTER

Ernst Van Dokkum

ABSTRACT

The predictive value of socioeconomic status and migration background for a complicated course of lower respiratory tract infections in primary care

E. Van Dokkum¹

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BACKGROUND

Evidence on risk factors for a complicated course of lower respiratory tract infections (LRTIs) in primary care remains limited and often consensus-based. While population-based studies have linked socioeconomic status (SES) and migration background to complicated LRTIs, their predictive value in primary care is still unclear. Consequently, these factors are not incorporated within current guidelines, which may contribute to health inequalities. We aimed to develop a prediction model for complicated LRTIs in general practice, integrating established risk factors and assessing the added value of SES and migration background.

METHODS

Routine care data from general practices from the ELAN-network (Leiden-The Hague-region) from 2014 to 2023, excluding the COVID-19 period, were linked to sociodemographic and hospital insurance claims data from Statistics Netherlands. Adults presenting with LRTI complaints were included. Complicated LRTI was defined as all-cause hospitalisation or mortality within 30 days. Logistic regression models were constructed with established risk factors; SES and migration background were subsequently added. LASSO selection refined the prediction model, and goodness of fit, discrimination, and calibration were compared between models, with internal and external validation.

RESULTS

Preliminary results identified 4,727 complicated LRTI episodes among 211,850 LRTI-related GP contacts. The final prediction model included SES, migration background, sex, age, comorbidities, oral corticosteroid use, antibiotics <30 days before visit, hospitalisation in the past year, current smoking, pneumonia diagnosis, and same-day antibiotic start. The lowest SES-quintile had an odds ratio of 1.50 (95%CI:1.34–1.68) compared to the highest. People with a Middle or Eastern European background had lower odds than those of Dutch origin (aOR 0.58, 95%CI:0.39–0.88). The model demonstrated good calibration and acceptable discrimination.

CONCLUSIONS

SES and Dutch background were predictive of complicated LRTI in primary care, even after adjusting for conventional risk factors. Integrating routinely available sociodemographic data into clinical decision tools could enhance early identification of at-risk patients, contributing to more equitable care.

KEYWORDS: Respiratory Tract Infections, Health Inequities, Socioeconomic Status, Primary Health Care, Predictive Learning Models

ABSTRACT ID: 398

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FIRESIDE SESSION 4

Day 1 | Wednesday 19 November | 14:00-15:30

Respiratory infections: evidence to practice

PRESENTER

Zeina Farah

ABSTRACT

Estimating the influenza disease burden averted through vaccination for children and elderly – Lebanon, 2016-2020

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BACKGROUND

Estimating the influenza burden averted through vaccination is important to guide evidence-based policies related to vaccination programs. In Lebanon, influenza vaccine is recommended for high-risk groups and mainly provided through the private sector. The objective of this study was to estimate the burden of influenza averted through vaccination in Lebanon between 2016/17 and 2019/20 for two high risk groups: children aged <5 years and elderly aged 65+ years.

METHODS

A static compartmental model was used to estimate the number of influenza-associated events (hospitalizations, medically attended illnesses and non-hospitalized illnesses) averted through vaccination. Different vaccine coverage and deployment strategies were also tested. We used as model inputs: influenza-associated events derived from a previous national study based on sentinel surveillance data; vaccine effectiveness estimated from meta-analyses; vaccine coverage estimated using vaccine sales data; and health indicators retrieved from national surveys.

RESULTS

During the study period, the average influenza vaccine coverage for the two populations was 24%. Among children under 5 years, influenza vaccination averted an annual mean of 8984 overall illnesses, 6648 medically-attended illnesses, and 61 hospitalizations during the study period, with a prevented fraction ranging between 8.7% and 13.1%. Among elderly adults, influenza vaccination averted an annual mean of 411 overall illnesses, 371 medically-attended illnesses, and 42 hospitalizations during the study period, with a prevented fraction ranging between 4.2% and 8.7%. For some seasons, an increase in averted illnesses would have been achieved using a different vaccine distribution strategy, such as increasing the proportion vaccinated earlier in the season, even with the same total cumulative coverage.

CONCLUSIONS

Influenza vaccination averted thousands of illnesses and hundreds of hospitalizations in Lebanon between 2016 and 2020. Improving vaccine coverage and using other deployment strategies would avert additional influenza illnesses. Estimates computed in this study could be used in future studies aiming to estimate the economic burden of influenza averted through vaccination.

KEYWORDS: Influenza-Human,Vaccination,Hospitalization

ABSTRACT ID: 684

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FIRESIDE SESSION 4

Day 1 | Wednesday 19 November | 14:00-15:30

Respiratory infections: evidence to practice

PRESENTER

Sandra Campos Mena

ABSTRACT

Monitoring nirsevimab effectiveness using surveillance data: a test-negative case-control study, Spain, October 2024-March 2025

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BACKGROUND

Population-based studies in Spain during the 2023/24 season estimated real-world nirsevimab effectiveness against respiratory syncytial virus (RSV) hospitalisations in under-1-year-olds at around 80%. The test-negative design (TND), widely used for influenza and COVID-19 vaccines, is a health-care-based less resource-intensive approach. We aimed to estimate nirsevimab effectiveness for the 2024/25 season using a TND and hospital-based surveillance data.

METHODS

Within the Spanish acute respiratory infections (ARI) surveillance system we selected children born ≥ 1 April 2024 and hospitalised with severe ARI (SARI) from the immunisation campaign start (regionally variable, 16 September–1 October 2024) until 31 March 2025. SARI patients were systematically RT-PCR RSV-tested within 10 days of symptom onset and classified as cases if positive or controls if negative. Effectiveness $[(1 - \text{Odds Ratio}) \times 100]$ for prior nirsevimab administration was estimated using logistic regression, adjusted for admission week, age, sex, high-risk factors and birth date. Catch-up (born from 1 April to campaign start) and at-birth (born after campaign start) groups were analysed.

RESULTS

We included 559 SARI patients: 249 in the catch-up group (102 cases/147 controls) and 310 in the at-birth group (97 cases/213 controls). Nirsevimab coverage (cases/controls) was 66.7%/84.4% for catch-up and 70.1%/87.8% for at-birth group. Effectiveness (95% Confidence Intervals) for catch-up immunisation was 68.6% (36.3%;84.6%) overall, and 85.6% (1.9%;97.9%), 79.0% (10.8%;95.1%), 78.7% (26.5%;93.8%) and -146.1% (-1245.3%;55.0%) for children aged 60-119, 120-179, 180-239 and ≥ 240 days at admission, respectively. At-birth immunisation effectiveness was 70.0% (42.0%;84.5%) overall, and 85.6% (49.6%;95.9%), 80.2% (38.7%;93.6%), 58.3% (-110.6%;91.8%) and -132.7% (-2381.3%;78.2%) for children aged 0-29, 20-59, 60-89 and ≥ 90 days.

CONCLUSIONS

The TND estimated slightly lower nirsevimab effectiveness against RSV hospitalisations compared to population-based studies. Moreover, an unexpected age-gradient was observed, albeit with wide 95%CI in older groups, warranting further research into challenges associated with the implementation of TND in the dynamic population of new-born children.

KEYWORDS: RSV, immunisation, nirsevimab, effectiveness, test-negative design

ABSTRACT ID: 470

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FIRESIDE SESSION 4

Day 1 | Wednesday 19 November | 14:00-15:30

Respiratory infections: evidence to practice

PRESENTER

Fredrik Oscarson

ABSTRACT

Subtyping of seasonal Influenza A: Assessing Wastewater for Enhanced Detection Methods and Surveillance in Sweden

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BACKGROUND

The predominant influenza A subtype affects epidemic progression, for instance due to vaccine effectiveness. Swedish subtype surveillance relies on primary care sentinel testing and laboratory reporting. In 2023–2024, 20% of positive influenza A samples were subtyped with significant regional variation. In a survey of the 21 Swedish regional infectious disease control units, 88% reported using subtype data, and 65% communicated it to clinicians, underscoring its public health importance. To investigate if wastewater data can improve the representativeness of subtype surveillance, we compared influenza A subtypes in wastewater and geographically matched laboratory data.

METHODS

Laboratory and sentinel influenza A data (week 40 2024 – week 13 2025) from 35 municipalities (4.018.932 residents – 38% of Sweden's population) was matched geographically to 8 wastewater treatment plant catchment areas. Weekly untreated and 24h flow-compensated wastewater samples were collected. Quantification of influenza A(H1N1)pdm09 and A(H3N2) was performed by RT-qPCR, normalized by pepper mild mottle virus. Descriptive and correlation analyses of subtype levels in wastewater and clinical data were performed based on the catchment area.

RESULTS

Data on 2.264 subtyped samples from laboratory and sentinel surveillance in the included municipalities were used in the analysis. Subtyped cases and subtype wastewater levels correlated well by catchment area: A(H1N1)pdm09, Spearman's $\rho = 0.68 - 0.85$ and A(H3N2), Spearman's $\rho = 0.69 - 0.90$ ($p < 0.01$ for all catchment areas).

CONCLUSIONS

The levels of influenza A subtypes in wastewater correlated well with clinical data. Wastewater analysis may be a usable tool to enhance surveillance of regional subtype distributions, especially in regions where clinical laboratories do not perform subtyping. Further on it could enhance the representativeness of national surveillance data. Wastewater can also be used to detect emerging subtypes before emergence of clinical cases (like a new pandemic), and particularly in periods when it is only feasible to subtype a share of clinical samples.

KEYWORDS: Influenza, H1N1 subtype, H3N2 subtype, Wastewater-Based Surveillance, Correlation of Data

ABSTRACT ID: 692

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FIRESIDE SESSION 4

Day 1 | Wednesday 19 November | 14:00-15:30

Respiratory infections: evidence to practice

PRESENTER

Vânia Gaio

ABSTRACT

Nirsevimab effectiveness against hospitalised Respiratory Syncytial Virus infection in Portugal, 2024/25 season

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BACKGROUND

Respiratory Syncytial Virus (RSV) is one of the leading causes of lower respiratory tract infections in younger children. In mainland Portugal, in order to reduce the risk of severe RSV post-infection complications, an immunisation strategy using Nirsevimab was implemented starting in October 2024, targeting all children aged less than 3 months, and those with high-risk conditions less than 24 months. We conducted a test-negative case-control study using the national hospital-based RSV surveillance network to estimate Nirsevimab effectiveness (NE).

METHODS

This multicentre study included children aged under 24 months hospitalised with severe acute respiratory infection in 14 hospitals. Cases were defined as children testing positive for RSV by RT-PCR or rapid antigen test (RAT), while controls tested negative. Immunisation status was obtained from electronic medical records. NE was estimated using logistic regression and estimated as $(1 - \text{adjusted odds ratio of immunisation}) \times 100$, adjusting for age group, sex, month of symptom onset date, low birth weight, prematurity, and chronic conditions.

RESULT

Between weeks 40/2024 and 12/2025, we included 111 cases and 110 controls. The median age for both groups was 2 months (IQR: 1–4). 44 (39.6%) RSV-positive and 80 (72.7%) RSV-negative infants received Nirsevimab at least 2 days before symptom onset. No significant differences were observed between cases and controls regarding sex or medical conditions. NE against RSV-associated hospitalisation was 85% (95% CI: 66–94) in the target population. Sensitivity analysis restricted to RT-PCR-confirmed cases yielded similar results.

CONCLUSIONS

During the first immunisation season in mainland Portugal, Nirsevimab conferred good protection against the most severe presentation of RSV infection in young children. Our results are aligned with those reported in other countries. Given the potential for viral evolution following the introduction of universal immunisation programmes, ongoing monitoring of NE is warranted.

KEYWORDS: Nirsevimab, effectiveness, RSV, multicentre study, case-control studies, test-negative design

ABSTRACT ID: 619

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FIRESIDE SESSION 5

Day 1 | Wednesday 19 November | 14:00-15:30

Vaccine research and immunisation programmes

PRESENTER

Kristyna Faksova

ABSTRACT

Brand-specific influenza vaccine effectiveness in three Nordic countries: estimates for the 2024-2025 season

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BACKGROUND

Seasonal influenza is a major public health concern, threatening older adults, who are recommended the seasonal influenza vaccine in the Nordic countries. Because influenza viruses evolve and new vaccine platforms emerge, continuous monitoring of vaccine effectiveness (VE) is essential. We aimed to assess brand-specific VE in preventing laboratory-confirmed outcomes in individuals aged ≥ 65 years in Denmark, Finland, and Sweden during the 2024–2025 season.

METHODS

In this multi-country register-based cohort (1 October 2024–21 March 2025), we included 2.6 million individuals. We matched vaccine recipients 1:1 with non-recipients, initiating follow-up on day 14 post-vaccination. National registers provided data on vaccination status and outcomes. Outcomes included laboratory-confirmed influenza, influenza-related hospitalization, and death. Using target trial emulation and time-to-event survival analysis, we estimated VE from cumulative incidences (1–risk ratio) with 95% confidence intervals (CI) at week 18 since start of follow-up, based on data availability. Country-specific results were meta-analysed. Quadrivalent vaccine brands included Efluelda Tetra (ET, high-dose), Fluad Tetra (FT, adjuvanted), Influvac Tetra (IT), and Vaxigrip Tetra (VT).

RESULTS

A total of 1,611,962 (62%) individuals were vaccinated. The overall VE against positive test was 39% (95%CI: 34%–44%). ET provided 54% (95%CI: 31%–77%) protection, FT 40% (95%CI: 35%–47%), VT 35% (95%CI: 23%–46%), and IT 26% (95%CI: 11%–50%). VE against hospitalization and death was 47% (95%CI: 39%–53%), and 63% (95%CI: 50%–75%), respectively. FT provided protection of 48% (95%CI: 41%–56%) against hospitalization, and 66% (95%CI: 55%–77%) against death.

CONCLUSIONS

Seasonal influenza vaccination remains an effective tool to prevent influenza infection, hospitalization, and death. High-dose and adjuvanted vaccines provided the highest protection and are recommended for use in the 2025–2026 influenza season. As the precision of our estimates depended on seasonal infection patterns and vaccine brand uptake in each country, continued annual monitoring using Nordic health registries remains crucial for informing evidence-based vaccination strategies and regulatory decision-making.

KEYWORDS: human influenza, influenza vaccines, vaccine effectiveness, registers

ABSTRACT ID: 279

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FIRESIDE SESSION 5

Day 1 | Wednesday 19 November | 14:00-15:30

Vaccine research and immunisation programmes

PRESENTER

Margarida Arede

ABSTRACT

Childhood vaccination coverage and completion in children born in Regensburg, Germany, between 2015 and 2019: Insights from a longitudinal cohort study

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BACKGROUND

In Germany, routine childhood vaccination is voluntary and free of charge, yet coverage remains below the 90–95% international immunisation target and is often delayed. In the absence of a national vaccination registry, we analysed indicators for all routine childhood vaccines, and assessed whether the 2020 introduction of compulsory measles vaccination before kindergarten/school entry increased measles-mumps-rubella (MMR) uptake in a cohort from Regensburg, Germany.

METHODS

We studied 631 children from the KUNO-Kids survey-based birth cohort (2015–2019), born at the University Children's Hospital Regensburg. Using pseudonymised self-report questionnaires available at 6 months, 2 years, and 4 years, we estimated vaccine coverage by 6 months, and completion (uptake of all doses) by 2 years (recommendations until 2020) and by 4 years. We used logistic regression to assess 6-month vaccination delays on completion by age 2.

RESULTS

At 6 months, only 66–69% of children were vaccinated on schedule with 2 doses of rotavirus and pneumococcal vaccines, and 3-dose Haemophilus influenzae B (HIB), hepatitis B (HEPB), diphtheria-tetanus-polio (DTP), and pertussis (PER). By age 2, series completion increased to 70–80% for the 4-dose HIB, HEPB, DTP, and PER vaccines; 3-dose pneumococcal; 2-dose MMR and varicella; and 1-dose meningococcal C vaccines. Children delayed at 6 months for HIB, HEPB, DTP, and PER had lower odds of completing vaccinations by age 2 (odds ratio: 0.23, 95%CI: 0.16–0.33). By age 4, completion increased to 98% for MMR and ranged 84–89% for all other vaccines.

CONCLUSIONS

Timely vaccination completion by 24 months fell short of international targets and was associated with delays at 6 months, highlighting this period as a critical window for intervention. The sharp increase of MMR completion by age 4 suggests compulsory measles vaccination improved uptake, although at a later age than recommended. The single-centre sample may limit generalisability, but allowed for early longitudinal follow-up.

KEYWORDS: vaccination coverage, birth cohort, Vaccine-Preventable Diseases, Germany

ABSTRACT ID: 307

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FIRESIDE SESSION 5

Day 1 | Wednesday 19 November | 14:00-15:30

Vaccine research and immunisation programmes

PRESENTER

Dimphey van Meijeren

ABSTRACT

Effectiveness of infant vaccination against pertussis in 1- and 2-year-olds, the Netherlands, 2013-2022

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BACKGROUND

Pertussis is a vaccine-preventable yet worldwide endemic respiratory disease, mainly caused by the bacterium *Bordetella pertussis* and sometimes *Bordetella parapertussis*. In the Netherlands, complete infant vaccination includes 4 vaccinations against pertussis for children born before 2020, and depending on maternal vaccination status 3 or 4 vaccinations for children born from 2020 onwards. We aimed to estimate vaccine effectiveness (VE) of complete infant vaccination against pertussis.

METHODS

We performed a case-control study, including all cases aged 12-35 months notified in 2013-2022 with laboratory confirmed pertussis, each matched on birth year and month with 4 randomly selected controls from the national vaccination register. Conditional logistic regression with interaction terms for age-group, sex, year of disease onset, causative pathogen, vaccine product and 3-or-4-dose schedule was used to estimate stratum specific odds ratios (ORs) with 95% confidence intervals (CIs). Sex and postal code were associated with the outcome and included as covariates. VE was calculated as $1 - \text{OR} \times 100$. Likelihood ratio tests were used to assess heterogeneity of VE across strata.

RESULTS

We included 675 cases and 2700 controls. 621 cases were infected by *B. pertussis*, 49 by *B. parapertussis* and 5 had unknown pathogen. Median age was 21 months. Yearly number of cases varied between 2 in 2021 and 128 in 2018. Proportion of girls was higher among cases (56%) than controls (48%). Overall VE was 99.2% (95% CI 98.5–99.5). VEs did not differ by age-group, sex, year of disease onset and pathogen. Statistical power was too low to detect VE differences by vaccine product and 3-or-4-dose schedule.

CONCLUSIONS

Complete infant vaccination proved highly effective against pertussis up to 36 months of age. We are extending the study period with epidemic years 2023-2024 to estimate VE in a high incidence period and to increase power to compare VE by vaccine product and 3-or-4-dose schedule.

KEYWORDS: Pertussis, Vaccine effectiveness, Whooping cough, *Bordetella pertussis*, *Bordetella parapertussis*, Vaccination

ABSTRACT ID: 395

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FIRESIDE SESSION 5

Day 1 | Wednesday 19 November | 14:00-15:30

Vaccine research and immunisation programmes

PRESENTER

Kevin Wassing

ABSTRACT

Immunity gaps despite high vaccination coverage: a mumps seroprevalence study in The Netherlands

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BACKGROUND

Despite the introduction of childhood mumps vaccination (Measles-Mumps-Rubella vaccine at 14 months and 9 years) in the Netherlands in 1987, mumps has re-emerged over the past two decades, likely due to waning immunity and gaps in population immunity. We aimed to estimate mumps seroprevalence in The Netherlands to identify potential immunity gaps.

METHODS

We used data from a sero-epidemiological study conducted in 2016/17 (age 0-89 years), with two main sampling strategies. For the national sample (NS), a representative estimate of the seroprevalence was estimated by weighting for age, sex, and region, and adjusting for study design. In the low vaccination coverage (LVC) areas, seropositivity was estimated without weighting. Specific serum IgG antibodies were measured using a bead-based multiplex immunoassay, applying a previously established cut-off for seropositivity.

RESULTS

In the NS (N = 5,146), overall seroprevalence was 87% (95% CI: 86–88). Among once-vaccinated seroprevalence decreased from 94% (95%CI: 82-98) at 14 months to 83% (95%CI: 72-91) at 9 years. Twice-vaccinated individuals, as of 9 years of age, showed a decline in seroprevalence from 98% (95%CI: 85-100) to 83% (95%CI: 73–90) once they had reached the age of (30–32). In LVC areas (n = 1,355), seropositivity was 58% (95%CI: 50-66) among 1 to 9 year old unvaccinated children. Among 10 to 32 year olds the seropositivity was 90% (95%CI: 87-92) and was 96% (95%CI: 95-98) in individuals >36 years.

CONCLUSIONS

We observed waning of vaccine-derived immunity to mumps in the Dutch population, explaining the increasing potential for resurgence of mumps outbreaks affecting immunized communities. In addition to waning immunity, pockets of unvaccinated individuals in low vaccination coverage areas, increase the pool of susceptible individuals who can become infected and spread the virus. We recommend ongoing monitoring and adaptive vaccination strategies are essential to control mumps circulation, identify at-risk populations, and prevent potential resurgence.

KEYWORDS: Vaccination Coverage,Public Health,Measles-Mumps-Rubella Vaccine,Mumps virus,Seroepidemiologic Studies

ABSTRACT ID: 531

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FIRESIDE SESSION 5

Day 1 | Wednesday 19 November | 14:00-15:30

Vaccine research and immunisation programmes

PRESENTER

Chiara Chiavenna

ABSTRACT

Psychological antecedents of vaccination: mapping social and demographic heterogeneity in six European countries

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BACKGROUND

Vaccination acceptance remains critical in Europe, yet uneven across populations. The 5C model identifies five psychological constructs—confidence, complacency, constraints, calculation, and collective responsibility—as key drivers of vaccination behaviour. However, little is known about how these antecedents vary by age, education, income, and minority status. To address this gap, we collected individual-level data in six European countries during the post-pandemic phase.

METHODS

Between March and June 2024, we surveyed 22,228 adults (18+) in Germany, Spain, France, Hungary, Italy, and the UK, using quota-representative samples by age, education, and region. The 5C constructs were measured on 7-point Likert scales (higher scores = greater readiness). We used ANOVA and linear regression to examine group differences, testing country × group interactions and pairwise contrasts, adjusting for other covariates.

RESULTS

Age was the most consistent predictor across all 5C constructs, with younger adults (18–29) showing lower confidence, higher complacency, and more perceived constraints than older adults (65+), particularly in the UK and Germany. Income and education gradients were strongest for vaccine confidence, notably in France and Hungary, but weaker or absent for other constructs outside Hungary and Italy. Minority patterns were country-specific: in Hungary, minorities reported lower confidence, while in France and the UK they reported higher collective responsibility and fewer constraints, suggesting country-specific dynamics. Overall, age-related disparities were broad and consistent, while socioeconomic gradients were mainly confined to confidence and complacency in certain countries. Country-level differences remained stark: Hungary and France showed the lowest confidence and highest constraints across groups, while Spain and the UK maintained higher confidence even among disadvantaged groups.

CONCLUSIONS

Our findings suggest that national context can amplify or buffer social disparities in vaccine acceptance, underscoring the need for interventions that address both structural and age-specific barriers.

KEYWORDS: Vaccine acceptance, Psychological antecedents, Health inequalities, Cross-country comparison

ABSTRACT ID: 774

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FIRESIDE SESSION 5

Day 1 | Wednesday 19 November | 14:00-15:30

Vaccine research and immunisation programmes

PRESENTER

Joana Gomes Dias

ABSTRACT

Impact of COVID-19 restrictions on invasive meningococcal disease notification in the European Union /European Economic Area: an interrupted time series analysis of surveillance data, 2013-2023

J. Gomes Dias¹

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BACKGROUND

Invasive meningococcal disease (IMD), caused by *Neisseria meningitidis*, is a severe bacterial infection causing meningitis and/or septicaemia with a high case-fatality ratio. Its epidemiology is driven by secular/seasonal trends, circulating variants, vaccination programmes and more recently by public health restrictions implemented as a response to the COVID-19 pandemic. We aimed to assess the impact of the COVID-19 restrictions on IMD trend notifications in the European Union /European Economic Area (EU/EEA).

METHODS

We conducted an interrupted time series analysis on monthly IMD notifications reported between 2013 and 2023 in EU/EEA using a negative binomial regression model to account for overdispersion, seasonality (Fourier terms), autocorrelation (one-month lag), country effects and population. Models included a pre/post-March 2020 indicator for COVID-19 restrictions. Results were presented as rate ratios (RR) with 95% confidence intervals (95%CI). Analyses were stratified by age-group and serogroup.

RESULTS

We analysed 19,152 IMD notifications reported by 22 countries. Overall notification rate increased before March 2020 (RR=1.002, 95%CI (1.001; 1.003)) with increases in serogroup W (RR=1.01, 95%CI (1.004; 1.009)) and Y (RR=1.01, 95%CI (1.01; 1.018)). There was an immediate decrease in March 2020 (RR=0.34, 95%CI (0.23; 0.37)) for all age-groups and serogroups. After March 2020, the overall notification rate increased (RR=1.26, 95%CI (1.21; 1.32)) with serogroup B (RR=1.33, 95%CI (1.267; 1.396)) and serogroup Y (RR=1.28, 95%CI (1.169; 1.412)) having the largest increase which was observed in all age-groups except the 0–4-year-olds for serogroup Y. Serogroup W notifications also increased (RR=1.10, 95%CI (1.0004; 1.209)) affecting adults aged ≥50-year-old. Serogroup C showed no significant trend after March 2020.

CONCLUSIONS

No increase in serogroup C IMD after March 2020 is the likely effect of long-lasting immunisation campaign across the EU/EEA. Further deployment of vaccination strategies against other vaccine-preventable serogroups should be carefully assessed and possibly revised to lessen the disease burden in the coming years.

KEYWORDS: Trends, Surveillance, COVID-19, Interrupted Time Series, Fourier ,invasive meningococcal disease

ABSTRACT ID: 512

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FIRESIDE SESSION 6

Day 2 | Thursday 20 November 11:00-12:30

Antimicrobial resistance

PRESENTER

Teresa Marie Nygren

ABSTRACT

Difficult-to-treat and pandrug resistance among carbapenem-resistant Enterobacterales and Acinetobacter spp. notifications in Germany, 2017–2024

T. Nygren¹

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BACKGROUND

Antimicrobial-resistant bacteria pose a public health threat, particularly when few or no treatment options remain. While carbapenem-resistant Enterobacterales (CRE) and Acinetobacter spp. (CRA) are notifiable in Germany, resistances to other antibiotics in CRE/CRA possibly leading up to panresistant strains were not monitored systematically. We assessed difficult-to-treat resistance (DTR) and suspected pandrug resistance (PDR) among CRE/CRA notifications, aiming to identify the most severely resistant cases as targets for public health action.

METHODS

In notifications 2017–2024, we defined DTR as resistance to all reported first-line carbapenems and fluoroquinolones, plus cephalosporins (for CRE) or aminoglycosides (for CRA). Suspected PDR required additional resistance to aminoglycosides and piperacillin-tazobactam (for CRE), colistin/polymyxin B, tigecycline, and zero non-resistant results in any of ≤22 reported antibiotics. We compared proportions using chi-squared tests.

RESULTS

Data was sufficient to assess 37,017/46,993 (79%) notifications for DTR, yielding 12,205/37,017 (33%) DTR cases. DTR was highest in 20–49-year-olds (40%), with 44% DTR among men in this age group. The annual proportion of DTR showed no clear trend, ranging between 26% ²⁰¹⁸ and 39% ²⁰²². DTR was 31% in cases without known exposure abroad, 57% with exposure in EU/EEA, 72% in Ukraine, and 60% in the rest of the world. Death was reported for 6.4% (351/5,498) of DTR infections versus 4.7% (484/10,326) of non-DTR infections ($p < 0.001$). Suspected PDR could be assessed in 33,982/46,993 (72%) notifications, identifying 70 cases (4–15 cases annually).

CONCLUSIONS

DTR affected a third of notified CRE/CRA in Germany, fluctuated annually, was more frequent with exposure abroad, and associated with higher mortality. We recommend monitoring DTR and confirmatory testing of suspected PDR cases among notifications. We have integrated DTR proportions and suspected PDR case alerts into routine surveillance. We plan communicating to local authorities about suspected PDR cases to guide intensified transmission prevention measures and reduce spread of these emerging resistance threats.

KEYWORDS: antimicrobial drug resistance, disease notification, Klebsiella pneumoniae, Escherichia coli, Germany

ABSTRACT ID: 165

PRESENTED BY: Teresa Marie Nygren - Germany - nygrent@rki.de

FIRESIDE SESSION 6

Day 2 | Thursday 20 November 11:00-12:30

Antimicrobial resistance

PRESENTER

Craig Hogg

ABSTRACT

Describing the establishment of a multi antimicrobial resistant strain of Escherichia coli in a hospital setting in North Wales; trends over time and patient outcomes

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BACKGROUND

A multi-drug resistant Escherichia coli phenotype defined by resistance to gentamicin, ciprofloxacin, and piperacillin-tazobactam appeared to be increasingly prevalent in a North Wales hospital since 2020. We aimed to quantify the phenotype over time, describe affected patients (demographics and outcomes) and compare them to patients with other phenotypes to support targeted control measures.

METHODS

Using data from the laboratory system, we conducted a retrospective cohort study on all inpatients with E.coli urine and blood sample isolates between 01 January 2023 and 31 December 2024, deduplicated by patient. We described proportions of the resistant phenotype over time and compared demographics. We conducted preliminary univariable and multivariable logistic regression, adjusting by age and sex, with the primary outcome of death within 28 days. Analyses were stratified by specimen type.

RESULTS

Of 3,126 isolates, 9% (n = 278; blood n = 85, urine n = 197) met the phenotypic definition. The proportion increased from 2 - 9% from 2020-2023. For urine isolates, patients with the resistant phenotype were older (median age (years): 80 v 70, p < 0.001), had a higher proportion of females (76% v 50%) and the adjusted 28 day mortality was significantly higher for resistant phenotype infections (OR:1.7, 95CI:1.1–2.7). No differences were found in blood isolates.

CONCLUSIONS

This preliminary study shows the resistant E.coli phenotype is well established in this hospital setting; trends identified suggest increased and sustained local transmission, and a pattern of local expansion. We have observed worse mortality outcomes in inpatients with urine isolates with this resistant phenotype. Work is ongoing to understand the impact of pre-existing comorbidities and hospital exposure on these outcomes. A larger study would be required to identify differences in blood infections. Enhanced surveillance, prompt identification, and isolation of affected patients are critical to prevent wider transmission and mitigate poor clinical outcomes.

KEYWORDS: Escherichia coli, Antimicrobial resistance, Bacteremia, Urinary Tract Infections, Epidemiologic Surveillance, Hospital mortality

ABSTRACT ID: 239

PRESENTED BY: Craig Hogg - United Kingdom - craig.hogg@wales.nhs.uk

FIRESIDE SESSION 6

Day 2 | Thursday 20 November 11:00-12:30

Antimicrobial resistance

PRESENTER

Lucy Findlater

ABSTRACT

Is mandatory surveillance of carbapenemase-producing Gram-negative organisms (CPOs) working? A surveillance evaluation, England, 2023

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BACKGROUND

Carbapenemase-producing organisms (CPOs), a group of antibiotic-resistant bacteria, are an increasing public health threat. In October 2020, English laboratories were mandated to report CPOs (colonisations or infections) into the existing national laboratory reporting system (SGSS). We aimed to evaluate laboratory coverage, simplicity, data quality, timeliness, and acceptability of the mandatory CPO surveillance system in England.

METHODS

We undertook a mixed-methods surveillance evaluation. Laboratory coverage was assessed as the proportion of laboratories reporting at least one CPO to SGSS in 2023. Data quality was assessed as completeness of variables. We conducted semi-structured interviews with 12 internal and external stakeholders engaged in clinical, laboratory, and epidemiological roles and assessed simplicity, acceptability, and perceived timeliness of the surveillance system and outputs via thematic analysis of interview transcripts.

RESULTS

In 2023, 72% (83/115) of laboratories reported at least one CPO or referred to another frontline laboratory for reporting, ranging from 38-100% by region. Not reporting was associated with technical difficulties with information management systems or referral to the reference laboratory instead. Completeness of data variables was high (99% patient name, sex, birthdate, postcode, organism species; 97% specimen type; 95% NHS number). Participants described delays in reporting into SGSS due to technical issues, limited staff capacity, or human error, potentially reducing the accuracy of weekly surveillance outputs. However, participants were satisfied with the timeliness of quarterly and annual outputs for monitoring longer-term trends. Mandatory CPO reporting was acceptable, and some participants experienced streamlined, automated reporting, whereas others noted complicated or manual workarounds using pre-existing laboratory systems. Participants used and appreciated surveillance outputs.

CONCLUSIONS

The CPO surveillance system is perceived as efficient, valuable, and acceptable to users. Despite being mandatory, reporting is still not comprehensive. We recommend investing in improvements to the existing surveillance system, ensuring that all laboratories have capacity and resources to report and to optimise processes.

KEYWORDS: Carbapenem-Resistant Enterobacteriaceae, Carbapenemase, Gram-Negative Bacteria, Surveillance, Mandatory Reporting, Evaluation Study

ABSTRACT ID: 537

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FIRESIDE SESSION 6

Day 2 | Thursday 20 November 11:00-12:30

Antimicrobial resistance

PRESENTER

Mirco Sandfort

ABSTRACT

Transmission of NDM-4-producing Enterobacterales across multiple hospitals and states – Insights from an outbreak investigation and surveillance in Germany between July 2023 and February 2025

M. Sandfort¹

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BACKGROUND

Carbapenemase-producing Enterobacterales cause infections, often nosocomial, with limited treatment options. National surveillance of notifiable colonisations and infections detected an increase in the rare New Delhi-metallo-beta-lactamase (NDM)-4 in October 2023 in Germany, prompting an outbreak investigation to halt transmission.

METHODS

Case definition: Individuals with NDM-4-Enterobacterales since July 2023, confirmed by overlapping hospital stays or isolates clustering with ≤ 15 allelic differences in core genome-multilocus sequence-typing. During the outbreak investigation, clinical and outpatient links between cases were assessed to locate transmission and coordinate infection prevention and control (IPC). Twenty-four isolates were Nanopore-sequenced for plasmid reconstruction.

RESULTS

Between July 2023-February 2024, we confirmed 68 cases in the outbreak investigation. Median age was 76 years, 34 (50%) were female, and 43 (63%) infected, including one infection-attributed death. Cases occurred in 6 hospitals in 2 states, mainly in two hospitals with 40 (59%) and 23 cases (34%), respectively. All cases had NDM-4-Klebsiella pneumoniae, in 11 cases additional NDM-4-producing species were detected. Sixty-six cases had overlapping hospital stays (the only identified epidemiological link). Only K. pneumoniae isolates clustered: 63 cases across three clusters, 4 singleton cases, and one without available sequence. A blaNDM-4-carrying IncFII-plasmid was reconstructed among the selected cases within and outside the clusters and in co-occurring species. When ward-based serial screening did not reveal new cases, the investigation and intensified IPC ended in February 2024. Until February 2025, routine surveillance sporadically detected 7 further cases with clustering NDM-4-K. pneumoniae but missing hospitalisation links to previous cases.

CONCLUSIONS

A large NDM-4-Enterobacterales outbreak in Germany involved multiple clones and species, demonstrating the synergism of epidemiological/genomic case identification. Hospitalisation histories were key to locate transmission and facilitate initial control, as this outbreak was driven by within-hospital patient-to-patient transmission and between-hospital patient transfers. New sporadic cases suggest undetected transmission and emphasise well-targeted screening to prevent NDM-4 establishment.

KEYWORDS: Disease Outbreaks,Hospitals,carbapenemase,Klebsiella pneumoniae,Genomics,Plasmids

ABSTRACT ID: 601

PRESENTED BY: Mirco Sandfort - Germany - sandfortm@rki.de

FIRESIDE SESSION 6

Day 2 | Thursday 20 November 11:00-12:30

Antimicrobial resistance

PRESENTER

Imme Roewer De Porto

ABSTRACT

Trends in Extended-Spectrum β -Lactamase and Carbapenem Resistance in Enterobacterales in the Paediatric patient population, Germany, 2018–2023: Findings from National Surveillance

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BACKGROUND

Antimicrobial-resistant (AMR) infections pose a growing threat to paediatric care, yet age-specific data remain scarce. We examined resistance patterns related to extended-spectrum β -lactamases (ESBLs) and carbapenem resistance (CR) in Enterobacterales from children in Germany to inform targeted antimicrobial stewardship interventions.

METHODS

We analysed data from health institutions continuously participating in the German Antibiotic Resistance Surveillance (ARS) between 2018-2023 (327 hospitals and 1,028 outpatient practices). Cases were defined as the first clinical isolate per -patient, -quarter, -species, and -specimen. Third generation-cephalosporin resistance represented ESBL-producing bacteria. Meropenem-resistance indicated CR. Resistance proportions were stratified by age group (<12 months (infants), 1-11 years (children), 12-17 years (adolescents)), sex (male/female), and care setting (inpatient vs. outpatient). Trends were assessed using stratified logistic regression and significance level, $p < 0.05$.

RESULTS

In total, 201,577 clinical isolates were analysed. Overall CR was low (0.1%, 93/179,264), but rising among paediatric inpatients from 0.07% in 2018 (10/15,044) to 0.13% in 2023 (18/13,971). This reflects a significant increase over the study period ($\beta = +0.213/\text{year}$, $p = 0.002$), with the highest increases in female ($\beta = +0.501/\text{year}$, $p = 0.012$) and infant ($\beta = +0.303/\text{year}$, $p = 0.016$) inpatients. In contrast, CR declined in paediatric outpatients ($\beta = -0.576/\text{year}$, $p = 0.045$). ESBLs were more frequent than CR (7.1%, 13,405/189,683). Among paediatric inpatients, ESBLs decreased, especially in adolescents ($\beta = -0.062/\text{year}$, $p = 0.032$). Among paediatric outpatients, ESBLs increased from 5.3% (957/18,777) in 2018 to 6.0% (1,131/18,891) in 2023 ($\beta = +0.003/\text{year}$, $p = 0.005$).

CONCLUSIONS

Increasing CR in paediatric inpatients– especially infants – alongside declining ESBLs may indicate selective pressure and a displacement effect, with decreased reliance on cephalosporins and increased use of last-resort antibiotics. Conversely, increasing ESBLs in outpatients reflect diverging AMR patterns between paediatric inpatient and outpatient groups, highlighting distinct dynamics and the need to strengthen paediatric-focused stewardship to preserve last-resort antibiotics.

KEYWORDS: AMR, Paediatrics, ESBL, Carbapenem resistance, logistic regression

ABSTRACT ID: 686

PRESENTED BY: Imme Roewer De Porto - Germany - roewer-de-portoi@rki.de

FIRESIDE SESSION 7

Day 2 | Thursday 20 November 11:00-12:30

Emerging and vector-borne diseases

PRESENTER

Justine Blanford

ABSTRACT

How has the spatial distribution of malaria changed in the past 20 years in Kenya?

J. Blanford¹

C. Kioko²

¹University Twente (UTwente)

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BACKGROUND

Malaria continues to rise worldwide, with over 263 million cases and more than 600,000 deaths reported during 2023. Geospatial information and technologies play a vital and central role in managing and reducing the burden of malaria. Here, we leverage malaria case data to show how the distribution of malaria has changed in Kenya over the past twenty years and how this change occurred with the use of different interventions.

METHODS

Twenty years of data on malaria clinical cases documented by the Malaria Atlas Project (MAP) were obtained for *Plasmodium falciparum* for Kenya between 2000 and 2020. Data are available annually. In addition, data on insecticide-treated nets (ITNs) and antimalarials were also obtained from MAP for the same period. Two space-time analyses were conducted to examine overall changes between 2000-2020 and then for each decade (2000-2009 and 2010-2020). The Emerging Hotspot Analysis (EHA) was used to identify the directional shift in malaria hotspot clusters while a Local Hotspot and Outlier Analysis (LHA) was used to identify significant clusters and outliers. For each cluster type ITNs and antimalaria use were examined.

RESULTS

Four main risk areas were identified. Two in the west along the Ugandan border (HH2 and HH3) and two along the coast (HH1 bordering Tanzania; HH4 bordering Somalia). Since 2010, malaria rates have increased in the northern and eastern part of Kenya, where two additional risk areas appeared. Overall, there has been an increase in bednet use and antimalarial use, plateauing around 2014.

CONCLUSIONS

The spatial distribution of malaria is changing in Kenya. Malaria is diminishing in well known malaria areas in southwestern and southeastern Kenya and rising in others. The changing distribution of malaria can be due to increases in local infrastructure developments, climate and political changes.

KEYWORDS: Malaria, antimalarials, spatial analysis, surveillance, geographic information systems, longterm effects

ABSTRACT ID: 58

PRESENTED BY: Justine Blanford - Netherlands - j.i.blanford@utwente.nl

FIRESIDE SESSION 7

Day 2 | Thursday 20 November 11:00-12:30

Emerging and vector-borne diseases

PRESENTER

Niamh McAuley

ABSTRACT

Risk factors for rodent-borne diseases: A cross-sectional study in rural Madagascar

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²University of Aberdeen (UoA)

BACKGROUND

Rodent-borne diseases (RBDs) pose a significant and underestimated threat to global health and the economy, particularly in low-income rural regions. In Madagascar, the invasive black rat (*Rattus rattus*) is a key reservoir for several zoonotic pathogens. This study aims to assess RBD prevalence and identify individual-level risk factors in rural communities.

METHODS

A cross-sectional study was conducted with 1056 participants across 20 villages. Blood samples were tested using enzyme-linked immunosorbent assays (ELISA) to detect IgG antibodies for leptospirosis, spotted fever group rickettsia (SFGR), typhus group rickettsia (TGR), and plague. Household surveys recorded demographic data, risk factors, and asset ownership. A pilot longitudinal component involved three repeated sampling points across 12 months in three villages. Data was analysed using generalised linear mixed models, with households and villages as random effects.

RESULTS

Seroprevalence was 8.6% for leptospirosis, 27.6% for SFGR, 7.4% for TGR, and 0.76% for plague. Seropositivity increased with age for leptospirosis, SFGR, and TGR. Males and those working in agriculture had significantly higher prevalence for leptospirosis and SFGR, but not for TGR. Regular bathing in freshwater was associated with higher risk of exposure to leptospirosis. SFGR exposure declined with increasing education, suggesting socioeconomic disparities in risk. In the longitudinal pilot, incidence rates were 1.8% for leptospirosis, 5.4% for SFGR, and 4.7% for TGR, with notable variation between villages.

CONCLUSIONS

RBDs are a significant yet under-recognised public health issue in rural Madagascar, with clear links to sex, occupation, and socioeconomic status. While this study identifies key risk patterns, it does not inform our understanding of long-term burden of RBDs. In response, a larger longitudinal study will launch in 2025, incorporating community- and clinic-based cohorts and cost-of-illness surveys to quantify both incidence and the economic impact of RBDs on vulnerable rural populations.

KEYWORDS: rodent disease, prevalence, cross-sectional studies, risk factors

ABSTRACT ID: 414

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FIRESIDE SESSION 7

Day 2 | Thursday 20 November 11:00-12:30

Emerging and vector-borne diseases

PRESENTER

Luca M. Zaeck

ABSTRACT

Serological evidence supports the transmission of clade Ib mpox virus by professional sex workers and spread within households in South Kivu, DRC

L. Zaeck¹

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BACKGROUND

The rapid spread of clade Ib mpox virus (MPXV) in Central Africa led to the declaration of a public health emergency of international concern by the World Health Organization in August 2024. As global smallpox vaccination efforts were halted around the 1980s, poxvirus-specific immunity among the general population became increasingly absent. With the Democratic Republic of the Congo (DRC) being the focal point of the ongoing outbreak, many questions remain regarding the seroprevalence of MPXV-specific antibodies, the extent of local clade Ib MPXV transmission in critical areas, and the role of sexual and non-sexual transmission.

METHODS

We developed serological assays to measure binding and clade Ib-specific neutralizing antibodies and report the first serological study performed in the South Kivu province of DRC. Sera were collected in November and December 2023 (n=120), and in May 2024 (n=48) from professional sex workers (PSW) and visitors of 25 bars with reports of mpox cases. Additionally, sera from 108 direct contacts of mpox cases from 34 households were collected between September 2023 and May 2024. Seropositivity was defined as a detectable titer in a cell lysate-based screening ELISA and confirmation by virus neutralization test.

RESULTS

We detected serological evidence for MPXV infection in 18% (November and December 2023) and 17% (May 2024) of the sera collected in bars, indicating that PSW played an important role in MPXV clade Ib transmission in this region. Serological evidence for MPXV infection was also found in at least one serum sample in 50% of households, including in nine households with seropositive minors, providing evidence for non-sexual close-contact household transmission.

CONCLUSIONS

This study emphasizes the importance of serological studies to comprehend the extent of the ongoing clade Ib MPXV outbreak, and provides evidence-based support to guide targeted vaccination strategies, particularly for high-risk groups.

KEYWORDS: Mpox (monkeypox), Monkeypox virus, Antibodies, Seroepidemiologic Studies, Disease Outbreaks, Democratic Republic of the Congo

ABSTRACT ID: 565

PRESENTED BY: Luca M. Zaeck - Netherlands - l.zaeck@erasmusmc.nl

FIRESIDE SESSION 7

Day 2 | Thursday 20 November 11:00-12:30

Emerging and vector-borne diseases

PRESENTER

Laura Bubba

ABSTRACT

A decade-long molecular epidemiological study of Enterovirus-C105 (2013–2023): Tracing its shift from rare detection to an outbreak in 2023 in Europe.

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BACKGROUND

Enterovirus (EV-) C105 is a non-polio enterovirus associated with respiratory infections, especially in children. Although previously rarely detected in Europe, a signal of its potential emergence was noted in 2023. Diagnostic challenges linked to mutations in the 5' untranslated region (UTR) region, commonly used for EV detection, were reported for EV-C105. To investigate the sudden increase and the virus's potential to spread more widely and cause severe disease, we have assessed this emergence and the genetic evolution of EV-C105 further.

METHODS

The European non-polio Enterovirus Network (ENPEN) laboratories were contacted to confirm and quantify EV-C105 circulation (2013–2023). Laboratories submitted aggregated data on case detections, age, clinical presentation, sample type, detection and typing methods. The same information was requested from those not reporting any EV-C105, to assess primer mismatches underlying possible zero-reporting. EV-C105 sequences (partial VP1 and complete genomes) were used for phylogenetic analysis and to study potential primer mismatches.

RESULTS

Twenty-three laboratories contributed data, with 14 laboratories from 9 countries reporting 138 EV-C105 cases. One hundred and eleven cases (80%) were detected in 2023, primarily in England (80/111; 72%). Clinical data for 42 cases revealed respiratory symptoms in 39 (93%) cases, and neurological signs in 3 (7%) cases; 103/138 (75%) cases were children <15 years old. Primers used in 11 laboratories, showed mismatches in the 5'UTR region. Two clades emerged in the 2023 upsurge: clade C1 (n=86), representing strains from multiple countries, and a new sublineage within clade C2 (n=20), predominantly from England (n=19).

CONCLUSIONS

This study highlights a significant European outbreak of EV-C105 in 2023. Primer mismatches in laboratories and the genetic evolution of EV-C105 illustrates its potential to emerge as a public health threat, emphasizing the necessity for ongoing genomic surveillance, diagnostic refinement, and early warning systems to enable timely interventions and mitigate future outbreaks.

KEYWORDS: non-polio enterovirus, enterovirus-C105, Europe, respiratory infections, outbreak

ABSTRACT ID: 635

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FIRESIDE SESSION 7

Day 2 | Thursday 20 November 11:00-12:30

Emerging and vector-borne diseases

PRESENTER

Luis Alberto Benegas Rodriguez

ABSTRACT

Characteristics of travellers who received post-exposure prophylaxis in a tertiary hospital in Barcelona after an animal-associated injury abroad

L. Benegas Rodriguez¹

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BACKGROUND

Rabies, a highly lethal and neglected tropical disease, remains enzootic in several popular tourist destinations. Returning travellers who sustain animal associated-injuries (AAIs) abroad require timely post-exposure prophylaxis (PEP) to prevent the onset of disease. However, various factors may hinder access to early vaccination. This study aimed to describe the characteristics of returning travellers who sought rabies PEP following an AAI abroad, at a tertiary hospital in Spain.

METHODS

We conducted a retrospective observational study at the vaccination centre of a tertiary hospital in Barcelona. We reviewed the records of international travellers who received PEP following an AAI abroad between 1 January 2023 and 31 March 2025. We extracted demographic, clinical, and exposure-related data from electronic health records. The descriptive analysis was conducted using RStudio to characterise patients, AAIs, and PEP management. The findings are preliminary.

RESULTS

We included a total of 146 travellers. The median age was 32 years (IQR 27–40); 53% were male and 44% were born overseas. Only 21% had received pre-travel advice at our centre, and 8.3% had received pre-exposure prophylaxis (PrEP). The majority (86%) had never received a rabies vaccine before. Most exposures occurred in South-East Asia (37%), followed by the Eastern Mediterranean (16%) and the Americas (14%). Most AAIs involved dogs (48%) and monkeys (27%) and the most common type of injury was due to bites (76%). Lower extremities were most affected (39%). The median time from AAI to first dose was 1 day (IQR 0–6). In 73% of cases, the first dose was given in the country of exposure; 31% received rabies immunoglobulin.

CONCLUSIONS

The observed gaps in prevention and variation in post-exposure care highlight persistent challenges in rabies risk mitigation for travellers. Strengthening access to timely care and reinforcing pre-travel guidance remain key priorities.

KEYWORDS: Rabies Vaccines, Post-Exposure Prophylaxis, Travel Medicine, Prevention and Control, Neglected Diseases

ABSTRACT ID: 734

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FIRESIDE SESSION 7

Day 2 | Thursday 20 November 11:00-12:30

Emerging and vector-borne diseases

PRESENTER

Katie Wrenn

ABSTRACT

National outbreak of iatrogenic botulism associated with cosmetic injections of botulinum neurotoxin-containing products in England, 2025

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BACKGROUND

Iatrogenic botulism is caused by the systemic spread of botulinum neurotoxin (BoNT) from therapeutic or cosmetic procedures. An outbreak of iatrogenic botulism following cosmetic BoNT injections occurred in England, over a four-month period (May-Aug 2025). We describe the outbreak investigation, including a case-control study to identify risk factors for illness and propose recommendations for minimising public health risk.

METHODS

The study population was adults (>18 years) in England who had received a cosmetic BoNT injection since 1st May 2025. We defined a confirmed case as a person with a clinical diagnosis of botulism and at least one compatible symptom (difficulty breathing, swallowing and/or changes in speech) within four weeks of a BoNT injection. Controls were recruited using a market research panel and self-completed an online questionnaire. Univariable logistic regression was used to determine risk factors for illness.

RESULTS

Overall, 42 cases (37/42 female (88%), median age 41 years (range 25-82)) were reported across five regions of England. Over half (30/42, 71%) were resident in the most deprived areas. Preliminary univariable results from the case-control study show that injection with an unlicensed product (OR=38.9, 95% CI 12.9-139), receiving an injection at home (OR=13.3, 95% CI 5.2-34.3) or the practitioner's home, (OR=15.1, 95% CI 6.7-35.2) and having more facial areas injected (4+ areas injected, OR=13.9, 95% CI 4.8-50.4) were associated with illness.

CONCLUSIONS

Study data suggest the cause of this outbreak was multifactorial, with both product and method of administration likely playing a role. Stronger regulation of cosmetic procedures should be introduced in the UK, where practitioners are currently not subject to any training or licensing requirements. Disrupting the supply of unlicensed products, as well as raising public awareness about the importance of choosing safe products and practitioners, will further help to reduce public health risk.

KEYWORDS: iatrogenic botulism; outbreak; botox; risk factors; cosmetic injections

ABSTRACT ID: 877

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FIRESIDE SESSION 8

Day 2 | Thursday 20 November 11:00-12:30

Food- and water-borne diseases

PRESENTER

Fatma Durmus

ABSTRACT

A foodborne outbreak of Salmonella Enteritidis in an institution – Honaz district, Denizli province, Turkiye, July 2024

F. Durmus¹

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¹General Directorate of Public Health, MoH

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BACKGROUND

Foodborne outbreaks pose a significant public health challenge. On July 22, 2024, we observed a notable rise in admissions for acute gastroenteritis symptoms specifically nausea, vomiting, abdominal pain, and diarrhoea at a facility housing 2,048 individuals (1,778 residents and 270 staff). In response, we initiated an investigation to identify the outbreak's source, causative agent, and to implement control measures.

METHODS

We conducted a retrospective cohort study, and interviewed 1761 residents and staff using a questionnaire on information on sociodemographic characteristics, symptoms, and meal items (soup, chicken, pasta, ayran). We defined a suspected case (n=1201) as a person who consumed lunch and exhibited at least one symptom of acute gastroenteritis. A probable case (n=755) was a suspected case with symptoms of vomiting and diarrhoea. We calculated attack rates and risk ratios with 95% confidence intervals (CIs) for probable cases. Adjusted odds ratios (ORadj) were derived through unconditional logistic regression that included soup, chicken, and pasta. Additionally, food (n=10), and stool (n=10) samples were tested by Real-Time Reverse Transcription–Polymerase Chain Reaction and culture.

RESULTS

The crude attack rate was 68.2% (n=1201/1761). Most common symptoms included diarrhoea (97.9%) abdominal pain (96.6%), nausea (87.6%), and vomiting (78.3%). The epidemic curve indicated a point source outbreak with a mean incubation time of 15±9.5 hours. The relative risk for consumption of pasta was 6.3 (95%CI:4.3-9.4), for chicken was 2.1(95%CI:1.5-2.9), and for soup was 1.4 (95%CI:1.2-1.6). After adjusting for soup and chicken, pasta remained significantly associated with illness (ORadj:46.3,95%CI:25.5-84.1) and a dose-response association was established (trend-test: p<0.001). Salmonella enteritidis was isolated from eight stool cultures, and one pasta sample.

CONCLUSIONS

The consumption of pasta contaminated with Salmonella enteritidis was the cause of this outbreak. However, we were unable to identify the source of the contamination. We recommended providing training for catering staff on hygiene practice and food safety.

KEYWORDS: Salmonella enteritidis, foodborne diseases, cohort studies, epidemiology

ABSTRACT ID: 153

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FIRESIDE SESSION 8

Day 2 | Thursday 20 November 11:00-12:30

Food- and water-borne diseases

PRESENTER

Ann Hoban

ABSTRACT

Multi-country outbreak of Salmonella Blockley, associated with tomato consumption in the United Kingdom, July to October 2024

A. Hoban¹

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BACKGROUND

In August 2024, a genetically related cluster of Salmonella Blockley (HC5_385614) was identified, with cases across England, Wales, and Scotland. Sharing of whole genome sequencing (WGS) data via an EU sharing platform identified further international cases. Salmonella Blockley is uncommon in the UK and cases are usually travel-associated. We undertook an outbreak investigation to identify the source.

METHODS

Cases were identified via routine analysis of WGS data, no signal of travel was associated with illness. Trawling questionnaires identified tomatoes as a possible vehicle of infection; a rapid case-control study was conducted to investigate this hypothesis, utilising case data from trawling questionnaires and pre-existing control data from a market research panel recruited for a previous Salmonella outbreak in 2023. Multivariable, first-penalised logistic regression was used to explore associations between illness, food exposures, and supermarket use. Microbiological investigations included testing of tomato samples taken from retailers for presence of Salmonella spp.

RESULTS

Phylogenetic analysis identified cases formed a distinct monophyletic clade. Between July-October 2024, 129 cases were identified in the UK, 56 cases in France and 30 cases in Germany. Twenty-nine cases and 87 controls from the UK were included in the analytical study. Tomato was most strongly associated with illness, eaten by 27/29 (93%) cases vs 52/86 (60%) controls (adjusted odds ratio (aOR) 3.80 (0.96 – 21.30)). Higher odds of tomato consumption and shopping at Supermarket A (aOR 10.75 (1.52 – 103.16)) was also observed in cases vs controls. Of 312 food samples, Salmonella spp was detected at a very low concentration in two samples (imported cherry tomato varieties) using PCR but not confirmed by culture.

CONCLUSIONS

The use of pre-existing case and control data allowed UKHSA to rapidly identify the likely food vehicle and supermarket associated with this domestic Salmonella Blockley outbreak. WGS continues to be useful tool to identify international spread.

KEYWORDS: Salmonella, Disease outbreak, Gastrointestinal Disease, foodborne disease

ABSTRACT ID: 710

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FIRESIDE SESSION 8

Day 2 | Thursday 20 November 11:00-12:30

Food- and water-borne diseases

PRESENTER

Celia Souque

ABSTRACT

Rapid genotyping of Salmonella using nanopore-only sequencing for outbreak investigation

C. Souque¹

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BACKGROUND

Whole genome sequencing of Salmonella using Illumina technology is a powerful tool for case identification during outbreak investigations. Long-read sequencing with Oxford Nanopore presents a promising alternative due to its speed and cost-effectiveness, albeit with the downside of high error rates which may wrongly exclude cases. Recent developments, however, have greatly increased Nanopore sequencing accuracy. In this study, we evaluated the accuracy and suitability of Nanopore-only sequencing for core genome multilocus sequence typing (cgMLST) of Salmonella during outbreak investigations.

METHODS

We selected 43 Salmonella isolates of six different serovars, representing both outbreak-associated and sporadic cases in Norway and previously sequenced using Illumina. Libraries were prepared using the Nanopore Rapid Barcoding kit and sequenced on a MinION flowcell. To evaluate performance, we tested different basecalling models (SUP vs HAC), filtering approaches (rasusa vs. filtlong), assemblers (raven, flye, and miniasm) and polishing models. For each resulting assembly, cgMLST was performed and allelic distances (AD) between Illumina and Nanopore assemblies were calculated.

RESULTS

Preliminary results from 19 isolates accurately clustered the outbreak samples using Nanopore-only assemblies. cgMLST typing was also in agreement with the Illumina references, with a maximum of one AD between the two technologies. Basecalling and polishing steps had the greatest impact on Nanopore genotyping accuracy, with the best performing options reducing average genotyping error by 0.71 and 0.98 AD respectively. In contrast, genotyping was unaffected by filtering method, assembler choice, or serovar. Finally, we found accurate genotyping could be obtained in as early as 5hrs of sequencing with Nanopore, compared to the 26h required for a full Illumina Nextseq run.

CONCLUSIONS

Nanopore-only sequencing is now a viable alternative to Illumina for Salmonella genotyping during outbreak investigations, offering comparable results in a rapid turnaround time. Implementation of Nanopore sequencing in public health laboratories may improve speed and permit immediate action during outbreak investigations

KEYWORDS: Nanopore Sequencing, Multilocus Sequence Typing, Salmonella, Disease Outbreaks

ABSTRACT ID: 361

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FIRESIDE SESSION 8

Day 2 | Thursday 20 November 11:00-12:30

Food- and water-borne diseases

PRESENTER

Grace King

ABSTRACT

A comparison of using online market panel members and traditional epidemiological methods in control recruitment for a case-control study during a national outbreak of STEC O145, United Kingdom.

G. King¹

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¹UK Health Security Agency

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^{14,15}Public Health Wales

¹⁶Public Health Agency

^{17,18}Public Health Scotland

BACKGROUND

National foodborne outbreaks of gastrointestinal disease require rapid case-control investigations to identify the source. Controls can be sourced from online market panels. The cost-effectiveness, representativeness and accuracy of these has not been evaluated since 2018. Here, we compare market panel controls to traditional controls in case-control recruitment during an outbreak of STEC O145 in the UK in 2024.

METHODS

Two case-control studies were conducted using online questionnaires for two different control groups a) Salmonella cases as case-controls and b) online market panel members. Controls were frequency matched on age, aiming for a 3:1 ratio. Both groups were compared on timeliness, cost and resources. The study findings were compared in a control-control analysis using firth logistic regression and false discovery rate (FDR) procedure to control for false positive results.

RESULTS

63 Salmonella case-controls and 93 panel controls were recruited. The final ratio of Salmonella controls to outbreak cases was 1.5:1 vs 2.2:1 for panel controls. Both groups did not reach the recruitment target for the younger adults age group despite extending survey time to 3 working days. Five staff members made 250 telephone calls, sent 26 emails and 206 text messages to recruit Salmonella cases. Salmonella case-controls had a nine-fold greater staff time to recruit and costed five times more than panel controls (£25.82 vs £4.99 per control). Both analytical studies identified the same variable as the outbreak source, with a similar odds ratios. There were no significant differences for exposures between the control groups following the FDR procedure.

CONCLUSIONS

This study demonstrates the value of both panels and case-controls where appropriate. The additional benefits in terms of cost and resource savings associated with panel controls justifies their use as standard procedure. We recommend exploring engagement with younger adult age groups that are difficult to recruit and assessing other methods to reach them.

KEYWORDS: Control Groups, Case-Control Studies, Disease Outbreaks, Gastrointestinal Diseases, Methods

ABSTRACT ID: 417

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FIRESIDE SESSION 8

Day 2 | Thursday 20 November 11:00-12:30

Food- and water-borne diseases

PRESENTER

Anika Meinen

ABSTRACT

Salmonella Infantis outbreak in young children caused by cashew butter with raspberry, Germany 2025

A. Meinen¹

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BACKGROUND

In May 2025, the National reference centre for salmonellosis and other enteric pathogens registered an unusual high number of Salmonella Infantis among young children prompting an immediate investigation in order to identify the outbreak vehicle and to protect this vulnerable population.

METHODS

Whole genome sequences were analysed by cgMLST. A reference sequence was shared internationally and cross-sectoral. We defined outbreak cases as 0 - 5 years old salmonellosis cases in Germany, with disease onset since April 2025, plus disease cases with an epidemiological link. Confirmed cases were those with isolates belonging to the outbreak cluster. We used descriptive epidemiology and exploratory patient interviews to generate a hypothesis. Results communicated to food safety authorities led to on-site inspections, sampling and analysis of food and environmental specimens.

RESULTS

In total, 147 outbreak cases were distributed all over Germany (median age: 1 year; age range 0-62 year). Females were slightly more affected than males (53% versus 47%). A high proportion of cases was hospitalized (69/118; 58%), partly with bloodstream infections. One child died. In other European countries outbreak cases occurred as well. In 73 of 80 interviews with cases' parents (first exploratory, later short interviews), consumption of cashew butter with raspberry distributed by a certain drugstore was named from which the outbreak strain was subsequently isolated. It had been distributed all over Germany. The suspected lots of this product, with a shelf life of one year, were probably not sufficiently heated. After recall, a public warning was published.

CONCLUSION

An unsuspecting food item caused a large outbreak mainly among young children; either due to special consumption patterns or different manifestation rates. Rapid sharing of data across sectors enabled timely measures. To date the product is no longer available on the market and the outbreak was stopped. We recommend heating during the production of such foods.

KEYWORDS: Salmonella Infantis; outbreak; ,rasperry,children

ABSTRACT ID: 856

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FIRESIDE SESSION 8

Day 2 | Thursday 20 November 11:00-12:30

Food- and water-borne diseases

PRESENTER

Joana Vidal-Castro

ABSTRACT

Disentangling two large hepatitis A outbreaks in a very low endemicity country: Portugal, Oct 2023–Aug 2025

J. Vidal-Castro¹

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BACKGROUND

Hepatitis A has historically a very low incidence in Portugal, with most cases being imported. Since October 2023, we have seen the largest rise in reported cases since 1996 . Genomic characterisation confirmed two distinct and concurrent autochthonous outbreaks in different regions. This analysis aims to disentangle their epidemiological profiles to best inform tailored outbreak responses.

METHODS

We conducted two separate retrospective case-case analyses using data from Portugal's National Epidemiological Surveillance System (01/01/2020-31/08/2025). Baseline cases (01/01/2020–06/10/2023) were compared with Outbreak 1 (began in 06/10/2023 in Lisbon/Porto) and Outbreak 2 (began in 30/04/2024 in southern Portugal) cases . Crude odds ratios (OR) and 95% confidence intervals (CI) were calculated for sociodemographic and contact history characteristics.

RESULTS

Baseline included 97 cases. Outbreak 1 comprised 500 cases of which 53% reported sexual transmission, 40% self-identified as gay, bisexual or other men who have sex with men (GBMSM). Compared with baseline, cases were more often male (OR=4.8; 95%CI:2.9–7.8), aged 18–44 years (OR=8.5; 95%CI:4.4–16.5), GBMSM (OR=68.4; 95%CI:15.1–1210), and had Brazilian nationality (OR=14.9; 95%CI:4.6–91.4). Outbreak 2 involved 554 cases, most were children (65% aged 0–17). Compared with baseline, they were more likely to report contact with a confirmed case (OR=21.5; 95%CI:11.1–45.2), non-sexual person-to-person transmission (OR=27.8, 95%CI:11.9-69.3) and less likely to have other nationality than Portuguese or Brazilian (OR=0.08; 95%CI:0.03–0.19).

CONCLUSIONS

Our analysis of these large concurrent hepatitis A outbreaks demonstrates distinct epidemiological patterns. These differences call for differentiated interventions for outbreaks, even when caused by the same pathogen, as targeted vaccination and awareness in GBMSM communities for Outbreak 1, and systematic contact tracing, vaccination and hygiene promotion in pediatric contexts for Outbreak 2. Our results provide timely evidence to inform national control and European preparedness efforts.

KEYWORDS: Hepatitis A, Disease Outbreaks, Public Health Practice, Surveillance, Epidemiological Monitoring

ABSTRACT ID: 842

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FIRESIDE SESSION 9

Day 2 | Thursday 20 November | 14:00-15:30

One Health

PRESENTER

Juthathip Khongpetch

ABSTRACT

Seasonal trends of sand fly abundance and Leishmania infection: The case of Bologna province, Italy (2016–2023)

J. Khongpetch¹

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BACKGROUND

Leishmaniasis, a vector-borne disease transmitted by sand flies, is expanding in Europe, including Italy, likely due to climate-driven ecological shifts. This study uses data from Bologna province (2016–2023) to examine the links between meteorological factors before sand fly activity period, sand fly abundance, Leishmania infection in vectors, and human visceral leishmaniasis (VL) cases.

METHODS

From July–September (2016–2023), sand fly abundance was defined as the highest number of sand flies captured per trap-night. Yearly abundance was calculated as the average of these monthly maxima. Leishmania infection rates were estimated with Maximum Likelihood Estimation, using the number of positive and tested pools and the average pool size. Yearly infection rates were computed from pooled data across July–September. Averages of temperature, humidity, and cumulative precipitation were calculated for each year from March–June. Spearman's correlation test was then used to examine relationships between meteorological factors, sand fly abundance, Leishmania infection rates, and human VL cases in the following year.

RESULTS

Sand fly abundance peaked between July and August, followed by a peak infection rate about one month later. Sand fly abundance was negatively correlated with spring cumulative precipitation ($r: -0.93$, 95% CI: $-1.00, -0.62$) and relative humidity ($r: -0.81$, 95% CI: $-1.00, -0.29$). In contrast, a positive correlation was observed between yearly sand fly abundance and the number of VL cases in the following year ($r: 0.82$, 95% CI: $0.34, 1.00$). A negative correlation was also found between spring cumulative precipitation and the number of VL cases in the following year ($r: -0.71$, 95% CI: $-1.00, -0.07$).

CONCLUSIONS

Reduced spring precipitation may increase sand fly abundance and elevate VL risk. These findings suggest meteorological variables could serve as early indicators for leishmaniasis risk. Strengthening public health responses, such as awareness campaigns and repellent use, during drier years may improve disease prevention, pending confirmation in other settings.

KEYWORDS: Leishmania, Sand fly, Climate change, Vector-borne diseases, One health

ABSTRACT ID: 253

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FIRESIDE SESSION 9

Day 2 | Thursday 20 November | 14:00-15:30

One Health

PRESENTER

Ameze Simbo

ABSTRACT

Swimmer's itch: a One Health approach to assess an emerging zoonosis at a reservoir in Wales

A. Simbo¹

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^{7,9}Public Health Wales (PHW)

BACKGROUND

Cercarial dermatitis, commonly known as swimmer's itch, is a papular rash caused by skin-penetrating larvae of avian schistosomes (zoonotic parasites), shed by intermediate snail hosts. In July 2023, control measures were implemented at a Welsh reservoir after swimmers reported such skin reactions. The following summer, we took a One Health approach to determine the prevalence of skin reactions and cercariae at the site.

METHODS

We surveyed swimmers on exposures and symptoms related to swimmer's itch via the reservoir online booking system (26/06/2024-23/12/2024). We compared the prevalence of episodes reported as "unusual skin changes" against exposures in a univariate analysis. We also performed qPCR-based cercariometry on 25L water samples taken bi-weekly from the reservoir (08/07/2024-09/12/2024). Schistosome larvae DNA were quantified as gene copies per 25L (gc/25L).

RESULTS

Among 6,574 bookings, we received 291 responses (4.4% response rate). Prevalence of episodes among respondents was 13.4% (39/291), of which 25/39 (64.1%) reported pimple-like spots. Episode prevalence was higher in females (PR=2.4, 95%CI:1.1–5.3, p<0.05) and lower in those wearing a full wetsuit (PR=0.5, 95%CI:0.3–0.8, p<0.05). Episodes were reported throughout the summer, with the highest reports occurring in August (n=19). Episodes were also reported in September (n=3) and October (n=2). Schistosome larvae concentrations fluctuated in the water samples, with steady increases observed in August (range:317-1150 gc/25L), and large spikes in October (range:0-3,285 gc/25L) and November (range:0-2,550 gc/25L).

CONCLUSIONS

Coinciding reports of skin reactions and the presence of schistosome larvae at the reservoir suggests that symptoms were consistent with swimmer's itch. Wearing a full wetsuit reduced the likelihood of symptoms. Although swimmer's itch is known as a summer ailment, the presence of cercariae in the winter months suggests the risks persist all year round. We recommend continuous environmental monitoring of schistosome activity to assess the risks to swimmers.

KEYWORDS: Zoonoses, Parasitic Skin Diseases, Swimming, One Health, Dermatitis, Environmental Monitoring, Prevalence

ABSTRACT ID: 419

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FIRESIDE SESSION 9

Day 2 | Thursday 20 November | 14:00-15:30

One Health

PRESENTER

Allegra Chatterjee

ABSTRACT

Rising scabies incidence in Spain, 2011–2023: a retrospective observational analysis of four national data sources

A. Chatterjee¹

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BACKGROUND

Scabies is a Neglected Tropical Disease which is not notifiable, therefore estimating the true incidence is challenging. However, over the past 10-20 years large rises have been observed across Europe, including Spain, with a shift in the profile of affected individuals. We aimed to characterise scabies epidemiology and identify potential risk settings in Spain from 2011–2023.

METHODS

We triangulated national data on primary care appointments, hospital admissions, occupational cases, and outbreaks and calculated mean annual incidence rates (IRs) per million for each source. We used joinpoint regression to calculate average annual percentage change (APC) in IR to identify significant trend changes. Time-series analysis explored seasonality in hospital admissions. Attack rates and duration including interquartile range (IQR) of outbreaks were calculated.

RESULTS

IR increased across all sources from 2011–2023, with marked acceleration from 2020–21. The largest rise occurred in primary care, where APC in IR increased from 23% (95%CI:7-32) in 2011–2020 to 66% (95%CI:48-97) in 2020–2023. IR was highest amongst 15-24-year-olds attending primary care (IR=3,311/1,000,000). Hospitalisation IR was highest among >65-year-olds (IR=17/1,000,000) and peaked each January. The Balearic Islands (IR=5,209/1,000,000) and Canary Islands (IR=2,971/1,000,000) had the highest primary care IR. Amongst occupational cases, 82% were in social- or healthcare settings. Of reported outbreaks, 40% occurred in households and 27% in nursing homes. Highest attack rates were in households (median=75%; IQR=57–100) and longest outbreaks occurred in healthcare settings (median=54 days; IQR=0.5–74).

CONCLUSIONS

The surge in scabies incidence in Spain, particularly since 2020, aligns with broader European trends. Potential drivers include socio-economic shifts, increasing sexual transmission, tourism, climate-related factors, and treatment resistance. Highest incidence among young adults, the elderly, and healthcare workers suggest enhanced surveillance and targeted interventions for those groups could mitigate spread. Analytical studies to identify risk factors could better inform prevention, diagnosis, and treatment of scabies.

KEYWORDS: scabies, *Sarcoptes scabiei*, Neglected Tropical Disease, Spain

ABSTRACT ID: 418

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FIRESIDE SESSION 9

Day 2 | Thursday 20 November | 14:00-15:30

One Health

PRESENTER

Antonio Sciurti

ABSTRACT

Seasonality and effects of climatic exposures on community-acquired Legionnaires' Disease incidence: an evaluation of the Italian surveillance data, 2005-2022

A. Sciurti¹

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BACKGROUND

In recent years, community-acquired Legionnaires' Disease (LD) incidence has risen globally and in Europe. Climatic conditions are increasingly recognized as potential contributors to this trend, yet evidence from high-incidence countries like Italy remains limited. This study aimed to evaluate community-acquired LD seasonality at a national level, and effects of climatic exposures – temperature, relative humidity, and precipitation – on weekly LD incidence at a municipality level in Italy.

METHODS

Community-acquired LD cases reported in Italy from 2005 to 2022 were included. Climatic data were sourced from the VHR-REA IT dataset. Seasonality of LD was assessed at a national level, while a Case Time-Series design with Distributed Lag Non-Linear Models was used to assess the 10 to 1-week lagged effects of climatic exposures on weekly LD incidence at a municipality level.

RESULTS

24,677 community-acquired LD cases were included. LD incidence showed a clear seasonal trend, peaking in autumn (week 40) and dipping in early spring (week 10), with a peak-to-trough ratio of 3.36 (95%CI: 2.24–5.06). The effect of temperature was more pronounced in earlier weeks, with higher temperatures associated with higher incidence [Incidence Rate Ratio (IRR) for a 5°C increase ten weeks before: 1.38, 95%CI: 1.26–1.52]. A similar, but less pronounced, pattern was observed for relative humidity (IRR for a 5% increase: 1.15, 1.08–1.23, ten weeks before), while the effect of precipitation was more evident in closer weeks (IRR for a 5mm increase: 1.08, 1.06–1.10, one week before). Similar results were found when restricting the analysis to individuals aged ≥60.

CONCLUSIONS

These patterns suggest that temperature and humidity may contribute to the environmental proliferation of Legionella over longer periods, while precipitation may act in the weeks immediately preceding diagnosis, by favoring mobilization and aerosolization from environmental reservoirs.

KEYWORDS: Legionnaires' Disease, Climatic Processes, Public Health Surveillance, Temperature, Humidity, Rain

ABSTRACT ID: 476

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FIRESIDE SESSION 9

Day 2 | Thursday 20 November | 14:00-15:30

One Health

PRESENTER

Bernadette Walter

ABSTRACT

Effectiveness of community trainings for population-based control of *Aedes albopictus*: Results of a pilot project in a town in Baden-Wuerttemberg, Germany in 2024

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BACKGROUND

The Asian tiger mosquito, *Aedes albopictus*, is a competent vector for arboviruses. Its successful establishment in Baden-Wuerttemberg, Germany presents a public health threat. As current measures face limitations due to labour-intensity and high costs, new strategies are needed. We evaluated the effectiveness of community trainings in reducing *Ae. albopictus* density in a town in Baden-Wuerttemberg, Germany, in 2024, to develop a community-based control strategy.

METHODS

We defined an intervention and an adjacent control area, similar in size and urban structure. Previous monitoring showed similar *Ae. albopictus* infestation in both areas. The municipality provided mosquito larvicides and access to information on breeding site control to every resident. In addition, residents in the intervention area were invited to in-person vector control trainings in April. We installed 45 egg-laying traps in May, spatially distributed throughout both areas. Eggs of *Ae. albopictus* were quantified in each trap biweekly between June and October, serving as a proxy for *Ae. albopictus* density. To assess the effect of the intervention on egg counts, we used a generalized linear mixed model with a negative binomial distribution, including area type and calendar week as fixed effects and accounting for inter-trap variability with a random effect.

RESULTS

Of 810 residents in the intervention area, 77 (9.5%) participated in a training. Median egg count over the entire monitoring period was 20 (IQR 0-97) in the intervention versus 46 (IQR 0-178) in the control area. Traps in the intervention area showed a statistically significant 38% reduction in egg counts (Rate Ratio=0.62, p=0.02).

CONCLUSIONS

Despite the small proportion of residents who participated in a training, the intervention was associated with a significant reduction in *Ae. albopictus* density. These findings indicate that community trainings may be a low-cost, scalable tool for mosquito control. Subject to further investigations, we recommend implementation of such trainings in affected areas.

KEYWORDS: Environment and Public Health, Climate Change, Vector Borne Diseases, Mosquito Vectors, *Aedes albopictus*, Vector Control

ABSTRACT ID: 150

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FIRESIDE SESSION 9

Day 2 | Thursday 20 November | 14:00-15:30

One Health

PRESENTER

Yasemin Inaç

ABSTRACT

Assessing the timeliness of the seasonal surveillance system for imported cases of dengue, chikungunya, and Zika in mainland France (2019–2024) at the national and regional level

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BACKGROUND

Since *Aedes albopictus* was detected in mainland France in 2003, seasonal surveillance (May–November) for dengue, chikungunya, and Zika has aimed to detect imported cases and prevent transmission during periods of high mosquito density. We assessed the timeliness of the surveillance system for imported cases at national and regional levels, and its development over time.

METHODS

We analysed cases from 2019–2024, calculating median time-intervals in days for key moments: symptom onset to sample collection, sample collection to test result, result to notification, notification to classification (probable/confirmed), and notification to vector control. We used multivariable linear regression to assess changes over time and by region (north, central [reference], south). Cases included probable (symptomatic with virus-specific IgM) and confirmed (RT-PCR, antigen detection, or IgG seroconversion/fourfold rise). Imported cases had travel to endemic areas within 15 days before symptom onset.

RESULTS

From 2019–2024, 6,874 imported cases were reported. The median time-interval from symptom onset to sample collection was 5 days, decreasing from 2019–2024 ($p<0.001$), with no regional differences. Sample collection to result took 6 days, decreasing across regions ($p<0.001$). Test result to notification was 2 days, improving only in the south ($p<0.001$). Notification to classification was 1 day, decreasing in the south ($p<0.001$). Notification to vector control was 1 day, decreasing overall from 2019–2024 ($p<0.001$) but increasing in the north ($p<0.001$).

CONCLUSIONS

Timeliness varied across the system, with national improvements observed; however, in the north, response times increased for two intervals. Regional health authorities can implement actions to address timeliness for these intervals, e.g. improving test result reporting through data feedback and addressing notification delays with outbreak simulations. Additionally, at the national and regional level, improved awareness among clinicians and travellers can ameliorate the time to sample collection and reduce the risk of autochthonous outbreaks.

KEYWORDS: Public Health Surveillance, France, Vector Borne Diseases, Arboviruses, Aedes

ABSTRACT ID: 588

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FIRESIDE SESSION 10

Day 3 | Friday 21 November | 11:00-12:30

Strengthening epidemic intelligence and surveillance

PRESENTER

Miriam Saso

ABSTRACT

Building resilient intelligence networks for Europe: strengthening governance of evidence for pandemic preparedness

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BACKGROUND

The COVID-19 pandemic and previous research highlighted the importance of intelligence networks that do not simply collect data but enable its effective translation into policy. However, many countries lacked structured processes for integrating evidence into real-time responses, resulting in fragmented and delayed actions. Responding to this challenge, we have examined how scientific evidence informed decision-making during the COVID-19 crisis in eight European countries. Our objective was to identify the governance structures, advisory mechanisms, and information flows that enabled or hindered the use of evidence in pandemic response, and to draw lessons that can inform the strengthening of intelligence networks in Europe.

METHODS

A systematic literature review and qualitative analysis were performed to identify strengths, gaps and lessons learnt from the advisory processes in the eight selected countries during COVID-19. Findings were supplemented by national and international evaluations, advisory body reports and interviews with experts and policymakers directly involved in the pandemic response.

RESULTS

These insights informed the development of a conceptual framework which will guide the design and evaluation of governance structures for pandemic intelligence networks. Several enablers of effective governance emerged, including: clearly defined legal mandates, formalised roles and responsibilities between experts and policymakers, advisory body independence, and transparent expert selection processes. Conversely, we found that persistent barriers such as fragmented coordination leading to duplication of work, limited integration of diverse disciplines, and a lack of structural resourcing impeded the timely and coherent use of evidence.

CONCLUSIONS

Building resilient and trusted pandemic response systems requires long-term investment in evidence-to-policy processes, fundamental for developing people-centred policies and protecting population health. The lessons from COVID-19 show that resilience is built between pandemics, not during them. Intelligence networks, grounded in interdisciplinary collaboration and supported by structured coordination, must become a core function of everyday public health, not just tools activated in times of crisis.

KEYWORDS: Pandemic Preparedness, Knowledge Translation, Public Health, Policy

ABSTRACT ID: 103

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FIRESIDE SESSION 10

Day 3 | Friday 21 November | 11:00-12:30

Strengthening epidemic intelligence and surveillance

PRESENTER

Laura Espinosa

ABSTRACT

Finding the needle in the haystack: using machine learning to detect signals of public health threats in the Epidemic Intelligence from Open Sources

L. Espinosa¹

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BACKGROUND

The European Centre for Disease Prevention and Control (ECDC) monitors the Epidemic Intelligence from Open Sources (EIOS) system daily, which collects and processes articles in near-real-time from several sources to detect potential public health threats. EI analysts must screen thousands of articles related to European signals on infectious diseases every day. This study aimed to support the prioritisation of articles screening and the detection of small signals, and assess its usefulness during the morning screening.

METHODS

We built a Python application using open-source technology to cluster EIOS articles, through unsupervised machine learning and natural language processing, and to detect anomalies in primary (based on tags, country and month) and secondary clusters (based on primary clusters and article title/description). We collected data on EIOS articles, clusters and anomalies between 16 and 22 April 2025 and evaluated the relevance of anomalies according to ECDC mandate.

RESULTS

We collected 7,715 deduplicated EIOS items, identifying 746 primary and 364 secondary anomalies. Most of the anomalies were not relevant: 96.2% of primary and 60.9% of secondary anomalies and most were not aligned with the ECDC mandate. Among the relevant anomalies, 12.5% (primary) and 20% (secondary) were not detected through manual EIOS screening, and the events or information included in these articles were shared internally or included in the daily EI reports.

CONCLUSIONS

While most anomalies were not relevant, this proof-of-concept solution showed that anomaly detection can complement EIOS manual screening by identifying otherwise undetected signals of public health importance. It highlighted the need to refine the filtering settings in the specific EIOS board used to reduce the number of irrelevant anomalies flagged by the tool. Future work includes the assessment of integrating the tool into epidemic intelligence workflows, exploring its scalability to longer time periods and broader geographic scopes, and further improving its precision.

KEYWORDS: machine learning, natural language processing, epidemic intelligence, surveillance

ABSTRACT ID: 379

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FIRESIDE SESSION 10

Day 3 | Friday 21 November | 11:00-12:30

Strengthening epidemic intelligence and surveillance

PRESENTER

Thomas Rowland

ABSTRACT

Community stool survey following detection of poliovirus in the environment in London, United Kingdom, October 2022 to April 2023

T. Rowland¹

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^{6,7,8}UKHSA and Manchester University Hospitals NHS Trust Medical Microbiology Partnership

^{9,10}Barts Health NHS Trust

BACKGROUND

Since 2024 vaccine-derived polioviruses (VDPVs) have been detected in wastewater in five European countries (Finland, Germany, Poland, Spain and the United Kingdom (UK)), but no cases have been identified. Following an outbreak, the World Health Organization (WHO) recommends a community stool survey to identify further cases. However, only one prior study reports a community survey based on environmental surveillance without an index case. This study aimed to opportunistically sample children living in the area of environmental detection in London, UK, during a similar cross-border environmental detection event involving Israel, the United States of America and the UK in 2022.

METHODS

We implemented an opportunistic, cross-sectional survey in areas where environmental surveillance indicated sustained VDPV transmission between October 2022 and April 2023. Residual stool samples taken from children < 16 years living in the area of wastewater detection presenting to primary or secondary healthcare were examined for enteroviruses, including poliovirus. Methods for poliovirus detection recommended by WHO, including virus isolation in cell culture, PCR and molecular characterisation, were applied to residual stool material on a daily basis with real-time clinical reporting.

RESULTS

We examined 1,251 stool samples from 1,051 children presenting to healthcare with illness over a 6-month period. A range of enteroviruses from groups A, B and C were found, but no poliovirus was detected. Documented polio vaccination coverage was high: between 95% and 98% in under 5-year-olds, and higher than the reported local vaccination rates (between 85% and 87%).

CONCLUSIONS

Poliovirus was not widespread in the area of environmental isolation. When poliovirus is detected in sewage but no cases are identified, opportunistically testing stools collected through routine clinical practice is a practical approach to looking for cases and can be rapidly implemented. However, untargeted sampling may not adequately capture populations at highest risk because of uneven vaccination coverage in the area under investigation.

KEYWORDS: poliovirus; , VDPV2,outbreak investigation,surveillance

ABSTRACT ID: 475

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FIRESIDE SESSION 10

Day 3 | Friday 21 November | 11:00-12:30

Strengthening epidemic intelligence and surveillance

PRESENTER

Rosaline van den Berg

ABSTRACT

Paper-based surveillance for infectious diseases in Dutch childcare: added value or added burden?

R. Van Den Berg¹

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BACKGROUND

Child daycare centres have increased risk for infectious disease transmission. In the Netherlands, these centres are legally required to report unusually high numbers of infections to Public Health Service (PHS). However, underreporting is common, limiting timely public health interventions. To improve surveillance and enable timely public health interventions in childcare settings, we piloted a paper-based syndromic surveillance system to monitor infectious disease trends over time.

METHODS

Large childcare centres (>75th percentile) in one Dutch PHS region (~470,000 population) were invited to participate. Staff recorded weekly counts of children (0–4 years) and staff with respiratory, skin, and gastrointestinal infections during 16 weeks in summer and winter. Incidence rates per 100 persons/week were calculated and compared between seasons (Wilcoxon signed rank test, on childcare centre level).

RESULTS

Twenty-six centres (2,480 children) participated in summer (21 May–12 July); 23 (2,208 children) in winter (21 October–13 December 2024). PHS received 7 mandatory infectious disease notifications in summer and 4 in winter from participating centres. Weekly tallies showed a median of 17 symptomatic persons/week/centre (IQR 8-28.25; incidence 18.9/100 persons/week) in winter and 5 (IQR 0.75-11; incidence 8.4/100 persons/week) in summer ($p=0.366$). Respiratory infections dominated in both seasons (winter: 13.1/100 persons/week; summer: 4.9/100 persons/week; $p=0.266$). Skin infections were more frequent in summer (2.3 vs 1.4/100 persons/week in winter; $p=0.008$), while gastroenteritis symptoms peaked in winter (2.5 vs 1.1/100 persons/week in summer; $p=0.153$) – as expected.

CONCLUSIONS

This simple paper-based surveillance system provided valuable insights in the incidence of infectious diseases in child daycare centres, revealing under-recognised illness trends missed by mandatory public health notifications. Notably, the number of respiratory symptoms reported during summer exceeded expectations based on national surveillance data. However, childcare staff perceived the paper-based surveillance system burdensome. Future research should focus on developing innovative, low-burden (digital) surveillance methods tailored to childcare settings.

KEYWORDS: child daycare, surveillance, communicable diseases, infectious diseases, incidence

ABSTRACT ID: 693

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FIRESIDE SESSION 10

Day 3 | Friday 21 November | 11:00-12:30

Strengthening epidemic intelligence and surveillance

PRESENTER

Beth Savagar

ABSTRACT

Harmonising the surveillance of respiratory viruses to monitor activity levels

B. Savagar¹

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BACKGROUND

The co-circulation of Influenza, RSV and COVID-19 in England demands integrated surveillance across respiratory viruses (RV) and epidemiological indicators. Simultaneously monitoring activity and integrating severity assessments is critical to inform public health policy and assess healthcare systems impacts. Activity level thresholds provide easily understandable metrics which are consistent and comparable across RV and indicators facilitating harmonised surveillance. Here, we develop an integrated approach to RV surveillance using activity level thresholds, aiming to apply established and novel threshold setting methods to monitor RV activity in England during the 2024-2025 winter season and to inform public health messaging and policy.

METHODS

RV surveillance systems were reviewed and suitable epidemiological indicators identified. Overall and age-stratified activity level thresholds were computed using either the established Moving Epidemic Method (MEM), or the novel Mean-Standard Deviation Method (MSD), for RV indicators with 5+ and 1+ years' of available historical data respectively. Both methods produced 5 activity level thresholds for each indicator: baseline, low, medium, high and very high which were applied to the 2024-2025 season's data.

RESULTS

Applying RV thresholds across viruses and indicators enabled harmonized surveillance throughout the season revealing sequential waves of RV with "baseline" COVID-19 activity throughout the winter underlying a "medium" RSV peak in late November and a "high" influenza peak in mid-December. Activity level thresholds directly informed public health messaging via an internal report, official statistics publications and social media communications, and shaped policy, including the transition of influenza activity from "baseline" to "low" across indicators denoting the start of the season and triggering antiviral prescribing.

CONCLUSIONS

Harmonising respiratory virus surveillance using threshold setting methods enabled simultaneous monitoring of RV activity and integrated and comparable severity assessment. Thresholds indicated the intensity of RV (co-)circulation and potential healthcare service impacts, representing a key tool for informing public health messaging and policy during the 2024-2025 season.

KEYWORDS: Respiratory virus surveillance, epidemic thresholds, influenza, COVID-19, RSV, moving epidemic method, mean standard deviation method

ABSTRACT ID: 717

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FIRESIDE SESSION 10

Day 3 | Friday 21 November | 11:00-12:30

Strengthening epidemic intelligence and surveillance

PRESENTER

David Kelly

ABSTRACT

The OECD PaRIS survey in 18 countries estimates that 7.2% of primary care patients aged 45 and older have experienced Long COVID as of 2024

D. Kelly¹

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BACKGROUND

Owing to lack of routine surveillance, Long COVID remains an under-recognised consequence of the COVID-19 pandemic. To better inform health policy, we used the OECD PaRIS survey to estimate the prevalence and patient-reported health outcomes of Long COVID.

METHODS

OECD PaRIS surveyed primary care patients aged 45 years and older in 18 countries from May 2023 to January 2024. Participants completed a self-administered questionnaire on sociodemographic characteristics, symptoms and duration of COVID-19, and employment status. We defined Long COVID using the World Health Organization case definition as symptoms persisting more than 3 months post-initial SARS-CoV-2 infection. We calculated Long COVID prevalence as the percentage of patients who fulfilled the Long COVID case definition divided by the total number of patients in the survey. We used a multilevel model to provide adjusted estimates of Long COVID prevalence, severe fatigue, and being unemployed or on sick leave.

RESULTS

In total 103,009 primary care patients participated, 56,017 (54.4%) reported ever having a COVID-19 infection, and 7,787 fulfilled the Long COVID case definition. The estimated prevalence of ever having Long COVID was 7.2% [CI 6.3–8.2], ranging from 3.9% [CI 3.3–4.7] in Greece to 10.8% [CI 9.7–12.0] in Norway. At the time of survey, 5.1% [CI 4.5 – 5.9] reported persisting Long COVID symptoms. The prevalence of Long COVID was significantly higher ($p < 0.001$) among patients who were female, younger (aged 45–54), of higher educational level, and living with chronic conditions. Patients with Long COVID reported higher rates of severe fatigue (20.3% [CI 18.0–22.9] versus 10.2% [CI 9.0–11.6]) and being unemployed or on sick leave (13.3% [CI 11.3–15.6] versus 10.8% [CI 9.2–12.8]), compared to those without.

CONCLUSIONS

The multi-country survey confirms that Long COVID is a prevalent condition in the primary care population in 2024, for which the long-term epidemiology and public health impacts remain uncertain and require continued surveillance.

KEYWORDS: surveillance, COVID-19, Long COVID, primary care

ABSTRACT ID: 179

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FIRESIDE SESSION 11

Day 3 | Friday 21 November | 11:00-12:30

Blood-borne and sexually transmitted infections

PRESENTER

Marta Bertran

ABSTRACT

New nationwide surveillance of chlamydia-related long-term complications using hospitalization data, The Netherlands, 2015-2022

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BACKGROUND

Untreated chlamydia infection in women can cause pelvic inflammatory disease (PID), tubal factor infertility, and ectopic pregnancy (EP). Since 2008, sexual health centers have screened for chlamydia, the most common bacterial sexually transmitted infection in the Netherlands, regardless of symptoms. In 2025, asymptomatic testing was discontinued due to unclear evidence of its effectiveness on preventing ongoing transmission or complications. We established a national surveillance system to monitor chlamydia-related complications and provide a baseline for assessing any unintended consequences of the policy change.

METHODS

We extracted the annual number of women with a primary diagnosis from the Dutch Hospital Data (DHD), which excludes outpatient visits, using International Classification of disease tenth revision (ICD-10) codes for PID (N70,N71,N72,N73,A56.1+N74.4), infertility (N97), and EP (O00) between 2015-2022. 2023-2024 data were unavailable given a two-year data lag. We estimated annual incidence per 100,000 population for PID and infertility, and per 1,000 live births for EP among women aged 15-44 years. We estimated the trends using linear regression.

RESULTS

Between 2015-2022, 656-984 (median=900; incidence=21.5/100,000) women were hospitalized with PID, 1413-3914 (median=1710; incidence=40.8/100,000) women were diagnosed with infertility, and 1592-1712 (median=1619; incidence= 9.6/1,000) with EP per year. PID incidence decreased by 1.7/100,000 (95%CI: -2.6 to -0.8; p=0.003) per year and infertility incidence decreased by 9.9/100,000 (95%CI: -15.2 to -4.5; p=0.003) per year. Incidence was stable for EP (-0.04/1,000; 95%CI:-0.1 to 0.05; p=0.3).

CONCLUSIONS

Downward trends were observed for PID and infertility. Codes were not chlamydia-specific and may be attributed to other causes, such as gonorrheal infection. We recommend shortening the DHD data lag for timely surveillance and initially focusing on PID surveillance which manifests earlier after infection, to assess whether discontinuing asymptomatic testing would lead to a reversal of downward trends. Additional data sources for PID, such as primary care data, should be considered given potential underestimation.

KEYWORDS: Chlamydia,STI,Infertility,Ectopic pregnancy,Complications

ABSTRACT ID: 204

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FIRESIDE SESSION 11

Day 3 | Friday 21 November | 11:00-12:30

Blood-borne and sexually transmitted infections

PRESENTER

Samuel E. Schulz-Medina

ABSTRACT

Targeting risk by connecting the dots: Molecular HIV transmission clusters enriched with people who use crystal meth in Mexico City (2022–2024) reveal behavioural and structural risk patterns

S. Schulz-Medina¹

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BACKGROUND

Crystal methamphetamine (CM) use increases HIV transmission risk through injection practices and modified sexual behaviors. Characterising people who use crystal methamphetamine (PWUCM) in molecular epidemiological studies is critical to inform targeted HIV prevention. We aimed to assess socio-demographic, clinical, and behavioural factors associated with PWUCM and their role in HIV transmission network in Mexico City (2022–2024).

Methods

We collected socio-clinical metadata and HIV pol sequences from individuals tested for HIV at Mexico City's largest testing center. Genetic transmission networks were inferred using Tamura-Nei genetic distances (threshold: 1.5%). Multivariable logistic regression models were developed to identify factors associated with PWUCM, adjusting for covariates selected via bivariate analysis and theoretical relevance. Cluster characteristics were compared based on PWUCM presence.

RESULTS

Among 5,773 individuals, 672 (11.6%) reported CM use. PWUCM were more often cisgender men (95%), aged >30 years (55%), reported recent high-risk sexual behavior (85%), and showed higher prevalence of NNRTI resistance (16%). PWUCM with CD4+ counts >500 cells/mm³ had higher viral loads. PWUCM were more likely to report commercial sex (aOR: 3.7), unemployment (aOR: 2.1), injectable drug use (aOR: 96.7), STIs (aOR: 1.6), and lower condom use (aOR: 0.6) than non-PWUCM. Clusters with PWUCM showed significantly greater size, median node degree, STI prevalence, trans women representation, and more frequent partner acquisition via dating apps and sex venues than clusters with no PWUCM. STI reports (syphilis, gonorrhea, hepatitis, chlamydia) were higher among clustered PWUCM compared to non-clustered PWUCM, regardless of administration route (all p<0.05).

CONCLUSIONS

CM use is linked to overlapping risk patterns, including unemployment, commercial sex, increased STI burden, higher viral load despite preserved immunity, reduced condom use, and greater size and degree. These findings highlight the need to prioritise PWUCM through tailored, integrated interventions, particularly via dating apps and sex encounter venues (e.g. PEP, PrEP, and DoxyPEP).

KEYWORDS: HIV-1, Methamphetamine, Molecular Epidemiology, Genetic Clustering, Transmission Network

ABSTRACT ID: 330

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FIRESIDE SESSION 11

Day 3 | Friday 21 November | 11:00-12:30

Blood-borne and sexually transmitted infections

PRESENTER

Jakub Czarnecki

ABSTRACT

Evaluating syphilis surveillance in Finland 2020-2024: identifying missed reinfections

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BACKGROUND

Although Europe has the lowest global prevalence of active syphilis, case numbers have been rising, including in Finland. We evaluated Finland's syphilis surveillance system, in place since 1995, to assess its current performance.

METHODS

Syphilis surveillance in Finland is integrated into the National Infectious Diseases Register (NIDR), maintained by the Finnish Institute for Health and Welfare (THL). It is a passive system based on mandatory electronic notifications from laboratories and clinicians. A laboratory-confirmed active case requires positive results in both screening and confirmatory tests. If only the screening test is positive, the case may be notified as a "serological scar," indicating a past, non-active infection. The combination period in NIDR is 50 years, as defined in the Communicable Diseases Decree (146/2017, §2), meaning that for the same person, positive results for syphilis are combined into a single case during the 50 years following the first positive result. We evaluated the system using data from 2020 to 2024, including both aggregated cases and individual clinician notifications.

RESULTS

NIDR recorded 1,541 syphilis cases linked to 1,541 individuals. However, 2,156 clinician notifications were submitted, suggesting that over 600 possible reinfections were aggregated with existing cases, 29% of all clinician notifications. Among NIDR cases, 11% were classified as serological scars, but this information was missing in 15% of records.

CONCLUSIONS

The system underestimates reinfections and is missing key information on whether cases are active or non-active, leading to inclusion of past infections with limited public health relevance. We recommend replacing the current 50-year combination period with a shorter one (e.g. 3 months). This would improve detection of reinfections and better reflect trends in high-risk groups. Until this change is made, we suggest monitoring individual clinician notifications. We also recommend improving completeness of serological scar classification.

KEYWORDS: syphilis, disease notification, public health surveillance, reinfection, Finland

ABSTRACT ID: 391

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FIRESIDE SESSION 11

Day 3 | Friday 21 November | 11:00-12:30

Blood-borne and sexually transmitted infections

PRESENTER

Sophie Harker

ABSTRACT

Introducing late HIV diagnosis cohort reviews in Wales: Exploring missed opportunities for testing

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BACKGROUND

For people living with HIV, receiving a late diagnosis is a key predictor of morbidity and premature mortality. Tackling late HIV diagnoses is a priority of the HIV Action Plan for Wales, 2023-2026. Reviewing late diagnoses has been found to be beneficial for training and policy changes, enabling earlier diagnoses and improving health outcomes for those living with HIV. Late HIV diagnosis cohort reviews were introduced in Wales to explore missed opportunities (MOs) for earlier HIV testing.

METHODS

Patients were identified for review if: resident in Wales; diagnosed at a Welsh site; no record of previous diagnosis; and a recorded CD4 count of <350 within 90 days of diagnosis. MOs and patient outcomes were recorded one year after diagnosis, by eform, and discussed amongst a group of HIV clinicians from across Wales to review possible actions and share lessons learned.

RESULTS

UK-wide official statistics reported 222 new diagnoses of HIV in Wales between 01/01/2022 and 31/12/2023 and 66 (30%) met the criteria for late cohort review. MOs for testing were identified for at least 21 cases (32%), more commonly in primary care settings (67%). Recurrent MOs included unexplained weight loss and the presence of other indicator conditions such as candidiasis. Investigations in gastroenterology and colposcopy were common in those eventually diagnosed late. Patient-related MOs included declining testing due to fear or stigma.

CONCLUSIONS

Exploring MOs in cohort reviews enabled actions to be taken to reduce the likelihood of reoccurrence. Patient outcomes were fed back to primary and secondary care teams involved with MOs to enable future earlier testing, and learning was shared to clinicians across Wales through opportunities to speak at conferences. Continued surveillance of late HIV diagnoses and the use of cohort reviews in Wales provide a national process for taking action on MOs and evaluating the impact of those actions.

KEYWORDS: HIV, Testing, Delayed Diagnosis, Peer Review

ABSTRACT ID: 638

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FIRESIDE SESSION 11

Day 3 | Friday 21 November | 11:00-12:30

Blood-borne and sexually transmitted infections

PRESENTER

Karolina Zakrzewska

ABSTRACT

Is the congenital syphilis (CS) elimination target fit for purpose? Insights from Polish neonates cohort (2017-2023) exposed to maternal *Treponema pallidum* seropositivity.

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BACKGROUND

The diagnosis of CS is particularly challenging due to the biological characteristics of *T.pallidum* (non-cultivable, its presence is mainly inferred indirectly via serological markers), nonspecific symptoms or passive maternal antibody transfer. WHO Europe aims to eliminate CS as a public health threat, targeting ≤ 1 case per 100,000 live births. This study assessed the relevance and limitations of the CS elimination target in 2030 in the context of national data from Poland.

METHODS

Case-based epidemiological surveillance data on neonates born between 2017-2023 with perinatal exposure to maternal *T.pallidum* seropositivity, as reported by physicians or identified through positive laboratory test results, were analysed. Cases were classified as confirmed or probable (EU 2018/945) and counted toward the WHO Europe elimination target. Aggregated live births and deaths (ICD-10: A50-A53 among children under 2 years) were obtained from Statistics Poland.

RESULTS

Among over 2.4 million live births in Poland between 2017 and 2023, 98 newborns were reported as perinatally exposed to *T.pallidum*, based on maternal seropositivity (88.5% of mothers were Polish). All exposed neonates received immediate postnatal treatment, in line with the treatment-as-prevention (TaSP) approach. One neonatal death from cardiorespiratory failure was noted. No CS-related deaths were reported. Nevertheless, 7 met the criteria for confirmed CS (7.1%), and 14 for probable CS (14.3%). Despite neonatal TaSP, the annual CS incidence exceeded 1/100,000 live births in 4 of 7 years (range: 0.000-1.835; median: 0.995), nearing or exceeding the WHO Europe elimination threshold.

CONCLUSIONS

This study assessed the applicability of the 2030 CS elimination target in the Polish context. Although the target was exceeded in some years, all reported neonates exposed to maternal *T.pallidum* seropositivity were treated prophylactically. Probable CS were based on non-specific symptoms without diagnostic confirmation. Tailored clinical guidelines linking surveillance definitions with clinical management are needed to support accurate classification and improve interpretability of the elimination target.

KEYWORDS: *Treponema pallidum*, congenital syphilis, Poland, surveillance, neonates

ABSTRACT ID: 662

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FIRESIDE SESSION 11

Day 3 | Friday 21 November | 11:00-12:30

Blood-borne and sexually transmitted infections

PRESENTER

Moses Njiru

ABSTRACT

Determinants of interruption in treatment among people living with HIV in Murang'a County, Kenya: a sequential explanatory mixed-method study.

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BACKGROUND

Globally, approximately one in four people living with HIV (PLHIV) experience interruption in HIV treatment (IIT) that may threaten sustained care continuity and viral suppression, and increase risks of onward HIV transmission, morbidity and mortality. Understanding factors associated with IIT is important to inform targeted interventions.

METHODS

We conducted a sequential explanatory mixed-method study across nine high-volume facilities in Murang'a County between January 2023 and June 2024. We compared PLHIV with missed scheduled clinical appointments by >30 days to PLHIV who remained in care. Multivariable logistical regression estimated the relative risk (aRR) of IIT. We conducted focus group discussions with those who returned to care after IIT. Audio recordings were translated, transcribed, coded and analysed thematically.

RESULTS

Among 11,472 PLHIV (mean age 45.7 years, 67% female), 742 (6.5%) experienced IIT. Of those, 377 (50.8%) did not return to care. Factors independently associated with IIT included ages 20–24 years (aRR = 2.02), 25–49 years (aRR = 2.27) compared to ≥50 years old, male sex (aRR = 1.42), viral non-suppression (aRR = 6.35), invalid viral load results (aRR=9.59), ART for a duration of 6–12 months (aRR=4.96) compared to those on ART for > 10 years, WHO stage 3&4 (aRR=2.08,) ($p<0.001$ for all). Recurrent themes were HIV knowledge gaps, especially on undetectable viral load equals untransmittable concept, alcohol and substance use, negative services experience, transport cost & mobility, frequent clinic visits, stigma, and religious influence.

CONCLUSIONS

PLHIV experienced prolonged disengagement with care, with potential determinants of IIT being younger age (20–49 years), men, unsuppressed & invalid viral load results, early in ART treatment, and advanced HIV disease with interplay of individual, systemic and socio-cultural factors. Strengthening early tracing mechanisms, differentiated service delivery care targeting younger PLHIV and men, fidelity to viral load monitoring, comprehensive U=U education & stigma reduction initiatives are recommended.

KEYWORDS: Continuity of Patient Care, HIV Infections, Focus Groups, Viral Load Logistic Models, and Morbidity

ABSTRACT ID: 826

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FIRESIDE SESSION 12

Day 3 | Friday 21 November | 11:00-12:30

Healthcare-associated infections

PRESENTER

Phillip Butterick

ABSTRACT

Identifying the optimal timeframe of potential *Clostridioides difficile* transmission events for genomically linked patients

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BACKGROUND

Since 2019 all *C. difficile* in Wales have been whole genome sequenced (WGS) by the Anaerobe Reference Unit (ARU). ARU alerts hospital infection prevention teams (IPCT) to clusters closely related genomically. This prompts local investigation to identify potential transmission events between genomically linked patients in hospitals, followed by targeted interventions. Because *C. difficile* spores persevere within the gut and environment, transmission events may not have been recent. With limited resources, identifying transmission from long ago may be neither practical nor useful for targeting interventions. We aimed to rapidly identify potential transmissions and determine the optimum timeframe over which this was useful.

METHODS

We linked ARU WGS data (01/04/19 – 01/04/2024) with location history from hospital administration systems, using National Health Service identifier. We used an R script to identify cluster patient time/location overlaps, producing graphical outputs for review. We expanded admission periods from 1-12 months to identify patient overlaps in common locations. Graphical outputs were manually reviewed to determine whether transmission was likely; high evidence was based on co-location around positive sample dates, or if environmental persistence was indicated from multiple cluster positives co-located within the timeframes.

RESULTS

We identified 477 national incidents of genomically linked patients co-located within 1 month; of these 389 (~80%) had high transmission evidence. Expanding to 3 months identified an additional 90 incidents; 28 (~30%) had high evidence. Using 6 months identified 52 more incidents, 5 (~10%) with high evidence, and at 12 months, none of the 49 incidents had high evidence.

CONCLUSIONS

We developed a more rapid and efficient process for identifying patient overlaps. Three months identified the greatest number of transmission events accurately. Longer periods identified more transmission events, however evidence of transmission was weaker and therefore not useful for timely IPC action. This process, using a 3 month timeframe, is now routinely used across Wales.

KEYWORDS: *Clostridioides difficile*, Wales, Whole genome sequencing, Healthcare associated infection, Infection prevent and control

ABSTRACT ID: 187

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FIRESIDE SESSION 12

Day 3 | Friday 21 November | 11:00-12:30

Healthcare-associated infections

PRESENTER

Maria Suau Sans

ABSTRACT

Infant Gram-negative bloodstream infections in England, 2011-2019: A population-based study of case characteristics and risk factors for mortality

M. Suau Sans¹

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BACKGROUND

Gram-negative bloodstream infections (GNBSI) in infants are on the rise globally. Predicting infants at higher risk of infection could help target interventions to prevent infection and enable early diagnosis and treatment. We aimed to characterize infants (<1-year-old) in England with GNBSIs caused by the three most common GNBSI pathogens (*Escherichia coli*, *Klebsiella* spp., *Pseudomonas aeruginosa*) and to identify risk factors associated with all-cause mortality.

METHODS

National mandatory surveillance data reported to the UK Health Security Agency for *E. coli* (2011-2019), *Klebsiella* spp., and *P. aeruginosa* (2017-2019) were linked to birth registrations, hospital admissions for infants and mothers, and mortality data. Descriptive analyses were conducted to characterise the demographic and clinical features of affected cases. Multivariable logistic regression to identify risk factors for all-cause mortality within 30 days of the first positive specimen was restricted to *E. coli* bacteraemia due to the limited number of events for the other pathogens.

RESULTS

The linked dataset comprised 3115 *E. coli*, 231 *Klebsiella* spp., and 64 *P. aeruginosa* cases, and case fatality rate was 10%, 13% and 34% respectively. Infants from the most deprived quintile accounted for 31% of *E. coli*, 35.95% of *Klebsiella* spp., and 32.78% of *P. aeruginosa* cases. For *E. coli*, extreme prematurity (<27 weeks) was the strongest predictor of mortality (Odds ratio (OR) 7.94; 95%CI:4.40–14.7); other risk factors included invasive ventilation (OR 2.37; 95%CI:1.43–3.94), maternal hospital stay >48 hours (OR 2.08; 95%CI:1.33–3.22), infant circulatory, endocrine, nutritional or metabolic comorbidities (OR 2.08; 95%CI:1.39–3.14) and having a mother of South Asian ethnicity (OR 1.94; 95%CI:1.04–3.53).

CONCLUSIONS

While GNBSI is a contributor to infant mortality, birth and postnatal factors significantly influence outcome. These demographic and clinical predictors should be leveraged to develop robust prognostic tools that support early intervention and enable the efficient allocation of clinical resources.

KEYWORDS: Gram-Negative Bacterial Infections, infant, *Escherichia coli* Infections, mortality, *Klebsiella* Infections, *Pseudomonas aeruginosa*

ABSTRACT ID: 709

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FIRESIDE SESSION 12

Day 3 | Friday 21 November | 11:00-12:30

Healthcare-associated infections

PRESENTER

Felipe Teixeira De Mello Freitas

ABSTRACT

Respiratory Syncytial Virus-associated hospitalizations in children younger than 5 years in Brazil using National Severe Acute Respiratory Infections Surveillance, 2013 - 2022.

F. Teixeira De Mello Freitas¹

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BACKGROUND

Respiratory syncytial virus (RSV) is the leading cause of respiratory tract infection in infants and young children across the globe. Its activity reduced during the COVID-19 pandemic, but emerging epidemics, out of usual seasonality, were seen after social isolation measures were withdrawn. As new technologies for RSV prevention become available, such as vaccine and new monoclonal antibodies, national data on its circulation is needed as baseline to future evaluation of their impact.

METHODS

We performed a descriptive study of RSV-related hospitalizations in children younger than 5 years-old in Brazil from 2013 to 2022. Data of RSV laboratory confirmed cases were obtained from the national Severe Acute Respiratory Infections (SARI) surveillance system. In Brazil, SARI requires compulsory notification, and cases are tested by PCR for a panel of respiratory viruses, including RSV, since 2012.

RESULTS

A total of 51,069 cases of RSV were detected in the period of study, 28,225 (55%) were male, the median age was 5 months (IQR 1.8 months to 1 year), 38,012 (74.5%) were below one year-old. The total number of ICU admissions and deaths were 16,233 (32%) and 803 (1.5%) respectively. RSV cases peaked during fall, between the months of February to July from 2013 to 2019. In 2020, no peak in cases was observed, but from 2021 and 2022, two peaks of cases occurred, during fall and summer, but the proportion of RSV positivity was lower when compared to pre-pandemic years.

CONCLUSIONS

RSV represent the main agent of SARI among children under 5 years-old in Brazil with significant morbidity and mortality. The COVID-19 pandemic changed the RSV patterns of circulation, posing new challenges to its control. These data also serve as a baseline after new technologies of RSV prevention are implemented.

KEYWORDS: Respiratory Syncytial Viruses, Respiratory Tract Infections, Hospitalization, Brazil

ABSTRACT ID: 494

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FIRESIDE SESSION 12

Day 3 | Friday 21 November | 11:00-12:30

Healthcare-associated infections

PRESENTER

Luke McGeoch

ABSTRACT

Prospective enhanced surveillance study of respiratory syncytial virus (RSV) outbreaks in care homes in England during winter 2024-25.

L. McGeoch¹

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⁸UK Health Security Agency (UKHSA)|University of Kent|Brighton and Sussex Medical School

BACKGROUND

Care home residents are vulnerable to respiratory syncytial virus (RSV) infection and adverse outcomes. Most residents (median age 86 years) are above RSV vaccination age (75-79 years) in England. Given limited evidence on RSV burden, we conducted enhanced surveillance of care home RSV outbreaks in England between October 2024 – February 2025.

METHODS

We extracted information on acute respiratory infection (ARI) outbreaks in care homes reported to UKHSA health protection teams (HPTs). RSV outbreaks were defined as ARI outbreaks with ≥ 1 confirmed RSV case. Confirmed cases had a positive RSV laboratory test; probable cases had ARI symptoms only. For 25% randomly sampled RSV outbreaks, enhanced surveillance questionnaires (ESQs) were completed with care home managers, including information on symptomatic individuals, testing, and disease outcomes. Frequencies and percentages were used to describe temporal outbreak trends, coinfections, attack rates (AR), and hospitalisations.

RESULTS

Of 2,420 ARI outbreaks, 222 (9%) were RSV outbreaks. RSV outbreaks peaked in December and January. In 69 (31%) RSV outbreaks, additional respiratory pathogens were identified, most commonly influenza (n=37), rhinovirus (n=14) or SARS-CoV-2 (n=9). ESQs were completed for 36/59 selected outbreaks. There were 258 RSV cases overall (median AR 15%, IQR 10-21), 82 confirmed cases (median AR 5%, IQR 3-7%), and 58 (22%) hospital admissions. Eleven (31%) outbreaks included symptomatic staff (median AR 4%, IQR 2-7).

CONCLUSIONS

We provide a systematic, real-world insight into RSV outbreaks in older adult care homes, highlighting resident vulnerability. Additionally, RSV infections in staff members may impair care provision. We will share findings with the UK's immunisation technical advisory group to inform decision-making regarding vaccination of adults aged ≥ 80 years. Further work to explore the impact of extending vaccine eligibility to care home residents is warranted. We recommend ongoing enhanced winter surveillance including, if introduced, examination of RSV vaccination impact on disease burden.

KEYWORDS: Respiratory Syncytial Viruses, Nursing Homes, Homes for the Aged, Residential Facilities, Public Health Surveillance, Disease Outbreaks

ABSTRACT ID: 448

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FIRESIDE SESSION 12

Day 3 | Friday 21 November | 11:00-12:30

Healthcare-associated infections

PRESENTER

Dominic Power

ABSTRACT

Gastrointestinal infections outbreak in a care home involving *C. perfringens* from an environmental source in Wales, UK

D. Power¹

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BACKGROUND

Clostridium perfringens (*C. perfringens*) is widely distributed in the environment. Most strains are not harmful to humans because they do not produce enterotoxin (CPE). Infection is usually food-associated following inadequate heating and cooling practices. Illness from environmental exposures is rarely reported. We describe the response to a care home outbreak of *C. perfringens* with potential environmental source.

METHODS

Cases were notified to Environmental Health Officers (EHOs). Local laboratories detected gastrointestinal pathogens by PCR, isolating bacteria by culture. Samples were sent to the UKHSA reference laboratory to detect CPE gene (PCR) and CPE toxin (ELISA) and genetic typing by fAFLP. Field Epidemiologists and EHOs inspected the site, taking environmental samples. They reviewed activities, incidents, food-history, stool-charts and medication of all residents for epidemiological links. An analytical study was based on ensuite and shared WC facilities and two social events.

RESULTS

Over three weeks, over half the residents experienced gastrointestinal illness (n=16): 13 had results for at least one pathogen. *C. perfringens* (n=11), norovirus (n=10), *S. aureus* (n=3) and *C. difficile* (n=1) were detected. CPE was detected in two of eight symptomatic residents. *C. perfringens* was isolated in 11 of 16 environmental samples. Clinical and environmental samples were genetically indistinguishable, all able to express the CPE gene. Likelihood of illness did not increase through specific food consumption or social events attendance.

CONCLUSIONS

This outbreak was likely due to norovirus infections causing faecal contamination across the home, creating an environmental exposure to CPE-producing *C. perfringens*. No associations were found with food items, nor problems with food safety, arguing against a common food source for any pathogen. The concordance of environmental and clinical samples and evidence of environmental contamination suggest that this was the vehicle of infection. IPC training, including correct use of sporicidal cleaning agents, was delivered and incorporated into future training.

KEYWORDS: Healthcare, *Clostridium perfringens*, Fluorescent Amplified Fragment Length Polymorphism (fAFLP) analysis, Norovirus, Environmental Exposure, Homes for the Aged

ABSTRACT ID: 590

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FIRESIDE SESSION 12

Day 3 | Friday 21 November | 11:00-12:30

Healthcare-associated infections

PRESENTER

Anna Gavan

ABSTRACT

Investigation of a multi cluster outbreak of emm-type 80.0 Group A Streptococcus in the West Midlands, England

A. Gavan¹

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BACKGROUND

In January 2025, an outbreak of Group A Streptococcus (GAS) involving invasive (iGAS) and non-invasive cases was identified in West Midlands. Confirmed cases were emm-type 80.0, a rare sequence type in England, although routine surveillance is limited to invasive cases. This investigation aimed to identify sources and inform control measures.

METHODS

A routine outbreak investigation was conducted, including epidemiological analysis using network diagrams, timelines and geographical mapping. Confirmed cases were individuals with laboratory confirmed emm 80.0 GAS or iGAS with epidemiological links to the outbreak. Possible cases were individuals with GAS or iGAS awaiting typing but were epidemiologically linked. Whole genome sequencing (WGS) assessed genetic relatedness between cases. Contact screening and enhanced surveillance was implemented.

RESULTS

Between October 2024 and April 2025, 12 confirmed and 4 possible cases were identified (7 iGAS and 9 GAS). Case ages ranged from 41 to 97 years and 56% were male. WGS for 11 typed cases showed isolates were within 8 single nucleotide polymorphisms (SNPs), indicating close genetic relatedness. Three separate clusters were identified. The first involved two genetically identical cases linked to an emergency department. Network diagrams identified 25 emergency department staff to be screened, and all tested negative. The second cluster included three residents in the same care home, two of which were genetically identical to the first cluster. The third cluster included ten cases receiving care from the same district nursing team, including a household cluster of three cases. Screening of the district nursing team was negative and further investigations continue.

CONCLUSIONS

A common source has not been identified, however genetic analysis suggests an unidentified transmission link. This outbreak highlights the complexity of GAS transmission and the need to develop surveillance for non-invasive GAS within the general population to improve understanding of transmission of different GAS emm-types and enhance response to complex clusters.

KEYWORDS: Streptococcus Group A, Outbreaks, Whole genome sequencing, Epidemiology, Surveillance

ABSTRACT ID: 645

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FIRESIDE SESSION 13

Day 3 | Friday 21 November | 14:00-15:30

Health inequalities and key populations

PRESENTER

Ernst Van Dokkum

ABSTRACT

Health disparities in complicated lower respiratory tract infections: the role of socioeconomic status

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BACKGROUND

International studies show that ethnic minority groups and individuals with lower socioeconomic status (SES) face higher severity of lower respiratory tract infections (LRTI). It is unclear whether these associations exist in The Netherlands and to what extent they are mediated through comorbidities and household composition. Therefore, our study investigates the relationship between sociodemographic factors and complicated LRTI before and during the COVID-19 pandemic in The Hague, the Netherlands.

METHODS

A population-based cohort study was conducted using sociodemographic and insurance claims data from Statistics Netherlands, covering The Hague's adult population in 2014-2019 (pre-COVID-19) and 2020 (COVID-19). The associations of structural determinants (age, sex, SES, migration background) and intermediary determinants (comorbidities, household composition) on complicated LRTI incidence and mortality were assessed using Poisson regression models. Complicated LRTI episodes were defined as hospital admission or death within 14 days after an emergency department visit.

RESULTS

In 2014-2019, individuals in the lowest SES quintile displayed the highest incidence of complicated LRTI (aIRR 2.26 [95%CI: 1.98–2.57]), and LRTI-associated mortality (aIRR 3.49 [95%CI: 2.28–5.34]), compared to the highest SES quintile, after adjusting for structural and intermediary determinants. Similar associations were observed in 2020. Furthermore, geographical hotspots concerning complicated LRTI incidence in The Hague were identified, which overlapped with neighbourhoods of greater socioeconomic deprivation. Individuals without a migration background were most affected in 2014-2019, while individuals with a migration background were more impacted in 2020.

CONCLUSIONS

These findings underscore the need to consider SES and migration background in targeted treatment, prevention and population health strategies. Adding residential location and/or SES as a risk factor in (flu) vaccination strategies and clinical decision-making (SES on top of existing risk factors) could potentially help reduce health disparities. Further studies are needed to confirm these findings and evaluate the impact of targeted measures.

KEYWORDS: Respiratory Tract Infections,Public Health,Health Inequities,Socioeconomic Status,Ethnicity

ABSTRACT ID: 181

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FIRESIDE SESSION 13

Day 3 | Friday 21 November | 14:00-15:30

Health inequalities and key populations

PRESENTER

Chiara Elisa Sabbatini

ABSTRACT

Decline in incidence and prevalence of hepatitis C virus infection among drug users in France, 2004-2023

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BACKGROUND

Hepatitis C virus (HCV) remains a major public health challenge, particularly among people who use and inject drugs (PWUD and PWID), who face a high risk of infection. Although direct-acting antivirals (DAAs) have revolutionized HCV treatment, meeting the World Health Organization's 2030 elimination target requires robust surveillance to track transmission and reduce new infections. Critically, accurate estimation of incidence and prevalence is needed to assess disease burden and guide scaling up of prevention, testing and cure strategies.

METHODS

We analyzed data from three cross-sectional surveys conducted in France in 2004, 2013, and 2023. These surveys included a time-location sampling plan to collect behavioral and biological data from PWUD recruited at harm reduction services. We estimated age- and time-dependent prevalence of HCV antibodies and RNA-HCV using multivariate regression models. HCV incidence was estimated for both biomarkers using two-state transmission models.

RESULTS

The demographic profile of PWUD has evolved over time: the mean age increased from 35 years in 2004 to 44 years in 2023, and the proportion of men rose from 71.6% to 84.6%. Injection drug use remained stable throughout the period. Between 2013 and 2023, both HCV prevalence and incidence declined significantly. Among PWID, RNA-HCV prevalence fell from a mean value of 29.6% to 14.5%, and incidence dropped from 6.5 [4.1, 8.0] (95% confidence interval) to 2.4 [1.4, 4.2] per 100 person-years. In the broader PWUD population, RNA-HCV prevalence decreased from 19.4% [16.3%, 23.0%] to 9.5% [7.2%, 12.3%].

CONCLUSIONS

The marked decline in HCV prevalence and incidence among PWUD and PWID in France reflects the impact of DAAs scale-up and harm reduction strategies. These results suggest meaningful progress toward HCV elimination. Yet, transmission persists—particularly among PWID—highlighting the need for targeted interventions in prevention and care. These findings provide timely insights for shaping future public health policies and help guide medium-term management plans.

KEYWORDS: hepatitis C virus, mathematical modeling, prevalence, incidence, drug users

ABSTRACT ID: 367

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FIRESIDE SESSION 13

Day 3 | Friday 21 November | 14:00-15:30

Health inequalities and key populations

PRESENTER

Fariya Abdullahi

ABSTRACT

Inequalities in a measles outbreak in the South West region of England, 2024-2025

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BACKGROUND

Between January and March 2025, the South West region accounted for one-fifth of all measles cases in England, driven by an outbreak centred around the city of Bristol. Despite the region's comparatively high measles vaccination coverage, inequalities in uptake are known. We described the epidemiology of this outbreak to identify inequalities and associations between deprivation, measles incidence and vaccination status.

METHODS

Demographics, exposure settings and vaccination status of confirmed (detection of measles IgM in blood/oral fluid or wild-type measles RNA) and probable cases (clinical evidence with epidemiological links) reported between 11th November 2024 and 16th March 2025 were described. Cases were deemed measles vaccine eligible if aged over 1-year. Deprivation quintile was determined using residential postcode. Poisson regression was used to compare measles incidence by deprivation quintile using incidence rate ratios (IRR), whilst associations between deprivation and vaccination were determined using odds ratios (OR) and logistic regression.

RESULTS

There were a total of 112 cases, with a median age of 11 years (IQR 2-25). Nearly all cases were vaccine eligible (101/112, 90%), of which 15% (15/101) were fully vaccinated, 8% (8/101) vaccinated appropriate for age, 7% (7/101) partially vaccinated and 70% (71/101) unvaccinated. Vaccine eligible cases residing in the most deprived areas had lower odds of having at least one dose of a measles vaccine compared to the least deprived (OR:0.18, 95% CI:0.09-0.95, p=0.041), with nearly seven times higher measles incidence (IRR:6.97, 95% CI:3.57-15.30, p<0.001). Measles incidence decreased by 39% (IRR:0.61, 95% CI:0.53-0.70, p<0.001) for each one-quintile decrease in deprivation, whilst odds of vaccination increased by 65% (OR:1.65, 95% CI:1.18-2.36, p=0.005).

CONCLUSIONS

Measles incidence was highest in the most deprived, and less likely vaccinated, communities. Despite good regional coverage, pockets of low uptake linked to deprivation can drive measles outbreaks. Targeted efforts to improve local coverage will be needed to curb future outbreaks.

KEYWORDS: Measles,Vaccination,Inequalities,Outbreaks,England

ABSTRACT ID: 410

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FIRESIDE SESSION 13

Day 3 | Friday 21 November | 14:00-15:30

Health inequalities and key populations

PRESENTER

Vanessa Piechotta

ABSTRACT

Ongoing outbreak of invasive *Haemophilus influenzae* type b in people using substances and experiencing homelessness in Northern Germany since September 2024

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BACKGROUND

Haemophilus influenzae type b (Hib) can cause severe invasive disease (IHibD), primarily affecting young children, elderly, and immunocompromised individuals. Hib outbreaks among adults are rare. In January 2025, three adult IHibD cases were notified in Hamburg within two weeks, indicating an unusual accumulation. We aimed to verify and describe the outbreak and case characteristics, and identify and implement control measures.

METHODS

Cases were defined as adults (18-65 years) diagnosed with IHibD since 01/09/2024, and residing in or visiting Hamburg. We conducted retrospective active case-finding and extended interviews of notified cases, inquiring about housing, substance use, co-morbidities, and vaccination-status. Microbiological investigations, performed at the national reference centre and Robert Koch Institute, included serotyping and whole-genome-sequencing of available *Haemophilus influenzae* isolates possibly related to the outbreak, and other nationally notified IHibD cases. Genomic information was compared to public typing data via PubMLST.

RESULTS

Between 01/09/2024-31/03/2025, we identified ten cases (three deaths) in Hamburg and neighboring states of Northern Germany, 50% female, 26-58 years old (median 45 years). Substance use was reported for all cases, 70% experienced homelessness, and 50% had known co-morbidities. Cases were unvaccinated (n=3) or vaccination-status was unknown. Phylogenetic analysis of all available outbreak isolates (9/10 cases) showed a genetic cluster, with ≤ 1 allele differences (AD). Other Hib isolates from Germany and Europe were genetically distinct by ≥ 144 AD's.

CONCLUSIONS

This is the first outbreak of IHibD in adults ≤ 65 years in Germany. Phylogenetic analysis confirmed, that as of 31/03/2025, the outbreak was restricted to individuals using substances and/or experiencing homelessness. Co-morbidities, generally poor health, and substance use might have contributed to increased vulnerability, including lethality, to IHibD. We recommend post-exposure chemoprophylaxis for close contacts, prevention and symptom awareness campaigns for staff and persons using shelters and drug consumption rooms, and Hib vaccination. We continue with active case-finding to evaluate control measures.

KEYWORDS: *Haemophilus influenzae* type b, outbreak, homelessness, substance use

ABSTRACT ID: 423

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FIRESIDE SESSION 13

Day 3 | Friday 21 November | 14:00-15:30

Health inequalities and key populations

PRESENTER

Fiona Alma Költringer

ABSTRACT

Zooming in on Genomics to See the Bigger Picture: Suspected Autochthonous Transmission of an Imported Tuberculosis Strain Affecting Migrants in Austria

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BACKGROUND

Tuberculosis (TB) predominantly affects vulnerable populations such as migrants. In 2024, increasing notifications among Somali-born migrants with suspected autochthonous transmission were detected in Vienna. To identify a cluster and assess the geographical extent, epidemiologic investigations were supplemented with whole genome sequencing (WGS).

METHODS

WGS data of 47 cases reported by Vienna in Somali-born migrants in 2023/2024 were analyzed using core genome Multilocus Sequence Typing and Single Nucleotide Polymorphism (SNP) analysis. Clustering isolates were compared against the sequencing database at the national reference center including TB cases in Austria since 2015 and linked to epidemiological records of local health authorities. Autochthonous transmission was suspected if cases were reported >18 months after date of entry. Cases detected through screening upon arrival or with reporting date <6 months after date of entry were considered imported.

RESULTS

We identified 20 cases of sequence type 215–Beijing/2.2.1 reported between 2021 and 2024 that clustered within 0–4 allelic differences and 0–3 SNPs. These included 14 cases among Somali migrants in Vienna. Six cases identified through the genomic database were reported by five other federal states in patients from Afghanistan (n=2), Somalia, Morocco, Yemen and Pakistan. All patients were male with a median age of 24.5 years (IQR:21–27.2). Median time between date of entry and reporting was 3.6 years (IQR:1.4–8.12). 14 cases were likely autochthonous, including three close contacts identified through epidemiological investigations; four were considered imported; two could not be classified.

CONCLUSIONS

Genomic investigations revealed that the outbreak among Somali migrants was linked to a larger TB cluster spanning Austria. While autochthonous transmission of an imported strain likely contributed to the outbreak in Vienna, multiple independent introductions from migrants of different nationalities suggest an origin along a migratory route. The findings underscore the significance of integrated genomic and epidemiologic methodologies to better understand transmission dynamics of TB in migrants.

KEYWORDS: Whole Genome Sequencing, Cluster Analysis, Molecular Epidemiology, Tuberculosis, Migrants

ABSTRACT ID: 532

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FIRESIDE SESSION 13

Day 3 | Friday 21 November | 14:00-15:30

Health inequalities and key populations

PRESENTER

Andreas Hoefer

ABSTRACT

Largest European *Corynebacterium diphtheriae* outbreak in 50 years leading to secondary cases in general population

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BACKGROUND

Increased numbers of cases of *Corynebacterium diphtheriae* infections were diagnosed in migrant related facilities of Europe since summer 2022. Most cases involved cutaneous diphtheria, although some respiratory cases and fatalities were reported. A pan-European consortium assessed the genetic relatedness and the antibiotic susceptibility of the isolates from the outbreak.

METHODS

All 363 toxigenic *C. diphtheriae* isolates between 1 January and 31 November 2022, from ten European countries underwent WGS analysis. A combination of cgMLST and SNP-based methods were used to outline phylogenetic relationships of outbreak isolates. Sequence, integron, toxin and antimicrobial resistance typing were performed with diphtOscan.

RESULTS

cgMLST analysis identified four genomic multicountry outbreak clusters (GC): GC795 (ST574, n=131), GC817 (ST377, n=110), GC671 (ST377, n=17), and GC217 (ST384, n=74). Notably, GC671 carried *ermX* and *blaOXA-2* genes. Strains harboring *ermX* were phenotypically resistant to erythromycin; isolates carrying *pbp2m* were resistant to penicillin, but susceptible to amoxicillin, and those carrying *blaOXA-2* remained susceptible to beta-lactams. SNP analysis within the four genomic clusters showed root-to-tip SNP distances of maximum 14 SNPs. The multi-country distribution of each cluster, with smaller scale genetic clusters observed within countries, demonstrated recent transmissions, likely occurring during travel and within migrant facilities.

CONCLUSIONS

The increased number of *C. diphtheriae* cases among migrants is a cause for concern, particularly considering the presence of antimicrobial resistance genes that threaten the efficacy of first-line treatments and lack of DAT global supply. The later detection of isolates genomically and epidemiologically linked to this outbreak in different populations raises additional concerns, including the unknown extent of ongoing transmission, the potential impact of waning immunity, and the consequences of introduction into unvaccinated populations. To reduce further transmission, we recommend: Increased clinical suspicion and testing, sequencing of isolates and routine administration of adult booster doses as per national programmes.

KEYWORDS: Diphtheria, Outbreak, Migrant health, Genomic epidemiology, AMR

ABSTRACT ID: 736

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FIRESIDE SESSION 14

Day 3 | Friday 21 November | 14:00-15:30

Late breakers

PRESENTER

Christina Frank

ABSTRACT

Ongoing large STEC/HUS outbreak centred on North-East-Germany (STEC O45:H2)

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BACKGROUND

In late August 2025 an outbreak of paediatric infections with shigatoxigenic *Escherichia coli* (STEC) was noted in north-east Germany (NEG), including cases of haemolytic uraemic syndrome (HUS). To actively prevent new infections, we initiated a multi-level (local, state and national) outbreak investigation integrating human health and food safety authorities. We present the preliminary epidemiology of the outbreak.

METHODS

Typing of STEC cases was intensified to differentiate outbreak cases from background. Any STEC infection matching the outbreak strain is considered a 'confirmed' case. We conduct exploratory interviews with cases or their parents using a 'shotgun' questionnaire to detect commonalities in terms of places, environmental or animal exposures, or food consumed in the week before diarrhoea symptom onset (DSO). Food safety authorities investigate suspected food items and their distribution patterns in NEG.

RESULTS

The outbreak strain was identified as STEC O45:H2, stx2a and eae positive. As of 22 September, 86 confirmed cases have been notified including a US-tourist and a child from Luxembourg (information received via EpiPulse). The majority of patients (both sexes) are children (median age: 4 years, range 0-88 years). Twenty-eight cases developed HUS, none have died so far. DSO currently ranges from August 11 to September 14. Of those with information, 82% have an association to NEG (45 residents, 11 visitors). Cases without NEG-association have later onsets than other cases. In over 50 interviews to date no single unifying property or food item among all cases interviewed was found. However, many of the frequently consumed meat (products).

CONCLUSIONS

At the time of writing, the large outbreak of STEC/HUS in Germany is ongoing, with 3-5 new cases notified daily. Scenarios with a protracted source and/or multiple contaminated food-items are being considered, also a strong tail of non-primary infections among later cases. A suspicious STEC isolate from beef in NEG is currently being investigated.

KEYWORDS: STEC HUS outbreak foodborne

ABSTRACT ID: 817

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FIRESIDE SESSION 14

Day 3 | Friday 21 November | 14:00-15:30

Late breakers

PRESENTER

Roberto Croci

ABSTRACT

Influenza vaccination attenuates acute myocardial infarction and stroke risk following influenza infection: a registry-based, self-controlled case series study, Denmark, 2014- 2025

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BACKGROUND

Influenza infection triggers acute myocardial infarction (AMI) and stroke, but whether vaccination modifies this risk remains unclear. One single previous study reported a non-significant effect modification. We aimed to quantify the short-term cardiovascular risk increase after PCR-confirmed influenza infection and assess whether vaccination attenuates it.

METHODS

We conducted a self-controlled case series study using Danish health registries (2014-2025), enrolling individuals aged ≥ 40 years with a first-ever hospital admission for AMI or stroke within ± 365 days of an influenza infection. The risk period was days 1-7 after specimen date. To reduce reverse causality, where cardiovascular symptoms prompt influenza testing, we excluded a 14-day pre-exposure period. Individual-level data on testing, hospitalisation, vaccination and mortality were linked deterministically via unique personal identifiers. We estimated incidence rate ratios (IRRs) and 95% confidence intervals (CI) with conditional Poisson regression. We tested effect modification by vaccination status with an interaction term and evaluated significance via likelihood ratio tests.

RESULTS

Among 1,221 individuals with a positive influenza PCR test within 365 days of a first-ever AMI ($n=429$, 35%) or stroke ($n=792$, 65%), median age was 75 years (interquartile range 66-82); 561 (46%) were female. After calendar-month adjustment, the IRR for cardiovascular events during risk period was 3.5 (95% CI 2.6-4.7), higher for AMI [4.7 (3.1-7.4)] than stroke [2.9 (2.0-4.2)]. Prior influenza vaccination, recorded in 50% of cases, reduced the event rate during risk period by 49% (29-91%) from 2.97 to 1.57 per person-year (interaction $p=0.020$). Results were robust in sensitivity analyses studying a negative control outcome, excluding fatal events, using pre-exposure or post-exposure control time, and shifting index date backwards to mirror symptom onset; they were consistent across subgroups.

CONCLUSIONS

Influenza infection conferred a transiently increased risk of first-time AMI and stroke. We demonstrate that vaccination substantially attenuated this risk, supporting its role in preventing cardiovascular complications after breakthrough infection.

KEYWORDS: laboratory-confirmed influenza; myocardial infarction; influenza vaccination; stroke; self-controlled case-series

ABSTRACT ID: 783

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FIRESIDE SESSION 14

Day 3 | Friday 21 November | 14:00-15:30

Late breakers

PRESENTER

Camelia Savulescu

ABSTRACT

Effectiveness of long-acting monoclonal antibodies against respiratory syncytial virus infection in hospitalised children <24 months from three European countries, winter season 2024-2025

C. Savulescu¹

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BACKGROUND

Guidelines for preventing respiratory syncytial virus (RSV) recently included long-acting monoclonal antibodies (mAb) according to national recommendations. We measured the mAb immunisation effectiveness (IE) against laboratory-confirmed RSV among eligible children <24 months hospitalised for severe acute respiratory infection (SARI), in a multicentre study during the 2024–2025 season.

METHODS

We conducted a test-negative case-control pilot study in three countries (Belgium, Spain and Portugal). We compared the immunisation status in cases (children < 24 months eligible for immunisation, hospitalised for SARI, PCR-positive for RSV) and controls (eligible SARI children PCR-negative for RSV). Time since immunisation was stratified in four groups: <30, 30–89, 90–149 and 150–215 days. Using logistic regression, we calculated IE for each country as (1-odds ratio of immunisation among cases and controls)*100, adjusting for age-group (0–6 vs 7–23 months), sex, underlying conditions, and date of onset/testing. We pooled site-specific IE estimates in a random-effects meta-analysis.

RESULTS

We included 2195 children: 785 cases and 1410 controls. Cases were less likely to present an underlying disease (10% vs 15%), more likely to present with shortness of breath (40% vs 22%) and more likely to be admitted in the intensive care unit (11% vs 7%). Overall IE was 79% (95% CI: 61–89); 80% (95% CI: 65–89) in 0–6-months and 77% (95% CI: 17–93) in 7–23-months. The overall IE by time since immunisation was 85%, 78%, 69%, and 18% at <30, 30–89, 90–149 and 150–215 days since immunisation, respectively.

CONCLUSIONS

Our results indicate a high overall effectiveness of long-acting monoclonal antibodies in children hospitalised for SARI laboratory-confirmed RSV during the 2024–2025 season. However, real-world studies remain important to address key public health questions, such as whether early-immunised infants remain protected throughout the entire RSV season, the IE by RSV type, and in older high-risk children.

KEYWORDS: monoclonal antibodies, effectiveness, RSV, nirsevimab, Europe

ABSTRACT ID: 843

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FIRESIDE SESSION 14

Day 3 | Friday 21 November | 14:00-15:30

Late breakers

PRESENTER

Hanne-Dorthe Emborg

ABSTRACT

Out-of-season influenza A(H1N1)pdm09 outbreak among >50,000 attendees of an open-air music festival in Denmark, August 2025

H. Emborg¹

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BACKGROUND

In week 33, 2025, a sharp, six-fold increase in influenza A(H1N1)pdm09 cases was observed in the integrated respiratory virus surveillance in Denmark. Whole genome sequencing showed a near-identical genetic cluster of cases. Interviews revealed attendance at a large open-air music festival on 6-10 August. We aimed to map the size and progression of the outbreak in order to help prevent future outbreaks.

METHODS

An online questionnaire was developed inquiring about age, sex, festival attendance, symptoms and symptom onset. In collaboration with the festival management, we distributed the questionnaire to festival staff/volunteers and those having purchased tickets online. National surveillance data were assessed.

RESULTS

On 11 September, 55,433 individuals were e-mailed the questionnaire. One week later 12,755 (23%) had responded. Among these 6,600 reported respiratory symptoms. Individuals with symptoms prior to the festival or not meeting the ECDC case definition for influenza-like illness (ILI) were excluded, leaving 10,526 festival attendees of whom 4,618 (44%) were ILI cases. The highest proportion of ILI cases was observed in the 15-24-year age group (attack rate 61%), declining with age. From 6-11 August, ILI cases increased exponentially from 89 to 1,026. National influenza notifications reverted to baseline within four weeks.

CONCLUSIONS

We document a highly unusual influenza outbreak with outdoor transmission during summer at a mass gathering event. Contributing factors to progression of the outbreak may have involved the close proximity of participants and party-style behaviour, which potentially increased the number of contacts, decreased the serial interval and increased host susceptibility to infection. A superspreading mechanism cannot be excluded. Despite the unprecedented magnitude of the outbreak, sustained community transmission was not observed. Throughout Europe, week-long, open-air festivals are common; and may promote local outbreaks. We recommend surveillance for disease outbreaks in relation to mass gatherings, year-round surveillance of airborne viruses and dissemination of relevant information on non-pharmaceutical interventions.

KEYWORDS: Influenza outbreak, out-of-season, mass gathering, online survey, transmission dynamics, influenza-like illness

ABSTRACT ID: 867

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FIRESIDE SESSION 14

Day 3 | Friday 21 November | 14:00-15:30

Late breakers

PRESENTER

Laura Paris

ABSTRACT

Protecting infants from respiratory syncytial virus (RSV) in Ireland: High impact of a novel infant immunisation with nirsevimab, 2024/2025

L. Paris¹

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BACKGROUND

To mitigate the substantial RSV disease burden amongst infants in Ireland, a national RSV immunisation programme was delivered from 01/09/2024–28/02/2025. The programme offered infants immunisation with nirsevimab, a long-acting monoclonal antibody. We aimed to estimate the programme's impact on RSV-related morbidity among eligible infants

METHODS

This retrospective, population-based ecological study included all infants born during the programme period. Immunisation uptake was monitored weekly. We used nirsevimab uptake and immunisation effectiveness estimates sourced from a published systematic review with meta-analysis to estimate averted cases, prevented fractions and the number needed to immunise (NNI) to prevent a single RSV notified case, emergency department (ED) presentation, hospitalisation, and intensive care unit (ICU) admission and their 95% confidence intervals (CI) using adapted Machado et. al formulas

RESULTS

Between 01/09/2024–28/02/2025, nirsevimab was administered to 22,444 infants, with an 84% uptake and 360 RSV cases were notified, compared with 1,142 in the same period in 2023/2024 representing a 68% decrease. Preliminary analyses estimated that the programme averted 1,030 (95%CI:1013-1047) notified cases, 440 (95%CI:432-447) ED presentations (non-hospitalised), 433 (95%CI:426-440) hospitalisations, and 79 (95%CI:77-81) ICU admissions among infants. To prevent one RSV case, the NNI was 23 (95%CI:22-24) for all notified cases, 53 (95%CI:49-57) for ED presentations, 54 (95%CI:50-59) for hospitalisations, and 300 (95%CI:242-397) for ICU admissions

CONCLUSIONS

Consistent with international studies, nirsevimab significantly reduced RSV-related morbidity in infants in Ireland, suggesting a high impact of immunisation in preventing cases and severe RSV outcomes. We recommend its use for future RSV seasons in newborns and expansion to catch-up infant cohorts born prior to the start of the RSV season

KEYWORDS: Respiratory Syncytial Virus Infections, Immunization Programs, Infant, Newborn, Monoclonal Antibodies, Program Evaluation

ABSTRACT ID: 788

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POSTER TOURS

POSTER TOUR 1

Day 1 | Wednesday 19 November 15:40-16:40

Sexually-transmitted infections

PRESENTER

Hassan Mahmood

ABSTRACTT

Hepatitis B and C Prevalence Among Transgender Individuals and Men Who Have Sex with Men in Pakistan

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BACKGROUND

In Pakistan, Transgenders (TGs) and Men who Have Sex with Men (MSM) are marginalized communities at high risk of sexually and parenterally transmitted infectious diseases. The prevalence of hepatitis B virus (HBV) and hepatitis C virus (HCV) infection in these populations has not been well described in Pakistan, and access to care and treatment is lacking.

METHODS

From 2020-2022, community health workers tested 2241 transgenders (TGs) and men who have sex with men (MSM) for hepatitis B and C. Those with hepatitis B were referred to provincial programs, while those with hepatitis C were linked to "One Stop Shop" community-based organizations for same-day testing, treatment, and care, including HCV RNA testing and 12-24 weeks of Sofosbuvir and Daclatasvir treatment based on APRI scores.

RESULTS

A total of 201/2241 (9%) tested positive for anti-HCV, and 69/2241 (3.1%) tested positive for HBsAg. All participants who tested HBsAg+ were referred to the provincial hepatitis control program for additional care. The 201 who tested anti-HCV+ were referred to CBOs for additional testing and care under One Stop Shop model. Of those, 161 (80%) were tested for HCV RNA, of which 99 (62%) tested positive for HCV RNA. Of these 87 (88%) initiated treatment and 77/87 (89%) completed treatment; all were tested for cure (sustained virologic response; SVR), of which 72 (94%) were HCV RNA negative (cured).

CONCLUSIONS

Outreach to marginalized populations with same day testing and referral for HBV and HCV is feasible and effective in Pakistan. Key populations were willing to be screened, tested and treated. Partnering with CBOs was key to the success in this pilot project in reaching "key" populations with limited access to health services and achieving high rates of linkage to care and adherence with treatment for HCV.

KEYWORDS: Key Populations, Transgender Individuals, Men who have sex with men, One Stop Shop Model, Community based Organizations, Hepatitis B, Hepatitis C, Evidence based Public Health Policy Formulation, Pakistan, Replicable and Sustainable Project Model in similar settings, Community Outreach, Community Mobilization

ABSTRACT ID: 347

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POSTER TOUR 1

Day 1 | Wednesday 19 November 15:40-16:40

Sexually-transmitted infections

PRESENTER

Lena Böff

ABSTRACT

Fitting beta distributions for the analysis of minimum inhibitory concentrations in *Neisseria gonorrhoeae*: insights from Germany's antimicrobial resistance surveillance, 2014–2023

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BACKGROUND

Neisseria gonorrhoeae (NG) causes the second-most-common bacterial sexually transmitted infection (STI) worldwide. Increasing antimicrobial resistance (AMR) threatens established treatment regimens. We analysed the temporal development of antibiotic susceptibility in NG in Germany and examined whether distinct shifts occurred in specific sexual networks.

METHODS

We analysed cross-sectional data from the German Go-Surv-AMR sentinel surveillance system (2014-2023), collected annually across 42 laboratories. The laboratory unit (FG18) tested NG isolates for phenotypic susceptibility to azithromycin (AZM), ceftriaxone (CRO) and ciprofloxacin (CIP) using E-tests to determine minimum inhibitory concentrations (MIC) in mg/L. We described patient demographics, and calculated MIC statistics (mean, median, quartiles) by year, sex, age group, specimen type, and urbanisation level. We examined temporal MIC distribution differences using Kolmogorov-Smirnov tests and assessed MIC development by fitting beta distributions to log-transformed MIC by antibiotic and epidemiologic strata.

RESULTS

We collected 5422 NG isolates in 2014-2023 across all German federal states, primarily from urethral specimens (76%), men (87%), individuals aged 30-39 years (28%) and residents of metropolitan cities (42%). CRO median MIC were low-level sensitive in all years (≤ 0.008) and increased significantly from 2022-2023 in men (0.0038-0.0049, $p < .001$) but not women (both: 0.0049). Among men, the increase was more pronounced in extragenital/screening isolates (0.0037-0.0052, $p < .004$) than urethral (0.0037-0.0048, $p < .001$). From 2016-2023, median MIC in both sexes for AZM almost quadrupled (0.1189-0.4450) and slightly increased (0.0050-0.0056) in CIP-sensitive isolates.

CONCLUSIONS

Complementing reported emerging resistance, we used Go-Surv-AMR to evaluate subtle temporal antibiotic susceptibility shifts. A recent MIC increase in CRO screening isolates from men suggests decreasing susceptibility in populations who are regularly screened for STI. MIC increases in CIP-sensitive isolates may precede further resistance development. Upcoming NG notification will essentially complement sentinel surveillance with epidemiologic data to better characterise emerging resistance in distinct sexual networks, informing guidelines for tailored screening strategies and targeted treatment options.

KEYWORDS: Minimum Inhibitory Concentration, Bacterial Sexually Transmitted Diseases, *Neisseria gonorrhoeae* Infection, Antimicrobial Drug Resistance

ABSTRACT ID: 162

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POSTER TOUR 1

Day 1 | Wednesday 19 November 15:40-16:40

Sexually-transmitted infections

PRESENTER

Clara Fappani

ABSTRACT

HPV35 dominance in high-grade cervical lesions in Eswatini: are the currently available vaccines enough?

C. Fappani¹

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BACKGROUND

Eswatini (southern Africa) has the highest cervical cancer (CC) incidence and mortality worldwide. Since May 2023, the 4-valent (4v, HPV-6, 11, 16, 18) HPV vaccine has been offered to girls aged 9–14, with 64% of the target population vaccinated by March 2024. However, prevention strategies must rely on locally acquired epidemiological data that are currently missing. This study describes HPV genotypes infecting adolescent girls and women (AGW) screened for CC at rural St. Philip's Clinic, Eswatini.

METHODS

Between January 2023–February 2024, 440 AGW aged 13–49 (mean age 29) self-presenting for any medical reason were enrolled for urine-based HPV-DNA testing. A subset of 208 AGW aged 21–49 was also screened through Pap test. Urine samples were dried on filter paper (dried urine spot) and shipped to Italy for HPV genotyping through in-house PCR and hybridisation-based methods targeting L1 region of HPV genome.

RESULTS

All AGWs enrolled were unvaccinated; 37% were HIV positive. HPV-DNA was detected and genotyped in 333 samples (333/440, 76%). HPV35 was the most prevalent genotype (80/333, 24%), followed by HPV16 (61/333, 18%). Among the 208 AGWs with known cytology status, 46 had high-grade lesions, including 7 CC. HPV35 was found in 33% (15/46), and was the only HR type in 7 cases (15%), including 1 CC. 37% (17/46) tested positive for 4v-covered HR-types (HPV-16, 18), 65% (30/46) for nonvalent-vaccine (9v, HPV-16, 18, 31, 33, 45, 52, 58) HR-types. Adding HPV35 to 9v vaccine formulation potentially raises coverage to 80% (37/46) (100% considering only CC).

CONCLUSIONS

The study revealed an alarming 76% HPV prevalence and a high prevalence of HPV35, associated with 4%–10% invasive CC cases in Sub-Saharan countries and not covered by currently available HPV vaccines. This suggests that to effectively eliminate CC, relying only on data collected on the “global North” is not enough; evidence-based CC prevention programs are crucial.

KEYWORDS: Papillomavirus Infections; ,Papillomavirus Vaccines,Cervical cancer,Genotype,Eswatini

ABSTRACT ID: 477

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POSTER TOUR 1

Day 1 | Wednesday 19 November 15:40-16:40

Sexually-transmitted infections

PRESENTER

Karolina Zakrzewska

ABSTRACT

Diagnostic confirmation, clinical characteristics and surveillance classification of suspected congenital syphilis in Poland, 2017-2024

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BACKGROUND

Syphilis notification rates among women of reproductive age have risen across Europe, increasing concern about congenital syphilis (CS). We aimed to assess the clinical profile, diagnostics and classification of CS cases reported to Polish national surveillance between 2017 and 2024.

METHODS

We analysed epidemiological surveillance data on suspected CS (sCS): 1) case-based, reported from 2017-2023 by physicians/laboratory (n=96); and 2) aggregate counts for 2024 (n=24, verification ongoing). Cases were classified as confirmed/probable (EU 2018/945) or possible according to the national definition (clinician-diagnosed). Linear regression (Stata 18.0) assessed trends in annual sCS counts.

RESULTS

No significant trend was observed in the number of reported sCS due to maternal seropositivity between 2017 and 2024 ($p=0.815$). Annual sCS case count ranged from 15 to 24, with a decline during the COVID-19 pandemic (6-7 cases). Between 2017 and 2023, 18.8% of sCS cases met the EU definition for probable or confirmed CS. Nearly all infants (99.0% sCS) received treatment, without waiting for diagnostic confirmation (Treatment-as-Prevention, TaSP). T.pallidum-specific-IgM testing was performed in 22.9% of sCS - 7.3% of all and 31.8% of tested were positive. Most cases were asymptomatic (78.1%), including 2.1% with IgM positivity. Symptoms were reported in 21.9% of sCS: mucocutaneous lesions (42.9% of symptomatic), jaundice (38.1%), and anaemia (19.0%). Among asymptomatic infants without IgM testing or maternal-infant serology comparison, 39.3% were definitively diagnosed as CS by physicians, although the findings may have reflected passive maternal antibody transfer.

CONCLUSIONS

Given the diagnostic uncertainty and asymptomatic presentation in most sCS, the current use of TaSP appears justified as a preventive strategy. However, it warrants careful evaluation. The development of clinical guidelines aligned with surveillance case definitions has become an urgent need to support clinicians in the management of sCS.

KEYWORDS: congenital syphilis, Treponema pallidum, Poland, surveillance

ABSTRACT ID: 668

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POSTER TOUR 1

Day 1 | Wednesday 19 November 15:40-16:40

Sexually-transmitted infections

PRESENTER

Marta Niedzwiedzka-Stadnik

ABSTRACT

Chlamydia in Poland, 2020–2024: emerging trends in incidence and national screening programme needs.

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BACKGROUND

Unlike in European countries, chlamydia is the least frequently diagnosed STI in Poland. This study aimed to describe temporal trends, demographic patterns, and reporting characteristics of chlamydia cases (ChC) between 2020 and 2024.

METHODS

Case-based epidemiological surveillance data on 3,071 new ChC reported in 2020-2024 by physicians and/or laboratories and classified as ChC in surveillance according to EU case definitions, 2018/945 (confirmed/probable) or national (possible: clinically diagnosed by a physician), were analyzed. Incidence rates (per 100,000) were calculated using mid-year population estimates from Statistics Poland and stratified by age and sex. Temporal trends in reporting districts were assessed with linear regression, and gender differences in presence of symptoms with the chi-square test. Analyses were performed in Stata 18.0.

RESULTS

Incidence increased from 0.37/100.000 to 3.11/100.000 (2020-2024), the overall M/F ratio was 1:1.4. Majority of cases were notified among 25-34 years old (44.1%), however, the highest grow in incidence was observed among youth <24 years (range: 0.06-7.08/100.000). The number of foreigners increased more than 3.5 times in 2023-2024 (vs. 2020-2022). Reporting districts expand (2020:15%→2024:48%, $\beta=36.7$, $p<0.001$; $R^2=97.3\%$). With no formal screening programme established, most ChC are identified through laboratory reports, while 36.7% are notified by clinicians. However, 19.2% of ChC lacked laboratory confirmation and were classified as possible based on clinical diagnosis. Clinicians were more likely to report symptomatic than asymptomatic cases (45.3% vs. 13.9%, data on symptoms were missing in 40.8% of clinician-reported cases). Men showed a significantly higher proportion of symptoms compared to women ($\chi^2=220.9$, $p<0.001$).

CONCLUSIONS

The increase in incidence, geographic spread, and foreign cases signals a growing public health concern. With surveillance remaining largely laboratory-based and limited clinical access, there is a need for accessible, tailored screening programmes that address the needs and comfort of diverse subpopulations, including sexual partners. Strengthening linkage-to-care is essential for timely diagnosis, treatment, and partner management.

KEYWORDS: Chlamydia trachomatis, Poland, STI infections, 2020-2024, screening

ABSTRACT ID: 760

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POSTER TOUR 2

Day 1 | Wednesday 19 November 15:40-16:40

Respiratory infections: evidence to practice

PRESENTER

Iris Ganser

ABSTRACT

Risk factors associated with laboratory-confirmed SARS-CoV-2 infection among healthcare workers: a European prospective multicentre cohort study, May 2021 - April 2024

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BACKGROUND

Healthcare workers (HCWs) face increased risk of SARS-CoV-2 infection, and evidence is still needed for health promotion policies. We aimed to identify risk factors for SARS-CoV-2 infection among hospital-based HCWs and characterise their evolution over time.

METHODS

This prospective multicentre cohort study recruited HCWs from 18 hospitals in eight European countries, who underwent weekly/fortnightly PCR testing and completed questionnaires on occupational, community, and individual exposures at enrolment and weekly during follow-up. We constituted separate cohorts of HCWs at risk of infection for three periods: pre-Omicron (May 2021-December 14, 2021), pandemic Omicron (December 15, 2021-April 2023), and post-pandemic Omicron (September 2023-April 2024). Using Cox proportional hazards models with calendar time as underlying scale, we calculated adjusted hazard ratios (aHRs) for associations between each occupational and community exposure and PCR-confirmed SARS-CoV-2 infection, adjusting for hospital, vaccination and additional confounders of each association exposure-infection.

RESULTS

We included 3253 HCWs in the study (1395, 2056, and 1254 in the three cohorts, respectively). Median age was 44 years, 2597 (80%) female, 740 (22%) medical doctors, 1399 (42%) nurses, and 113 (3%) ancillary personnel. Compared to medical doctors, ancillary hospital personnel presented the highest risk (aHR 8.0, [95% CI 2.2-29.0]) in the pre-Omicron period, but not in later periods. Contact with a COVID-19 case at work did not significantly increase risk in any period (aHRs 1.2 [0.4-3.4], 1.0 [0.8-1.2], 1.0 [0.8-1.3]). In contrast, contact with a case at home had an aHR of 3.7 (1.5-9.2) pre-Omicron, and 1.7 [1.3-2.3] and 1.4 [CI 0.9-2.1] during Omicron periods.

CONCLUSIONS

HCWs' infection risk factors evolved over time and infection prevention and control protocols remain important for all occupational groups. Household exposure was the most important factor, but the effect size decreased over time. Differences across roles highlight the need to reinforce prevention efforts beyond clinical staff and require further evidence.

KEYWORDS: SARS-CoV-2 Infection, Healthcare Workers, Vaccine Effectiveness, COVID-19 Vaccine, Active surveillance

ABSTRACT ID: 137

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POSTER TOUR 2

Day 1 | Wednesday 19 November 15:40-16:40

Respiratory infections: evidence to practice

PRESENTER

Sebastian von Schreeb

ABSTRACT

Individual and seasonal determinants of death among influenza patients admitted to intensive care units, Portugal 2012–2024

S. von Schreeb¹

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BACKGROUND

Portugal's sentinel surveillance for influenza in intensive care units (ICU), established following the H1N1 pandemic, has operated since 2012. We aimed to identify individual and seasonal determinants of death to inform ICU triage and capacity planning.

METHODS

We conducted a retrospective analysis of laboratory-confirmed influenza patients admitted to the 27 ICUs during 2012–2024. Covariates included comorbidities, influenza peak weeks with most ICU admissions, ICU occupancy level and high caseload seasons defined as those with influenza ICU admissions above the median. We calculated case fatality and adjusted risk ratios (aRR) for death during ICU admission using multivariable log-binomial regression. Directed acyclic graphs informed adjustments, including age, sex, influenza type and comorbidities.

RESULTS

Of 1,071 patients, 262 (24%) died. Case fatality increased with age (aRR:1.02, 95%CI:1.02–1.02) and was highest among individuals aged ≥80 years (aRR:11, 95%CI:2.4–184), compared with those aged 0–19 years. Case fatality was higher among patients with chronic liver disease (aRR:2.0, 95%CI:1.5–2.6), cancer (aRR:1.6, 95%CI:1.1–2.1), and during high caseload seasons (aRR:1.52, 95%CI:1.16–2.05). Compared with the latest season (2023–2024), case fatality was lower in 2021–2022 (aRR:0.12, 95%CI:0.02–0.85) and 2022–2023 (aRR:0.46, 95%CI:0.23–0.91), while no differences were observed for other seasons. In 2020–2021, two cases were reported, and none died. ICU occupancy (aRR:1.00, 95%CI:0.98–1.01) and influenza peak week (aRR:0.82, 95%CI:0.66–1.03) were not associated with death.

CONCLUSIONS

Influenza case fatality in the ICU was consistent with previous studies. Liver disease, cancer and advanced age were associated with increased case fatality, which should be considered in ICU triage. Few influenza cases and lower case fatality during 2020–2023 suggest reduced influenza activity and strict prioritizations during the COVID-19 pandemic. Case fatality was higher in seasons with high caseload but did not increase during peak influenza weeks or with increasing ICU occupancy, indicating consistent ICU triage throughout seasons. These findings may contribute to optimizing ICU triage and capacity planning for future seasons.

KEYWORDS: Intensive Care Units, Influenza Human, Health Services Needs and Demand, Mortality

ABSTRACT ID: 140

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POSTER TOUR 2

Day 1 | Wednesday 19 November 15:40-16:40

Respiratory infections: evidence to practice

PRESENTER

Malorie Perry

ABSTRACT

Impact of RSV Vaccination in Wales – Maternal programme to protect infants

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BACKGROUND

Assessing impact of vaccination programmes after introduction is an effective way to monitor progress, enable adjustments and advocate for continuing support. From September 2024, pregnant women in Wales were offered RSV vaccination at 28 weeks' gestation but remained eligible for vaccination until discharge from midwifery. Uptake in women giving birth has stabilised at around 40%. We assessed the impact of the maternal programme on RSV related hospitalisations in infants in the post-vaccination period.

METHODS

Using an Interrupted Time Series (ITS) approach, we aimed to detect if there was a step change in admissions in infants from 7 October 2024 to 31 March 2025. Data from 2010 was extracted from the All-Wales hospital admissions database to construct a weekly time series. RSV-related admissions were defined as those with primary diagnosis of ICD-10 code J12, J18, J20, J21 or J22. Using the field "diagnosis description", admissions that were due to a specified organism other than RSV were excluded. A Poisson regression model was fitted with the count of RSV related admissions as the outcome. The model included the log of the population in the age year as an offset term. We accounted for seasonality using 2 pairs of sine and cosine. We also accounted for the effect of the COVID-19 pandemic in the final model.

RESULTS

There was a 43.3% decrease in hospital admissions (95%CI: -55.3% to -28.1%), $p < 0.001$ in infants under 3 months from 7 October 2024 to 31 March 2024, compared to the estimated admissions in the absence of vaccination. Similar reduction was observed for infants under 6 months while considerably lower reductions were seen in older age groups (6-12 months and 1-4 years).

CONCLUSIONS

This result highlights the early impact of the programme. Continued monitoring will help motivate uptake in future seasons.

KEYWORDS: RSV Respiratory Syncytial Virus, Immunization, Interrupted Time Series Analysis, Infant, Pregnancy

ABSTRACT ID: 274

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POSTER TOUR 2

Day 1 | Wednesday 19 November 15:40-16:40

Respiratory infections: evidence to practice

PRESENTER

Héloïse Lucaccioni

ABSTRACT

Seasonal influenza vaccine effectiveness estimates in primary care, 2024/25 season, Europe

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BACKGROUND

High levels of influenza activity have been reported in Europe in 2024/25. We estimated vaccine effectiveness (VE) against primary care-attended influenza, by (sub)type, age group and in the vaccination target group (older adults ≥ 60 -65 years, individuals with chronic conditions, pregnant, healthy children with age-based recommendation, varying by country).

METHODS

We conducted a multicentre test-negative case-control study among individuals presenting to primary care with acute respiratory infection in 10 European countries. Cases were RT-PCR positive for influenza; controls were negative. All or a systematic sample of viruses were sequenced in each site. Vaccination was ascertained from electronic medical records, registry linkage or self-reported. The VE was calculated using logistic regression as (1-odds ratio of vaccination) $\times 100$, confounding-adjusted for site, age, sex, onset date, and chronic conditions.

RESULTS

We included 6,416 cases and 13,294 controls from weeks 40-2024 to 12-2025. The VE against influenza A(H1N1) pdm09 was 29% (95%CI: 16–39) overall, 30% (95%CI: 0–52), 30% (95%CI: 12–44), and 14% (95%CI: -17–37) in 0–17, 18–64 and ≥ 65 -year-olds, respectively, and 24% (95%CI: 9–38) in the target group. The VE against influenza A(H3N2) was 34% (95%CI: 19–48) overall; 70% (95%CI: 48–85), 12% (95%CI: -17–35), and 18% (95%CI: -29–48) in 0–17, 18–64

and ≥ 65 -year-olds, respectively, and 26% (95%CI: 4–44) in the target group. The VE against influenza B was 78% (95%CI: 71–83) overall, ranging 72–85% by age and target group. Of sequenced viruses, 90% A(H1N1)pdm09 were clade 5a.2a (C1.9), antigenically different from the vaccine; 83% A(H3N2) were 2.a3a.1 (J.2) and 51% B/Victoria were V1A.3a.2 (C.5.1), 26% V1A.3a.2 (C.5.7), 22% V1A.3a.2 (C.5.6), all similar to the vaccine.

CONCLUSIONS

We observed low VE against influenza A subtypes, particularly in ≥ 65 -year-olds, and high protection against influenza B. Investigation of potential antigenic divergence between circulating viruses and vaccine components is warranted. In low VE seasons, appropriate use of antivirals and non-pharmaceutical interventions should complement vaccination.

KEYWORDS: influenza, influenza vaccine, vaccine effectiveness, multicentre study, case control studies, test-negative design

ABSTRACT ID: 373

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POSTER TOUR 2

Day 1 | Wednesday 19 November 15:40-16:40

Respiratory infections: evidence to practice

PRESENTER

Ka Chun Chong

ABSTRACT

Association of nirmatrelvir/ritonavir and molnupiravir with long COVID in patients with chronic liver disease: cohort study

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BACKGROUND

Patients with chronic liver disease (CLD) are at a higher risk of severe COVID-19 as well as long COVID due to compromised liver function and related comorbidities. Our study examined the association of nirmatrelvir/ritonavir and molnupiravir with post-COVID-19 conditions among patients with CLD.

METHODS

This is a retrospective cohort study using real-world data obtained from the healthcare officials in Hong Kong. Patients were included if they were tested positive for SARS-CoV-2 between Feb 26, 2022 and Nov 9, 2023, aged ≥ 18 years, hospitalized with COVID-19, and had CLD prior to their COVID-19 diagnosis. We compared patients who received nirmatrelvir/ritonavir and molnupiravir against no antiviral treatment. Post-acute mortality (i.e., 21-365 days post infection), all-cause hospitalization, and hospitalization due to 13 selected sequelae were the study outcomes. Standardized-mortality-ratio weighting with doubly robust adjustment was applied to control for confounders. Cox models were used to estimate hazard ratios (HR) for the outcomes.

RESULTS

Of the screened patients with COVID-19, 442 and 750 CLD patients were prescribed nirmatrelvir/ritonavir and molnupiravir, while 821 and 1,702 CLD patients were in the control groups, respectively. Compared to patients receiving no treatment, CLD patients receiving nirmatrelvir/ritonavir had significantly lower risk of post-acute mortality (HR, 0.47 [95% CI, 0.33 to 0.67]; $p < 0.0001$), all-cause hospitalization (HR, 0.84 [95% CI, 0.71 to 0.99]; $p = 0.043$), and hospitalization due to chronic pulmonary disease and acute respiratory distress syndrome (ARDS). Compared with nirmatrelvir/ritonavir, molnupiravir was generally less effective. Molnupiravir was significantly associated with lower risk of post-acute mortality (HR, 0.70 [95% CI, 0.56 to 0.87]; $p = 0.0015$) and hospitalization due to ARDS, compared to no antiviral treatment.

CONCLUSIONS

While nirmatrelvir/ritonavir and molnupiravir are associated with reduced risk of post-COVID-19 conditions in patients with CLD, molnupiravir was generally less effective. Our findings suggest nirmatrelvir/ritonavir should be prescribed over molnupiravir for patients with stable hepatic conditions.

KEYWORDS: long covid; antiviral; paxlovid; post-covid

ABSTRACT ID: 399

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POSTER TOUR 2

Day 1 | Wednesday 19 November 15:40-16:40

Respiratory infections: evidence to practice

PRESENTER

Susana Monge

ABSTRACT

Two-season effectiveness of a single nirsevimab dose against RSV hospitalisation in healthy term-born infants: a population-based case-control study in Spain, October 2023 – March 2025

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BACKGROUND

In autumn 2023, Spain recommended nirsevimab, a monoclonal antibody against respiratory syncytial virus (RSV), to all infants born ≥ 1 April 2023, either at-birth or as catch-up immunisation. Initial effectiveness was high, but long-term protection remains unclear. We estimated effectiveness of a single nirsevimab dose in preventing RSV hospitalisations throughout two seasons in healthy term-born infants.

METHODS

Cases were children born 1 April 2023 through 31 March 2024 after 35 gestation weeks without major comorbidities, RSV PCR-positive, and hospitalized for respiratory symptoms, apnoea or sepsis between the 2023 immunisation campaign onset and 31 March 2025. For each case, we selected four healthy population density controls matched by birthdate (± 2 days) and province. Target trial emulation per-protocol effectiveness was estimated for at-birth immunisation (within 14 days of life) and catch-up immunisation (within 30 days of 2023 campaign onset) through inverse-probability-weighted conditional logistic regression, controlling for sex, gestational age, birthweight, multiple pregnancy, and previous non-RSV-related hospitalisation.

RESULTS

We included 334/1,292 cases/controls during first season and 328/1,269 during second season for at-birth immunisation group, and 235/905 and 188/713, respectively, for catch-up immunisation group. Two-season effectiveness (95%CI) was 68% (59;74%) for at-birth immunisation and 64% (52;72%) for catch-up immunisation, compared to 84% (79;88%) and 78% (70;84%) during first season and 19% (-21;46%) and -8% (-88;38%) during second season, respectively. Excluding cases with co-detection of non-RSV viruses increased effectiveness for at-birth and catch-up immunisation, respectively, to 74% (66;80%) and 69% (58;77%) overall, 84% (78;88%) and 78% (69;84%) during first season, and 37% (-3;62%) and 26% (-44;62%) during second season.

CONCLUSIONS

Nirsevimab was an effective long-term population-level intervention, decreasing by two-thirds the RSV hospitalisation rate during the first two seasons of life. Effectiveness during second season was low or null, particularly when not restricted to RSV single infections. Differential depletion of susceptibles during first season likely underestimated any subsequent protection.

KEYWORDS: Respiratory syncytial virus (RSV), Hospitalisation, Immunisation, Nirsevimab, Long-term effectiveness, Pediatric

ABSTRACT ID: 454

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POSTER TOUR 3

Day 1 | Wednesday 19 November 15:40-16:40

Outbreaks of food-borne diseases

PRESENTER

Syamend Saeed

ABSTRACT

Outbreak of Salmonella Agona linked to cross-contamination via doner kebab and electric knives in Hesse and Baden-Wuerttemberg, Germany, January 2022 - December 2024

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BACKGROUND

Salmonella enterica subsp. enterica (S.) serovar Agona, a rare serovar in Germany (2017-2021: 355/68,592 cases), was identified in an accumulation of 29 cases in Hesse in January 2024. Twenty cases occurred in only one district (District A1) over two years. This prompted an investigation by the Hessian State Office for Health and Care (HLfGP) with the aim to identify the source of the outbreak and implement control measures.

METHODS

We included laboratory-confirmed cases of S. Agona that were notified between 01/01/2022-31/12/2024. These cases were either: ¹ without isolate (probable case) or ² assigned to the outbreak strain (ct20182) based on WGS (confirmed case), who residing in District A1 and A2 in Hesse and B in Baden-Wuerttemberg, or in surrounding districts but within a distance of 50 km from, or visiting these districts. We analysed epidemiological data, including case consumption histories, to identify potential risk factors, and used WGS to trace the genetic relatedness of isolates.

RESULTS

A total of 63 S. Agona cases (Hesse: 25 confirmed, 18 probable; Baden-Wuerttemberg: 14 confirmed, 6 probable) were identified, with 89% (39/44) of sequenced isolates showing close genetic linkage. Cases were more likely to have consumed doner kebab compared to a population-based food survey, as determined using the screening method (OR 6.7, CI 2.66-16.9). Product and environmental investigations repeatedly detected the outbreak strain in doner kebab meat and electric knives.

CONCLUSIONS

The outbreak indicates the role of poor hygiene in doner kebab preparation, particularly contaminated electric knives. Previous research indicated that contaminated utensils (doner cutting knives) and contaminated food items (poultry) can be associated with inadequate cleaning protocols. Enhanced hygiene measures, stricter cleaning protocols, targeted sampling, and improved surveillance are recommended to prevent future outbreaks and ensure food safety.

KEYWORDS: Salmonella Agona, outbreak investigation, cross-contamination, electric doner knife, doner kebab

ABSTRACT ID: 56

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POSTER TOUR 3

Day 1 | Wednesday 19 November 15:40-16:40

Outbreaks of food-borne diseases

PRESENTER

Arthur Rakover

ABSTRACT

A large outbreak of multiple *Salmonella* serovars linked to alfalfa sprouts in Norway, October to December 2024

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BACKGROUND

In Norway, salmonellosis remains an important public health concern, ranking among the most reported gastrointestinal infections. Between October and December 2024, we investigated the largest nationwide *Salmonella* outbreak in Norway since 1980, involving multiple serovars. The investigation aimed to assess the outbreak's scope, identify the source, and implement control measures.

METHODS

Epidemiological analyses included trawling and targeted questionnaires, a matched case-control study (calculating odds ratio's using Lasso regression), and grocery receipt analysis. Whole-genome sequencing (WGS) was used to determine genetic links between *Salmonella* isolates from human cases, food, and environmental samples. Traceback investigations identified potential contamination sources.

RESULTS

We identified 230 cases (69% female, median age: 48 years), of which 33% (n=76) required hospitalization. Four *Salmonella* serovars—*S. Newport*, *S. Typhimurium*, *S. Kisarawe*, and *S. Kinondoni*—were involved, linked to same exposure. Sprout consumption was reported by 69% of the 26 cases interviewed using trawling or targeted questionnaires. Grocery receipts were collected from 17 cases, 9 of which had purchased sprouts. The matched case-control study included 47 participants—12 cases and 35 controls—and found that sprouts consumption was significantly associated with illness (penalized adjusted odds ratio 3.13). WGS established genetic links between clinical, food, and environmental isolates, identifying alfalfa sprouts as the outbreak source. Traceback investigations identified risk associated with seeds from an Italian supplier, previously associated with two *Salmonella* outbreaks in Norway in 2024 and multiple outbreaks across the European Union. The Italian supplier reported negative findings for *Salmonella* in their self-monitoring checks on seeds sent to Norway. Control measures included product withdrawal, seed batch quarantine, and public health advisories.

CONCLUSIONS:

This multi-serovar outbreak highlights the public health risks linked to the consumption of raw sprouts and emphasizes the importance of integrated surveillance, improved detection methods and stricter regulations when importing sprout seeds to prevent future outbreaks.

KEYWORDS: *Salmonella*, outbreak, sprouts, whole genome sequencing, case-control study, Norway

ABSTRACT ID: 148

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POSTER TOUR 3

Day 1 | Wednesday 19 November 15:40-16:40

Outbreaks of food-borne diseases

PRESENTER

Gülşen Barlas

ABSTRACT

Foodborne outbreak in 12 construction sites in Ankara province-Türkiye, August 2023

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BACKGROUND

Acute gastroenteritis is an important public health problem worldwide and in Türkiye. We received information from the notification system that there was an increase in admissions to various hospitals in Ankara province on August 13, 2023 with symptoms of nausea and vomiting. The cases were at construction sites in different regions, but they all consumed the same lunch menu. We investigated the outbreak to reveal its source and causative agent, and to prevent the recurrences.

METHODS

We defined patients as those who ate lunch on 13 August 2023, in 12 construction sites and had vomiting or diarrhoea. In this retrospective cohort study, we interviewed 201 individuals who had lunch. A catering company had prepared and distributed the food. We asked the company for a list of the sites and visited all. We calculated crude and food-specific attack rates, and Relative Risks (RR) with 95%CI. We tested 2 stool, and 2 food samples (chicken liver and soup). We inspected the company's environment.

RESULTS

Crude attack rate was 52.2%(105/201). Most common symptoms were nausea (88.6%) and vomiting (81.0%). Epidemiological curve indicated a point-source outbreak with a mean incubation of 3.2±2.2 hours. Eating of chicken liver (RR:3.2, 95%CI:1.3–7.8) was associated with illness. 2 stool samples tested positive with RT-PCR for Salmonella, Enteropathogenic E.coli, Enterotoxigenic E.coli. Chicken liver food sample tested positive for E.coli O157, coagulase positive Staphylococcus, Staphylococcal enterotoxin, anaerobic bacteria. Water samples of construction sites and the company's kitchen were negative for pathogens. The catering company's environment had a poor hygiene, and no temperature chart in storages.

CONCLUSIONS

In this point-source food outbreak, the short incubation period, symptoms and presence of the agent in food samples support the identification of S.aureus and its enterotoxin as the causative agent. We recommended hygiene training for employees, keeping a temperature chart in storages.

KEYWORDS: Staphylococcal Food Poisoning, Gastroenteritis, Cohort Studies, Disease Outbreaks

ABSTRACT ID: 152

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POSTER TOUR 3

Day 1 | Wednesday 19 November 15:40-16:40

Outbreaks of food-borne diseases

PRESENTER

Kate Liljepold

ABSTRACT

Multi-cluster outbreak of Salmonella Typhimurium sequence type 36 linked to alfalfa sprouts, Sweden, August – November 2024

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BACKGROUND

Salmonella Typhimurium sequence type (ST) 36 is rare in Sweden, with 3-13 cases reported per year between 2019-2023. In August 2024, we identified two genetic clusters of ST36 separated by 38 single nucleotide polymorphisms (SNPs), each clustering within 0-5 SNPs. By 09-09-2024, when the clusters had reached 17 isolates total, an outbreak investigation aiming to remove a possible common source was initiated.

METHODS

We defined a case as a person with a laboratory-confirmed ST36 infection reported in Sweden as of 01-08-2024. We excluded imported cases and cases with isolates >53 SNPs to the initial clusters. We performed a case-control study to test if consumption of food exposures more frequently identified in trawling questionnaires were associated with illness. Controls from a national web panel were matched 1:10 on age group, sex, and region. We used conditional logistic regression to estimate adjusted odds ratios (aOR) and 95% confidence intervals (95%CI). We conducted trace-back investigations using purchase information from cases and restaurants. We shared findings through international exchange platforms.

RESULTS

By 02-12-2024, 100 cases were reported, comprising nine clusters and five individual strains. Consumption of alfalfa sprouts was reported by 25% (8/32) of cases in the study and was the only exposure associated with illness (aOR = 4.15, 95%CI: 1.15-15.1). Trace-back investigation identified two Swedish alfalfa sprout producers using seeds from one European supplier. Salmonella was not detected in the sprouted seeds. Similar outbreaks in other European countries detected Salmonella in sprouted seeds from the same supplier. The Swedish outbreak ceased after recall of sprouts from the implicated seed batch on 26-11-2024.

CONCLUSIONS

Alfalfa sprouts were the likely outbreak vehicle. Our investigation highlights the importance of multifaceted approaches for identifying vehicles prone to poor recall, including garnishes. We emphasize the need for primary producers of alfalfa seeds and sprouts to identify and prevent possible contamination points.

KEYWORDS: Salmonella, outbreak, sequence typing, alfalfa sprouts, case-control study

ABSTRACT ID: 186

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POSTER TOUR 3

Day 1 | Wednesday 19 November 15:40-16:40

Outbreaks of food-borne diseases

PRESENTER

Thomas Thackray

ABSTRACT

Listeria monocytogenes (L. monocytogenes) CC217 outbreak linked to ready-to-eat smoked fish products in Great Britain, 2020-2025

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BACKGROUND

Listeria monocytogenes infection is a principally foodborne illness that primarily affects vulnerable individuals, including pregnant women, the elderly and immunocompromised. Listeriosis can be fatal and severe clinical outcomes make collection of reliable case histories challenging. In December 2020, a cluster of two cases was identified in England and an outbreak investigation initiated.

METHODS

Confirmed cases across GB were identified through routine whole genome sequencing (WGS). Case information (demographics, clinical severity, food history) was collected via enhanced surveillance questionnaires, descriptive epidemiological analyses were undertaken, the results informing food chain analysis and food safety interventions, including microbiological sampling of food and environment.

RESULTS

To date, 25 confirmed cases have been identified across GB; 56% were female (n=14), the median age was 78 years (range: 35-97 years), one was pregnancy-related and four died. Descriptive analyses identified ready-to-eat (RTE) smoked-fish as the likely vehicle, with 88% (n=22) of cases reporting consumption but from multiple retailers. The outbreak strain was detected in smoked-fish products sampled from; one retailer, the home of a case and RTE food company, but all tested prior to product use-by dates were below the legal limit. GB public health and food safety authorities reiterated guidance to pregnant and immunocompromised individuals on the risk of developing listeriosis when handling or consuming smoked-fish. Several retailers added warning labels to their smoked-fish products highlighting these risks. GB food authorities changed consumer guidance to avoid consumption of RTE smoked-fish, unless thoroughly cooked.

CONCLUSIONS

This is the largest Listeria outbreak identified through WGS in Great Britain and remains ongoing despite extensive risk communication. It outlines the difficulties of managing prolonged outbreaks of listeriosis, particularly given its persistence within food-processing environments and the allowance for low levels of Listeria at retail, while also highlighting the importance of effective control measures by industry to ensure RTE food is safe for consumers.

KEYWORDS: Listeria; surveillance; outbreak; smoked fish; salmon

ABSTRACT ID: 665

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POSTER TOUR 3

Day 1 | Wednesday 19 November 15:40-16:40

Outbreaks of food-borne diseases

PRESENTER

Ella Rodwell

ABSTRACT

Outbreak of Salmonella Saintpaul in the UK likely associated with watermelon consumption

E. Rodwell¹

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BACKGROUND

Non-typhoidal Salmonella is a leading cause of foodborne illness, often self-limiting and resolving within 7 days. In March-April 2025, the UK Health Security Agency identified and investigated a Salmonella Saintpaul cluster, genetically linked at the 5-single nucleotide polymorphism (SNP) level using whole genome sequencing.

METHODS

Cases were defined as resident in the UK and Crown Dependencies, belonging to the SNP designation 1.416.480.571.608.945.% and the first case in the household. Questionnaires (exploratory and trawling) were conducted with cases to gather exposure information and support hypothesis generation. A case-control study (frequency matched on age and sex, using market research panel from a previous Salmonella outbreak as the control group) tested our hypothesis that the outbreak was associated with watermelon consumption. Univariable and multivariable first logistic regression were conducted. Microbiological testing of supermarket watermelons was undertaken

RESULTS

The cluster comprised of 29 cases across the UK (n=28) and Crown Dependencies (n=1). Most cases were among children under 5 years old (13/29, 45%), and female (17/29, 59%). There were no genetic markers of antimicrobial resistance. Exploratory and trawling questionnaires revealed a fresh fruit products signal. Univariable analysis highlighted watermelon [OR 7.81, 95% CI 1.95-35.1]. Watermelon was the only exposure meeting inclusion criteria for the multivariable analysis (exposures declared by ≥50% of cases and p<0.2 in univariable analysis) and was associated with higher odds of being a case [adjusted OR 8.20, 95% CI 1.98-41.12]. Microbiological testing revealed no Salmonella in products tested.

CONCLUSIONS

This study highlights the complexities around obtaining a positive isolation from fresh produce with a short shelf life. Analytical epidemiology revealed that the likely source of the outbreak was associated with watermelon consumption, and this is not the first Salmonella Saintpaul outbreak associated with melon consumption in the UK. Descriptive epidemiology continues to be a powerful tool for formulating hypotheses.

KEYWORDS: Salmonella infections, epidemiology, disease outbreaks, foodborne diseases

ABSTRACT ID: 683

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POSTER TOUR 4

Day 1 | Wednesday 19 November 15:40-16:40

Surveillance of antimicrobial resistance

PRESENTER

Paulius Greicius

ABSTRACT

Endemic IncN plasmid caused the majority of blaKPC-2 Enterobacterales cases in Lithuania since 2019

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BACKGROUND

IncN plasmids are key vectors for blaKPC-2 spread amongst Enterobacterales worldwide. In Lithuania, their presence was first detected during a 2019 outbreak of ST392 *Klebsiella pneumoniae*. Since 2019, most instances of blaKPC-2-producing Enterobacterales identified through national genomic surveillance have been associated with an IncN replicon. In this study, we investigated the role of IncN plasmids in disseminating blaKPC-2 in Lithuania.

METHODS

Complete plasmid assemblies were generated by combining Oxford Nanopore and Illumina sequencing for 17 *Klebsiella pneumoniae* and *Escherichia coli* blaKPC-2-positive isolates collected between 2019 and 2025 from clinical specimen and municipal wastewater samples. Comparative plasmid analysis was performed with Pling. A multilocus sequence typing scheme based on 48 conserved plasmid backbone genes was developed and applied to confirm the presence of the same plasmid in short-read IncN-positive isolates identified through national surveillance.

RESULTS

All 17 complete IncN plasmid assemblies carried the blaKPC-2 gene and clustered within the same subcommunity of closely related mobile genetic elements. Although multiple structural rearrangements were observed, a conserved backbone of 48 genes with 0 allelic differences remained intact across all plasmids. This backbone was also detected in 142 of 147 blaKPC-2-positive clinical isolates identified through national genomic surveillance, spanning 5 cities, 8 Enterobacterales species and 2 distinct *K. pneumoniae* outbreaks.

CONCLUSIONS

Our findings demonstrate that the endemic circulation of a single IncN plasmid caused majority of blaKPC-2-producing Enterobacterales cases in Lithuania. This plasmid has persisted since at least 2019, conjugating across multiple sequence types and species. Importantly, it has spread beyond healthcare settings and is detectable in municipal wastewater of major cities. Similar dissemination of blaKPC-2 by IncN plasmids has been reported in other countries, including Germany and the Czech Republic, underscoring the central role of such plasmids in the spread of carbapenem resistance.

KEYWORDS: Carbapenem-Resistant Enterobacteriaceae, Plasmids, beta-lactamase KPC-2, Whole Genome Sequencing, Nanopore Sequencing

ABSTRACT ID: 105

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POSTER TOUR 4

Day 1 | Wednesday 19 November 15:40-16:40

Surveillance of antimicrobial resistance

PRESENTER

Carsten Van Rossum

ABSTRACT

An update on a regional AMR surveillance network in the Netherlands: challenges and opportunities

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BACKGROUND

Antimicrobial resistance rates in the Netherlands are among the lowest in Europe due to infection prevention and control (IPC) measures and national surveillance. Systematic and early genetic typing of multidrug resistant organisms (MDRO) on a regional level could help with early outbreak detection. We established a regional typing network (~2.1M inhabitants) in which we sequenced MDRO isolates from hospitals, general practitioners and care homes. We assessed the added value of early genetic typing in a regional surveillance network.

METHODS

Genomes of *Klebsiella pneumoniae* MDRO isolates (ESBL and CPE) – the first isolate/patient/year – were sequenced using Illumina NextSeq500 (regional, Radboudumc) and Illumina NextSeq550 (national, Type-Ned) Whole Genome Sequencing. Bioinformatic analysis was performed using 1928Dx software and included read cleaning, de novo assembly, MLST and resistance analysis. A genetic cluster was defined using a threshold of 20 alleles difference (cgMLST). Epidemiological data from Electronic Health Records was used to assess likelihood of transmission within genetic clusters.

RESULTS

From June 2023 to May 2025 we sequenced 199 samples from 192 patients. The most frequent sequence types were 307(n=27), 15(n=23) and 45/147/219(n=10). We identified 18 genetic clusters involving 64 isolates (median: 2, range: 2-22) and 15 sequence types. CPE resistance was found in three clusters. So far, two genetic clusters had probable epidemiologic links, one of which had not been identified through routine IPC investigations.

CONCLUSIONS

Implementing a genotyping network enhances MDRO cluster detection, allows for extended outbreak detection, provides insight into MDRO isolate's sequence types and resistance patterns and facilitates data sharing. Combining patient-related and geographic epidemiological with genetic data is crucial to eliminate duplicate isolates/patients and verify cluster plausibility in the context of clonally expanding sequence types. However, General Data Protection Regulation complicate data sharing and epidemiologic investigations between institutes. We will continue regional typing to evaluate long-term benefits, representativeness of isolates and cost-effectiveness.

KEYWORDS: *Klebsiella pneumoniae*, Public Health Surveillance, Drug Resistance Bacterial, Whole Genome Sequencing, Multilocus Sequence Typing

ABSTRACT ID: 290

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POSTER TOUR 4

Day 1 | Wednesday 19 November 15:40-16:40

Surveillance of antimicrobial resistance

PRESENTER

Jasmin S. Kutter

ABSTRACT

Nationwide Retrospective Study on the Performance of the WHO Mutation Catalogue for Genomic Prediction of Antibiotic Resistance in the *Mycobacterium tuberculosis* Complex in Spain, 2022-2025

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BACKGROUND

Effective treatment and control of drug-resistant tuberculosis (DR-TB) depends on rapid and accurate detection of antibiotic resistance, which is often constrained by traditional drug susceptibility testing (DST) methods. To address this, the WHO developed a mutation catalogue based on a globally sourced dataset enabling genomic prediction of phenotypic drug resistance for more than 30.000 variants of 13 anti-TB therapeutics. We assessed the performance of this catalogue using an independent, real-world dataset from across Spain collected over a three-year period.

METHODS

Culture-positive *Mycobacterium tuberculosis* Complex (MTBC) isolates submitted to the National Mycobacteria Reference Laboratory between 01.01.2022 and 15.02.2025 were included if whole-genome sequencing and phenotypic DST (pDST) data for at least one first- or second-line antibiotic were available. Genotypic drug resistance profiles (gDST) were predicted by matching MTBseq-identified single nucleotide polymorphisms with variants in the catalogue. gDST profiles were subsequently compared with phenotypes (pDST). Catalogue performance was determined by computing sensitivity, positive predictive value (PPV), and specificity with binomial exact 95% confidence intervals (CI). gDST/pDST discrepancies were studied to investigate country-specific differences in resistance.

RESULTS

We analysed 5122 gDST/pDST associations from 1223 TB strains. Sensitivity was highest for fluoroquinolones (100%;CI:79.41-100) and PPV was highest for first-line drugs (92.12%;CI:88.67-94.79). Specificity exceeded 94% for both drug categories. Analysis of gDST/pDST discrepancies revealed five phenotypically susceptible strains harbouring variants (*rpoB*_p.His445Asn, *rpoB*_p.Leu430Pro) associated with phenotypic borderline rifampicin resistance. The variant *ethA*_p.Leu272Pro, classified as "uncertain significance" was exclusively detected in phenotypically ethionamide-resistant strains (n=8).

CONCLUSIONS

The WHO catalogue is a valuable tool complementing pDST. Genomic prediction accelerates and substantially improves detection of DR-TB, including resistance potentially missed by pDST. This enables more accurate diagnosis and patient-tailored treatment, ultimately advancing DR-TB control. Future research should validate the catalogue using real-world datasets from different locations to refine region-specific resistance profiling and strengthen national and global surveillance efforts.

KEYWORDS: Drug-Resistant Tuberculosis, *Mycobacterium Tuberculosis* Complex, Antimicrobial Resistance, Drug-Susceptibility Testing, Whole-Genome Sequencing, Genomic Prediction

ABSTRACT ID: 479

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POSTER TOUR 4

Day 1 | Wednesday 19 November 15:40-16:40

Surveillance of antimicrobial resistance

PRESENTER

Jacquelyn McCormick

ABSTRACT

The epidemiology of sterile site acquired carbapenemase-producing Gram-negative organisms in England, October 2020 – September 2024

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BACKGROUND

Acquired carbapenemase-producing Gram-negative organisms (CPOs) are an increasing global public health threat. While in England 95% of CPO reports are from non-sterile sites, sterile-site CPO reports have increased since mandatory reporting began in October 2020. Sterile-site infections are associated with increased morbidity and mortality, and have limited treatment options. We investigated demographics of CPO sterile-site cases to improve understanding of CPO epidemiology.

METHODS

CPO laboratory reports from October 2020-September 2024, classified as sterile-site (e.g. blood, bone) or non-sterile site, were extracted from UKHSA's national laboratory database. Patient demographics, carbapenemase families and organisms were analysed and compared to UKHSA published all specimen-type CPO data.

RESULTS

There were 24,526 CPO records reported from 14,151 patients; 741 patients had sterile-site isolates (termed 'cases'). Cases increased 123% from n=121 in 2020/21 to n=270 in 2023/24. Half of cases (51.6%) were aged ≥65y and 43.9% aged 18-64y (versus 60.0% and 37.5% for all specimen types); 65.1% of cases were male (versus. 55.8% for all specimen types). London reported the most cases (37.4%, versus 30.8% for all CPO specimen types). NDM was the most common carbapenemase family (42.5%), followed by OXA-48-like (37.8%) and KPC (15.5%); 58 cases (7.8%) had two families with NDM/OXA-48-like the most common (n=42), other combinations were ≤5 cases each. The most common organisms from sterile-sites were *Klebsiella pneumoniae* (47.2%), *Escherichia coli* (23.4%) and *Enterobacter* spp. (17.4%) compared with all CPO specimen types where *K. pneumoniae* and *E. coli* accounted for 30-35% each.

CONCLUSIONS

Cases with sterile-site records were disproportionately younger, male, in London, and more likely to have *K. pneumoniae* versus reports from all specimen types. Given the difference between sterile-site and all specimen types and the increase in sterile-site cases, further work examining clinical risk factors, drivers and outcomes of sterile-site cases is imperative to identify interventions to reduce burden and transmission in England.

KEYWORDS: Antimicrobial Resistance, Surveillance, Carbapenemase-Producing Enterobacterales, United Kingdom

ABSTRACT ID: 667

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POSTER TOUR 4

Day 1 | Wednesday 19 November 15:40-16:40

Surveillance of antimicrobial resistance

PRESENTER

Sebastian Haller

ABSTRACT

Majority of cases with carbapenemase-producing *Klebsiella pneumoniae* are part of genomic clusters deriving from either regional, national, or international spread in Germany, 2022-2023

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BACKGROUND

The emergence and spread of carbapenemase-producing Enterobacterales (CPE) pose a major threat to public health. Over the last decade, numbers of infections with CPE have increased, particularly with *Klebsiella pneumoniae* (CP-Kp). We analysed data from the Integrated-Genomic-Surveillance (IGS) to understand the spread of CP-Kp in Germany.

METHODS

In the IGS, mandatorily notified cases, containing comprehensive information about CPE infections and colonisations in Germany, are linked through probabilistic matching to isolate data from the National Reference Centre (NRC), including Illumina whole-genome sequences (WGS). We selected CP-Kp cases from notifications and, for clustering analysis, those WGS-confirmed by the NRC. Clustering was determined through core-genome multilocus sequence typing (cgMLST), using a threshold of ≤ 15 allelic differences. Clusters were compared by cases' location/date of detection and exposure.

RESULTS

From 2022-2023, notified cases with CP-Kp increased from 2,349 to 2,931 (+25%), while numbers of non-duplicate CP-Kp isolates received at the NRC increased from 1,322 to 1,486 (+12%). In 2023, 1,276/1,486 CP-Kp (86%) isolates were available for WGS and 68% sequences could be matched to notification data. Analyses of cgMLST showed that 69% (884/1,276) of cases were found within genomic clusters. For CP-Kp, we found a total of 155 clusters with the largest consisting of 72 cases of *K. pneumoniae* ST395, many of which harboring carbapenemases NDM-1 and OXA-48. Spatiotemporal cluster analyses revealed three patterns of transmission: imported cases from ongoing outbreaks abroad, transmission in German hospitals from imported cases, or regional and local outbreaks.

CONCLUSIONS

CP-Kp are strongly increasing in Germany with unexpectedly high numbers of genomic clusters. Reasons for spread and appropriate control measures differ according to the patterns of transmission. This highlights the necessity of a WGS-based surveillance, but also indicates that much effort is needed in investigating the cluster signals to identify ongoing chains of infection which may be interrupted through infection prevention and control.

KEYWORDS: *Klebsiella pneumoniae*, Antimicrobial resistance, cluster, genomic surveillance

ABSTRACT ID: 716

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POSTER TOUR 5

Day 1 | Wednesday 19 November 15:40-16:40

Preparedness

PRESENTER

Motuma Guyassa

ABSTRACT

Intra-Action Review IAR of Cholera emergency response in Malawi: Country experience

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BACKGROUND

Malawi, as with many African countries, is vulnerable to natural disasters like floods, cyclones, and associated hazard related epidemics. In March 2022, due to the storm there was a cholera outbreak which had become protracted and continued till August 2023. On November 20, 2022, the government decided to conduct an Intra action review (IAR) with the support of Africa Centres for Disease Control and Prevention, World Health Organization and key partners to document key lessons and implement short, midterm and long-term recommendations to the ongoing emergency response.

METHODS

The IAR review, adapted from the World Health Organization (WHO) guideline working group discussions and document review, focused on the eight response pillars that included country-level coordination, planning and monitoring, surveillance, case and contact tracing, case management, infection prevention and control, operational support and logistics, national laboratories, points of entry, risk communication and community engagement, and vaccination. We also visited two of the affected districts, Salima and Nkhosakota.

RESULTS

Lessons learnt were identified from each pillar and recommendations were derived. challenges included: the need to strengthen coordination of stakeholders, access to funds for better coordinated response, the need to conduct studies to address the risk communication issues and main drivers of outbreaks in hotspot areas. Main recommendations of IAR included the need to fully operationalize the cholera incident management team with multisectoral engagement, to involve all relevant stakeholders in cholera daily update meetings, to avail public health emergency operating centre with readily available funding for response, and to conduct a knowledge, attitude, and practice (KAP) survey on affected communities along the lake Malawi to understand contributing factors to the outbreak.

CONCLUSIONS

Conducting an IAR is important during an ongoing outbreak to improve response. IAR should also be routinely conducted in protracted outbreaks as they allow an opportunity to adjust and apply effective control measures

KEYWORDS: Key Words: Intra-action review, Cholera, public health emergency, public health emergency operating centre, outbreak, global health security, emergency preparedness

ABSTRACT ID: 542

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POSTER TOUR 5

Day 1 | Wednesday 19 November 15:40-16:40

Preparedness

PRESENTER

Femke Overbosch

ABSTRACT

Advancing integrated scientific advice in pandemic preparedness

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BACKGROUND

A whole-of-society approach to infectious disease outbreak management requires balanced input from diverse disciplines. However, scientific advisory bodies for pandemics often underrepresent social and behavioural sciences, limiting the range of response or mitigation strategies. This ongoing study explores how simulation exercises can support multidisciplinary collaboration to deliver integrated policy advice. Key questions include: ¹ Is timely, integrated, and actionable multi-disciplinary advice feasible during outbreaks? ² Which scientific components are best delivered integrated versus in parallel?

METHODS

Three simulation exercises are conducted involving a zoonotic disease X, which is later revealed to be a less severe Ebola variant with asymptomatic and pre-symptomatic transmission. We incorporated insights from previous research and simulations. Policymakers develop advice questions and participate in interdepartmental policy tables to evaluate the advice. Experts from biomedical, behavioural and social sciences and humanities collaborate: real-time behavioural data, transmission models, and resilience strategies. Multidisciplinary teams develop policy advice using the WHO-INTEGRATE framework. Sessions are recorded and analysed, followed by surveys and interviews.

RESULTS

Preliminary findings show that integrated advice is feasible when preparedness infrastructure is in place. Topics with diverse and potentially opposing perspectives, such as proposed public health measures affecting children, the proportionality of measures, and stigmatization, benefited most from integration. Success factors include shared terminology, knowledge exchange, collaborative experience, and structured deliberation frameworks.

CONCLUSIONS

Our study suggest that integrated scientific advice is valuable. Integration is most effective when preparedness infrastructure supports cross-disciplinary interpretation of data. These insights inform future outbreak preparedness, providing actionable guidance on organizing multidisciplinary advisory bodies.

KEYWORDS: pandemic preparedness,interdisciplinary research,advisory committees,infectious disease outbreak,public health

ABSTRACT ID: 568

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POSTER TOUR 5

Day 1 | Wednesday 19 November 15:40-16:40

Preparedness

PRESENTER

Neema Kamara

ABSTRACT

Prioritisation of epidemic-prone diseases for emergency preparedness and response in Southern Africa, 2024

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BACKGROUND

Disease prioritisation is important for public health strategic planning. The Africa Centres for Disease Control and Prevention in collaboration with the European Centre for Disease Prevention and Control, conducted a prioritisation exercise for epidemic-prone diseases in Southern Africa, to determine priorities for the region, inform preparedness planning, guide resource allocation and strengthen risk ranking methodology knowledge among Member States.

METHODS

We employed a risk ranking methodology based on Multi-Criteria Decision Analysis, previously used by the Africa CDC. We held a workshop in Gaborone, Botswana from 25-27 November 2024, inviting multidisciplinary public health experts from 10 Southern Africa countries. During the workshop, experts selected epidemic-prone diseases and then scored them against 17 pre-defined criteria assessing risk⁸ and preparedness and response⁹. We calculated median scores, interquartile ranges, and overall risk as the product of risk trajectory-epidemic potential and disease severity. Using the Delphi approach, we presented the risk ranking to the participants to reach a consensus on the outcome.

RESULTS

Eighteen diseases were selected. Overall, the top five risk-ranked diseases were cholera (10.56), rabies (10.35), influenza (10.03), malaria (9.50) and measles (8.44). Measles scored the highest risk trajectory-epidemic potential score (3.38), followed by cholera (3.17), influenza (3.17) and malaria (3.17). Ebola Virus Disease (EVD) received the highest severity score (4.00), followed by Crimean-Congo Haemorrhagic Fever (CCHF) (3.67) and rabies (3.50). The highest preparedness score was for measles (3.73), while the lowest was attributed to unknown disease (0.69), CCHF (1.24), and EVD (1.33). The top five risk-ranked diseases scored higher in preparedness.

CONCLUSIONS

The exercise revealed heterogeneous preparedness levels for priority diseases. The results underscore the necessity of strengthening integrated intersectoral approaches to health emergencies preparedness and response. In the context of reduced global funding for health, the outcomes of the exercise can guide resource allocation, preparedness planning and response in Southern Africa.

KEYWORDS: risk prioritization, risk ranking, epidemic-prone diseases, emergency preparedness, emergency response, Southern Africa

ABSTRACT ID: 629

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POSTER TOUR 5

Day 1 | Wednesday 19 November 15:40-16:40

Preparedness

PRESENTER

Maude Montani

ABSTRACT

From influenza to COVID-19 to future pandemic threats: Revising the Swiss national pandemic plan

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BACKGROUND

The COVID-19 pandemic revealed gaps in pandemic preparedness and response, highlighting the need for robust, adaptive planning tools. In response, the Swiss Federal Office of Public Health (FOPH) initiated a comprehensive revision of the national pandemic plan. Unlike previous editions, which focused solely on influenza, the new plan adopts a generic approach applicable to pathogens with pandemic potential, with a focus on respiratory infections as a model. It serves as a strategic and operational framework for coordinated preparedness and response across all levels of government and the healthcare system.

METHODS

The revision process started in 2022 and was led by the FOPH, in close collaboration with the Federal Commission for Pandemic Preparedness (FCP). Numerous federal, cantonal, and non-governmental stakeholders were involved through a participatory, consultative process. An important step was a systematic review of a draft version by the stakeholders in 2024, which governed the further revision process. A first final version was published in mid 2025.

RESULTS

The new plan is structured around three modules: strategic planning principles, operational themes for surveillance, prevention and response, and cross-cutting themes, such as security of supply and communication. The plan is newly published in the form of a modular, digitally accessible platform to facilitate regular updates and integration with other preparedness instruments. The revised pandemic plan defines roles and responsibilities of key actors, supports coordinated response planning, and provides practical tools such as checklists and implementation guides. It promotes interoperability between national and subnational preparedness structures and emphasizes the importance of readiness exercises.

CONCLUSIONS

The new Swiss national pandemic plan represents a shift toward a collaborative, digitally enabled, and adaptable preparedness framework. By integrating lessons learned from recent crises, in particular the Covid-19 pandemic, the plan lays the groundwork for a more resilient pandemic response system in Switzerland.

KEYWORDS: Pandemic Preparedness Plan; Pandemics; Communicable Disease Control; Administration; Public Health; Intersectoral Collaboration; Health Policy; Switzerland

ABSTRACT ID: 731

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POSTER TOUR 5

Day 1 | Wednesday 19 November 15:40-16:40

Preparedness

PRESENTER

Kirsten Bisschops

ABSTRACT

Infodemic preparedness through social listening: Generating insights into (mis)information about measles vaccination in Amsterdam, August-September 2024

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BACKGROUND

Suboptimal vaccination coverage for Measles, Mumps, and Rubella (MMR) and recent increases in measles cases in the Netherlands, prompted innovation to support informed vaccine decision-making. This project at the Public Health Service Amsterdam (PHSA), responsible for local outbreak response and vaccination programs, aims to: ¹ establish social listening for infodemic management; ² generate insights into measles-related narratives and (mis)information influencing confidence in MMR-vaccination.

METHODS

First, we identified potential social listening data sources and tools within the PHSA. Second, in August-September 2024, we gathered data from sources that provide contextual and substantive information, covering perspectives of citizens, medical and communication professionals and media for measles vaccination specifically. Third, we generated insights through quantitative and qualitative (thematic) analysis for insights reporting.

RESULTS

We identified 20 sources for social listening. From these, 7 were selected for active listening based on cost, availability and relevance. Sources that were monitored included PHSA internal sources, e.g. youth nurses observations, website statistics, source and contact tracers' inbound phonelines and press requests, and media sources, e.g. social media (via Coosto), news media (LexisNexis), and Google Trends. Through inductive thematic analyses, we observed a variety of online and offline questions, concerns, narratives, mis- and disinformation regarding measles (vaccination). Prevalent identified themes concern: 1) false claims (misinformation) alleging COVID-19 vaccines caused immunodeficiency,

leading to measles and Mpox, 2) narratives suggesting that vaccination against measles is unnecessary or ineffective (misinformation), and 3) concerns about combining vaccines. Moreover, low search activity and contextual (e.g. articles on reported cases, interventions and policy changes) themes were detected.

CONCLUSIONS

We established real-time insight generation during an anticipated measles outbreak, capturing relevant narratives that can guide an interdisciplinary response. The established structured social listening framework is essential for understanding public needs, addressing misinformation, and is currently re-activated to inform effective communication during a cluster of measles cases in Amsterdam.

KEYWORDS: Communication, Infodemic, Measles Vaccine, Infodemiology

ABSTRACT ID: 775

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POSTER TOUR 6

Day 1 | Wednesday 19 November 15:40-16:40

Surveillance of infectious diseases

PRESENTER

Antonia Genath

ABSTRACT

Human Q fever cases in Germany (2001-2023): A 23-year descriptive overview of national surveillance data

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BACKGROUND

Q fever, caused by *Coxiella burnetii*, is a zoonotic disease affecting humans and animals worldwide, with major reservoirs in ruminants and potential for large outbreaks in humans. In Germany, Q fever has been notifiable since 2001, but comprehensive epidemiological studies are scarce. This study analyses the epidemiology of human Q fever cases from 2001-2023 to assess temporal trends, identify affected groups, and inform prevention and control strategies.

METHODS

We conducted a descriptive analysis of Q fever cases reported through national surveillance (SurvNet) in Germany from 01.01.2001–31.12.2023. We compared sporadic and outbreak-associated cases, and analysed incidences and distributions across demographic and clinical characteristics. We assessed temporal trends by aggregating data into 5-year periods and using Mann-Kendall tests.

RESULTS

From 2001-2023, 4,718 Q fever cases (60% male, mean age: 46 years) were reported, with an average annual incidence of 0.25 per 100,000 inhabitants. The annual incidence varied considerably (0.07-0.5) but declined overall (2001-2005:0.34 - 2021-2023:0.09), primarily due to a notable reduction of outbreak-associated cases. The stable incidence of sporadic cases led to their rising proportion (2001–2005:28% - 2021–2023:89%). Over time, mean age (2001-2005:46 - 2021-2023:52), hospitalisation rate (27%-63%), case fatality (0.36%-0.42%), and proportion of travel-associated cases (2.4%-12%) increased, particularly among sporadic cases.

CONCLUSIONS

Preliminary results suggest a shift from predominantly middle-aged male outbreak-associated cases to more sporadic, older, and severe cases suggesting a need for adapted risk communication. The decline in outbreak-associated cases may reflect improved public health measures, including ruminant vaccination since 2010, which could have prevented larger outbreaks. However, potential underreporting of moderate cases and outbreaks cannot be excluded, underscoring the potential need for surveillance evaluation. In the event of frequent sporadic cases, close coordination between health and veterinary authorities and increased awareness in regional healthcare facilities should be ensured to detect further potential cases.

KEYWORDS: Q fever, Surveillance, Trend analysis, Epidemiology

ABSTRACT ID: 164

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POSTER TOUR 6

Day 1 | Wednesday 19 November 15:40-16:40

Surveillance of infectious diseases

PRESENTER

Lilas Mercuriali

ABSTRACT

20 years of hepatitis C surveillance in correctional facilities in Lower Saxony, Germany – A surveillance system evaluation

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BACKGROUND

Correctional facilities (CF) are disproportionately affected by hepatitis C virus infection (HCV) and are key settings for HCV elimination according to Germany's Strategy for the prevention and control of HIV, HBV, HCV, and other STIs. However, the 2024 ECDC led mid-term review of the strategy highlighted the lack of recent HCV data in CF. We conducted an initial evaluation of the 2005-established HCV surveillance system in CF of Lower Saxony.

METHODS

Following ECDC and CDC guidelines, we assessed the system's simplicity, data quality, flexibility, representativeness and usefulness, by reviewing system documentation and conducting informal interviews, during 2024. Additionally, during October-November 2024, we conducted two online surveys aimed at users of the system (health and judicial authorities), and health professionals (CFHP).

RESULTS

We assessed the system to be simple, as it relies on completing a low-threshold questionnaire (LTQ) on HCV risk factors upon patient sampling. LTQ availability for cases ranged from 46% ²⁰⁰⁸ to 8% ²⁰¹⁶. Amongst those, data quality was moderate, with LTQ-item completeness ranging from 15% (piercings acquired in CF) to 96% (presence of tattoos). Flexibility was constrained with no adaptation to evolving surveillance needs, including discovery of direct-acting antivirals. Representativeness was limited due to inconsistent participation, with 3/16 facilities in Lower Saxony never completing the LTQ. We obtained 32 responses (22 CFHP and 10 users) in the online surveys). In total 14/22 and 9/10 respondents respectively knew about the LTQ. Usefulness was constrained by infrequent analyses (5 pooled analyses over 20 years, focused on prevalence and risk factor quantification), and a case definition relying solely on serostatus.

CONCLUSIONS

The HCV surveillance system provides valuable information but is hindered by incomplete participation, inconsistent data quality and a need to adapt to new surveillance objectives. Addressing the identified issues is essential to align with hepatitis elimination goals in Germany.

KEYWORDS: Hepatitis, Correctional Facilities, Surveillance, Germany

ABSTRACT ID: 268

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POSTER TOUR 6

Day 1 | Wednesday 19 November 15:40-16:40

Surveillance of infectious diseases

PRESENTER

Larisa Savrasova

ABSTRACT

Invasive pneumococcal disease in Latvia and factors associated with fatal disease outcome, 2012-2022

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BACKGROUND

Streptococcus pneumoniae is the major pathogen responsible for invasive pneumococcal disease (IPD), manifesting as bacteremic pneumonia, septicemia, and meningitis. The introduction of pneumococcal conjugate vaccines (PCVs) has significantly reduced the incidence of IPD caused by vaccine-covered serotypes. Age, common chronic diseases (not specified), oncology, immunosuppression, HIV infection, nosocomial infection, and sepsis as clinical presentation are described as associated with lethal IPD outcomes. The objectives of our study were to investigate factors associated with death from IPD based on surveillance data in Latvia over 11 year period.

METHODS

We conducted a retrospective population-based cross-sectional study using IPD surveillance data from Latvia over 11 years (2012-2022). IPD cases were defined according to the European Union case definition. Multivariable logistic regression was used to explore associations between case lethality and various risk factors including IPD clinical presentations, comorbidities, *S. pneumoniae* serotypes, and age groups (0-17, 18-64 and 65+).

RESULTS

811 IPD cases were reported during the study period (males, 60,2%). The highest IPD rate was reported in 2022 (6,7 cases per 100,000 inhabitants). The highest mean annual incidence during the study period was reported in infants and those aged 65 or more. The most common serotypes were 3 and 19A, 17,4% (131/752) and 10,9% (82/752) respectively. Reported total case lethality was 34.4% (279/811). The highest, at 51.4% (36/70), was reported in 2021. After adjusting for meningitis as clinical presentation and comorbidities (HIV and hepatitis C), PCV13nonPCV10 serotypes (adjusted OR 1.42, 95%CI 1.021-1.985 p-value 0.037) and age 65+ (adjusted OR 1.77, 95%CI 1.295-2.43 p-value <0.001) were associated with fatal IPD outcome.

CONCLUSIONS

The findings highlight the importance of *S. pneumoniae* serotype monitoring and the necessity of IPD continuous surveillance and age-targeted vaccination strategies to mitigate the impact of IPD in Latvia.

KEYWORDS: IPD, *S. pneumoniae* serotypes, PCV, Latvia

ABSTRACT ID: 321

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POSTER TOUR 6

Day 1 | Wednesday 19 November 15:40-16:40

Surveillance of infectious diseases

PRESENTER

Maria Gori

ABSTRACT

Integrated genomic surveillance of pregnancy-associated *Listeria monocytogenes* infections in northern Italy, 2021–2024

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BACKGROUND

Pregnant women have up to 18-fold greater risk of acquiring *Listeria monocytogenes* infection compared to the overall population, due to decreased cellular immunity. Listeriosis in pregnancy is associated with major adverse outcomes, including preterm birth and foetal death. This study presents the findings from a 4-year integrated genomic surveillance for listeriosis in Lombardy (northern Italy, ~10 million population), focusing on the clinical and molecular characteristics of the pregnancy-associated cases to identify possible sources of exposure and preventive measures.

METHODS

All clinical samples collected from patients hospitalised with a diagnosis of invasive listeriosis were typed with whole-genome sequencing using Illumina technology. Cluster analysis was performed with cgMLST and SNPs approaches. Demographic, clinical, and microbiological data were collected from a standardised report form. Laboratory data of human isolates were combined with those of food collected as part of outbreak investigations.

RESULTS

Out of 271 cases, 14 (5.2%) were pregnancy-associated, all occurred after the 24th week of gestation. The median age of the mothers was 34 years (range 23–41). All pregnancies with known outcome (11/14, 78.6%) resulted in preterm birth. Six sequence types (STs) were recognized. Five pregnancy-associated cases fell into 4 clusters. Epidemiological investigation revealed that 3 of these clusters were part of strong-evidence outbreaks at national scale, with links to food isolates (ST1-black olives, ST1-porchetta, ST155-frankfurters).

CONCLUSIONS

The percentage of pregnancy-associated listeriosis was slightly higher than those reported by the ECDC in the EU (~4%). All identified cases occurred in the second half of gestation. This could be explained by the fact that earlier stages miscarriage is seldom investigated. This study underlines the importance of genomic surveillance and the urgent need for revised, evidence-based dietary guidelines tailored to pregnant women. Future research should explore food habits and communication barriers, providing insights for targeted control strategies to protect this high-risk group and prevent severe outcomes.

KEYWORDS: *Listeria monocytogenes*, Pregnancy, Genomics, Cluster Analysis, Listeriosis

ABSTRACT ID: 464

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POSTER TOUR 6

Day 1 | Wednesday 19 November 15:40-16:40

Surveillance of infectious diseases

PRESENTER

Anne-Sophie Barret

ABSTRACT

Changing epidemiology of invasive meningococcal disease in France, 2023 - 2025

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BACKGROUND

In France, the incidence of invasive meningococcal disease (IMD) dropped during the COVID-19 period and subsequently increased following the relaxation of control measures. Prior to 2025, the vaccination strategy targeted serogroup C IMD (since 2010) and serogroup B IMD (since 2022). The changing epidemiology of IMD post-COVID-19 prompted to revise these recommendations. Our objective was to describe the post-COVID-19 epidemiology of IMD in France in 2023-2025 compared to pre-COVID-19.

METHODS

We used surveillance data based on mandatory notification of IMD, along with typing and sequencing data from the National Reference Center for Meningococci and Haemophilus influenzae. We compared the 2023-2025 (up to June 2025) period to 2018-2019, and presented data by age group and main serogroups.

RESULTS

In 2024, 616 IMD cases were notified – the highest number since 2010 – with an incidence rate of 0.9 per 100,000 inhabitants. The increase continued during the 2024-2025 winter, with an exceptionally high peak in January-February 2025. Compared to 2018–2019, serogroups W and Y cases more than doubled in 2023–2024, while serogroup B rose slightly (+18%) and serogroup C declined markedly (–88%). Between 2023 and 2025, there were several IMD serogroup B clusters among young adults prompting local vaccination campaigns, albeit with low uptake.

CONCLUSIONS

The post-COVID period was characterised by a shift in IMD epidemiology, with emerging strains and an exceptionally high incidence in 2024-2025. In response to the increase in W and Y IMD cases, in January 2025, the French Ministry of Health reinforced the vaccination strategy introducing mandatory vaccination for infants for both MenB and MenACWY (replacing MenC), with a catch-up for children up to 4 years. In addition, ACWY vaccination for adolescents aged 11 to 14 with a catch-up campaign up to 24, and reimbursement of the MenB vaccine for those aged 15 to 24 have also been recommended.

KEYWORDS: Meningococcal infections, Neisseria meningitidis, immunization programs, vaccination

ABSTRACT ID: 589

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POSTER TOUR 6

Day 1 | Wednesday 19 November 15:40-16:40

Surveillance of infectious diseases

PRESENTER

Laure Mortgat

ABSTRACT

Age-standardised mortality rates related to viral hepatitis B and C in Belgium

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BACKGROUND

As 2030 approaches, Belgium must assess its progress toward eliminating hepatitis B and C, a commitment made in 2015. While hepatitis-related deaths are rising globally, Belgium lacks data documenting hepatitis-attributable mortality. Since 2021, the World Health Organization (WHO) recommends using absolute rather than relative mortality targets. Our objective was to estimate age-standardised hepatitis B and C mortality rates in Belgium and assess progress towards elimination.

METHODS

Mortality and population data were obtained from Statistics Belgium. We analysed the Belgian national cause-of-death registry data from 2008 to 2022. Hepatitis B and C deaths were identified using ICD-10 codes: B16.2, B16.9, B16.0, B16.1, B18.1, B18.0 (hepatitis B) and B17.1, B18.2 (hepatitis C). Deaths were included if any of these codes were listed in any causes of death. National and regional crude and age-standardised mortality rates were calculated using the Belgian mid-year 2015 population as reference.

RESULTS

During these 15 years, hepatitis B and C were reported in 2231 and 655 death certificates, respectively. In 2022, Belgium's age-adjusted hepatitis C mortality rate was 0.76 per 100,000, compared to 2.78 in 2008. This rate showed a decreasing trend and met the WHO 2030 target ($\leq 2/100,000$) since 2010, except in Brussels. Hepatitis B mortality rate was 0.35 in 2022, compared to 0.72 in 2008. From 2009 to 2022, the trend fluctuated but remained below the 2030 target ($\leq 4/100,000$) across all regions. For both infections, mortality was highest in Brussels, followed by Wallonia and Flanders.

CONCLUSIONS

Hepatitis B and C related mortality are low in Belgium, and below the 2030 WHO targets. Despite these positive findings, efforts are still needed to reduce the burden of hepatitis in Belgium. Alternative methods to estimate hepatitis attributable deaths should be implemented to validate these results.

KEYWORDS: Hepatitis B, Hepatitis C, Mortality, Belgium

ABSTRACT ID: 779

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POSTER TOUR 7

Day 1 | Wednesday 19 November 15:40-16:40

Late breakers 1

PRESENTER

Umalkhair Jama Mohamoud

ABSTRACT

Outbreak investigation of visceral leishmaniasis in Sanaag Region, Somaliland, December 2024–August 2025

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BACKGROUND

Visceral leishmaniasis (VL) has been documented in northern Somalia, including 118 confirmed cases in Bosaso, Bari, during 2013–2019. In late December 2024, a suspected case at Erigavo General Hospital led to rapid supply of rK39 rapid diagnostic tests and initiation of an outbreak investigation with enhanced facility-based surveillance.

METHODS

We analysed routine hospital line-list data from December 2024 to August 2025. A suspected case was defined as fever ≥ 2 weeks with splenomegaly and/or wasting and malaria excluded; confirmation required a positive rK39 rapid diagnostic test. All suspected patients were tested, and all confirmed cases were treated according to national guidelines. Weekly trends were compiled by report date (or admission when report date was missing) and interpreted alongside clinical and logistics notes.

RESULTS

Among 143 patients tested, 41 (28.7%) were rK39-positive; six died (case-fatality 14.6%). Children predominated: 35/41 (85.4%) were <10 years and 30/41 (73.2%) were <5 years; only 6/41 (14.6%) were ≥ 15 years. Males accounted for 24/41 (58.5%). Cases clustered in coastal and sub-coastal Guban settlements, with the largest shares in Maydh (24.4%) and Laasasurad (22.0%), and smaller clusters in Erigavo, Kulmiye, Xiis, Gudmo Biyo Cas and Hluul. Intermittent stock-outs of rK39 tests and antileishmanial drugs constrained timely case confirmation and treatment.

CONCLUSIONS

Facility-based surveillance in Erigavo revealed a persistent, pediatrics-predominant VL focus likely under-ascertained because of access and supply constraints. Priorities are to ensure uninterrupted rK39 testing and treatment, strengthen community case-finding and engagement, and implement targeted vector control to curb morbidity and mortality and interrupt transmission across northern Somalia.

KEYWORDS: Leishmaniasis, Visceral; Epidemiologic Surveillance; Outbreaks; Somalia; Immunochromatography; Child, Preschool

ABSTRACT ID: 828

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POSTER TOUR 7

Day 1 | Wednesday 19 November 15:40-16:40

Late breakers 1

PRESENTER

Fanny Chereau

ABSTRACT

Local multistrain outbreak of Shiga toxin-producing *Escherichia coli* (STEC) linked to the consumption of meat from butcher shops, France, June to July 2025

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BACKGROUND

On June 17, 2025, the regional health agency of Hauts-de-France was notified of 3 cases of STEC infection in children residing in the same city, including one death from hemolytic uremic syndrome (HUS). The French national public health agency initiated epidemiological investigations to describe cases, identify a common contamination source, and implement appropriate control measures.

METHODS

Epidemiological investigations using a standardized questionnaire collected food and environmental exposures prior to diarrhea onset. Food and environmental samples were collected at suspected establishments. Human and food isolates were compared using whole-genome sequencing.

RESULTS

Between June 17 and July 18, 2025, 34 cases were identified, including 11 HUS and 1 death, median age 6 years (range: 9 months to 73 years). Among 31 interviewed cases, 83% had consumed meat products, mostly purchased from local butcher shops in the same city. Based on initial epidemiological data, inspections and product traceback, control measures were taken within 48 hours of the start of investigations, with preventive closure of the suspected shops. Two outbreak strains were ultimately identified from cases, a predominant O26:H11 strain (20 cases) and a O146:H21 strain (1 case), and detected in multiple meat samples from 3 butcher shops, confirming the epidemiological link. Additionally, STEC strains of 5 other serotypes were isolated from cases, including some cases of multistrain infection.

CONCLUSIONS

Epidemiological investigations rapidly identified a suspected contamination source and guided health authorities to implement timely control measures. Rapid closure of the suspected establishments was key for limiting further spread as investigations continued. Multistrain contamination in both cases and food was unusual. Investigating products from butcher shops was challenging for traceback as cases consumed multiple meat types. This outbreak highlights the importance of hygiene in meat production and distribution, while improve public awareness of the risks associated with undercooked meat and cross-contamination between raw and cooked products.

KEYWORDS: Shiga toxin-producing *Escherichia coli*, hemolytic uremic syndrome, outbreak, foodborne infection, butcher shops, northern France

ABSTRACT ID: 853

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POSTER TOUR 7

Day 1 | Wednesday 19 November 15:40-16:40

Late breakers 1

PRESENTER

Clara Mazagatos

ABSTRACT

Large outbreak of severe Shiga toxin-producing *E. coli* O157:H7 infections in multiple nursing homes in Belgium, August 2025

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BACKGROUND

Shiga toxin-producing *Escherichia coli* (STEC) infections pose elderly at higher risk of severe outcomes. In August 2025, multiple cases of gastroenteritis, some STEC-confirmed, were reported in different nursing homes (NH) in Belgium raising public health concerns. The outbreak team aimed to identify the source through multidisciplinary methods in order to implement measures and prevent further transmission.

METHODS

We defined suspected cases as NH residents presenting gastrointestinal symptoms from 13.08.2025. The National Reference Centre analysed stool samples of suspected cases for confirmation of STEC O157:H7 stx1/stx2a-positivity (confirmed cases). We compared food menus in all affected NH and conducted a retrospective case-control study in three NH, 2 weeks after suspected exposure. We surveyed 32 cases and 73 controls selected from the same NH regarding food exposures. Additionally, we trained a random forest prediction model. We used both methods to rank the most probable food items as the outbreak source. Food trace-back was also conducted.

RESULTS

Among 1,195 residents in 11 NH, we identified 66 suspected cases (attack rate: 5.5%), including 28 confirmed and 10 deaths (case fatality: 15.2%). Among surveyed cases median age was 89 years and 8 (35%) presented bloody diarrhoea. Raw minced beef was the most probable source of infection according to both methods (OR: 3.8, 95% CI: 1.1-13.3). It was delivered to 104 institutions nationwide, including all affected NH. No leftovers from the suspected batch were available for microbiological investigation.

CONCLUSIONS

This STEC outbreak is among the most severe outbreaks in Belgium displaying a high case fatality. Multidisciplinary collaboration enabled a timely and coordinated investigation. Despite recall bias and restricted diets complicating exposure assessment, epidemiological investigations, with two analytical approaches, pointed to raw minced meat as the most likely source. The outbreak yielded communications to facilities caring for at-risk groups to avoid serving raw or undercooked beef products in Belgium.

KEYWORDS: Shiga-Toxigenic *Escherichia coli*, Disease outbreaks, Epidemiology, Foodborne Diseases, Gastrointestinal diseases

ABSTRACT ID: 866

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POSTER TOUR 7

Day 1 | Wednesday 19 November 15:40-16:40

Late breakers 1

PRESENTER

Ioannis Karagiannis

ABSTRACT

Epidemiology and Characteristics of Mpox virus Clade I Importations and Onward Transmission in the WHO European Region, 2024-2025

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BACKGROUND

On 14 August 2024, WHO declared a public health emergency of international concern (PHEIC) due to a sharp rise of mpox cases linked to the emergence of a new strain, monkeypox virus (MPXV) clade Ib spreading from person to person. We aimed to describe the epidemiology and characteristics of mpox virus (MPXV) clade I cases reported in the WHO European Region since August 2024.

METHODS

Between 14 August 2024 and 27 August 2025, we noted key information of index cases of clade I MPXV reported by member states of the WHO European region through International Health Regulations. We followed up with countries to collect or confirm, age, gender, travel history, possible exposures, most likely route of transmission, clinical course, number and age of contacts and type of exposure, and on implemented control and prevention measures.

RESULTS

Since August 2024, 46 cases of MPXV clade I infection have been reported; 32 were imported cases and 14 were acquired in Europe, including six children and two cases with no identified epidemiological link to endemic countries. Most imported cases reported heterosexual contact or other close physical contact as likely exposure. Secondary transmission occurred in five households, with one instance of probable second-generation spread. Two cases were typed as clade Ia. No deaths were reported.

CONCLUSIONS

MPXV clade I in the WHO European Region (Aug 2024–Aug 2025) remained rare and mostly imported, with limited onward spread in households. Heterosexual/other close-contact exposures among importations, two clade Ia detections, and two cases without links to endemic countries indicate occasional undetected chains and multiple sub-lineages. Compared with published data on the 2022 clade Ib outbreak, exposures appear broader than single sexual networks. These data justify continued surveillance at national level, rapid case finding and contact tracing, routine clade assignment, and inclusive risk communication.

KEYWORDS: Mpox/epidemiology, Contact Tracing, International Health Regulations, Public Health Surveillance, Infection Transmission

ABSTRACT ID: 874

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POSTER TOUR 7

Day 1 | Wednesday 19 November 15:40-16:40

Late breakers 1

PRESENTER

Maria Saavedra-Campos

ABSTRACT

Descriptive analysis of invasive Group A streptococcal infection outbreaks and their management in London and the South East Region, UK, April 2024-July 2025

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BACKGROUND

Outbreaks of invasive Group A streptococcal (iGAS) infections are associated with morbidity and mortality particularly in vulnerable settings. To prevent transmission, screening and potentially prophylaxis of contacts and staff is undertaken. We described recent iGAS outbreaks to assess their impact and outcome.

METHODS

We identified outbreaks of iGAS infections from April-2024 to July-2025 in London and the South East region from the case management database. We summarised the setting and impact of each outbreak and reviewed case data for a random sample to ascertain the screening outcome.

RESULTS

Of 59 outbreaks identified, the majority were in healthcare settings (n=22), including 10 linked to community health services. Six were in care homes and accommodation for people experiencing homelessness respectively. The median age of the 134 linked cases identified was 60 years (IQR:45, 84). Forty cases were known to be hospitalised, and 9 died. The most common emm types were 89.0 (n=5) and 83.13 (n=4). The median duration of investigation was 83 days (Range: 2, 400). Some had multiple episodes of screening and prophylaxis. Screening took place in 16 of the 39 outbreaks reviewed: seven in community health service settings, two in care homes, two in nurseries and the rest in healthcare settings. On average, each outbreak had three cases. Where known, screening was universal, (ie. throat swab) or targeted where contacts had skin lesions. Screening identified positives in four outbreaks: six and three patients in two care homes, and one staff member each in a hospital and community health service.

CONCLUSIONS

Outbreaks can be prolonged but typically involve few cases. Limited data availability hindered assessment of screening completeness, positivity rates, and time between case identification, outbreak declaration and screening. A prospective risk assessment questionnaire is recommended to standardise screening and outcome tracking. Qualitative assessment may be more appropriate to reveal vulnerabilities.

KEYWORDS: Group A Streptococcal Infections, screening, outbreaks

ABSTRACT ID: 875

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POSTER TOUR 7

Day 1 | Wednesday 19 November 15:40-16:40

Late breakers 1

PRESENTER

Raquel Mulongeni

ABSTRACT

An outbreak of impetigo during June-July 2025 in a semi-urban setting in Portugal: the putative role of insect bites

R. Mulongeni¹

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BACKGROUND

Impetigo is a common skin infection among children, especially in warmer months, and climate change may increase its incidence. There was an unusual increase in reporting impetigo outbreaks to Directorate General of Health, from different regions in Portugal, in kindergartens and similar institutions in summer heatwaves of 2025 (June 15th –20th and June 27th– July 9th). We aimed to understand risk factors underlying an impetigo outbreak, occurring from 27th May to 30 July, across institutions in Mangualde, Portugal.

METHODS

Retrospective cohort study, with a self-administered questionnaire, sent to the institutions and parents. A case was an individual who self-reported clinically confirmed impetigo. Risk ratios, using univariate analysis, for exposures with 95% confidence intervals and Chi-squared test p-values, alpha set at 0.05, were computed. Skin swabs were collected from two patients.

RESULTS

The cohort comprised of 416 individuals with 59 (14%) cases, response rate was high at 80.6% (n=416/516) across four institutions, with 85% (n=352/416) being parents of children and the remainder being kindergarten staff members. The median child age was 3 (IQR:5 - 2) and 51.1% of children reported female. The sole exposures with a significant association with impetigo were prior insect bites (RR 2.37; 95% CI: 1.71 – 4.37) and prior varicella infection (RR 1.43; 95% CI: 1.43 – 4.69). The laboratory results were of two different strains of *Staphylococcus aureus* with two different resistance profiles.

CONCLUSIONS

This cohort study elucidated the association of past varicella infection and insect bites with impetigo in the context of heat-waves. This finding mobilised the public health unit to identify and control mosquito breeding grounds near institutions. We recommend strengthened monitoring for insect breeding grounds near educational settings during summer, and increased awareness of varicella history as a risk factor, to prevent future impetigo outbreaks.

KEYWORDS: impetigo, risk factors, insect bites, Disease Outbreaks

ABSTRACT ID: 891

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POSTER TOUR 8

Day 1 | Wednesday 19 November 15:40-16:40

Late breakers 2: Vaccine preventable diseases

PRESENTER

Jin-Min Yuan

ABSTRACT

Carriage of *Corynebacterium diphtheriae* in people experiencing homelessness in London, England – interim findings from a rapid prevalence study in spring/summer 2025

J. Yuan¹

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BACKGROUND

Corynebacterium diphtheriae outbreaks affecting people who experience homelessness have been reported globally in recent years. The UK Health Security Agency were notified of five people with severe infective endocarditis secondary to non-toxicogenic *C. diphtheriae* infection between July 2024-January 2025. Four were typed by multilocus sequence typing as ST559 and one as ST8. All cases used drugs non-intravenously and had links with London, with three cases experiencing street homelessness there. We therefore investigated the prevalence of *C. diphtheriae* carriage amongst homeless people in London to understand the need for further public health interventions, given the dearth of literature on carriage in this population.

METHODS

We partnered with 'Find & Treat', a specialist health outreach team, recruiting participants by convenience sampling at homeless hostels, day centres, and drug/alcohol services across London. Nurses took nasal, pharyngeal and skin wound swabs for microbiological testing and collected demographic/risk factor information. Prevalence was calculated with 95% confidence intervals.

RESULTS

179 participants were recruited from 17 sites between April-June 2025. 94% were male. Median age was 44 years. 98% were homeless with 55% reporting recent non-intravenous drug use. 46% had English as a second/other language. Wound swabs were taken from 19 participants. 17% reported symptoms: these were generally non-specific, such as coughs/coryza. One participant with no symptoms tested positive for non-toxicogenic *C. diphtheriae*, with carriage in their nose, pharynx and skin wound. The skin isolate was typed as ST559. Prevalence of *C. diphtheriae* was 0.56% (95% CI 0.00-2.23%).

CONCLUSIONS

We found a very low prevalence of *C. diphtheriae* carriage and no evidence of toxigenic or non-toxicogenic *C. diphtheriae* circulation amongst homeless people across London, which was surprising given the initial cluster but reassured against implementing further public health interventions. However, given the disease severity of the initial cluster, ongoing surveillance of non-toxicogenic *C. diphtheriae* strains, including sequencing, is recommended.

KEYWORDS: *Corynebacterium diphtheriae*, Prevalence, Non-toxicogenic, Ill-Housed Persons

ABSTRACT ID: 821

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POSTER TOUR 8

Day 1 | Wednesday 19 November 15:40-16:40

Late breakers 2: Vaccine preventable diseases

PRESENTER

Norman Galea

ABSTRACT

Out-of-Season Surges: Unprecedented Summer Peaks of Influenza in Malta, 2024-2025

N. Galea¹

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BACKGROUND

Malta, the most densely populated EU country, experienced a 14% population increase in the last 5 years, with 30% of the population being foreigners, mostly third country nationals. Influenza is typically seasonal, leading to substantial morbidity and mortality in winter months, however unusual surges in Influenza activity were recorded during summer in 2024-2025 in Malta unlike in other EU/EEA countries. We analysed surveillance data to assess comparability between summer and winter peaks to inform public health preparedness measures.

METHODS

We analysed surveillance data from January 2023–September 2025. Data included influenza-positive respiratory screens and typing by PCR carried out at the Pathology Department that processes samples from government hospitals and long-term care facilities. Test results were linked with patient demographics, hospitalisation and mortality data using unique identifiers and analysed using R, producing descriptive and inferential statistics.

RESULTS

Influenza epidemics occurred between December–March in winter and June–September in summer. Winter 2023–2024 had 907 cases (158/100,000; peak week 52), summer 2024 had 751 cases (131/100,000; peak week 30); winter 2024–2025 had 1,170 cases (203/100,000; peak week 50), summer 2025 had 830 cases (144/100,000; peak week 30). Influenza A predominated in each season (84–98%; H1N1 28–52%). Hospitalisations ranged from 65–75% in both seasons with similar odds of hospitalisation (OR 0.91, 95% CI 0.80–1.04), whereas mortality ranged from 2–8%, being lower in summer (OR 0.65, 95% CI 0.49–0.84). Similar age patterns were noted across seasons, with children (<5 years) and elderly (65+ years) accounting for 56–73% of cases.

CONCLUSIONS

Summer flu epidemics are comparable to those in winter leading to a burden on the healthcare system. The high population density coupled with increased mass gatherings, travel and high tourist influx during summer potentially fuel transmission. This highlights the need for stringent public health interventions to counteract summer epidemics and further virological characterisation to better understand transmission patterns.

KEYWORDS: Influenza A(H1N1), Summer influenza, Epidemiologic surveillance, Hospitalization, Mass gatherings

ABSTRACT ID: 847

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POSTER TOUR 8

Day 1 | Wednesday 19 November 15:40-16:40

Late breakers 2: Vaccine preventable diseases

PRESENTER

Erjola Hani

ABSTRACT

Containing Measles: Outbreak Dynamics and Control in the Charedi Jewish Community, England, 1st April 2025 to 31st August 2025

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BACKGROUND

The Charedi Orthodox Jewish community (OJC) in England is an underserved population with sub-optimal MMR vaccine coverage. Although largely unaffected during the 2024 national measles outbreak in England, the OJC experienced an outbreak between April and August 2025 following importations from Belgium and Israel. We describe the epidemiology, transmission, and interventions that limited spread.

METHODS

The UK Health Security Agency (UKHSA) conducts enhanced surveillance of all suspected measles cases. Cases were defined as laboratory-confirmed or clinically-compatible with epidemiological links. OJC cases were flagged in UKHSA's case management system, which provided incubation data for transmission analysis. N-gene sequencing data were obtained from MeaNS2, and vaccination records from the Immunisation Information System. This analysis includes cases in England reported between 1 April and 31 August 2025.

RESULTS

756 measles cases were reported, of which 24.6%¹⁸⁶ occurred in the OJC. Most cases were in London (143/186) and the North West (43/186). All cases were 25-years-and-under. Transmission was dominated by children under 10 (175/186, 94.1%). Almost all cases (184/186, 98.9%) had no MMR vaccine recorded. A further 32 linked cases occurred outside the OJC, from contact in shared community spaces such as schools. All cases were B3 genotype, with four sequences detected. Sequencing did not separate transmission chains, reflecting cocirculating strains in international OJC hubs from which cases were imported.

CONCLUSIONS

Despite low vaccine coverage, the outbreak was smaller than expected, likely due to targeted interventions including vaccinating over 1,000 OJC children in London through walk-in and pop-up clinics. Transmission was concentrated in schools, underscoring their role as intervention points in future outbreaks. The decline also coincided with school closure for the summer holidays, likely interrupting transmission. Though largely contained in the OJC, spillover highlights the need for higher MMR coverage nationally. Until sustained high MMR coverage, importations risk leading to outbreaks, particularly in underserved communities.

KEYWORDS: Measles/epidemiology,Disease Outbreaks,Molecular Epidemiology,Vaccination Coverage,Health Services

Accessibility,Measles/prevention & control

ABSTRACT ID: 861

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POSTER TOUR 8

Day 1 | Wednesday 19 November 15:40-16:40

Late breakers 2: Vaccine preventable diseases

PRESENTER

Annika Erdwiens

ABSTRACT

Effectiveness of Nirsevimab against RSV infection in primary and secondary care: a test-negative case-control study in infants in Germany, November 2024 – May 2025

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BACKGROUND

Respiratory syncytial virus (RSV) is a leading cause of severe respiratory illness in young children. In June 2024, the preventive monoclonal antibody Nirsevimab was recommended for all infants in Germany to reduce severe RSV-related illness during their first RSV season. Therefore, we aimed to evaluate RSV activity and effectiveness of Nirsevimab against symptomatic, laboratory-confirmed RSV infections in infants in both primary care (PC) and secondary care (SC) in the first season after Nirsevimab implementation in Germany.

METHODS

In 2024/25, we conducted a nationwide test-negative case-control study within our PC and SC surveillance systems, focusing on infants born on or after April 1, 2024, presenting with acute respiratory symptoms. Cases were defined as RSV-positive and controls as RSV-negative by qPCR. Odds ratios were estimated using logistic regression, adjusting for age, sex, month of symptom onset and underlying diseases. Effectiveness was calculated as $(1 - \text{adjusted odds ratio}) \times 100$. RSV activity in seasons 2023/24 and 2024/25 was evaluated.

RESULTS

In PC, 186 infants were enrolled of whom 24 (13%) tested RSV-positive. In SC, 109 infants were included with 25 (23%) RSV-positives. Nirsevimab coverage was higher among controls than cases in both systems (PC: 46% vs. 32%; SC: 27% vs. 8%). Adjusted effectiveness was 44% (95%CI: -48 to 79) in PC and could not be estimated in SC due to the low number of cases who had received Nirsevimab. However, a 38% and 15% reduction in RSV activity in PC and SC, respectively, was observed compared to the previous season.

CONCLUSIONS

In the first season following Nirsevimab implementation, RSV activity was lower among infants in both PC and SC compared to the previous season. Preliminary data indicate moderate protection of Nirsevimab against RSV infection in PC. Further RSV surveillance is essential for evaluating the sustained impact of Nirsevimab on RSV epidemiology and for informing public health decisions.

KEYWORDS: effectiveness | Nirsevimab | prophylaxis | RSV | primary care | hospitalisation

ABSTRACT ID: 868

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POSTER TOUR 8

Day 1 | Wednesday 19 November 15:40-16:40

Late breakers 2: Vaccine preventable diseases

PRESENTER

Anke Meyers

ABSTRACT

Wastewater surveillance as a public health tool for measles monitoring in Belgium

A. Meyers¹

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BACKGROUND

Despite certified measles elimination in 2020, Belgium counted the third-highest measles notification rate among European countries in 2024. To maintain elimination status, it is paramount to confirm interruption of transmission chains and absence of endemic circulation. This study explores the potential of wastewater-based surveillance as a complementary tool to clinical surveillance for monitoring measles. Specifically, it examines whether the detection of measles virus in Belgian wastewater correlates with reported clinical case data.

METHODS

Wastewater samples were collected from the influents of six wastewater treatment plants selected based on three criteria: high population coverage, proximity to identified risk areas and geographic distribution across the Brussels-Capital, Flemish and Walloon regions. Samples were collected weekly from May to September 2025 and concentrated using ultrafiltration. RNA was extracted and analysed using reverse transcription digital polymerase chain reaction (RT-dPCR). The clinical case data were retrieved from mandatory notifications and lab testing at the National Reference Centre.

RESULTS

Measles virus was detected in 28 percent of the 110 samples analysed, and in five out of six locations sampled between May 5th (week 19) and September 8th (week 37) 2025. At a national level high case numbers were observed in May and June through clinical surveillance, with a marked decrease from week 24 onwards.

CONCLUSIONS

Measles virus was successfully detected in Belgian wastewater, and qualitative trends mirrored those observed in clinical surveillance at a national level. Further data consolidation is required to conduct a correlation study at the provincial level. Results of the correlation analysis will be presented at the ESCAIDE conference. Furthermore, the perspectives of wastewater data to fill knowledge gaps belonging to the clinical-based surveillance will be discussed in this work.

KEYWORDS: Wastewater-based epidemiological monitoring; public health; measles; epidemiology

ABSTRACT ID: 871

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POSTER TOUR 8

Day 1 | Wednesday 19 November 15:40-16:40

Late breakers 2: Vaccine preventable diseases

PRESENTER

Hendrik Sauskojus

ABSTRACT

Herpes Zoster Vaccination and Risk of Dementia – Updated Evidence from a Systematic Review and Meta-Analysis

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BACKGROUND

Incidence of Herpes Zoster (HZ) and prevalence of dementia have been increasing across ageing populations globally. As countries roll out or update HZ vaccination programmes, recent studies, the latest one published in June 2025, suggest that HZ vaccination may reduce the risk of dementia, which studies suggest HZ may be pathologically implicated in. We aimed to assess the latest evidence to inform decision-making on HZ vaccination programmes.

METHODS

We conducted a systematic literature review and meta-analysis aimed at investigating the effect of HZ vaccination on dementia across Pubmed, Embase and Cochrane Library up until August 2025 according to PRISMA guidelines. Two independent reviewers performed study selection, data extraction, and quality assessment. Adjusted hazard ratios (HRs) were pooled using a random-effects meta-analysis with subgroup and sensitivity analyses; other measures of association were narratively synthesized.

RESULTS

Of 60 studies identified, five reporting HRs were included in the meta-analysis, yielding a pooled adjusted HR of 0.71 (95%CI: 0.67-0.75), indicating a 29% reduction in dementia risk among vaccinated individuals. Sub-group analyses showed a significant difference between the European (HR: 0.75, 95%CI: 0.71-0.79) and American (HR: 0.68, 95%CI: 0.65-0.72) WHO regions. A leave-one-out sensitivity analysis confirmed robustness and no publication bias was detected. The narrative synthesis included four studies which supported the findings of a protective effect, with estimates of up to 20%-reductions in dementia risk. Protective effects were found for both Zostavax and Shingrix vaccines.

CONCLUSIONS

There is increasing evidence that HZ vaccination not only reduces herpes zoster infections and associated complications, including postherpetic neuralgia, but could also prevent dementia in ageing populations. The estimated reduction in dementia risk among vaccinated individuals, and similar protective findings from additional studies, represents a highly public health and policy-relevant finding with significant implications for vaccination strategies. These findings should urgently be integrated into cost-benefit analyses and HZ vaccination programme decision-making.

KEYWORDS: Dementia, Herpes Zoster, Vaccination, Health Policy

ABSTRACT ID: 881

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POSTER TOUR 9

Day 2 | Thursday 20 November 15:40-16:40

Emerging and vector-borne diseases

PRESENTER

Luís-Jorge Amaral

ABSTRACT

High epilepsy prevalence and excess mortality in onchocerciasis-endemic counties of South Sudan: A call for integrated interventions

L. Amaral¹

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BACKGROUND

Epilepsy is a major public health concern in onchocerciasis-endemic regions, where intense *Onchocerca volvulus* transmission—still affecting 20 million people in 2021—is linked to high epilepsy prevalence, including nodding syndrome (NS). To inform WHO-2030 elimination goals and integrated care strategies, we quantified epilepsy prevalence and mortality in five highly endemic counties of South Sudan and examined the association with onchocerciasis transmission.

METHODS

Between 2021 and 2024, door-to-door surveys screened 34,345 residents, identified suspected persons with epilepsy (sPWE) and retrospectively recorded deaths among sPWE and individuals without epilepsy (IWE). Clinicians confirmed epilepsy diagnoses, including NS. Anti-Ov16 seroprevalence in children aged 3-9 years served as a proxy for *O. volvulus* transmission. Prevalence and mortality indicators were age- and sex-standardised. Standardised mortality ratios (SMRs) and 95% confidence intervals (95%CI) were calculated using IWE as a reference population. Weighted arcsin-transformed linear regression assessed associations between epilepsy prevalence and anti-Ov16 seroprevalence.

RESULTS

Epilepsy prevalence was 4.1% (site range: 2.3-7.1%) and NS prevalence was 1.5% (range: 0.6-2.2%). Anti-Ov16 seroprevalence in children was 23.3% (range: 1.4-44.1%). Each 1% increase in standardised seroprevalence was statistically significantly associated with epilepsy and NS prevalence increased by approximately 0.10 and 0.04 percentage points, respectively. During 4,069 person-years for sPWE, 211 deaths occurred versus 701 deaths in 82,177 person-years for IWE. Median age at death was lower for sPWE (20 years) than for IWE (39 years, $p < 0.0001$). The standardised mortality rate among sPWE was 48.4 per 1,000 person-years (95%CI: 41.9-55.8) versus 6.1 (95%CI: 5.6-6.7) among IWE, yielding an overall SMR of 6.8 (95%CI: 5.8-7.8), indicating sPWE were seven times more likely to die.

CONCLUSIONS

Onchocerciasis-endemic communities face a dual burden of elevated epilepsy prevalence and excess mortality. Strengthening ivermectin coverage, adding vector control where feasible and guaranteeing uninterrupted access to antiepileptic medication are urgent, actionable steps to reduce new epilepsy cases and deaths in endemic regions.

KEYWORDS: epidemiology,epilepsy,river blindness (onchocerciasis),mortality,burden of disease,neglected tropical diseases

ABSTRACT ID: 70

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POSTER TOUR 9

Day 2 | Thursday 20 November 15:40-16:40

Emerging and vector-borne diseases

PRESENTER

Francesco Menegale

ABSTRACT 9

Risk assessment and perspectives of local transmission of chikungunya and dengue in Italy, a European forerunner

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BACKGROUND

Aedes-borne arboviral infections are an emerging threat in Europe, as highlighted by the growing frequency and size of the outbreaks occurred in the recent years. Italy is a forerunner country in Europe for chikungunya and dengue transmission, having experienced the largest epidemics of both diseases in mainland Europe.

METHODS

We retrospectively analysed dengue and chikungunya transmission in Italy from 2006 to 2023. We applied generalized additive models to records of travel-related cases to highlight the spatiotemporal patterns of disease importation. We computed reproduction numbers for six local outbreaks based on autochthonous case data and mapped current transmission risks by applying a computational model that integrates human density, entomological, and climate data.

RESULTS

Between 2006 and 2023, higher numbers of imported chikungunya and dengue cases were reported in northern and central Italy and between June and October. We found a general uptrend in the number of imported dengue cases in Italy across the years and a notably higher incidence of dengue importation compared with chikungunya. Locations of autochthonous outbreaks appeared primarily driven by case importation rather than higher local transmission risks, as many areas in Italy showed similar permissive conditions for local transmission after case importation. Although reporting delays and favourable temperatures allowed onward transmission for several generations from mid-August to mid-November, upon outbreak detection control of transmission was achieved within 15 days. In high-risk areas, significantly longer time-windows of epidemic risks were found for chikungunya (over 4 months). Considering importation trends, increasingly frequent local dengue outbreaks are expected.

CONCLUSIONS

Case detection should be prioritized in areas and during periods where environmental and climate conditions are permissive for autochthonous transmission, regardless of prior outbreaks history in those regions. The case of Italy could anticipate scenarios that may emerge in the future in other European countries facing introduction or increasing colonization of Aedes mosquitoes.

KEYWORDS: Infectious Disease Transmission, Risk Assessment, Epidemics, Disease Outbreaks, Chikungunya Fever, Dengue Fever

ABSTRACT ID: 128

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POSTER TOUR 9

Day 2 | Thursday 20 November 15:40-16:40

Emerging and vector-borne diseases

PRESENTER

Alexandra Czerniewska

ABSTRACT

Emergence and epidemiology of *Trichophyton indotineae* in the United Kingdom and Republic of Ireland, 2017–2025

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BACKGROUND

Trichophyton indotineae is an emerging dermatophyte fungus causing often severe, treatment-resistant skin infections. First reported in India in 2014, where it is now endemic, it is increasingly detected worldwide. We describe cases since 2017 in the UK and Republic of Ireland (ROI) to inform clinical and public health responses.

METHODS

We extracted data on demographics, infection site(s), and travel history from laboratory forms submitted with confirmed *T. indotineae* isolates to the UK Health Security Agency's Mycology Reference Laboratory between 1 August 2017 and 4 March 2025. We deduplicated and, where possible, linked to ethnicity data and current postcode.

RESULTS

There were 258 confirmed cases. Numbers rose each quarter throughout 2023-24, from one case in January-March 2023 to 53 in October-December 2024, and with 28 more confirmed by 4 March 2025; only 44 cases were referred during 2017–2022 (0–3/month). In 2024, *T. indotineae* comprised 40% of all referred dermatophyte isolates. We mapped cases to 10 of 13 UK/ROI regions, and 54 of 181 local areas in England and Wales. The three highest rates (3.1 to 8.0 cases/100 000 population) were in urban areas. Of 225 cases with known gender, 55% were female. Median age was 38.5 years (range: 2–82); 80% were aged 20–59. Among 157 recorded infection sites, 57% were groin, buttocks or thigh. Travel history was available for 36 cases (14%) with 34 linked to South Asia. Six pairs of cases shared a postcode; four other cases had notes indicating affected family members. Of 80 cases with known ethnicity, 84% self-identified as Asian/Asian British (71% stated 'South Asian'; 13% 'Other Asian background').

CONCLUSIONS:

We confirm a rapid emergence of *T. indotineae* infections in the UK and ROI. However, the importance of international importation versus domestic transmission remains unclear. Enhanced surveillance and further research could clarify transmission patterns, risk factors, and public health impact.

KEYWORDS: *Trichophyton*; Tinea; Dermatomycoses; Arthrodermataceae; Mycology

ABSTRACT ID: 457

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POSTER TOUR 9

Day 2 | Thursday 20 November 15:40-16:40

Emerging and vector-borne diseases

PRESENTER

Nadezhda Zhgenti

ABSTRACT

Occult Transmission of Crimean-Congo Hemorrhagic Fever Virus among Farm Animal Owners in Rural Villages, Georgia, 2024

N. Zhgenti¹

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BACKGROUND

Crimean–Congo hemorrhagic fever (CCHF) is a viral tick-borne disease. Individuals in close contact with livestock have higher risk of infection. No internationally approved vaccine or treatment exists. Since the first CCHF human case in Georgia was identified in 2009, 221 cases have been reported through 2024 (case fatality rate - 10.9%). As many CCHF human infections are asymptomatic or mild, the actual spread of CCHF virus (CCHFV) may be greater and include areas where cases have not been detected. Our study aimed to determine possible occult CCHF infection among farm animal owners in rural villages of Georgia.

METHODS

A seroepidemiological study was conducted during May-July 2024, in 13 villages: 12 had no reported CCHF cases, located near the villages with documented CCHF among humans and/or animals; one village had documented CCHF infection among animals. The study population included owners of at least one farm animal (cattle, sheep, goat) and their households were randomly selected from study villages. Within selected households, we selected and enrolled the individual who reported the most animal contact. Each participant completed a risk factor questionnaire and provided a blood sample. Samples were tested to detect IgG antibodies against CCHFV using in-house ELISA (U.S CDC).

RESULTS

Of 412 participants, 23 (5.6%; 95%CI: 3.8%–8.2%), from 6 of the 13 study villages, tested positive for anti-CCHFV IgG. Seropositivity rate ranged from 2% to 36% across villages. The median age of seropositive individuals was 61 years. Seropositivity was higher in persons with history of tick bite (10.3%; 95%CI: 5.1%-19.2%) versus not (3.1%; 95%CI: 1.5%-5.8%) (Fisher p-value=0.025) and raw milk consumption (16.3%; 95%CI: 7.8%-30.3%) versus not (4.3%; 95%CI: 2.6%-7.0%) (Fisher p-value=0.011).

CONCLUSIONS

The survey confirmed occult transmission of CCHFV in villages near areas with known transmission. We recommend enhancing preventive measures and considering CCHF in differential diagnosis beyond the areas defined as endemic.

KEYWORDS: Zoonotic Diseases, Crimean-Congo Hemorrhagic Fever (CCHF), Seroepidemiological Study, Georgia

ABSTRACT ID: 616

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POSTER TOUR 9

Day 2 | Thursday 20 November 15:40-16:40

Emerging and vector-borne diseases

PRESENTER

Ofelya Harutyunyan

ABSTRACT

Tularaemia as a persistent problem: a study of the prevalence of tularaemia in Armenia

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BACKGROUND

Tularaemia is a serious bacterial zoonosis typically transmitted by an arthropod bite, exposure to infected animals or by ingestion of contaminated water or food. It can lead to large epidemics and epizootics in the northern hemisphere. The aim of the study is to assess the distribution of tularaemia cases in Armenia by region and age group.

METHODS

Descriptive study was conducted based on tularaemia reported cases data of NCDC of Armenia. The percentage changes in the number of cases over time were calculated. The distribution of cases by year, region, and age group from 2014 to 2024 was studied.

RESULTS

A total of 94 (0.3/100000) tularaemia cases were registered in the 11 provinces of Armenia from 2014 to 2024. Highest number of cases was registered in 2017 (n=32), in 2023 (n=14) and in 2024 (n=12). Regionally, there were each 5 cases (5.3%) in 5 provinces (Gegharkunik, Lori, Kotayk, Shirak, and Syunik). 2 cases (2.1%) were in Ararat, 4 cases (4.2%) in Aragatsotn. No cases have been reported in Armavir and Vayots Dzor provinces. Most cases were recorded in Yerevan (n=7) and in Tavush (n=56). It is notable that 71.8% (n=23) in 2017, 85.7% (n=12) in 2023 and 41.6% (n=5) in 2024 of total cases were in Tavush region. Of all cases, 5.3% (n=5) were children 3-5 years of age, 25.5% (n=24) were aged 7-18 and 69.1% (n=65) were 19 or older.

CONCLUSIONS

In Armenia, tularaemia is most prevalent in Tavush endemic region and among adults. It is necessary to strengthen control of animals and arthropods, raise awareness about water and food protection. To establish an appropriate priority for preventive measures, we recommend including the clinical forms of tularemia in official records of NCDC of Armenia and conduct additional research to find out the reason of the highest rates of tularemia in Tavush.

KEYWORDS: tularaemia, distribution, endemic region, preventive measures

ABSTRACT ID: 282

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POSTER TOUR 9

Day 2 | Thursday 20 November 15:40-16:40

Emerging and vector-borne diseases

PRESENTER

Martina McMenamin

ABSTRACT

Development of a WHO Global Arbovirus Surveillance System in Response to an Increasing Global Threat

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(GROUP) WHO Dengue Emergency Incident Management Support T

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BACKGROUND

In 2024, a record 14.3 million cases of dengue fever were documented globally following annual doubling of cases since 2021. In response to this global health crisis, the World Health Organization (WHO) determined dengue to be a Grade 3 emergency, which is the highest internal designation of its kind, and together with Member States, established the first real-time global dengue surveillance system.

METHODS

The integrated surveillance platform combines human case data, genomic epidemiology, national seasonality patterns, high resolution estimates of probability of presence of disease and other factors to present a comprehensive risk profile for countries. We triangulate this with other available data, to estimate changes over time in average incidence, geographic spread, and season timing and length.

RESULTS

The system currently captures data from 182 countries, areas and territories, 107 (59%) of which documented local transmission in 2024. Prior to 2024, a record of 86 countries reported cases, compared to 113 in 2024. Among 46 countries with available data, 35 (76%) saw an increase in cases between 2020-2024 compared to previous 5-year period, with a 3.8-fold increase in cases. Additionally, peak transmission timing varies in recent years highlighting the unpredictable impact of climate and other environmental changes favouring the proliferation of vectors on established seasonal patterns. Other contributing factors include spread within some endemic countries and newer regions, changes in circulating serotypes and improved surveillance.

CONCLUSIONS

Multiple interconnected factors are likely responsible for the global surge in dengue, underlining the need for enhanced consistent real-time surveillance and risk profiling to better understand the main drivers and mitigate impact in the presence of changing arbovirus landscape. Changes in the transmission and geographic range of other arboviruses such as chikungunya, yellow fever and Zika viruses implicate the same determinants and demonstrate the need to expand the global dashboard to enable integrated arbovirus surveillance.

KEYWORDS: arbovirus,dengue,surveillance,risk

ABSTRACT ID: 705

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POSTER TOUR 10

Day 2 | Thursday 20 November 15:40-16:40

Research to policy and practice

PRESENTER

Ilse Hazelhorst

ABSTRACT

Urinary tract infections and antibiotic overuse in a long-term care facility, The Netherlands, May 2024-March 2025

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BACKGROUND

Urinary tract infections (UTIs) are highly prevalent healthcare-associated infections (HAI) among residents in long-term care facilities (LTCF). Dipstick tests, which measure leukocytes and nitrites, are quick and easy for detecting signs of infection in urine. However, the Dutch Association of Elderly Care Physicians (Verenso) guidelines recommend prioritizing clinical assessment over dipstick tests for UTI confirmation. Relying on dipstick tests for diagnosing, rather than excluding UTIs, can lead to antibiotic overuse and therefore contribute to antimicrobial resistance. Our study aimed to estimate UTI prevalence and to evaluate testing and treatment practices in Dutch LTCFs.

METHODS

In the pilot phase, which was set up in collaboration with the Surveillance Network on Infectious diseases and HAI in LTCFs (SNIV), one LTCF with 296 residents participated between May 2024 and March 2025. Upon suspicion of an UTI the clinician notified the local principle investigator who completed a questionnaire based on the Electronic Client Record covering patient characteristics, clinical symptoms, testing and treatment practices. Each suspected UTI was compared with the guideline to determine if it met the clinical criteria. Data analysis was conducted using Microsoft Excel.

RESULTS

A total of 65 UTIs were notified in 60 (20%) residents, of which 41 (63%) were based on a positive dipstick. According to Verenso guidelines, only 14 UTIs (22%) met the clinical criteria, while 45 (69%) did not and 6 (9%) had missing values. Of 45 misclassified UTIs, 30 (67%) were treated with antibiotics. Overall, 44 UTIs (68%) were treated with antibiotics, of which the reason for prescription in 30 (68%) cases was due to the UTI and 14 (32%) for other reasons.

CONCLUSIONS

This study shows that UTIs are often misdiagnosed, with treatment decisions based more on dipstick tests than clinical evaluation. LTCFs should educate medical staff on the importance of guideline-based clinical assessments when prescribing antibiotics for UTIs.

KEYWORDS: urinary tract infections, healthcare-associated infections, antimicrobial resistance, antibiotic resistance, dipstick, long-term care facility

ABSTRACT ID: 413

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POSTER TOUR 10

Day 2 | Thursday 20 November 15:40-16:40

Research to policy and practice

PRESENTER

Hassan Mahmood

ABSTRACT

Linkage to care and health education for promoting water, sanitation, and hygiene (WASH) and primary healthcare services in underserved communities of Islamabad, Pakistan

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BACKGROUND

Over 50,000 Islamabad residents live in underserved communities ("slums") in extremely poor WASH conditions. These include limited access to potable water, poor handwashing practices, and inadequate healthcare access. Given the rise of extensive drug-resistant typhoid and high rotavirus prevalence, this project – in partnership with the John C. Martin Foundation - aims to improve immunization rates and WASH practices to decrease the burden of preventable waterborne disease.

METHODS

In this prospective cohort study, a baseline survey was conducted by community health workers to assess childhood vaccination coverage and WASH knowledge, attitudes, and practices (KAPs). Interventions implemented include educational programming in schools, text messaging, and printed materials. A preliminary descriptive analysis was completed and a comparative statistical analysis to track changes in KAPs will be conducted following survey re-administration.

RESULTS

A total of 9,451 households were surveyed across 15 slums. Over 90% were aware of handwashing importance, but only 67% consistently treat their water due to lack of fuel and time. 40% faced difficulties in accessing healthcare due to cost-related issues. 20% of households report washing hands because they were told to do so by a parent, while only 5% cited CHWs. Approximately 1 in every 5 households do not know where to obtain vaccinations. Through IEC awareness campaigns, 32 schools were targeted and over 127,000 WASH-related SMS messages have been sent out.

CONCLUSIONS

Despite general awareness of safe WASH practices, critical gaps remain in access. Many households attribute handwashing to parent instruction, suggesting that family influence is a strong driver of behavioral change, offering key opportunities for intervention in family-centered settings like primary schools. Community-tailored messaging with specific locations, public messaging on water treatment, and addressing cost barriers may improve vaccine uptake and decrease disease burden. Further research on slum-specific metrics is necessary to target communities with the highest risk.

KEYWORDS: Waterborne diseases, Linkage to care, Underserved and marginalised communities, Data digitalization, KAP survey, Community mobilization, Community outreach services, School health education, Water Sanitation and Hygiene (WASH)

ABSTRACT ID: 449

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POSTER TOUR 10

Day 2 | Thursday 20 November 15:40-16:40

Research to policy and practice

PRESENTER

Nienke Van Schaik

ABSTRACT

Lessons learned from a cluster of invasive group A streptococcal infections related to an elementary school in the Netherlands, June 2024

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BACKGROUND

In June 2024, the Public Health Service (PHS) South Limburg, the Netherlands, was notified of a single case of invasive Group A Streptococcus (iGAS) in a 5-year-old schoolchild. 'Warn and inform' letters were sent to parents and staff within the same classroom setting as recommended by national infection control guidelines. A second iGAS case (case 2) was reported 10 days later in a 47-year-old female. When PHS incidentally learned that both children of case 2 attended the same school (234 pupils) but not the same class as the index, a cluster was suspected. We describe lessons learned from this cluster.

METHODS

Cluster investigation included laboratory testing of all 5 household and close contacts of case 2. Emm-typing and whole-genome sequencing in positive individuals confirmed a school-related cluster. This prompted PHS to extend 'warn and inform' letters to the entire school, followed by 3-months retrospective and prospective surveillance of school-related cases. An online questionnaire assessed Group A Streptococcus (GAS) infections, GAS-like symptoms and antibiotic treatment in schoolchildren, siblings, parents and staff.

RESULTS

Two contacts of case 2 tested GAS-positive, including one of her children. All available isolates (two cases, two contacts) were bioidentical (emm 87.0 cluster E3). This emm type had not previously been reported in the region. Questionnaire data was available for 61 children from 40 families and 66 adults. Overall, 21 of 127 individuals (17%) (10 adults; 11 children) reported GAS-like symptoms for which 8 (38%) received antibiotic treatment. Furthermore 16 (13%) (2 adults; 14 children) reported chickenpox (iGAS risk factor). No further iGAS cases were reported.

CONCLUSIONS

Existing guidelines might not be sufficient to timeously prevent GAS/iGAS-clustering in schools. For each iGAS-notification, we recommend that applicable school-links be recorded. Single iGAS-cases at school should prompt enhanced surveillance and informing of parents and staff beyond the case's classroom.

KEYWORDS: Streptococcus pyogenes, Outbreak, Whole Genome Sequencing, Elementary school, Infection Control

ABSTRACT ID: 488

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POSTER TOUR 10

Day 2 | Thursday 20 November 15:40-16:40

Research to policy and practice

PRESENTER

Malorie Perry

ABSTRACT

Hospital admissions for respiratory infections in those with lived experience of homelessness, evidence for vaccine policy from Wales; UK

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BACKGROUND

In Wales, homeless populations are eligible for free influenza vaccination but not pneumococcal polysaccharide vaccine, unless they meet other eligibility criteria. These individuals often have several vulnerabilities and likely have increased susceptibility to respiratory infections. The burden of severe acute respiratory infection (ARI) in this group has not been previously quantified.

METHODS

Those aged 18+ years with lived experience of homelessness between 01/01/2014 and 31/12/2023, registered for NHS care in Wales as at 31/12/2023, were identified by linking four national healthcare datasets. The number of hospital admissions per 1,000 population, between 01/01/2014 and 31/12/2023, was calculated with the general population as a comparison group. Relevant hospital admissions were identified using ICD-10 codes: J09-J18 (influenza and pneumonia) or J20-J22 (other acute lower respiratory infections) as the primary diagnosis.

RESULTS

In the cohort of 15,678 individuals, there were 96.9 (95%CI:91.8-101.6) admissions per 1,000 population, compared to 26.9 (26.7-27.1) in the general population. This ranged from 38.8 (33.6-44.5) in 18-29-year-olds to 311.9 (280.8-345.4) in those aged 70+ years. Admissions in the 30-39-year-old homeless population were equivalent to the 70+ general population. Pneumonia (unspecified organism) was the cause for 63.4% of admissions, 26.1% were due to COVID-19, 3.6% influenza, 1.3% streptococcus pneumoniae, 3.4% other viral or bacterial pneumonia and 2.2% acute bronchitis/bronchiolitis.

CONCLUSIONS

Ascertainment of the denominator is challenging and health seeking behaviour may vary compared to the general population. This population may have a higher proportion of co-morbidities and poorer general respiratory health. A more robust study is needed. Findings suggest that it is correct to consider homeless populations in respiratory infection vaccination policy and to prioritise outreach.

KEYWORDS: Ill-Housed Persons ,Vaccination,Influenza,Pneumonia

ABSTRACT ID: 525

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POSTER TOUR 10

Day 2 | Thursday 20 November 15:40-16:40

Research to policy and practice

PRESENTER

Aigul Mamatova

ABSTRACT

Evaluation of the measles surveillance system in the Kyrgyz Republic, 2024

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BACKGROUND

In 2023, the Kyrgyz Republic reported over 7,000 cases of measles, including 9 fatalities. In 2022, an integrated electronic case reporting system for notifiable diseases, including measles, was introduced to enhance monitoring and response capabilities. This study aimed to evaluate the surveillance system, identify strengths and weaknesses, and develop actionable recommendations for improvement.

METHODS

Using the U.S. Centers for Disease Control and Prevention (CDC) updated surveillance system evaluation guidelines, we evaluated Kyrgyzstan's measles surveillance system in February and April 2024. Two of ten healthcare centers and the Bishkek State Sanitary and Epidemiological Surveillance Center (SES) participated. Data were ABSTRACTed from the national electronic case reporting system, weekly paper-based case reporting forms, medical records, and reports from >1,700 medical organizations.

RESULTS

The electronic case reporting system recorded a total of 8,224 emergency notifications for measles, of which 7,046 were confirmed. Case notification data were transmitted in real time from healthcare facilities, with 94% (2,170/2,308) of emergency notifications received by the SES within 12 hours of diagnosis. However, 7% (159/2,308) of these notifications contained errors in diagnosis dates. Of all emergency notifications, 92% (7,582/8,244) were investigated within 48 hours, and 2.1% (n=176) contained errors in registration dates. Of 4,245 laboratory samples collected, 66% had been taken within the median of 10 days after the appearance of rash, the laboratory received 71% within 24 hours of collection, and 99% were tested within 24 hours.

CONCLUSIONS

The evaluation indicates that the surveillance system effectively facilitates rapid notification of measles cases. However, weaknesses in data completeness, quality, and timeliness of sample collection were identified. Implementing additional data entry checks could enhance data quality. At the same time, further training for healthcare providers and laboratory personnel may help reduce delays in sample collection and transport, ultimately improving the overall effectiveness of the measles surveillance system in Kyrgyzstan.

KEYWORDS: Measles, outbreak, assessment, epidemiological surveillance, Kyrgyz Republic

ABSTRACT ID: 617

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POSTER TOUR 10

Day 2 | Thursday 20 November 15:40-16:40

Research to policy and practice

PRESENTER

Yingshih Su

ABSTRACT

First evaluation of Somaliland's national HIV surveillance system

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BACKGROUND

Somaliland introduced antenatal sentinel surveillance in 2004 and conducted its first key population surveys in 2008 and 2014. In 2020, the country launched a national HIV surveillance system to generate actionable data for public health decision-making. This is the first formal evaluation of that system, applying the European Centre for Disease Prevention and Control (ECDC) and WHO guidelines to assess seven core attributes: simplicity, acceptability, data quality, timeliness, sensitivity, representativeness, and stability.

METHODS

A qualitative evaluation was conducted between January and March 2025 using document review, semi-structured stakeholder interviews, and facility-level observations across multiple reporting sites. Thematic analysis was used to assess system strengths and limitations.

RESULTS

The system demonstrated moderate simplicity through structured forms and demographic dashboards. However, data correction processes remain dependent on supervisory input. Acceptability was generally high among healthcare providers, though lower among populations with male sexual health vulnerabilities due to stigma and limited access to anonymous testing. Data quality was strengthened by quarterly audits and supervisory checks, but undermined by inconsistent documentation and staff shortages. Manual entry and spreadsheet-based reporting contributed to delays, affecting timeliness. Sensitivity was moderate: most cases were detected through TB or ANC clinics, while nomadic and marginalised populations were insufficiently captured. Representativeness was constrained by exclusion of private-sector data. Stability remained limited by a reliance on paper-based infrastructure.

CONCLUSIONS

While nominally a national system, HIV surveillance in Somaliland is largely donor-driven, with UNICEF and international partners playing key roles in funding and implementation. This has shaped priorities, reporting structures, and data flow—emphasising the need for long-term sustainability planning and local ownership. Despite limitations, the system provides a functional foundation. The Ministry of Health's 2024 Digital Health Strategy presents a timely opportunity to strengthen integration, equity, and continuity. This evaluation offers transferable insights for fragile settings seeking to institutionalise HIV surveillance beyond external funding cycles.

KEYWORD: HIV Infections / epidemiology, Somaliland, Surveillance system evaluation, Social Stigma, Health Policy

ABSTRACT ID: 707

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POSTER TOUR 11

Day 2 | Thursday 20 November 15:40-16:40

Social determinants of infectious diseases

PRESENTER

Pontus Christopher Hedberg Wang

ABSTRACT

Factors associated with lack of evidence of successful tuberculosis treatment in regional surveillance data, Saxony, Germany, 2012–2023

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BACKGROUND

Unsuccessful treatment outcomes (UTO) of tuberculosis (TB) prolong disease and increase duration of infectiousness and risk of drug resistance. To inform targeted care retention strategies, we aimed to identify factors associated with UTO in Saxony, Germany. We focused on adverse outcomes likely to be modifiable from a public health perspective, including treatment discontinuation and loss to follow-up (LTFU).

METHODS

We included TB cases meeting the national case definition notified to the Saxon state authority in 2012–2023. UTO were defined as treatment failure, interruption for ≥ 2 consecutive months, ongoing treatment after 24 months (36 months for multidrug-resistant [MDR]-TB) and outcomes indicating LTFU without a documented transfer of care. Successful treatment outcomes (STO) were defined as treatment completion regardless of evidence of culture negativity. Other outcomes included death and transfer of care. We calculated yearly UTO proportions among all cases and compared UTOs and STOs with logistic regression analyses. Factors investigated were age group, sex, place of birth, previous TB, notification year, incarceration status, case-finding method, disease site and bacteriological status, and drug resistance. Adjusted odds ratios (aOR) with 95% confidence intervals (CI) were calculated using separate models and confounder selection for each exposure.

RESULTS

Among 1913 included cases, 221 (12%) UTOs, 1480 (77%) STOs, and 212 (11%) other outcomes were recorded. The UTO proportion ranged from 8.3% (12/145) in 2022 to 15.5% (23/148) in 2023. Factors associated with increased odds of UTO vs STO included birth in the WHO-Europe region outside Germany (OR=4.26; 95% CI: 2.77–6.56), incarceration at time of notification (aOR=3.57; 95% CI: 1.87–6.83), previous TB (aOR=2.95; 95% CI: 1.82–4.79), MDR-TB (aOR=2.62; 95% CI: 1.20–5.72), and male sex (OR=2.00; 95% CI: 1.41–2.84).

CONCLUSIONS

These findings reinforce the need for tailored TB case management in low-incidence settings, including people-centred approaches such as peer support services and care coordination across health, social, and correctional services.

KEYWORD: Tuberculosis; Treatment Outcome; Risk Factors; Multidrug-Resistant Tuberculosis

ABSTRACT ID: 285

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POSTER TOUR 11

Day 2 | Thursday 20 November 15:40-16:40

Social determinants of infectious diseases

PRESENTER

George Ahern

ABSTRACT

Predictors of poor outcome in people with tuberculosis disease, Wales 2012-2022

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BACKGROUND

The incidence of tuberculosis disease (TB) in Wales is low (<10 per 100,000 per year) but increasing. Whilst incidence is low, a significant proportion of patients are recorded as having a poor treatment outcome, such as mortality, loss to follow-up (LTFU) and treatment cessation. We investigated determinants of an unfavourable treatment outcome.

METHODS

We conducted a retrospective observational cohort study using TB notification data drawn from the National TB Surveillance system (NTBS) from 2021-2022, supplemented by enhanced case data from Wales TB cohort review. Univariable and multivariable Firth's logistic regression models were created to estimate association between poor outcomes and demographic and clinical factors. Variables with significant odds ratios (ORs) were selected for multivariable analysis on theoretical association with poor outcomes.

RESULTS

A total of 1,118 notifications were included, of which 147 (13%) had a poor outcome; 95 deaths, 40 LTFU and 12 ceased treatment. White ethnicity and being born in the UK were associated with an increased odds of poor outcomes in univariate analysis but was not found to be significant in multivariable model (OR 2.03, 95% CI: 1.43-2.91, OR 1.58, 95% CI: 1.12-2.25 respectively). Poor outcomes were identified amongst: those aged 65 or older compared to 25-34 year olds (OR 4.1, 95% CI: 2.46-6.99; aOR 4.37, 95% CI: 2.06-9.54); those with multiple self-reported social risk factors (history of prison, drug use, alcohol use and homelessness) (aOR 16.2, 95% CI: 3.50-78.0); and those presenting through secondary care compared to those who presented in primary care (aOR 2.32, 95% CI 1.33-4.06).

CONCLUSIONS

These findings provide further evidence for the need to target interventions to reduce poor outcomes at older individuals with tuberculosis and those with multiple social risk factors. Further qualitative research into the barriers associated with treatment completion is needed to inform the development of novel interventions in these groups.

KEYWORD: Tuberculosis, Epidemiology, Public Health Surveillance, Logistic Regression, Treatment Outcome, Wales

ABSTRACT ID: 571

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POSTER TOUR 11

Day 2 | Thursday 20 November 15:40-16:40

Social determinants of infectious diseases

PRESENTER

Emomali Kurbonov

ABSTRACT

Predictors of mortality among adult PLHIV receiving antiretroviral therapy in AIDS centers in Sughd Province, Tajikistan: a retrospective cohort study

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BACKGROUND

Despite significant advances in antiretroviral therapy (ART), HIV-related mortality remains a significant global health problem in low-income countries, including the Sughd region of Tajikistan. Our study aimed to assess mortality rates among people living with HIV (PLHIV) on ART and to identify key factors influencing mortality in Sughd, Tajikistan.

METHODS

We conducted a retrospective cohort study among PLHIV (≥ 18 years) who received ART for ≥ 6 months in 2013–2022 in the Sughd region. Data were extracted from the national electronic HIV case registry. Descriptive statistics were used to summarize the characteristics of study participants. Multivariable Poisson regression was used to estimate the adjusted relative risks (aRR) and 95% confidence intervals (CI) associated with HIV mortality.

RESULTS

A total of 1,871 PLHIV received ART for ≥ 6 months in 2013–2022. Of whom, 57% were men, the mean age was 31 years (standard deviation=9.8), 96% had secondary education, 68% lived in rural areas, and 38% were migrants. One-third (32%) were diagnosed with late-stage HIV (23% in stage 3 and 9% in stage 4). Overall, 163 (9%) died (cohort mortality rate of 17.4 deaths per 1,000 person-years). Mortality was associated with age 40–49 years (aRR=1.8, 95% CI=1.1–3.0) and 50 years vs <40 (aRR=2.5, 95% CI: 1.4–4.4) migration after HIV diagnosis vs no migration (RR=1.6, 95% CI=1.1–2.2), HIV stage 4 (aRR=4.6, 95% CI=2.9–7.3) and stage 3 vs stage 1 (aRR=2.3, 95% CI: 1.5–3.5), viral load >1000 copies/mL vs ≤ 1000 (aRR=4.8, 95% CI=3.5–6.7), and ART initiation ≥ 7 days after diagnosis vs <7 days (aRR=1.7, 95% CI=1.2–2.4).

CONCLUSIONS

The HIV mortality rate is high in the Sughd region. Late initiation was an important risk factor for mortality. Interventions to increase earlier diagnosis and timely initiation of ART, especially among older and migrant PLHIV, may reduce mortality.

KEYWORD: HIV infection, survival, retrospective studies, viral load, Tajikistan, risk factors

ABSTRACT ID: 584

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POSTER TOUR 11

Day 2 | Thursday 20 November 15:40-16:40

Social determinants of infectious diseases

PRESENTER

Zulfiya Tilloeva

ABSTRACT

THE MULTIDRUG-RESISTANCE CHARACTERISTICS OF EXTRAPULMONARY TUBERCULOSIS, TAJIKISTAN, 2017-2022

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BACKGROUND

Extrapulmonary tuberculosis (EPTB) represents an escalating concern in public health, particularly with multidrug-resistant tuberculosis (MDR-TB). The World Health Organization indicated in 2019 that EPTB constituted 16% of all tuberculosis cases worldwide. In the capital city of Dushanbe, Tajikistan, EPTB comprised 21.2% of the total MDR-TB cases in the cohort 2017-2022. There exists a paucity of data regarding the treatment outcomes for MDR-EPTB in settings characterized by limited resources. We assessed the characteristics of MDR-EPTB and the effectiveness of treatment in Dushanbe during the period from 2017 to 2022.

METHODS

We conducted a retrospective cohort study. Data were collected from medical recording forms and comprehensive medical histories. Odds ratios (OR), 95% confidence intervals (CI), and p-values were computed to investigate the associations between demographic and clinical factors and treatment outcomes.

RESULTS

Among the 91 patients evaluated, 46.2% were identified as female, with a mean age of 27.7 years. A majority (76.9%) were categorized as new cases; 21.9% were classified as underweight, and 72.5% had clinically confirmed tuberculosis. Co-infection rates included HIV (6.6%), HCV (8.8%), and diabetes (3.3%). Social determinants included unemployment (44.8%), migration status (15.4%), and residence in rental accommodations (17.5%). The overall rate of treatment success was recorded at 87.9%. Short treatment regimens achieved a perfect success rate of 100%, while longer regimens based on bedaquiline exhibited a success rate of only 58.3%. Unfavorable outcomes were found to be significantly correlated with HIV infection (OR = 9.6; p = 0.02), migration status (OR = 6.57; p = 0.011), and unemployment (OR = 16.41; p = 0.003).

CONCLUSIONS

Despite demonstrating a high overall success rate, patients infected with HIV, those from migrant backgrounds, and individuals who are unemployed exhibited increased risks of unfavorable outcomes. Targeted interventions—including the integration of HIV/TB care, support for migrants, and socioeconomic assistance—are imperative for enhancing treatment outcomes for MDR-EPTB.

KEYWORD: Extrapulmonary tuberculosis, MDR-TB, treatment outcomes, HIV, Tajikistan

ABSTRACT ID: 713

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POSTER TOUR 11

Day 2 | Thursday 20 November 15:40-16:40

Social determinants of infectious diseases

PRESENTER

Maria Tseroni

ABSTRACT

Tuberculosis in Greek correctional facilities: A nationwide mapping of epidemiological burden and system responses

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BACKGROUND

Incarcerated populations face a heightened risk of tuberculosis (TB) due to overcrowding, limited access to healthcare, and high concentration of vulnerable individuals. In Greece, national data on TB in correctional facilities (CFs) remain limited. This study aimed to map the TB burden and assess institutional responses across all CFs in Greece over a five-year period.

METHODS

A nationwide mixed-methods study was conducted in all 34 CFs in Greece. Quantitative data were gathered through structured forms on infrastructure, staffing, screening practices, TB detection, and treatment continuity. Epidemiological data (2019–2023) were retrieved from facility-level health records. Semi-structured interviews with CF staff provided qualitative insights.

RESULTS

Sixty-eight TB cases and three TB-related deaths were recorded over five years, yielding a TB-specific mortality rate of 4.4%. The incidence was 125.0 per 100,000 person-years (ranging from 88.1 to 199.1 by facility type), and 224.3 per 100,000 based on the estimated cumulative incarcerated population—over 20 times higher than that observed in the general population. Permanent overcrowding (average occupancy rate of 126%), chronic understaffing (27.1% vacancy rate in the approved staffing positions is uncovered), substandard infrastructure (75%), and limited adherence to internationally recognised prevention and control procedures were highlighted as major barriers. These factors may partly account for the observed increase in incidence. Moreover, insufficient implementation of standardised practices may contribute to missed diagnoses and underreporting of cases.

CONCLUSIONS

Significant systemic deficiencies in TB control persist within Greek CFs. There is a need to restructure the health framework in correctional facilities by integrating timely TB diagnosis, prevention, and care—an approach that would not only improve health outcomes for incarcerated individuals, but also contribute significantly to public health by limiting transmission during incarceration and following release.

KEYWORD: Tuberculosis, Correctional Facilities, Incidence, Public Health, Greece

ABSTRACT ID: 743

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POSTER TOUR 11

Day 2 | Thursday 20 November 15:40-16:40

Social determinants of infectious diseases

PRESENTER

Teresa Marie Nygren

ABSTRACT

Pharmacies supply needles and syringes for safer injecting drug use: a cross-sectional study in Germany, 2024

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BACKGROUND

To prevent transmission of blood-borne infections, WHO recommends 300 sterile needles and syringes annually per person who injects drugs (PWID) by 2030. In Germany, low-threshold services are mainly concentrated in large cities and have distributed fewer needles/syringes than the WHO target (2021: 127 needles, 85 syringes). However, provision via pharmacies remains unknown. We aimed to estimate the proportion of pharmacies selling or providing for free needles/syringes to PWID to inform harm reduction programmes.

METHODS

We invited German pharmacies to a cross-sectional study in April–May 2024 through federal state pharmaceutical chambers. We defined areas with <5,000 inhabitants as rural. An online questionnaire gathered information on pharmacy characteristics, monthly numbers of needles/syringes likely intended for injecting drugs, and reasons for not providing needles/syringes. Pharmacies providing ≥10 needles/syringes supplied an additional dataset with numbers of needles/syringes and PWID during the two prospective weeks.

RESULTS

Twelve of 17 chambers participated, potentially reaching 66% (11,618/17,575) of pharmacies, of which 9.5% (1,102/11,618) completed the online questionnaire. Of these, 83% (n=918) reported providing needles/syringes; 89% (787/889) in urban and 73% (117/160) in rural areas. Of 1,102 pharmacies, 6.6% (n=73) provided >100 needles/syringes per month; 69 of those were urban. Of 130 (12%) pharmacies not providing needles/syringes to PWID, 60% (78/130) mentioned as reasons low demand and 18% (24/130) not wanting PWID in their premises. Of invited pharmacies, 58% (98/170) supplied an additional dataset; those provided a median of 7.7 (interquartile range (IQR): 3.5–13.2) syringes and 10 (IQR: 4.7–16.0) needles per PWID per month.

CONCLUSIONS

Most participating pharmacies provided PWID with safe drug paraphernalia, improving access in urban, but also in rural areas, where low-threshold services are sparse. Addressing stigma barriers that prevent PWID from entering pharmacy premises, e.g. through vending machines outside pharmacies, could improve access to safe needles/syringes and reduce blood-borne infections in this vulnerable population.

KEYWORD: intravenous drug users, blood-borne infections, harm reduction, surveillance, pharmacies

ABSTRACT ID: 154

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POSTER TOUR 11

Day 2 | Thursday 20 November 15:40-16:40

Social determinants of infectious diseases

PRESENTER

Rianne Reijts

ABSTRACT

Access to sexual health services among ethnic minorities under the age of 25 years in the Netherlands

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BACKGROUND

Migration is a growing phenomenon and has impact on sexual and reproductive health outcomes, such as an increased burden for STIs, sexual violence and unintended pregnancies. Equitable access to sexual health care is of great importance for young people from ethnic minorities (EMs). In this study, we aimed to determine the proportional representation of first- and second generation EMs under 25 years at Dutch Sexual Health Centers (SHCs) compared to ethnic Dutch citizens.

METHODS

In this retrospective cohort study, coded surveillance data of 270.927 persons under the age of 25 visiting SHCs between 2016 and 2021 were included. Surveillance data was combined with census tract data (Statistics Netherlands) to calculate consultation rates, i.e, dividing the number of first consultations of a patient in the study period belonging to a specific EM by the total number of citizens in the age group of 15 till 24 years belonging to that EM in the Netherlands in 2021, multiplied by 1000.

RESULTS

The consultation rate for ethnic Dutch patients was 22.0 per 1000 person-years (95%CI: 21.8-22.2, 18.9, 19.8 (95%CI: 19.8-20.4) for first-generation EMs and 18.4 (95%CI: 18.0-18.8) for second-generation EMs. In both first- and second generation EMs, consultation rates for patients from Turkey, Morocco, Eastern Europe and Asia were lower than for ethnic Dutch patients. Consultation rates among patients from Africa were lower for first-generation EMs than ethnic

Dutch patients. Consultation rates among patients from Indonesia, Suriname/Dutch Antilles, Latin America and other western countries were equal or higher than among ethnic Dutch patients.

CONCLUSIONS

Our study showed that several EMs were underserved in Dutch sexual health care, suggesting lower access to care and indicating the need for culturally sensitive approaches to increase access. Using consultation rates is informative to indicate inequalities in access to sexual health care among EMs.

KEYWORD: Migrants, Youth, Health Services Accessibility, Sexual Health

ABSTRACT ID: 94

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POSTER TOUR 12

Day 2 | Thursday 20 November 15:40-16:40

Surveillance of respiratory infections

PRESENTER

Miguel Angel Sanchez Ruiz

ABSTRACT

Assessment of the timeliness of reporting severe acute respiratory infections in five European Union countries, 2024-2025: an electronic health record-based surveillance study

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BACKGROUND

Timely reporting of severe acute respiratory infections (SARI) is essential for effective surveillance and public health response. Countries report weekly SARI data to The European Surveillance System (TESSy). Studies on SARI reporting timeliness in electronic health records (EHR)-based systems are scarce, with differing methods. We evaluated the timeliness of reporting SARI cases across five European Union countries using EHR-derived data for surveillance.

METHODS

We analysed SARI data reported to TESSy by Austria, Belgium, Germany, Malta, and Spain, from week 40/2024 to week 52/2024. Retrospective updates in weekly case counts were tracked until week 6/2025. Counts reported at that point defined the total number of SARI cases hospitalised each week. We assessed timeliness by measuring the cumulative proportion of cases reported each week after hospitalisation. Results were summarised over the study period and by country (median, interquartile range [IQR]).

RESULTS

Overall, the median proportion of cases reported in the first, second, and third week after hospitalisation was 60% (IQR 38–79), 78% (IQR 70–94), and 96% (IQR 84–99), respectively. Across countries, the median proportion of cases reported after one, two, and three weeks varied from 46% (45–48) to 94% (88–96), 61% (45–70) to 99% (99–100), and 66% (53–81) to 100% (99–100), respectively.

CONCLUSIONS

Preliminary results suggest near-complete (96%) reporting of SARI cases within three weeks of hospitalisation. Cross-country variability may reflect differences in case identification at admission or discharge, data processing, and availability of human resources. To improve timeliness, further research should investigate reporting delay drivers and methods to adjust for expected delays. Assessing timeliness at the weekly level was a study limitation. Our approach is replicable across seasons and non-EHR-based surveillance systems, supporting cross-country comparisons.

KEYWORD: Respiratory Tract Infections, Hospitalisation, Public Health Surveillance, Electronic Health Records, Programme evaluation, Time Factors

ABSTRACT ID:174

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POSTER TOUR 12

Day 2 | Thursday 20 November 15:40-16:40

Surveillance of respiratory infections

PRESENTER

Andrzej Jarynowski

ABSTRACT

Pre-Event Social Dynamics Dominate Potentially Infectious Contacts at Mass Gatherings: Insights from UEFA EURO 2024

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BACKGROUND

Mass gathering events (MGEs) contribute to communicable (such as respiratory) disease transmission, particularly through superspreading. However, the precise mechanisms underlying their infectious potential remain poorly understood, largely due to limitations in traditional contact-tracing, experiment and survey methodologies.

METHODS

We employed GPS-based individual-level location data collected with extensive nationwide coverage in Germany (~1% of population), achieving an unprecedented spatio-temporal resolution. This dataset encompassed a variety of MGEs during spring and summer 2024, including the UEFA EURO 2024 football championship, Bundesliga games, major concerts, festivals, and fairs. Contacts induced by these events were quantified and contextualized by normalizing for participants share. We performed sensitivity analysis using various co-location definitions of contacts duration from 10 to 60 min and distance from 8x8 to 64x64m.

RESULTS

During UEFA EURO 2024, we observed no substantial increase in the nationwide number of contacts in contrast to notable local spatiotemporal changes. Specifically, we identified approximately 32% more contacts than a baseline in host cities during matches involving the German football team, with a peak in contacts occurring 1–3 hours before events (maximum at 2 hours prior, 95% increase over baseline, $p = 0.044$). Remarkably, gathering places (i.e. pubs, viewing areas) exhibited a 49.8% increase in contacts during German team games compared to the baseline days ($p = 0.014$).

CONCLUSIONS

Our findings highlight internal and collateral dynamics specific to MGEs, challenging the common assumption that single-event dynamics can represent MGEs broadly. The preparatory phases of events (in Germany post event dynamics was negligible which may not be the case in other cultural setups), rather than the events themselves, emerged as critical periods of heightened infectious contact due to crowding. Our findings are highly relevant for the modelling of disease transmission as well as planning of interventions (NPI) and event management in general context with social dynamics before and after an event.

KEYWORDS: Mass Gatherings, Social Behavior, Respiratory Tract Infections, Contact Tracing, Geographic Information Systems

ABSTRACT ID 246

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POSTER TOUR 12

Day 2 | Thursday 20 November 15:40-16:40

Surveillance of respiratory infections

PRESENTER

Gloria Pérez Gimeno

ABSTRACT

Vaccine effectiveness against influenza infection and hospitalization in older adults in Spain: Analysis of surveillance data from 2022/23 to 2024/25 seasons

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BACKGROUND

Older adults are especially susceptible to severe outcomes from influenza infection and are targeted for periodic seasonal vaccination. Monitoring influenza vaccine effectiveness (IVE) is needed to help inform vaccine recommendations. We aimed to estimate IVE between 2022/23 and 2024/25 seasons, using data from Spain's acute respiratory infection (ARI) surveillance system among older adults.

METHODS

We conducted a test-negative case-control study among patients aged ≥ 65 years presenting at primary care (PC) or hospitalised due to ARI. Patients were systematically selected and classified as cases if RT-PCR influenza was positive or as controls if negative. The odds of influenza vaccination in the current season and ≥ 7 days before symptom onset was compared between cases and controls using a logistic regression, adjusting by sex, age (splines), chronic conditions and epidemiological week (splines), with robust standard errors by region. IVE for each season was derived as $(1 - \text{Odds Ratio}) \times 100$, separately for PC and hospitals, overall and subtype-specific.

RESULTS

We included 986/8,723 and 2,532/10,849 cases/controls in PC and hospitals, respectively. In seasons 2022/23 and 2024/25 influenza A(H1N1)pdm09, A(H3N2) and B co-circulated, whereas in 2023/24, influenza A(H1N1)pdm09 predominated. In PC, overall IVE (95% Confidence Interval) was 34% (14;50), 41% (23;55) and 29% (-14;56) for seasons 2022/23, 2023/24 and 2024/25, respectively, while in hospitals, it was 34% (16;49), 42% (28;53) and 39% (27;49). IVE

against A(H1N1)pdm09 was similar to the overall, but A(H3N2) was generally lower albeit with wide confidence intervals. IVE against influenza B was particularly high during 2024/25 season, of 69% (23;88) and 77% (60;87) in PC and hospitals, respectively.

CONCLUSIONS

From 2022/23 to 2024/25 seasons, influenza vaccination reduced by 30%-40% the risk of presenting in PC or requiring hospitalization due to influenza infection in ≥ 65 -year-olds, without large differences across seasons. IVE was higher against influenza B and lower against influenza A(H3N2).

KEYWORDS: Influenza, influenza vaccines, public health, Case-Control Studies, elderly

ABSTRACT ID:468

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POSTER TOUR 12

Day 2 | Thursday 20 November 15:40-16:40

Surveillance of respiratory infections

PRESENTER

Elsa Negro Calduch

ABSTRACT

Qualitative evaluation and SWOT analysis of the Spanish SARI surveillance system

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BACKGROUND:

The Spanish Severe Acute Respiratory Infection (SARI) surveillance system was established in 2020 following ECDC and WHO recommendations. After the initial implementation phase, we evaluated the system's qualitative attributes to identify strengths, weaknesses, threats, and opportunities for improvement.

METHODS

A cross-sectional evaluation study was conducted (January-March 2025) using SurveyJS online questionnaires distributed to SARI surveillance coordinators from 18 Autonomous Communities and 51 participating hospitals within the Spanish Acute Respiratory Infection Surveillance System (SiVIRA). Six qualitative attributes (usefulness, acceptability, simplicity, flexibility, stability, and resilience) were evaluated using Likert scales, multiple-choice, and open-ended questions. T-tests assessed significance of hospital-coordinator differences, with Mann-Whitney U tests used for small samples or heterogeneous variances.

RESULTS

Response rates were 100% for coordinators and 88.2% for hospitals. The system received a positive overall assessment (mean: 4.0/5, SD=0.6). Acceptability was highest-rated (4.3/5), though significantly lower among clinical services (3.8/5) than among coordinators (4.4; $p=0.027$) and preventive medicine departments (4.7; $p=0.001$). Coordinators rated usefulness higher than hospitals (4.1 vs 3.7, $p=0.031$). The remaining attributes received moderate ratings: stability (3.9/5, SD=1.0), resilience (3.5/5, SD=1.5), flexibility (3.6/5, SD=1.1), and simplicity (3.4/5, SD=1.0). SWOT analysis identified qualified, dedicated staff professionals as the main strength (88% of mentions), and human resource shortages as the primary weakness (76%). System interruptions, reported by 40% of hospitals, were primarily attributed to staff absences and IT issues. Integration of digital technologies including AI emerged as key opportunities (94%), while staff turnover represented the main threat (41%).

CONCLUSIONS

The Spanish SARI surveillance system received generally positive ratings despite challenges related to specialized personnel dependence and manual processes. Improving the system requires automation, standardization of procedures, enhanced communication channels, and contingency planning for staffing shortages. These improvements would enhance data quality and sustainability while reducing demands on healthcare personnel. Regular evaluations are essential to standardize operations across hospitals and Autonomous Communities.

KEYWORDS: Public Health Surveillance; Respiratory Tract Infections; SARS-CoV-2; Influenza, Human; Health Information Systems; Qualitative Research

ABSTRACT ID: 490

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POSTER TOUR 12

Day 2 | Thursday 20 November 15:40-16:40

Surveillance of respiratory infections

PRESENTER

Francesco Baglivo

ABSTRACT

Assessing children's RSV clinical presentation across 5 seasons in primary care setting in Italy

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BACKGROUND

Respiratory syncytial virus (RSV) is one of the leading causes of acute respiratory infection (ARI) in children; however, there is no common case definition adopted across Europe, where some countries rely on ARI case definitions and others on influenza-like illness (ILI).

METHODS

We conducted a prospective, multicenter cohort study across five Italian regions, enrolling children under 5 years old presenting to primary care pediatricians who met the WHO-ARI criteria. At enrollment (T0), nasopharyngeal swabs were tested by multiplex RT-PCR for RSV and other respiratory pathogens. RSV-positive children underwent follow-up at 14 and 30 days (T14 and T30). Primary outcomes included illness duration, symptom persistence, RSV-attributable hospitalization rate, and length of stay.

RESULTS

From 2019-20 to 2024-25 (excluding 2020-21), 1767 subjects were enrolled, and 711 (40.2%) tested RSV-positive. At T0, both the overall cohort of ARI children and RSV+ patients most commonly reported cough (93% overall, 95% RSV), coryza (85% overall and RSV), and fever (57% overall, 56% RSV). However, a different pattern emerged with less common symptoms, like dyspnea (36% overall, 44% RSV), wheezing (25% overall, 33% RSV), and sore throat (26% overall, 21% RSV). 636 (89%) RSV patients completed both follow-up interviews. The mean RSV illness duration was 15.5 days (SD 8.9), with 38.4% of children still symptomatic at T14 and 15.9% at T30. Hospitalization occurred in 32 (5%) of RSV-positive cases, with a median stay of 6 days (IQR 4.5-7).

CONCLUSIONS

Our findings support the adoption of the WHO ARI case definition, which does not mandate fever, for consistent RSV surveillance in primary care settings. The adoption of standardized surveillance definitions is needed for assessing vaccine effectiveness and understanding the broader public health impact of preventive measures recently implemented to contrast RSV.

KEYWORDS: Respiratory Syncytial Virus, Infant, Child Preschool, Epidemiology, Public Health Surveillance, Primary Health Care

ABSTRACT ID: 518

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POSTER TOUR 12

Day 2 | Thursday 20 November 15:40-16:40

Surveillance of respiratory infections

PRESENTER

Claudia Cozzolino

ABSTRACT

Quantifying the Underestimation of RSV-Associated Respiratory Hospitalisations in Older Adults: A Time Series Modelling Study in the Veneto Region, Italy

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BACKGROUND

Respiratory syncytial virus (RSV) infection can cause serious complications in adults/older, multi-pathological, and immunocompromised subjects, leading to increased morbidity and hospitalisation rates. However, the true burden in adults remains difficult to assess due to the absence of a clear case definition, non-specific symptoms, and limited diagnostic testing. Administrative hospital records often fail to capture RSV as a cause of admission, especially in patients with comorbidities, resulting in significant underestimation.

METHODS

We conducted a time series analysis of hospital discharge records from the Veneto Region, Italy, covering the period 2018–2024. Acute respiratory infection (ARI) and RSV admissions were identified using ICD-9 codes. The number of RSV-attributable hospital admissions was estimated by fitting a generalised additive mixed model (GAMM) to weekly counts of ARI admissions, with circulating respiratory pathogen activity from RespiVirNet surveillance system as explanatory variables, while adjusting for seasonal trends and age-specific differences.

RESULTS

More than 4.2% of ARI-related hospitalisations in adults aged 65 years and older were attributable to RSV. Incidence rates increased with age, reaching 26.8, 109.4, and 317.4 per 100,000 person-years in the 65–74, 75–84, and 85+ age groups, respectively. RSV-coded hospitalisations underestimated the burden by factors of 2.9, 6.6, and 7.6 across these age groups, with greater underreporting observed during the post-pandemic seasons (2022–2024).

CONCLUSIONS

Statistical modelling provides an accurate approach for estimating the RSV burden among older adults, revealing substantial underreporting in administrative data. These findings highlight the need to strengthen RSV surveillance systems. Prospective studies of adults hospitalised with ARI are also essential to improve understanding of diagnostic test sensitivity and validate modelling approaches. Improved burden estimates are essential to guide healthcare resource allocation, inform prevention strategies, and evaluate the impact of future RSV vaccination programmes targeting both adults and infants.

KEYWORDS: Respiratory syncytial virus, Hospital admissions, Adults, Surveillance, Underreporting, Respiratory infection

ABSTRACT ID: 283

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POSTER TOUR 12

Day 2 | Thursday 20 November 15:40-16:40

Surveillance of respiratory infections

PRESENTER

Elin Moverf

ABSTRACT

Combined monitoring of individuals and wastewater for a strategic genomic surveillance of SARS-CoV-2 in Sweden 2025

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BACKGROUND

In the extended standing recommendations for COVID-19 the WHO describes critical actions that should be undertaken by the States Parties in the transition from the emergency response to COVID-19. Countries should strengthen their integrated infectious disease surveillance and prepare for potential worsening situations caused by new variants of the SARS-CoV-2 virus. While maintaining robust genomic surveillance is central to achieving these goals, there is significantly reduced funding for comprehensive COVID-19 surveillance on a global scale in 2025 compared to the emergency phase of the pandemic, necessitating evaluation of the goals and of systems used for monitoring.

METHODS

During 2021-2024, Sweden has maintained large scale genome sequencing on samples from infected individuals on a national level, ranging between 1000-15 000 sequences per month. From 2023, bi-weekly sequencing of wastewater, covering an estimated 43% of the Swedish population, was introduced as a complementary system. For the 2025 genomic surveillance program, we evaluated the Swedish systems used for COVID-19 by assessing each system in relation to their cost and ability to fulfil our established surveillance goals.

RESULTS

We observed moderate to strong correlation (Spearman) in variant prevalence for samples from individuals and wastewater monitored during 2024. Thus, in our 2025 program, wastewater-based genomic surveillance is used as the primary system to monitor the introduction, prevalence and spread of new SARS-CoV-2 variants. The national program also relies on a one tenth volume of data from individuals (approximately 200 sequences per month) compared to the previous year to fulfil our additional surveillance goals such as sharing of data internationally for vaccine content and vaccine efficacy assessment.

CONCLUSIONS

Genomic surveillance of wastewater and the establishment of international data reporting can provide a cost-effective approach to track SARS-CoV-2 variant introduction and prevalence, while data from individuals remains essential for additional surveillance goals such as severity assessments.

KEYWORDS: Public Health Surveillance ,Wastewater-Based Surveillance,Whole Genome Sequencing,SARS-CoV-2,Cost-Effectiveness Analysis,Correlation of Data

ABSTRACT ID: 622

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POSTER TOUR 13

Day 2 | Thursday 20 November 15:40-16:40

Surveillance of healthcare-associated infections

PRESENTER

Sooria Balasegaram

ABSTRACT

Investigating the source of 12-year long outbreak of a unique genotypic strain of Salmonella Montevideo in a hospital in , England

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BACKGROUND

In 2013, the UK national public health body was notified of 3 cases of Salmonella Montevideo in paediatric inpatients in a single hospital. Further cases were reported in 2016-17, 2019 and 2022-25. Typing by pulse field gel electrophoresis (PFGE) in 2013 and subsequently by whole genome sequencing (WGS) established that all 12 reported cases represented a unique genotypic variant with no other cases in England being genomically related. We summarise investigations into the potential source.

METHODS

Demographic data on cases were collected using routine questionnaires. Details of inpatient stay, medications, procedures and ward movements were obtained from hospital records. Environmental sampling of sinks, fridges, freezers, patient and parent areas, including in the paediatric intensive care unit (PICU), was undertaken at three time points (2013, 2024 and 2025).

RESULTS

Of the 12 cases, 9 were hospital inpatients identified on investigation of diarrhoea. The median age was 7 months (range 5 months to 16 years). Eight were primary cases. A secondary case may have been linked to a sink identified with the same strain of S. Montevideo, in a room occupied by a previous case. A family cluster (adult and a child) were linked to another inpatient case. A further secondary case was identified following a hospital transfer. Inpatient cases were admitted to different paediatric wards, eight had been in PICU. No common feeds, including milk products, medications or procedures were identified. Two other sinks, on different paediatric wards all outside of PICU were also positive

CONCLUSIONS

Although numbers are small, the persistence of the outbreak suggests a possible environmental reservoir(s) on a paediatric ward(s) or PICU. Positive environmental samples from sinks are likely to be due to seeding from recent cases, rather than the ongoing point source. Following identification of the latest case, further environmental sampling and targeted staff screening are being considered.

KEYWORDS: Salmonella; Health Care Associated Infection; Infection Prevention and Control; Hospital Outbreak

ABSTRACT ID: 655

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POSTER TOUR 13

Day 2 | Thursday 20 November 15:40-16:40

Surveillance of healthcare-associated infections

PRESENTER

Dunja Said

ABSTRACT

Recent trends and current situation of invasive Methicillin-resistant *Staphylococcus aureus* (MRSA) infections in Germany: An epidemiological description for the years 2015–2024

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BACKGROUND

Methicillin-resistant *Staphylococcus aureus* (MRSA) is among the most common antibiotic-resistant pathogens responsible for hospital-acquired infections. In recent years, there has been a decline in the incidence of invasive MRSA in Germany and Europe. We analysed recent developments and the current situation regarding MRSA infections in Germany to monitor the progress towards reducing MRSA incidence.

METHODS

We used surveillance data on cases of invasive MRSA infections (blood or cerebrospinal fluid), mandatorily reported to the Robert Koch Institute. The observation period covers 2015–2024. We calculated incidences per 100,000 inhabitants and analysed cases' notification year, federal state of residence, sex, age, and documented connections to an outbreak. We used chi-squared tests to assess significant differences.

RESULTS

During the observation period, 19,486 invasive MRSA cases were reported. We observed a significant decrease in incidence between 2015 and 2020, from 4.4 to 1.4 cases per 100,000 inhabitants, after which it levelled off. We found significant differences across regions and over time ($p < 0.001$): states in the north have higher incidences, but also sharper decreases in incidence - for example, a decline from 8.4 to 1.1 cases per 100,000 inhabitants in Mecklenburg-Western Pomerania between 2015-2024 compared to a decline from 1.5 to 0.9 in Baden-Württemberg. Incidence was highest among men >60 years with an increasing sex difference in older age groups reaching 14.3 cases per 100,000 inhabitants in males aged ≥ 80 , compared to 0.1 to 0.8 in women between 20 and 60 years. During the observation period, 161 (1%) cases of invasive MRSA infection were marked as being connected to an outbreak.

CONCLUSIONS

The incidence of invasive MRSA infections in Germany stabilised at a low level. However, differences remain between federal states and patient groups. Further investigation of the largely unknown reasons is needed to guide infection prevention and control efforts towards reducing MRSA incidence even further.

KEYWORDS: Public Health Surveillance, Disease Notification, Incidence, Disease Outbreaks

ABSTRACT ID: 523

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POSTER TOUR 13

Day 2 | Thursday 20 November 15:40-16:40

Surveillance of healthcare-associated infections

PRESENTER

Zahin Amin-Chowdhury

ABSTRACT

Ethnicity and Deprivation: Association with Escherichia coli Bloodstream and Antimicrobial-Resistant Infection Burden in England

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BACKGROUND

Escherichia coli (E. coli) bloodstream infections (BSI) disproportionately affect individuals in more deprived areas of England and the Black and Asian ethnicities (after adjusting for differences in age structure). Deprivation and ethnicity are closely interlinked, combining these factors will provide a greater understanding of those populations at greatest risk and underlying drivers of this disparity.

METHODS

Case-level data reported to UKHSA Mandatory Healthcare-Associated Infections surveillance programme were extracted and enriched with Hospital Episode Statistics and national laboratory resistance data and, Office for National Statistics geographical data, for ethnicity, AMR and deprivation data, respectively. Negative binomial regression models were used to estimate incidence rate ratios (IRR) of overall and resistant E. coli BSI by ethnic group, with the White group as reference, adjusting concurrently for age group and Index of Multiple Deprivation (IMD) quintile.

RESULTS

Between April 2017 and March 2024, 242,464 E. coli BSIs were reported. Age- and IMD-adjusted rates of overall E. coli BSI were greatest in Mixed (IRR 9.71 (95%CI 7.91-11.9, p<0.001), Black (IRR, 3.43 (95%CI 2.85-4.14, p<0.01) and Asian (2.01 (95% CI 1.70-2.39, p<0.001) ethnicities compared to the White group. The same was seen for resistant E. coli BSIs, with IRR 7.34 (95%CI 6.02-8.97, p<0.001), 3.68 (95%CI 3.09-4.37, p<0.001) and 2.71 (95%CI 2.32-3.17, p<0.001), respectively. Overall 41.8% of cases were caused by E. coli resistant to one or more key antibiotics. This was greatest for those of Asian (51.9%), followed by Black (47.0%) and White (41.1%) ethnicities. Resistance to third-generation cephalosporins was notable in the Asian ethnicity, particularly vs their White counterpart, Cefotaxime 13.5 vs 5.2% and Ceftriaxone 8.6 vs 2.8%.

CONCLUSIONS

Incidence and antibiotic resistance varied by ethnicity. Thus, universal approaches to interventions to drive down burden maybe suboptimal and likely would not address the ethnicity associated variation highlighted here.

KEYWORDS: Health inequalities, deprivation, ethnicity, E. coli bacteraemia

ABSTRACT ID: 570

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POSTER TOUR 13

Day 2 | Thursday 20 November 15:40-16:40

Surveillance of healthcare-associated infections

PRESENTER

Aishwarya Krishna

ABSTRACT

Genomic and epidemiological patterns in *Staphylococcus aureus* bacteraemia: A national surveillance study, England, 2017-2024

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BACKGROUND

Staphylococcus aureus (SA) bacteraemia causes significant morbidity and mortality. Monitoring clonal complex (CC) trends through whole genome sequencing (WGS) of methicillin-resistant- and methicillin-susceptible-SA (MRSA and MSSA) enhances understanding of its epidemiology to inform public health strategies.

METHODS

National mandatory surveillance of MRSA and MSSA bacteraemia (April 2017-March 2024) was enhanced to include CC and mortality data from UKHSA *Staphylococcus* and *Streptococcus* Reference Service and NHS Spine. Mixed-effects multinomial logistic regression identified factors associated with one of the top five versus other CCs, while binomial logistic regression analysed factors associated with 30-day mortality.

RESULTS

In England, 5,538 MRSA and 86,927 MSSA bacteraemias were identified, with 3,504 (63.3%) and 5,577 (6.4%) linked to WGS, respectively. Linked MRSA cases showed similar sex and onset distributions but lower proportions by region and age; linked MSSA showed lower proportions across all categories. Common MRSA CCs were CC22 (31.6%), CC5 (23.5%), CC8 (10.3%), CC1 (8.4%), and CC59 (5.4%). Adults ≥ 75 had higher risk of CC22 versus those aged 15–44 (aRRR 3.56, 95%CI 2.42-5.23) but lower likelihood of Asian or Black ethnicity (aRRR 0.43 and 0.42). Female cases were more associated with CC1 and CC59 (aRRR 1.66, 1.46). CC59 and CC22 had the highest 30-day case-fatality rates (30.1%, 29.7%) and elevated mortality risk (aOR 2.03, 1.61). Among MSSA, CC45 (12.4%), CC398 (12.0%), CC30 (11.1%), CC15 (10.6%), and CC5 (9.5%) were prevalent. CC30 and CC15 showed increased risk among those aged 1-4 years (aRRR 2.26, 95%CI 1.25-4.01; aRRR 2.23, 95%CI 1.19-4.29, respectively). Cases ≥ 65 years, particularly those aged 65-74 years (aRRR 0.60, 95%CI 0.43-0.84) and of Asian ethnicity (aRRR 0.61, 95%CI 0.40-0.91), were less likely to present with CC398. CC15 had lower odds of death (aOR 0.63, 95%CI 0.45-0.85) in comparison.

CONCLUSIONS

Linking genomic and epidemiological data of MRSA and MSSA bacteraemia highlight key patterns for further investigation.

KEYWORDS: *Staphylococcus Aureus*, Whole-genome sequencing, Hospital- Acquired Infections, Surveillance

ABSTRACT ID: 659

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POSTER TOUR 13

Day 2 | Thursday 20 November 15:40-16:40

Surveillance of healthcare-associated infections

PRESENTER

Phillip Butterick

ABSTRACT

Higher burden of co-morbidities increases *Clostridioides difficile* cause-specific mortality in under 80 but not in the very elderly: Findings from mandatory surveillance in Wales, 2020-2024

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BACKGROUND

Mortality is an important indicator for monitoring disease outcome. Routine *Clostridioides difficile* infection (CDI) surveillance in Wales measures all-cause mortality (ACM), which is simple to collect but may overestimate severity. Cause-specific mortality (CSM) provides more precise estimates. We aimed to compare ACM and CSM among individuals with CDI and identify risk factors associated with CSM.

METHODS

We conducted a retrospective cohort study on individuals with CDI between 01/04/2020-31/03/2024. We linked test results, hospital admissions (to classify likely acquisition), comorbidities (to calculate Charlson comorbidity index (CCI)), and death certificates (for date/cause of death). We calculated ACM and CSM at 90-days post last positive specimen. We defined hospital acquired as specimens taken more than two days into inpatient stays. We defined CSM as ICD-10 code A04.7 on the death certificate. We computed adjusted hazard ratios (aHR) for risk factors using multivariate Cox regression.

RESULTS

Among 3,649 individuals, ACM was 26% (n=957). 23% (224/957) of deaths were CDI attributed; CSM=6%. In univariate analysis, older age groups (65+, 80+), hospital acquisition, higher CCI, and specimen year were significantly associated with CSM. In multivariate analysis, aged 65+ or 80+ years (80+: aHR 3.6; 95% CI: 2.2–5.8; p<0.01), CCI ≥4 (aHR 1.8; 95% CI: 1.1–3.0; p= 0.02), and specimen year (2021/22: aHR 0.6; 95% CI: 0.4–0.9; p= 0.02) were independently associated. CSM increased as age and CCI increased, but the CCI association was only significant in those aged <80 years (CCI 1–2: aHR 3.4; CCI 3–4: aHR 3.6; CCI 4+: aHR 6.4).

CONCLUSIONS

Approximately one quarter of deaths in individuals with CDI were due to CDI, and we recommend CSM is used for routine surveillance. Being aged 65+/80+ and having multiple comorbidities were independently associated with CDI-attributed death, highlighting the importance of targeted prevention and treatment interventions, particularly for older people and those with multiple comorbidities.

KEYWORDS: *Clostridioides difficile* infections, Comorbidity, Cause of Death, Risk factors, Population Surveillance

ABSTRACT ID: 313

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POSTER TOUR 13

Day 2 | Thursday 20 November 15:40-16:40

Surveillance of healthcare-associated infections

PRESENTER

Lara Ricotta

ABSTRACT

Active surveillance of healthcare-associated infections in Pediatric Intensive Care Unit: a two-year study period (January–March), 2023-2024

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BACKGROUND

Healthcare-associated infections (HAIs) are a significant concern in pediatric intensive care units (PICUs), contributing to increased morbidity and mortality. Blood stream infections (BSIs) are among the most common, accounting for approximately 45% of HAIs. This study aimed to assess the incidence of HAIs over two consecutive years in two PICUs of an Italian pediatric hospital during three-month period, identifying trends and comparing infections rates to better understand possible infection patterns.

METHODS

This descriptive study was conducted in 2024 and 2023, January to March, at a tertiary care Children's Hospital with 627 beds. Data on demographic information and types of infections were collected for all the patients in two PICUs from 1 January to 31 March, using patient's folders and medical advice. HAIs were defined using ECDC HAI-net ICU (v2.2) protocol; infection rates were calculated, and statistical significance was evaluated (p value $\leq$ 0.05).

RESULTS

In total, 160 in 2024 and 176 patients admitted for more than two days in PICUs were included, respectively with 1411 (median 2; range 3-61) and 1297 (median 4; range 3-60) hospital days. HAIs incidence was 4.4 (7/160) per 100 patients in 2024 and 4.5 (8/176) in 2023 (p=0.9); HAIs incidence density in 2024 was 4.9 (7/1411) per 1000 hospital days and 6.2 (8/1297) in 2023 (p=0.7). The most represented HAI were blood stream (BSI), 50% (4/8) in 2024 and 57% (4/7) in 2023; followed by pneumonia (PN).

CONCLUSIONS

Over the two years period, HAI incidence in PICUs was stable, in line with lower reported incidence in literature (from 2% up to 34.9%), with BSI the most common HAIs in children. These findings confirm the importance of strong infection prevention and control (IPC) practices. Further investigation into specific risk factors is necessary to improve patient outcomes and reduce infections rates in PICUs.

KEYWORDS: Healthcare-associated infections, pediatric ICU, active surveillance, infection rates

ABSTRACT ID: 765

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POSTER TOUR 14

Day 2 | Thursday 20 November 15:40-16:40

One Health

PRESENTER

Paul Reidy

ABSTRACT

Pilot Assessment of Antimicrobial Resistance Gene Detection in Hospital & Urban Wastewater to compare AMR Ecology using Molecular Methods

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BACKGROUND

Antimicrobial resistance (AMR) is a critical public health issue. Antimicrobial consumption in healthcare is a significant driver and may affect the ecology of AMR. While monitoring antibiotic prescribing is routine practice, there are no established methods for directly assessing the impact of clinical prescribing on environmental AMR levels. This pilot study explores whether molecular quantification of antimicrobial resistance genes (ARGs) in wastewater could serve as a feasible indicator of these impacts of antimicrobial usage patterns, ultimately aiming to provide a potential tool for evaluating antimicrobial stewardship measures.

METHODS

Wastewater samples were collected from two distinct locations: a tertiary academic referral hospital (high antibiotic exposure) and an urban university site (low antibiotic exposure). Samples were collected from two sites at each location, over two days, with multiple biological replicates. ARG presence and abundance were quantified using Resistomap SmartChip quantitative PCR (qPCR), targeting 72 common ARGs. Relative abundance of each ARG was calculated using the 2-ΔCt method, normalising gene abundances to the 16S rRNA gene. Statistical analyses included Wilcoxon rank-sum tests with Benjamini–Hochberg corrections for gene-level comparisons and principal component analysis (PCA) for multivariate data exploration.

RESULTS

Clear differentiation between hospital and urban wastewater resistomes was observed. Principal component analysis indicated that the primary variance (44.4%) distinctly separated hospital-derived from urban-derived ARG profiles. Gene-level comparisons revealed significant differences (adjusted $p < 0.0001$) across all ARGs tested, with substantial hospital enrichment noted in clinically relevant resistance classes, including aminoglycoside, β-lactam, and macrolide antibiotics.

CONCLUSIONS

This pilot study suggests the feasibility of using molecular ARG quantification in wastewater to distinguish antibiotic-exposed (hospital) from less-exposed (community) populations. Given these clear distinctions, future work will evaluate correlations between wastewater ARG abundances and local antimicrobial prescribing patterns. If confirmed, ARG monitoring could become a valuable tool in assessing and guiding clinical antimicrobial stewardship interventions.

KEYWORDS: Antimicrobial Stewardship, Waste Water, Antimicrobial Resistance, Bacterial, Surveillance

ABSTRACT ID: 222

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POSTER TOUR 14

Day 2 | Thursday 20 November 15:40-16:40

One Health

PRESENTER

Salma Mohasseb

ABSTRACT

Seasonal Variations and reported rates of Human Brucellosis in Egypt: A Three-Year Study (2021-2023)

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BACKGROUND

Brucellosis is one of the most common zoonotic infections worldwide and is transmitted to humans by contact with infected animals or their products. Brucellosis is endemic in Egypt and is often underdiagnosed and underreported. We aimed to describe seasonal variation and characteristics of human brucellosis cases over three years (2021-2023).

METHODS

We described human brucellosis cases notified to the National Electronic Disease Surveillance System (NEDSS) between January 2021 and December 2023 (n=15,649). We defined a probable case according to WHO as a suspected case with positive screening Rose Bengal test but showing negative blood culture and standard agglutination test (SAT) showing low titer; SAT³160 or more. We defined a confirmed case as a suspected or probable case with laboratory confirmation, a positive blood culture, or a four-fold SAT.

RESULTS

Of the 15,649 reported cases, 56.9% (9,906/15,649) were males. The median age was 32 years [IQR=23] and almost half of the cases, 45.4% (7110/15,649), were in the age group 15-35 years. There were 19.9% (3,130/15,649) suspected cases, 76.7% (12,050/15,649) probable, and 3.3% (522/15,649) confirmed. Farmers and agriculture workers were the highest occupations 24.4% (3,818/15,649) reported. Cases occurred in summer 31.6% (4,942/15,649), particularly in July (1,603/15,649) and August (1,751/15,649). 85.9% of the cases (13,445/15,649) recovered. There were only 0.1% deaths (13/15,649), most of which occurred in summer and early autumn 69.2% (9/13).

CONCLUSIONS

Similar to other studies, there was no large seasonal variation in cases. However, the high number of cases in July (2021-2023) could be related to an Islamic event "Eid Al Adha", where sheep and cattle are sacrificed. Public health recommendations could focus on awareness campaigns during Eid Al-Adha to promote livestock vaccination, minimize human-animal contact, and enhance supervision of fresh meat handling.

KEYWORDS: Brucellosis,zoonotic,Surveillance,NEDSS,Egypt

ABSTRACT ID: 474

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POSTER TOUR 14

Day 2 | Thursday 20 November 15:40-16:40

One Health

PRESENTER

Stanislaw Maksymowicz

ABSTRACT

Floodborne Infections and One Health Responses: Lessons from Poland's 2024 Disaster

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BACKGROUND

The 2024 flood in southern Poland exposed significant public health vulnerabilities, particularly related to waterborne infectious diseases. This study, embedded in a One Health framework, investigates the flood's societal and health impacts, highlighting the interconnectedness of human, animal, and environmental health.

METHODS

We employed a mixed-methods design, integrating quantitative survey data, microbiological assessments, and qualitative interviews with affected residents, health professionals, sanitary or veterinary inspectors, and emergency responders. Media discourse was also analyzed to assess public risk perception and crisis communication effectiveness. Focus was placed on microbial water contamination, outbreak risk, and population-level health threats.

RESULTS

Traditional and non-traditional surveillance shows no significant increase in typical waterborne infections, however localized non-specific diarrhoea were mapped. Postexposure vaccination and functioning field hospitals were received positively by respondents. There were multiple complaints about water testing procedures. Even public understanding of water safety risks was fragmented, exacerbated by misinformation in social media. Notably, One Health surveillance was inconsistently applied across sectors, limiting real-time response. The lack of procedures for the immediate implementation of a state of natural disaster limits the initiative of One Health inspection services. We were surprised by the low awareness of epidemiological threats, as well as gaps in the education of medical students in this area.

CONCLUSIONS

Floods must be recognized as complex health emergencies requiring interdisciplinary, preemptive responses. One Health-informed strategies—especially coordinated water testing, targeted vaccination, and mental health support—should be embedded in future preparedness plans. Media monitoring revealed a need for clearer water safety messaging and rapid rumor control mechanisms. Greater emphasis is needed on translating scientific risk assessments into actionable, public-friendly information. The results of this full investigation were published in a report in Polish. Recommendations from the report emphasize strengthening interdisciplinary cooperation among human and veterinary medical professionals, environmental specialists, and emergency services.

KEYWORDS: Disasters, One Health, Social Determinants of Health, Waterborne diseases

ABSTRACT ID: 530

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POSTER TOUR 14

Day 2 | Thursday 20 November 15:40-16:40

One Health

PRESENTER

Miriam Van den Nest

ABSTRACT

Winter wonderland in Austria - an outbreak of Legionnaires' disease due to a cooling tower in Vorarlberg, 2024/2025

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BACKGROUND

Legionnaires' disease (LD) characterized by serious pneumonia, is primarily caused by *Legionella pneumophila* serogroup 1 (LP1). Most cases are sporadic and occur in the warmer months. Starting at the end of December 2024, cases of LP1 LD in the Austrian federal state Vorarlberg began to increase. This surprisingly and continuous rise was followed by an extensive investigation to find the source and terminate the outbreak.

METHODS

We included cases of LD caused by LP1 in Vorarlberg from 20/12/24 to 11/03/25. Confirmed cases had either stayed in Bregenz in their infection period or matched the genetic outbreak cluster. To identify potential (outdoor) sources, we conducted standardized case interviews and used Google Maps Satellite View, ECDC's LD GIS tool and meteorologic data. Core genome Multilocus Sequence Typing with an allelic threshold of ≤ 4 was used to characterize isolates as being outbreak-related.

RESULTS

We identified 37 confirmed cases, with a median age of 63 years (13 female, 24 male). Interviews revealed that most cases spent time outdoor in Bregenz, Vorarlberg, in their infection period, clustering within a radius of 2km. There were inversion weather conditions, with high inversion fog and mainly southeastern wind. Of 85 environmental sites tested, five were positive for LP1, one was a cooling tower (CT) not adhering to reprocessing standards, located at the southeastern border of Bregenz. All patient isolates (n=9) and isolates sampled from the CT were outbreak-related, resulting in two genomic clusters. After shutting down and reprocessing the unit, no further cases appeared.

CONCLUSIONS

This is the largest known Legionellosis outbreak in Austria, presumably caused by a single CT. Two major factors impacted on the outbreak and investigation: a) unusual weather conditions favouring spread of LP1, b) lack of registry for CT, hindering identification of potential sources. Following the outbreak more strict policies for CTs are being discussed in Vorarlberg.

KEYWORDS: Legionellosis, Infectious Disease Outbreak, Austria, Cooling Tower, cgMLST

ABSTRACT ID: 658

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POSTER TOUR 14

Day 2 | Thursday 20 November 15:40-16:40

One Health

PRESENTER

Raquel Barba Sanchez

ABSTRACT

Mortality risk attributable to high temperatures from 2021 to 2024 in Spain: the effect of heat waves

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BACKGROUND

Exposure to extreme heat and heatwaves, which are expected to become more intense and frequent due to climate change, increase morbidity and mortality, especially among vulnerable individuals such as those over 65 years old, infants, pregnant women, and those with chronic illnesses. MoMo system is a daily all-cause mortality surveillance system that provides estimates of mortality attributable to high temperatures in Spain. This study analyses the recent evolution of these estimates during the summers of the period 2021-2024, considering sex and age groups.

METHODS

The main information sources used by MoMo include population and daily mortality data provided by the National Institute of Statistics and death from civil registries from the Ministry of Justice, alongside daily temperatures from the State Meteorological Agency. Estimates of all-cause excess mortality and mortality attributable to high temperature are based on Poisson mixed generalised additive models that include terms for mortality trends, seasonality, accumulated thermal overcharge, and offset population. Monthly heat-attributable estimates were described by sex and age groups for the overall country. Geographic patterns were explored by calculating standardized mortality ratios for summer periods.

RESULTS

Over the four summers analysed, 11,684 deaths attributable to high temperature were estimated by the model, 59.2% in women and 40.9% in men. Mortality progressively increased with age, most heat-attributable deaths corresponding to groups over 74 years old. The highest number of deaths attributable to high temperature ^{4,732} was estimated in 2022. By regions, in 2021, 2022 and 2024 excess of mortality risks were mainly located in inland provinces, while coastal regions generally showed lower than average risks, except in certain provinces in the East and South.

CONCLUSIONS

Momo has shown the impact of rising temperatures and heat waves in mortality. It is essential to implement public policies focused on adaptation, especially in the most vulnerable populations and in the at-risk areas.

KEYWORDS: Heat, Mortality, Public Health Surveillance, Real-time mortality surveillance

ABSTRACT ID: 664

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POSTER TOUR 14

Day 2 | Thursday 20 November 15:40-16:40

One Health

PRESENTER

Idris Nasir Abdullahi

ABSTRACT

Guts of healthy humans, livestock and pets harbor critical priority and pandemic *Escherichia coli* clones

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BACKGROUND

In May 2024, the World Health Organization classified carbapenem (CARB)- and third-generation cephalosporin (3GC) resistance (R) in *Escherichia coli* as a critical priority, whereas colistin (COL) is a "last resort" antibiotic for their treatment. This meta-analysis evaluated the pooled prevalence, high-risk lineages, genetic relatedness, and mechanisms of CARBR, COLR, and 3GCR in *Escherichia coli* from healthy humans and animals.

METHODS

We conducted a systematic review and meta-analyses following the PRISMA criteria on all eligible studies that reported the analysis of *E. coli*, and antimicrobial susceptibility to CARB, COL and 3GC in *E. coli* from gut samples of clinically healthy humans, livestock, and pets from June 2014 to June 2024. Random-effect models and CSI Phylogeny 1.4 were used to determine pooled prevalence rates (PPs) and the relatedness of publicly available *E. coli* genomes, respectively.

RESULTS

Of the 5034 identified articles, 55 studies were deemed eligible. The overall PPs of 3GCR, CARBR, and COLR *E. coli* were 19% (95% CI, 14.5%-24.4%), 1.6% (95% CI, 0.8%-3.5%), and 13.3% (95% CI, 8.4%-20.9%), respectively. The PPs of 3GCR, COLR, and CARBR *E. coli* significantly varied by hosts, continent, and year of studies ($p < 0.001$). Diverse *E. coli* lineages were found, including 13 high-risk sequence types (STs), within which ST10 predominated. Phylogenomic analyses produced 4 clusters of related CARBR- and COLR *E. coli* strains (< 25 SNP): ST940-blaOXA-181 from humans in Lebanon, ST617-mcr-1 from pigs in China, ST46-mcr-1 from poultry in Tanzania, and ST1720-mcr-1 from goats in France.

CONCLUSIONS

COLR and 3GCR are more frequent than CARBR in gut *E. coli*. These 10-year epidemiological data highlight the persistence and transmission of critical priority and high-risk *E. coli* strains in healthy humans and animals, raising significant One Health concerns.

KEYWORDS: *Escherichia coli*, Gut microbiota, One Health, Carbapenem resistance, Colistin resistance, Third-generation cephalosporin

ABSTRACT ID: 323

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POSTER TOUR 14

Day 2 | Thursday 20 November 15:40-16:40

One Health

PRESENTER

Evangelos Mourkas

ABSTRACT

Genomic overlap and antimicrobial resistance of *Campylobacter jejuni* in poultry and wild birds around organic farms in Sweden

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BACKGROUND

Antimicrobial resistance (AMR) in foodborne pathogens such as *Campylobacter jejuni* poses a major public health concern, particularly when transmission occurs across livestock, wildlife, and environmental interfaces. While poultry is a well-known reservoir for *C. jejuni*, the role of organic farming systems in shaping pathogen diversity, transmission, and AMR dynamics remains poorly understood. This study investigates the genomic population structure and AMR profiles of *C. jejuni* in organic poultry and wild birds near organic farms in Sweden, a country with low background AMR prevalence.

METHODS

We performed whole-genome sequencing of *C. jejuni* isolates sampled from organic chickens and wild birds near organic farms. Comparative genomics and phylogenetic analysis were used to characterize clonal relationships and lineage overlap between sources. Shannon diversity indices were used to evaluate within-group diversity. Genomes were screened for AMR genes and plasmids. Comparative analyses included *C. jejuni* genomes from conventional chickens and wild birds sampled at Ottenby, Sweden.

RESULTS

Swedish poultry was dominated by generalist lineages ST-21 and ST-45, with a notable absence of poultry-adapted specialist lineages in organic systems. Evidence of clonal overlap between organic chickens and wild birds near farms revealed highly similar strain clusters, suggesting recent transmission. Wild birds near farms displayed higher lineage diversity than birds from remote areas. AMR prevalence was consistently higher in poultry and wild birds near farms, with frequent detection of plasmid-associated resistance genes.

CONCLUSIONS

Our findings highlight an ecological interface between organic poultry and wild birds near farms, shaped by shared *C. jejuni* lineages and resistance determinants. Elevated AMR and plasmid prevalence in wild birds near farms suggest environmental exposure and potential spillover from agricultural sources, reinforcing the need for integrated One Health surveillance.

KEYWORDS: Organic poultry, wild birds, antimicrobial resistance, transmission, One Health

ABSTRACT ID: 777

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POSTER TOUR 15

Day 2 | Thursday 20 November 15:40-16:40

Antimicrobial resistance

PRESENTER

Hong Fang

ABSTRACT

Genomic surveillance of vancomycin-resistant *Enterococcus faecium* reveals shift of dominant clones between ST80 and ST117, and from vanB to vanA in Stockholm, Sweden, 2018-2024

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BACKGROUND

Vancomycin-resistant *Enterococcus faecium* (VREfm) has been successfully disseminating in hospital settings and become endemic in many countries. Spread of VRE is a global concern in healthcare-associated infections. This laboratory-based surveillance study aimed to investigate the predominating strains in Stockholm during 2018-2024.

METHODS

Non-duplicate consecutive VREfm isolates (N=631) detected in the Stockholm area from 2018 to 2024 were included in the study. All isolates were subjected to whole-genome sequencing (WGS) by using an Illumina platform. Isolates were verified to be positive to vanA, vanB or vanD gene by PCR or WGS, resistant to vancomycin by Etest, and determined as *E. faecium* by MALDI-TOF. All isolates were analyzed by multi-locus sequence typing (MLST).

RESULTS

The incidence of VRE in Stockholm varied between 1.17 and 6.23/100,000 inhabitants during 2018-2024. In 2020, the incidence of VRE decreased to the lowest level since 2007 when VRE became notifiable in Sweden. Top incidence was observed in 2018 (6.23/100,000) and followed by 2024 (5.22/100,000). vanB-type VREfm predominated in 2018 (76%), while vanA-type was dominant in 2019 and 2022 - 2024. Fifty-one different STs were detected among the 631 isolates investigated, with a clear predominance of ST80 and ST117. ST80 isolates accounted for 74% of all isolates in 2018, being predominant till 2020. The predominant type was shifted to ST117 (51%) in 2021, returned to ST80 in 2022 and 2023, and again to ST117 (55%) in 2024. Two vanD-type VREfm isolates were identified in 2018 and 2020, being ST1495 and ST263, respectively. Two isolates carrying both vanA and vanB genes were identified in 2024, being ST80 and ST1903, respectively.

CONCLUSIONS

ST80 and ST117 predominated alternatively among VREfm isolates in Stockholm during 2018-2024. In the study period, the dominant genotype shifted from vanB to vanA. A continuous surveillance helps to prevent the further spread of VRE.

KEYWORDS: genomic surveillance,VRE,ST80,ST117

ABSTRACT ID: 217

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POSTER TOUR 15

Day 2 | Thursday 20 November 15:40-16:40

Antimicrobial resistance

PRESENTER

Márton Falus

ABSTRACT

A nationwide study of antimicrobial stewardship tools and activities coordinated by Infection Control and Antibiotic Committees in Hungarian hospitals, 2023

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BACKGROUND

Antimicrobial stewardship (AMS) policies at national and hospital level are key to preventing antimicrobial resistance (AMR), a critical public health problem worldwide. In Hungary, legislation has required hospitals to operate an Infection Control and Antibiotic Committee (ICAC) since 2009, with detailed tasks since 2018. We aimed to assess the AMS tools/activities of the ICACs and identify challenges nationally.

METHODS

In 2023, all hospital with at least 30 acute/chronic beds were asked to complete a self-assessment ICAC questionnaire. Topics included institutional policies on microbiological sampling and antimicrobial use (AMU), pre- and postprescription controls, laboratory support, AMU monitoring overall and by ATC subgroup, IT tools, and needs assessment. Proportions of positive answers were calculated.

RESULTS

Overall, 103 hospitals (95%) replied. Of them, 41% met at least 6 of the 8 assessed elements, the rest varied in their performance. Both groups were heterogeneous in size, level of care and geographical location. Protocols for microbiological sampling and AMU were available in 86% and 80% of hospitals, respectively. Preprescription authorisation for selected antimicrobials and routine postprescription review were in place in 48% and 47% of hospitals, respectively. AMU was monitored in 89% of hospitals, mostly focusing on specific wards and number of packages used. Of these, 53% monitored at least one systemic antimicrobial by ATC subgroup. The laboratory (in-house or contracted) provided aggregate AMR data to facilitate AMS in 57% of hospitals. IT tools for AMS were available in 15% of hospitals. Understaffing as main obstacle to AMS activities and need for national methodological guidance were reported by 95% of hospitals.

CONCLUSIONS

We found substantial variability in the implementation of most AMS tools/activities by the ICACs. To ensure that AMS efforts facilitate better clinical care and reduction of AMR, future developments should focus on human resources, IT capabilities, patient-level interventions and methodological support from national bodies.

KEYWORDS: Antimicrobial stewardship, Infection control, Organisational policy, Antibiotic resistance, Survey

ABSTRACT ID: 327

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POSTER TOUR 15

Day 2 | Thursday 20 November 15:40-16:40

Antimicrobial resistance

PRESENTER

Tjaša Žohar Cretnik

ABSTRACT

Clonal structure and mechanisms of resistance of carbapenemase-producing Enterobacterales from two regions in Slovenia

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BACKGROUND

Carbapenemase-producing Enterobacterales have become an increasing problem in Slovenia in the last five years, as we entered the exponential phase of the epidemic curve. Based on the EARS-Net data, the estimated incidence of carbapenem-resistant *Klebsiella pneumoniae* isolates from bloodstream infections per 100.000 inhabitants increased by 1140 % from 2019 to 2023. The aim of this study was to analyze the clonal structure and resistome of carbapenemase-producing Enterobacterales from 2024 from the Savinjska and Posavska regions, which represent one-fifth of the Slovene population and to assess the role of plasmid versus clonal spread of this group of bacteria

METHODS

Whole-genome sequencing using short-read technology on the Illumina platform and bioinformatic analyses were used to determine sequence types, genetic relatedness, resistance genes, and plasmid content. Plasmids were grouped into MOB secondary clusters based on a MASH distance threshold of 0.025. Reconstructed plasmid sequences were aligned to a reference plasmid and SNP-based phylogeny was constructed to assess their relatedness.

RESULTS

The 77 isolates belonged to 14 bacterial species, with *K. pneumoniae* (n=21), *Citrobacter freundii* (n=20), and *Escherichia coli* (n=17) being the most prevalent. Of the 37 MLST sequence types, 26 were represented by only one isolate. Eleven isolates harboured genes encoding two different carbapenemases (combinations of OXA-48+VIM-1, OXA-48+NDM-5, and GES-5+VIM-1), and 65 isolates carried genes encoding a single carbapenemase. Gene for OXA-48 was detected in 49 isolates belonging to 11 species and 25 STs. Further analysis of 42 plasmid sequences carrying blaOXA-48 gene demonstrated two closely related MOB clusters, AH529 and AH539, with the maximum difference of four SNPs across all 42 plasmids.

CONCLUSIONS

These results suggest that this very complex epidemiological situation is most probably a consequence of predominant plasmid spread carrying blaOXA-48 gene across bacterial species.

KEYWORDS: carbapenemase, clone, Enterobacterales, plasmid, Slovenia

ABSTRACT ID: 508

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POSTER TOUR 15

Day 2 | Thursday 20 November 15:40-16:40

Antimicrobial resistance

PRESENTER

Hannah Charles

ABSTRACT

Epidemiology of extensively-drug resistant *Shigella* in England: 2017 to 2024

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BACKGROUND

Shigella spp., Gram-negative bacteria transmitted through faecal-oral contact, cause acute bacillary dysentery. In England, shigellosis has been associated with travel to endemic regions, it is now a leading cause of sexually transmissible gastroenteritis among men who have sex with men (MSM). Among *Shigella* spp. isolates, antimicrobial resistance (AMR) is a key public health concern. We investigate the epidemiology of XDR *Shigella* in England between 2017 and 2024.

METHODS

Shigella spp. isolates referred by diagnostic laboratories to the reference laboratory in England for species identification and antimicrobial resistance (AMR) profiling using whole genome sequencing (WGS) between January 2017 and December 2024 were included. XDR was defined as non-susceptibility to at least one agent in all but two or fewer antibiotic classes¹.

RESULTS

The number of *Shigella* spp. detections have increased, as has the proportion of isolates that are XDR (15.2% in 2017 to 26.4% in 2024) (Figure 1). There were 2,673 XDR detections, most (70.0%) were among males, the median age was 35 years (IQR: 25-48), and 14.3% (363/2,673) were children under 10 years. Most XDR *Shigella* cases (75.9%) did not report international travel in the past month and were speciated as *S. sonnei* (83.2%), followed by *S. flexneri* (14.8%). Most XDR *Shigella* cases were reported from London, North West and South East of England, mirroring the epidemiology overall. Resistance determinants detected in most XDR strains of *Shigella* spp. using WGS are presented in Table 1.

CONCLUSIONS

The widespread national increase in cases, coupled with the increasing frequency of XDR infections, leads to concerns of treatment failures and untreatable infections. Treatment recommendations currently include carbapenems for severe infections, and pivmecillinam and fosfomycin for uncomplicated XDR shigellosis. Further understanding of the factors that facilitate the development of AMR and their transmission is needed to implement intervention strategies to stop dissemination.

KEYWORDS: *Shigella*, shigellosis, antimicrobial resistance

ABSTRACT ID: 672

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POSTER TOUR 15

Day 2 | Thursday 20 November 15:40-16:40

Antimicrobial resistance

PRESENTER

Veronica Mixao

ABSTRACT

Characterization of azole resistance in Portuguese *Candida parapsilosis* isolates

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BACKGROUND

Candida parapsilosis is an opportunistic pathogen associated with an increasing number of nosocomial infections, being a special concern in Southern Europe due to its increasing resistance to fluconazole. In this context, we aimed to characterize the Portuguese *C. parapsilosis* population by determining the frequency of fluconazole-resistant isolates, perceiving the molecular mechanisms associated with these phenotypes, and integrating the Portuguese isolates within the worldwide *C. parapsilosis* genomic diversity.

METHODS

We performed antifungal susceptibility tests (screening and microdilution tests) on 95 *C. parapsilosis* isolates (from biological and environmental samples) that integrate the collection of the Portuguese National Reference Laboratory. Whole-Genome Sequencing (WGS) analysis of all resistant isolates was performed with a read-mapping approach using the NCBI *C. parapsilosis* reference genome, allowing the identification of Single-Nucleotide Polymorphisms (SNPs) and copy number variations (CNVs). FungAMR database was used to determine the possible association between SNPs/CNVs and the resistant phenotype. To integrate the Portuguese fluconazole-resistant *C. parapsilosis* isolates in the worldwide species genetic diversity, we analyzed publicly available WGS data and reconstructed a phylogenetic tree.

RESULTS

The frequency of fluconazole-resistant *C. parapsilosis* isolates in this study was 8.4%. All fluconazole-resistant isolates presented the Y132F mutation, which was previously associated with this phenotype, in combination with R398I. The reconstructed *C. parapsilosis* phylogeny showed that the Portuguese isolates are distributed across 3 out of the 4 *C. parapsilosis* clades described to date, being more closely related to USA and German isolates than to the ones from Spain. Indeed, all Spanish isolates with publicly available WGS data formed a very distinct genetic cluster, which we propose to be *C. parapsilosis* clade 5.

CONCLUSIONS

This study represents a first step towards the full characterization of Portuguese *C. parapsilosis* isolates gathered in a reference collection, providing valuable information about the fluconazole-resistance rates in Portugal and the molecular mechanisms involved.

KEYWORDS: *Candida parapsilosis*, AMR, WGS

ABSTRACT ID: 751

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POSTER TOUR 16

Day 2 | Thursday 20 November 15:40-16:40

Food - and water-borne diseases

PRESENTER

Piotr Polanski

ABSTRACT

Factors associated with the presence of anti-hepatitis A virus antibodies in Poland's population- results from a 2023 cross-sectional study

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BACKGROUND

Years 1978-1998 were the transition period from very high to low circulation of hepatitis A virus (HAV) in Poland. It is very likely that persons born after this period had no contact with the virus in childhood and thus are less protected against hepatitis A. We aim to estimate anti-HAV seroprevalence and to identify subpopulations with lower prevalence, for vaccination prioritization in case of outbreak.

METHODS

We conducted a country-wide, cross-sectional study in the general population in Poland using a stratified random sampling with Random Digit Dialing method. We tested participants for anti-HAV antibodies using two-step competition enzyme immunoassay method, collected data on socio-demographic characteristics (from participants of all ages), and previous anti-HAV vaccination and infection statuses (from participants over 20 years old). We counted age-group seroprevalences and performed multivariable logistic regression, with age group, sex, settlement/area type (city/non-city), previous infection or vaccination status, voivodeship/region as predictors to calculate odds ratios (OR) with 95% confidence intervals (95% CI) for being seropositive.

RESULTS

In total 7437 persons aged between 0-94 years old were tested (3353 males and 4084 females). Seroprevalence increased with age from 7.5% in 0-19 age group (95% CI=6.3-8.9) to 88.4% in 70+ age group (95% CI=86.7-90.0) and within these age groups no differences were found between voivodeships/regions. Odds of being seropositive rose with age: from 3.4 (95% CI=2.4-4.9) in 40-59 age group to 89.1 (95% CI=60.9-133.5) in 70+ age group. Furthermore, vaccinated persons had 10.3 more odds of being seropositive (95% CI=6.2-17.3), however this effect was weaker in the older age groups.

CONCLUSIONS

At present in case of an outbreak vaccinations are offered to all persons exposed, regardless of their age. Our study shows that more effort should be made to reach younger age groups for vaccination irrespective of their socio-demographic characteristics, especially when availability of vaccines is limited.

KEYWORDS: Hepatitis A, Cross-Sectional Studies, Poland, Seroepidemiologic Studies, Logistic Models

ABSTRACT ID: 90

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POSTER TOUR 16

Day 2 | Thursday 20 November 15:40-16:40

Food - and water-borne diseases

PRESENTER

Lea-Elisa Heinz

ABSTRACT

Detection of non-tuberculous mycobacteria and other bacterial pathogens in dental unit waterlines, 2024, Germany: a microbiological single-centre study

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BACKGROUND

Dental unit waterlines (DUWLs) might pose infection risks due to the presence of biofilms. A global outbreak of *Mycobacterium chimaera* through water-carrying medical devices in cardiac surgery underscored the importance of water for pathogen transmission. We aimed to assess the presence of non-tuberculous mycobacteria (NTM), *Legionella* spp., and *Pseudomonas* spp. in DUWLs in one Medical Centre in Germany to evaluate their potential role as causative agent of infections linked to dental procedures.

METHODS

We conducted a cross-sectional, microbiological single-centre study at Saarland University Medical Centre from May to July 2024, examining 42 DUWLs once before patient care started. After DUWL flushing, 500 mL water samples were collected. *Legionella* spp. were detected after up to 10 days of incubation, *Pseudomonas* spp. via membrane filtration and 48-hour incubation, and NTM using liquid and solid cultures with up to eight weeks of incubation. Clinically relevant NTMs, e.g. *M. chimaera*, *M. chelonae*, were identified using a GenoType line probe assay. Frequencies and proportions of positive samples were calculated.

RESULTS

Among the 42 samples collected, 83% (n=35) tested positive for NTM, while *Pseudomonas* spp. were detected in only one sample. One sample was positive for both *Legionella* spp. and NTM. Most NTM isolates were identified as *M. chimaera* (n=27) isolates, followed by *M. chelonae* (n=6).

CONCLUSIONS

The large proportion of NTM detection highlights the need for frequent bacterial monitoring in DUWL water quality controls, which is not routinely implemented in most testing protocols. Regular NTM testing should be incorporated into standardized DUWL monitoring protocols to ensure patient safety. The findings suggest a need to update and implement DUWL testing protocols across Germany. To prevent potential infections, it is crucial to keep dental clinics safe. Further research is warranted to elucidate whether these findings are applicable to outpatient dental treatment centers.

KEYWORDS: atypical mycobacteria, *Mycobacterium chimaera*, dental units, DUWL, public health, biofilms

ABSTRACT ID: 129

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POSTER TOUR 16

Day 2 | Thursday 20 November 15:40-16:40

Food - and water-borne diseases

PRESENTER

Gulsum Zoroglu

ABSTRACT

An outbreak of waterborne tularaemia in 6 districts in Sivas province, Turkiye, case-control study, January 2024

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BACKGROUND

On January 24, 2024, Sivas Provincial Health Directorate reported 8 confirmed cases of tularaemia from 6 districts. We investigated to identify the source of the outbreak, and implement control measures.

METHODS

We conducted 1:4 unmatched case control study in six districts. For case-finding, we reviewed Tularaemia Surveillance Information System (TSIS) and laboratory records, and conducted door-to-door searching in villages. We interviewed 34 confirmed cases that we detected from TSIS and 23 confirmed cases, among 43 suspected cases we found in the field investigation, and their neighbourhood controls. Confirmed case was a suspected case plus positivity of *F.tularensis*-specific antibody by microagglutination test (titre $\geq$ 1:160 or four-fold rise in convalescent sera) between November 1, 2023, and February 9, 2024. We analysed 57 confirmed cases and their controls. We calculated ORs with 95%CI. We tested water samples from tap water (n=48), neighbourhood fountains (n=13), and water tanks (n=20) by culture.

RESULTS

Crude attack rate was 0.01%. Most common symptoms were swollen oropharyngeal lymph nodes (89.5%), sore throat (82.5%), and fever (80.7%). Neighbourhood fountain water consumption was 2.6(95%CI:1.4-5.1), tap water was 1.2(95%CI:0.6-2.3), and bottled water was 0.3(95%CI:0.1-0.9) times higher in cases compared to controls. When compared to bottled water, odds of tularaemia were 15.4(95%CI=2.7-88.6) for mixed (Fountain+tap water); 5.5(95%CI=1.1-27.7) for fountain, and 2.9(95%CI=0.7-12.9) for tap water. Epidemic curve indicated an intermittent-source exposure. *F.tularensis* was isolated in fountain (n=6), tap water (n=12), and water tanks (n=7). Free chlorine level was low prior to outbreak, automatic and solar-powered chlorination devices malfunctioned and water tanks were inadequate. Neighbourhood fountains were mostly fed from the water network system.

CONCLUSIONS

Fountain and tap water contaminated with *F.tularensis* due to malfunctioned chlorination devices caused this outbreak. We chlorinated water after chlorination devices were repaired. We recommended closure of fountains, to keep spare chlorination devices, monitor free chlorine levels regularly and improve water tanks.

KEYWORDS: Tularaemia, Outbreaks, Case-Control Studies, Waterborne Diseases

ABSTRACT ID: 219

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POSTER TOUR 16

Day 2 | Thursday 20 November 15:40-16:40

Food - and water-borne diseases

PRESENTER

Laura Giese

ABSTRACT

Survey on the impact of the increased use of multiplex PCR on the surveillance and control of foodborne pathogens in Germany

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BACKGROUND

In 2022, Germany introduced reimbursement for multiplex polymerase chain reaction (PCR) testing to detect gastrointestinal pathogens including Salmonella and Campylobacter, which account for a large proportion of foodborne illnesses and outbreaks. While PCR offers rapid, simultaneous detection of multiple pathogens, its increasing use may lead to reductions in culture-based diagnostics. This could limit the availability of clinical isolates for genomic surveillance, which is considered an effective public health strategy to detect and prevent foodborne outbreaks.

METHODS

We conducted an online survey among diagnostic laboratories in Germany from May-July 2024 (n=75). The questionnaire primarily addressed laboratory characteristics, diagnostic procedures and the use of genome sequencing for multiple pathogens. Participation was voluntary and questions could be left unanswered, resulting in varying sample sizes for each question. Descriptive analysis was performed to assess diagnostic trends and pathogen-specific testing practices.

RESULTS

Altogether, 48/75 (64%) laboratories perform diagnostics for Campylobacter and 49/75 (65%) for Salmonella. Of 40 responding laboratories, 24 (60%) see an impact of multiplex PCR on culture-based diagnostics in recent years. Among Salmonella-diagnosing laboratories, 15/39 (38%) perform both PCR and cultivation, 14/39 (36%) only cultivation, and 10/39 (26%) only PCR. Similar patterns were seen for Campylobacter (16/39 vs. 13/39 vs. 10/39). From 2021 to 2023, the proportion of positive samples with an associated clinical isolate decreased for both Campylobacter (85% to 70%) and Salmonella (94% to 85%).

CONCLUSIONS

While culture-based diagnostics remain in use, a large proportion of laboratories already perform PCR only, suggesting a continuing trend in this direction. This shift compromises the availability of clinical isolates for genomic surveillance in future. To ensure timely outbreak detection and the identification of sources of infections, it is crucial that healthcare providers, laboratories and health insurance companies recognize the importance of culture-based diagnostics for public health and consumer protection and support appropriate reimbursement strategies.

KEYWORDS: Genomic Surveillance, Foodborne outbreaks, Polymerase Chain Reaction, Salmonella Infections, Campylobacter Infections

ABSTRACT ID: 365

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POSTER TOUR 16

Day 2 | Thursday 20 November 15:40-16:40

Food - and water-borne diseases

PRESENTER

Fanny Chereau

ABSTRACT

Nationwide outbreak of haemolytic uraemic syndrome in adults linked to an atypical strain of Shiga toxin-producing *Escherichia coli*, France, December 2024-January 2025

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BACKGROUND

French Shiga toxin-producing *Escherichia coli* (STEC) surveillance is based on voluntary paediatric haemolytic uraemic syndrome (HUS) notifications and microbiological surveillance (HUS, non-HUS). Documented outbreaks have been largely limited to children and top-5 serogroups. On 8 January 2025, the National Reference Center (NRC) for *E. coli* alerted Santé publique France of four STEC isolates non-serotypable by PCR, identified in elderly patients with HUS in December 2024. Isolates carried the *stx2* gene alone and presented similar profiles by multilocus variable-number tandem-repeat (MLVA). Investigations aimed to identify a common contamination source and implement control measures.

METHODS

We used trawling STEC questionnaires for exposures, and supermarket loyalty card data for food traceback. The NRC conducted MLVA and whole genome sequencing (WGS) for cluster determination. A specific PCR was developed to detect cases with no strain isolation. We defined cases as patients ill from December 2024, with outbreak strain isolated (confirmed), or positive specific PCR, but no strain isolation (possible).

RESULTS

We identified 17 confirmed and four possible cases, ill from 9 December to 29 January. Median age was 72 years old (range: 34-89). WGS identified the atypical outbreak strain belonging to serotype O17/O44/O77/O106:H18:K92 and carrying *stx2d* alone. All patients were hospitalized for HUS, eight with neurological complications. Three patients died. Exposure to a specific raw cow's milk cheese prior to illness was documented for 15 of 17 investigated cases. Traceback identified a common manufacturer and recall/withdrawal of incriminated cheeses began on 24 January.

CONCLUSIONS

This outbreak was highly unusual as cases were primarily elderly adults with HUS, infected with an atypical STEC strain. This is the first documented STEC outbreak exclusively in adults in France and highlights the outbreak potential of atypical STEC strains and severe clinical impact. It reaffirms the pertinence of the recent decision to extend French STEC-HUS surveillance to all ages.

KEYWORDS: Shiga toxin-producing *Escherichia coli*, haemolytic uraemic syndrome, foodborne outbreak, whole genome sequencing

ABSTRACT ID: 621

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POSTER TOUR 16

Day 2 | Thursday 20 November 15:40-16:40

Food - and water-borne diseases

PRESENTER

Yanshi Yanshi

ABSTRACT

Estimating under-diagnosis of Hemolytic Uremic Syndrome attributable to Shiga toxin-producing Escherichia coli infections in England

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BACKGROUND

Hemolytic Uremic syndrome (HUS) is a notifiable severe systemic condition with over 90% of cases thought to be caused by Shiga toxin-producing Escherichia coli (STEC). In England, HUS surveillance is incorporated into the UKHSA's enhanced surveillance system for STEC, which may have led to the assumption that only STEC-HUS should be reported. We assess the completeness of UKHSA's HUS surveillance to determine if there were case characteristics to improve reporting.

METHODS

We used the Hospital Episode Statistics Admitted Patient Care dataset (HES-APC), for hospital admissions for patients in public hospitals in England. We extracted confirmed HUS cases from 01/01/2009 to 31/12/2023. We matched cases to records in UKHSA's enhanced surveillance system using the unique patient identifier, or postcode and date of birth. The ascertainment of cases was estimated using numbers and proportions. We described HUS cases by age, sex and proportion confirmed with STEC.

RESULTS

We identified 1834 confirmed HUS cases in HES-APC dataset. Over half (63%) of HUS cases were unknown to UKHSA. This under-ascertainment was not associated with age-group, sex, geographical region of treatment, or year of report. Overall, 37% of HUS cases had confirmed STEC infection. Over half (51%) of HUS cases were 0-9 years and they had the highest STEC confirmation rate (50%). Confirmation rates were lower in other age groups, for example 12% in 20-49 years and 23% in 50+ age group. There were no time trends with case reporting, other than reduced numbers in the pandemic years.

CONCLUSIONS

We found no case characteristics to target improvement in case reporting. We recommend raising awareness to test HUS cases for STEC confirmation; particularly in older adults where STEC may not be suspected. Furthermore, we reiterate the importance of notifying all HUS cases to UKHSA among clinicians and incorporating the HES-APC HUS notifications within the routine HUS surveillance.

KEYWORDS: HUS, STEC, Surveillance, England

ABSTRACT ID: 654

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POSTER TOUR 17

Day 3 | Friday 21 November 08:30-09:15

Vaccination acceptance and uptake

PRESENTER

Francisco Rios

ABSTRACT

Estimation of vaccination coverage from mandatory notification data using a reversed Farrington screening method, exemplified by Mpox data from Berlin, Germany, in 2023.

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BACKGROUND

Early knowledge of vaccination coverage (VC) and the size of the population at risk is crucial for managing containment efforts and allocating resources (e.g., personnel, vaccines, and medical supplies) during ongoing outbreaks of vaccine-preventable diseases (VPDs), such as Mpox. In 2022, a multi-country Mpox outbreak occurred almost exclusively among men who have sex with men (MSM); Berlin reported 1,666 cases that year, peaking between June and July. A vaccination campaign was launched in Berlin in July 2022 with a two-dose vaccination scheme targeting the population at risk, primarily MSM with multiple sexual partners. We developed a method to estimate VC and the size of the population at risk for future reference.

METHODS

We adapted the Farrington screening method to estimate the proportion of the population vaccinated (PPV): $PPVi = (PCVi) / ((1 - VEi) + (PCVi * VEi))$ where "i" denotes the number of doses. We calculated the proportion of cases vaccinated (PCVi) using 2023 mandatory notification data of the ongoing Mpox outbreak in Berlin. The German Vaccination Monitoring Program provided the number of administered vaccinations in Berlin. Using PPVi and the latter, we estimated the population at risk for Mpox, and VC for at least one dose (VC1+). As vaccination effectiveness (VEi), we used literature-reported values for one and two doses. We performed the Bayesian modelling using RStan.

RESULTS

We estimated the population at risk of acquiring Mpox to be 22,344 individuals (95% confidence interval [CI]: 20,188-26,566). The estimated VC1+ was 82% (95% CI: 69%-91%). Previous surveys validate the estimated size of the population at risk, since they fall within the estimated CI.

CONCLUSIONS

The reverse Farrington screening method allowed us to estimate VC1+ and the size of the population at risk of acquiring Mpox. It provides estimates needed to target public health interventions and manage vaccination and personnel capacities in Mpox outbreaks. It could be adapted for other VPDs.

KEYWORDS: Vaccine-Preventable Diseases, Mpox, Vaccination Coverage, Bayesian Estimation, Epidemiologic Methods

ABSTRACT ID: 213

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POSTER TOUR 17

Day 3 | Friday 21 November 08:30-09:15

Vaccination acceptance and uptake

PRESENTER

Malorie Perry

ABSTRACT

A large data linkage study to quantify waning of MMR vaccine against mumps, Wales, UK

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BACKGROUND

Uptake of MMR vaccine in Wales is high, although mumps continues to be endemic, with large outbreaks every few years. The aim of this study was to assess long term Vaccine Effectiveness (VE) of MMR against mumps, as current evidence from outbreaks suggests waning but this has not been robustly quantified in the literature.

METHODS

In a retrospective cohort study, 822 116 individuals aged 1 to 30 years as at 31 December 2020 were followed up between 01 January 2007 and 31 December 2020. The study population was identified using the Welsh Demographic Service dataset and vaccination status linked from the national vaccination register and Primary Care records. Outcomes were identified by linking to laboratory confirmations and clinical notifications data. Complications were sourced from hospital admissions and Primary Care data. Extended Cox regression was used to calculate hazard ratios with vaccination included as a time varying covariate.

RESULTS

Overall adjusted VE (aVE) for confirmed mumps infection declined over time; 93.6% (95% CI 90.2-95.8) for those vaccinated with two doses less than 5years previously, 64.3% (95% CI 54.1-72.2) after 10 to 14years and 49.9% (95% CI 34.4-61.8) after 14years. A third dose of mumps vaccine appeared to offer a longer-term increase in protection (84.1% (95% CI 68.2-92.1) 10 to 14years after dose three). aVE estimates for mumps were lower when based on clinical notification rather than confirmed cases only. VE was shown to be high against complications, 94.4% (95% CI 86.4-97.7) overall after two doses.

CONCLUSIONS

This is the largest known VE study for mumps infection and associated complications. High VE for mumps vaccines against complications is encouraging. Evidence for significant waning 10years post dose two may be important when deciding whether to implement a third dose in outbreak settings. This study also highlights the importance of accurate classification of cases in VE studies.

KEYWORDS: Vaccination, Measles-Mumps-Rubella Vaccine, Effectiveness, Mumps, MMR, Immunisation

ABSTRACT ID: 541

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POSTER TOUR 17

Day 3 | Friday 21 November 08:30-09:15

Vaccination acceptance and uptake

PRESENTER

Laure Fonteneau

ABSTRACT

First school-based HPV vaccination campaign in France : at last some progress !

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BACKGROUND

Since 2007 for girls, 2021 for boys, human papillomavirus (HPV) vaccination (two doses) has been recommended between 11 and 14 years. Self-employed healthcare professionals usually perform vaccinations. On 30/09/2023 one dose vaccination coverage (VC) was only 38% in girls and 26% in boys aged 12. A national school-based vaccination campaign, targeting students aged 12 was implemented in 2023-24: the first phase from 01/10/2023 to 31/12/2023, the second phase, from 31/03/2024 to 30/06/2024. The aim of this study was to measure the impact of this campaign on VC.

METHODS

We estimated the number of children aged 12 vaccinated by self-employed healthcare professionals from exhaustive individual data on vaccine reimbursements. We estimated the number of students vaccinated in schools through the campaign from two data sources: reporting from Regional Health Agencies and the aggregated number of vaccines reimbursed to vaccination centres. We estimated VC before and after each phase. We divided the sum of students vaccinated in schools and by self-employed professionals by the population of children aged 12, by sex.

RESULTS

The number of students vaccinated in schools was 106,346 for the first phase, and 85,470 for the second. At the end of the first phase, taking into account vaccination in schools and by self-employed healthcare professionals, one dose VC was 41% in boys and 55% in girls, respectively 15 and 17 points higher compared to the pre-campaign period. At the end of the second phase, one dose VC was 48% in boys and 62% in girls, respectively 22 and 24 points higher compared to the pre-campaign period. The two-dose VC was 30% in boys and 38% in girls.

CONCLUSIONS

This study confirms the effectiveness of school-based campaigns in raising HPV VC levels in France and underlines the importance of repeating such campaigns to reach the target of 80% for two doses by 2030

KEYWORDS: Vaccination coverage, Human papillomavirus viruses, Schools, Children, France

ABSTRACT ID: 653

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POSTER TOUR 17

Day 3 | Friday 21 November 08:30-09:15

Vaccination acceptance and uptake

PRESENTER

Álvaro Serrano-Ortiz

ABSTRACT

Algorithm-based identification of high-risk patients requiring meningococcal vaccination: coverage assessment and implications for catch-up programmes

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BACKGROUND

Invasive meningococcal disease (IMD) poses significant mortality and morbidity risks, particularly for vulnerable populations. Meningococcal vaccines (MenB and MenACWY) are recommended for high-risk individuals, yet coverage remains poorly documented. We aimed to develop and validate a systematic approach to identify high-risk patients through medical coding systems and assess vaccination coverage across different risk groups.

METHODS

We conducted a retrospective observational study at a tertiary hospital in Córdoba, Spain (2000-2023). We developed an algorithm using R to systematically extract records from national clinical databases and identify patients with conditions conferring increased IMD risk. Vaccination status was determined through linkage with the regional electronic immunisation registry. We calculated vaccination coverage for both MenB and MenACWY vaccines and performed statistical analyses to explore associations between coverage rates, demographic factors, and timing of risk-condition diagnosis.

RESULTS

Our algorithm identified 2689 individuals with 2,710 high-risk conditions requiring meningococcal vaccination. MenB coverage was suboptimal, with only 624 of the 1,755 eligible patients (35.6%) receiving at least one dose and 558 of these patients (31.8%) completing the two-dose schedule. MenACWY coverage was even lower, with 784 of the 2,710 eligible patients (28.9%) receiving at least one dose and 520 (19.2%) completing the two-dose regimen. Patients with complement deficiencies demonstrated the poorest vaccination rates (<10%). For other risk groups, vaccination rates were significantly higher when conditions were diagnosed after relevant immunisation guidelines were published ($p < 0.001$).

CONCLUSIONS

Our validated algorithm successfully identified high-risk patients requiring meningococcal vaccination and revealed substantial gaps in vaccine coverage. This approach enables targeted catch-up vaccination programmes and continuous monitoring of at-risk populations. The methodology developed could be adapted by other healthcare systems to identify vulnerable patients for meningococcal and other vaccines, thereby strengthening preventive strategies against vaccine-preventable diseases.

KEYWORDS: Neisseria meningitidis, Immunization programs, Vaccination, Vaccination coverage

ABSTRACT ID: 696

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POSTER TOUR 17

Day 3 | Friday 21 November 08:30-09:15

Vaccination acceptance and uptake

PRESENTER

Arlinda Ramaj

ABSTRACT

Factors associated with influenza vaccination among healthcare workers in three hospitals in Albania, September 2023- March 2024

A. Ramaj¹

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BACKGROUND

Healthcare workers (HCWs) are at high risk of acquiring and spreading influenza virus infection. Despite the vaccination programme, HCW influenza vaccine uptake remains low in Albania. We aimed to assess barriers and facilitators of influenza vaccination to identify strategies for improving uptake.

METHODS

Between September 2023 and March 2024, we carried out a cross-sectional survey of HCWs in Albania's three largest hospitals (Tirana, Durres and Fier). Participants completed a structured questionnaire covering vaccination status, demographics, occupational and health-related factors, influenza vaccination knowledge and attitudes. Vaccination was defined as self-reported receipt of the 2023-2024 seasonal influenza vaccine. We used multivariable logistic regression to calculate adjusted Odds Ratios (aOR) with 95% Confidence Intervals (CI) to estimate factors associated with vaccine uptake. The final model was adjusted for age, sex, chronic condition, occupation, hospital site, and care for pregnant women.

RESULTS

A total of 1377 HCWs responded to the survey (36.8%). Median age was 45 years (IQR:34-53), and 79% were females. Overall vaccination coverage was 45.2% and varied by hospital: Tirana 33.4%, Durres 52.5%, and Fier 80.2%. Factors significantly associated with vaccination included being ≥ 35 years (aOR=2.18; 95%CI=1.63-2.92), previous influenza vaccination (aOR=2.92; 95%CI=2.20-3.90), excellent self-rated health (aOR=2.69; 95%CI=1.02-7.5), and working at Fier's Hospital (aOR=3.98; 95%CI=2.62-6.13). Males (aOR=0.72; 95%CI=0.53-0.98), and those performing aerosol-generating procedures (aOR=0.70; 95%CI=0.52-0.93) had lower odds of being vaccinated. Reasons for non-vaccination included fear of side effects (13%), perception of not being-at-risk (7.7%), inclination towards natural immunity (26%), and recent COVID-19 vaccination (5.1%).

CONCLUSIONS

Although influenza vaccination was free and available at the workplace in Albania, coverage remained low. We recommend further qualitative research to understand the significant differences between hospitals. Tailored strategies should address hospital-specific barriers such as side effect concerns, low risk perception, and vaccine fatigue, focusing on younger HCWs, males, and those in high-risk clinical settings.

KEYWORDS: Influenza, Vaccination, Healthcare Workers, Albania, Occupational Health

ABSTRACT ID: 309

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POSTER TOUR 18

Day 3 | Friday 21 November 08:30-09:15

Childhood and maternal immunisation

PRESENTER

Monika Liptáková

ABSTRACT

Measles – analysis of data reported in the national surveillance system, Czech Republic, 2018–2024

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BACKGROUND

In response to increasing number of measles cases and reported outbreaks across Europe, Czech epidemiological data were analysed. Our aim was also to assess the effect of vaccination on measles complications and hospitalisation.

METHODS

The measles cases reported to the Czech nationwide surveillance system during 2018-2024, based on the EU case definition, were analysed using logistic regression with an odds ratio (OR) supplemented with the 95% confidence interval (95% CI) to measure the association between vaccination status and the occurrence of complications or hospitalisation.

RESULTS

A total of 837 measles cases were reported, of which 94% were laboratory confirmed and 437 (52%) were male. The most cases (590; 71%) occurred in 2019. An epidemiological link was found in 407 cases. The median age of the cases was 34 years (range: 0-75). In total, 111 (13%) measles cases were imported (62 from Ukraine and smaller numbers from 26 other countries; 59 of the imported cases were unvaccinated). In total, 41% of all cases were known to have been vaccinated, of which 62% with two doses and 23% with one dose. A total of 561 (67%) cases required hospitalisation. Measles complications occurred in 11% of cases. The highest proportion of complications was reported in infants (<1 year; 28%) and in adults aged 55-64 years (27%). The most frequent complication was pneumonia, reported in 23 (3%) cases. Two doses of vaccine reduced significantly the risk of any complications compared to unvaccinated cases: OR 0.39 (95% CI: 0.21-0.72, $p=0.002$) and the likelihood of hospitalisation: OR 0.50 (95% CI: 0.34-0.73, $p<0.001$).

CONCLUSIONS

Our findings demonstrated a protective effect of two-dose vaccination against measles complications and hospitalisation for measles. To prevent further cases, increased awareness and promotion of measles vaccination is recommended for all individuals, including travellers, as a substantial proportion of cases occurred in unvaccinated.

KEYWORDS: measles, measles complications, hospitalisation, vaccination

ABSTRACT: 69

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POSTER TOUR 18

Day 3 | Friday 21 November 08:30-09:15

Childhood and maternal immunisation

PRESENTER

Margrethe Greve-Isdahl

ABSTRACT

Establishing Timely Surveillance of Maternal Pertussis Vaccine Uptake

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BACKGROUND

Maternal vaccination against pertussis (whooping cough) was introduced in Norway in May 2024, recommended at gestational week (GW) 24. We recently developed a method to identify women with ongoing pregnancies based on procedure codes for ultrasound examination in the second trimester (GW 17-19), which has an attendance rate >90%. This provides an opportunity to monitor vaccines administered during pregnancy, months before information on pregnancies is available from birth registries. The aim of our study was to establish a novel and timely surveillance for maternal pertussis vaccine uptake.

METHODS

In this nationwide population-based study, we linked data from the Norwegian Immunisation Registry (SYSVAK) and the Norwegian Patient Registry (NPR). We retrieved ultrasound procedure codes specific for the second trimester examination from NPR to identify ongoing pregnancies, and vaccine codes and date of vaccination from SYSVAK. We calculated vaccine uptake estimates (proportion of pregnant women) by calendar month and cumulative vaccine uptake for the period from 01 May 2024 until 01 March 2025. To assess the timing of vaccination during pregnancy, we calculated uptake by GW.

RESULTS

A total of 54,796 pregnant women at ≥ 22 weeks' gestation were identified during the observation period. Of these, 72.9%^{39,948} received the pertussis vaccine by 01 March 2025. The vaccine uptake has increased each month, from 48.7 % at introduction in May. Most vaccines were administered according to recommendations in GW 24 (21.3%; 8,500/39,948) or 25 (16.2%, 6,460/39,948).

CONCLUSIONS

We demonstrate that using specific second-trimester ultrasound codes to identify ongoing pregnancies provides a new approach that allows for timely surveillance of maternal pertussis vaccine uptake in Norway. By monitoring monthly vaccine uptake, we can report a successful introduction of the maternal pertussis vaccine programme. Timely estimates for vaccine uptake in pregnancy provide "data for action" and enable health authorities to adapt public health recommendations if necessary.

KEYWORDS: Whooping cough, Pregnancy, Vaccine coverage, Vaccine Programme

ABSTRACT ID: 277

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POSTER TOUR 18

Day 3 | Friday 21 November 08:30-09:15

Childhood and maternal immunisation

PRESENTER

Katarina Widgren

ABSTRACT

One year of maternal pertussis vaccination in Stockholm region- a success with challenges

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BACKGROUND

Pertussis, or whooping cough, is a highly contagious respiratory disease caused by the bacterium *Bordetella pertussis*. Pertussis in infants (< 6 months) can lead to severe complications including apnoea, pneumonia, and in rare cases, death. Maternal vaccination is an important preventive measure to passively protect newborns until they are old enough to be vaccinated. Stockholm Region introduced free-of-charge maternal pertussis vaccination in March 2024. Vaccination are offered from pregnancy week 16 in accordance with national recommendations. The women book their own vaccination appointment at contracted clinics. The department of Communicable Disease Control and Prevention in Stockholm have monitored vaccination coverage since the start of the program.

METHODS

Pregnancies were defined through the region's inpatient care database, using ICD-10 code for delivery. Vaccination status was obtained from Stockholm's vaccine register. Population data was accessed from Stockholm region population database. Data from these three registers were matched on each individual's personal identity number. Women vaccinated within 24 weeks prior to delivery were considered vaccinated. Vaccination coverage by geographical area, age, and socio-economic status was monitored.

RESULTS

Overall, vaccination coverage reached 70% one year into the program. However, large discrepancies were observed, with coverage ranging from 33% to 90% between geographical areas. Differences were also seen between age groups with the lowest coverage among those younger than 25 years (43%) and the highest among 30–34-year-olds (72%). Women with a higher education and income had a coverage of 84% and women with lowest education and income had a coverage of 45%.

CONCLUSIONS

In only one year the coverage of maternal pertussis vaccination has reached a relatively high coverage. However, the significant difference in coverage needs to be addressed to achieve health equity. Our data will help identify areas where additional work is needed.

KEYWORDS: Pertussis, maternal vaccination, vaccination coverage

ABSTRACT ID: 461

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POSTER TOUR 18

Day 3 | Friday 21 November 08:30-09:15

Childhood and maternal immunisation

PRESENTER

Ameze Simbo

ABSTRACT

Estimating age-specific seroprevalence of measles IgG antibodies among adult blood donors in Wales, January – July 2024

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BACKGROUND

The rise in measles infections within countries with established vaccination programmes highlights the potential risk of transmission among susceptible individuals. Public Health Wales established serosurveillance to monitor population prevalence, identify immunity gaps and address inequalities. We present age-specific seroprevalence of measles IgG antibodies in adult blood donors to inform national immunisation and elimination programmes.

METHODS

Welsh residents aged 17+ donating to the Welsh Blood Service (January-July 2024) were eligible for inclusion. We collected anonymised residual blood samples, aiming for 2,500 minimum, and tested for measles IgG by ELISA. Results were classified as detectable (positive) or undetectable (equivocal/negative). Donors were deduplicated and described by age and sex. In a univariable analysis, we compared detectable seropositivity estimates across six age cohorts based on historical UK immunisation schedules to generate odds ratios (OR). We used those eligible for 2-dose measles-mumps-rubella vaccine (MMR2) plus two catchup campaigns (aged 17-28) as a baseline.

RESULTS

Of 3,353 samples tested, the median age of individuals was 51 years (range:17–86), 53% were female. Measles IgG seroprevalence was 80% (95%CI:79%-81%, n=2,684). Among seropositives, donors born before an available measles vaccine (aged 58+) had the highest odds (OR:5.3, 95%CI:3.9-7.3, p<0.001). Those eligible for single-antigen (aged 47-57) and measles-rubella (MR) vaccines (aged 41-46) were significantly associated with seropositivity (OR:2.8, 95%CI:2.1-3.7, p<0.001; OR:2.0, 95%CI:1.4-2.8, p<0.001). Those eligible for 1-dose MMR (aged 35-40) and MMR2 (aged 29-34) had non-significant reduced odds (OR:0.7, 95%CI:0.5-1.0, p=0.06; OR:0.8, 95%CI:0.6-1.2, p=0.28).

CONCLUSIONS

Seropositivity among blood donors was high and varied by age. Pre-MMR cohorts were significantly associated with being seropositive. Measuring IgG against measles in a population helps identify cohorts with immunity below the 95% threshold for preventing sustained transmission, such as the first cohort eligible for MMR in our study. Drivers of lower seropositivity among younger cohorts (e.g.suboptimal vaccine uptake) should be addressed to prevent future outbreaks.

KEYWORDS: Measles,Seroprevalence,Vaccine-preventable diseases,Blood Donors,Seroepidemiologic Studies

ABSTRACT ID: 586

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POSTER TOUR 18

Day 3 | Friday 21 November 08:30-09:15

Childhood and maternal immunisation

PRESENTER

Heili Poolsaar

ABSTRACT

Assessment of population immunity to measles in Canada, 2023: a Canadian Immunization Research Network study

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BACKGROUND

Although Canada eliminated measles in 1998, it is still endemic in many countries. Canada's elimination status is threatened due to repeated measles importations. Assessing measles population immunity is key to identify susceptible groups and monitor elimination status. We conducted a national measles serosurvey using residual specimens collected by Canadian Blood Services and Héma Québec. We present an interim analysis of results for nine Canadian provinces, with results for all 10 provinces forthcoming.

METHODS

We aimed to test de-identified 8,874 specimens collected in 2023 from individuals >16 years, with equal number of specimens between males and females and by province. We tested for measles antibody levels at the National Microbiology Laboratory using the BioRad BioPlex 2200 MMRV IgG enzyme immunoassay, retesting equivocal results using a plaque reduction neutralization test.

RESULTS

We tested 8,776 specimens. Seropositivity increased with age-group, ranging from 74.0% (95%CI 72.3-75.7) in individuals aged 17-29 years to 98.5% (95%CI 97.6-99.1) in individuals aged ≥60 years. Seropositivity was higher in females compared to males, at 82.4% (95%CI 81.2- 83.5) and 79.9% (95%CI 78.7-81.1), respectively. Of those who self-reported to be white, 81.8% (95%CI 80.9-82.6) were seropositive, compared to 78.3% (95%CI 76.15-80.37) of those who self-reported to be racialized. Seropositivity did not differ greatly by material deprivation quintiles, ranging between 80.0% (95%CI 77.3-82.4) and 82.4% (95%CI 80.3-84.2) in all quintiles.

CONCLUSIONS

Our results indicate that seroprevalence was <95%, the threshold thought to be required to sustain measles elimination, in several population groups. Despite this, cases in a large ongoing measles outbreak in Canada are mostly unvaccinated children, suggesting that despite low seroprevalence, adult groups with sub-optimal seroprevalence may be protected from infection, likely through previous vaccination. Further analyses will include post-stratification weighted estimates using 2021 Canadian Census data to generate overall national and provincial estimates.

KEYWORDS: measles,vaccines,immunity,serology

ABSTRACT ID: 728

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POSTER TOUR 18

Day 3 | Friday 21 November 08:30-09:15

Childhood and maternal immunisation

PRESENTER

Raquel Eusébio

ABSTRACT

Measles clinical presentation by vaccination status in Portugal, 2015-2025: implications for case definition in elimination settings

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BACKGROUND

In countries with high measles vaccination coverage, cases among vaccinated individuals often present with attenuated symptoms, potentially failing to meet the classical case definition. This may challenge timely detection and response. Our study aimed to describe the clinical features of cases reported in Portugal over the past decade, and the extent to which laboratory-confirmed measles cases fulfilled clinical case definition, comparing presentations across vaccination status.

METHODS

We conducted a retrospective descriptive analysis of all laboratory-confirmed measles cases notified to the National Surveillance System (SINAVE) in Portugal, between January 2015 and March 2025. Cases were grouped by vaccination status; variables included clinical features (fever, rash, cough, coryza, conjunctivitis, Koplik spots), hospitalisation, complications, and fulfilment of clinical case definition. We used Fisher's exact test to compare clinical characteristics by vaccination status, using Bonferroni correction for multiple testing.

RESULTS

Of 249 laboratory-confirmed measles cases reported, 209 had known vaccination status, and were included: 64 (28%) unvaccinated, 25 (11%) vaccinated with one dose, and 143 (61%) vaccinated with two or more doses. Cough, coryza, conjunctivitis, Koplik spots, hospitalisation and complications were more frequent among unvaccinated compared to vaccinated individuals ($p < 0.001$). The clinical case definition was fulfilled by 92% of unvaccinated individuals, versus 54% in both one-dose and ≥ 2 -dose groups ($p < 0.001$).

CONCLUSIONS

Our findings indicate that vaccinated individuals with measles often present with attenuated symptoms, aligned with existing evidence from countries with elimination status, and frequently do not meet the current clinical criteria of case definition. This underlines the need to revisit clinical criteria, to avoid missed diagnosis and ensure timely public health action to sustain measles elimination status.

KEYWORDS: measles, surveillance, measles vaccine, measles diagnosis, disease elimination

ABSTRACT ID: 754

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POSTER TOUR 19

Day 3 | Friday 21 November 08:30-09:15

Social and behavioural perspectives

PRESENTER

Jorg Van Beek

ABSTRACT

Co-creation of a toolbox to improve infection prevention and control behaviour in general practice care: a qualitative study

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BACKGROUND

General practice care professionals are at the forefront of the Dutch healthcare system. Therefore, it is important to protect both these professionals and their patients by implementing adequate infection prevention and control (IPC). However, prior research has shown that IPC is currently suboptimal in general practice care. In a previous qualitative study, general practice care professionals expressed the need for coherent guidelines for IPC. To support this, we designed an IPC 'toolbox' that follows varying levels of respiratory infection pressure. To strengthen future implementation, we aimed to involve end users in its development by examining factors that may shape implementation of the toolbox in professionals' daily practice.

METHODS

A qualitative study with semi-structured in-depth interviews was conducted, in which general practitioners and medical assistants were asked about their feedback and insights on a concept version of the toolbox, as well as their intention to use it. Interviews were performed using a topic list informed by various theories on behavioural- and implementation science. Data was analysed inductively and deductively using thematic analysis.

RESULTS

17 interviews were conducted. All respondents worked in general practices in the South of the Netherlands. Most participants indicated a positive attitude towards the toolbox, and their intention to use it was high. Moreover, it was viewed as a clear and compatible tool to facilitate communication between professionals regarding the internal IPC measures of their practice. Lastly, participants recommended adding a regional surveillance of respiratory infection pressure by public health services to support the toolbox.

CONCLUSIONS

Professionals viewed our toolbox as a useful instrument to support IPC behaviour in their daily practice. Using collected feedback and recommendations, it can be adapted to support IPC in GP care. This will increase the odds of success for future implementation of the toolbox, which may contribute to improved levels of IPC across GP care.

KEYWORDS: Prevention and control,behaviour,general practice,implementation science,disease transmission infectious,respiratory tract infections

ABSTRACT ID: 234

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POSTER TOUR 19

Day 3 | Friday 21 November 08:30-09:15

Social and behavioural perspectives

PRESENTER

Vittoria Offeddu

ABSTRACT

Integrating epidemic modelling with human behaviour: An interdisciplinary framework for the collection of empirical data

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BACKGROUND

Understanding the bidirectional relationship between human behaviour and disease transmission is crucial for effective public health interventions. However, integrating behaviour change into epidemic models remains limited by a lack of appropriate and theory-informed data. Here, we present newly collected cross-country data designed to inform novel behavioural-epidemic model components.

METHODS

Between March and June 2024, we conducted a survey on COVID-19 vaccination behaviours in representative adult samples from Germany, Spain, France, Hungary, Italy, and the UK. The questionnaire was grounded in the Capability, Opportunity, Motivation–Behaviour (COM-B) framework, widely adopted in behavioural science to understand mechanisms of behaviour change. We illustrate selected aspects of the dataset to investigate time-sensitive dynamics, validate behavioural proxies, and characterize patterns of opinion and information diffusion. To this aim, we examined changes in perceived risk and willingness, comparing these with actual vaccination uptake and timeliness. Social contacts and discussions contacts within participants' social groups were also quantified.

RESULTS

Among 22,228 respondents, initial willingness to get vaccinated ranged from 45% (France) to 76% (UK), and generally declined over time with perceived severity. Higher initial willingness was strongly associated with greater uptake and more timely vaccination. Age-related delays in vaccination ranged from 4.3-5.6 months for 18–29 years old to 2.2-4.3 months for 60 years and older. Despite initial willingness, a proportion of respondents remained unvaccinated (5.1% in France-9.8% in Hungary) or discontinued vaccination (8.0% in Germany-18.9% in Spain). Discussions contacts declined with age in Germany and Spain, mirroring traditional in-person contact patterns. In contrast, France, Hungary, and Italy showed a bell-shaped trend, peaking in middle aged groups.

CONCLUSIONS

Our interdisciplinary approach yielded a rich, dynamic dataset capturing the complexity and heterogeneity of behavioural responses during an epidemic. These insights provide a valuable foundation for the development of more realistic, behaviourally informed, epidemic models with direct relevance to public health policy.

KEYWORDS: Human Behavior, Models, Cross-Sectional Studies, Infectious diseases

ABSTRACT ID: 558

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POSTER TOUR 19

Day 3 | Friday 21 November 08:30-09:15

Social and behavioural perspectives

PRESENTER

Veja Widdershoven

ABSTRACT

Enhancing Vaccine Uptake: A Randomized Trial of Active Invitation, Motivational Interviewing, and On-Site Vaccination Among Hesitant Parents – The MICK Study

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BACKGROUND

Vaccine hesitancy remains a significant challenge, contributing to suboptimal uptake of DT-IPV/MMR and HPV vaccines in the Netherlands. Given the crucial role of healthcare professionals in parental decision-making, motivational interviewing (MI) has shown promise in addressing hesitancy. This study evaluates the impact of a multicomponent intervention combining active invitation, motivational interviewing sessions, and on-site vaccination on parental vaccination behavior.

METHODS

A three-arm randomized controlled trial was conducted among parents of 9- and 10-year-old children who missed their March 2023 DT-IPV/MMR or HPV vaccination appointment in the South Limburg region, the Netherlands. Participants were assigned to: ¹ the intervention group (telephone invitation for a face-to-face MI session with a trained healthcare professional and possible vaccination appointment), ² the flyer group (enhanced vaccination information flyer), or ³ the control group (standard care). The primary outcome was vaccination uptake within seven months; the secondary outcome was self-reported vaccination intention.

RESULTS

Of 2,387 eligible parents, 570 were allocated to the MI group, 707 to the flyer group, and 700 to the control group. Intention-to-treat analysis showed significantly higher DT-IPV/MMR uptake in the MI group (OR: 1.69; 95% CI: 1.20-2.37). A total of 114 parents participated in the MI sessions (20%). Per-protocol analysis demonstrated substantial increases in overall vaccination uptake (not specified for DT-IPV/MMR or HPV) (OR: 10.15; 95% CI: 6.05-17.03), DT-IPV/MMR uptake (OR: 88.62; 95% CI: 12.12-648.08), and HPV uptake (OR: 5.39; 95% CI: 2.94-9.88). Vaccination intention significantly increased following MI for DT-IPV/MMR ($p < .001$) and HPV ($p = .009$).

CONCLUSIONS

This RCT confirms the effectiveness of combining active invitation, MI, and on-site vaccination in improving vaccination uptake and intention. Future research should focus on disentangling the effects of each intervention component to optimize implementation strategies.

KEYWORDS: Vaccine hesitancy, Intervention study, vaccination, motivational interviewing

ABSTRACT ID: 144

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POSTER TOUR 19

Day 3 | Friday 21 November 08:30-09:15

Social and behavioural perspectives

PRESENTER

Larisa Vujnovic

ABSTRACT

Factors associated with intention to be vaccinated against seasonal influenza in healthcare workers: a cross-sectional study assessing Health Belief Model constructs in Serbia

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BACKGROUND

Although seasonal influenza vaccination is mandatory for healthcare workers (HCWs) in Serbia, vaccine coverage in this population remains low, fluctuating between 12% and 31% in 2018-2023. We aimed to identify factors associated with HCWs' intention to be vaccinated for the season 2024/2025 ("vaccination intention").

METHODS

We conducted a cross-sectional survey in 2024 using multi-stage sampling stratified by geographical region and healthcare level. From the list of state healthcare institutions, we selected randomly institutions in each stratum, using probability proportional to the institution size. All consenting HCWs present on the survey day completed self-administered questionnaires. The associations between vaccination intention (yes, hesitant, no) and occupation, as well as five dichotomised Health Belief Model constructs (perceived susceptibility to influenza, severity of the disease, vaccine benefits, HCW recommendation as a cue for action, and physical barriers) were assessed using age-adjusted multinomial logistic regression.

RESULTS

Among 1919 respondents, median age 44 (range 18–68) years, 81.58% (1541/1889) were female, 21.04% (402/1911) were physicians or dentists, 78.96% (1509/1911) were nurses or medical technicians. Thirty percent (572/1906) declared positive vaccination intention, 52.52% (1001/1906) no intention, while 17.48% (333/1906) were hesitant. Nurses had significantly lower odds of vaccination intention versus no intention than physicians and dentists (adjusted odds ratio (aOR)=0.53, 95%CI=0.35–0.80). Compared with no intention, vaccination intention was positively associated with perceived influenza susceptibility (aOR=3.16, 95%CI=2.18–4.57), potential severity (aOR=2.09, 95%CI=1.43–3.05), and vaccination benefits (aOR=9.62, 95%CI=5.57–16.61). A recommendation for vaccination by another HCW increased the odds of showing hesitancy instead of no vaccination intention at all (aOR=2.31, 95%CI=1.28–4.15).

CONCLUSIONS

Targeted campaigns for increasing awareness of own influenza susceptibility, potential disease severity, and vaccine benefits may increase the low HCWs seasonal influenza vaccination intention, particularly among nurses. Additionally, pro-vaccination HCWs should be prompted to advocate for yearly vaccination among HCWs with no vaccination intention, to sway them towards being tentative.

KEYWORDS: Health behaviours, vaccine hesitancy, influenza vaccine, intention, health workforce

ABSTRACT ID: 776

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POSTER TOUR 19

Day 3 | Friday 21 November 08:30-09:15

Social and behavioural perspectives

PRESENTER

Noé Hernández Valdivia

ABSTRACT

Contesting global health governance: Opposition to the WHO pandemic agreement in online media

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BACKGROUND

The negotiations surrounding the World Health Organization (WHO) Pandemic Agreement have become a focal point for wider debates about sovereignty, globalisation, and the legitimacy of multilateral cooperation. Opposition has framed the Agreement as a threat to national sovereignty, individual freedoms, and moral order. Digital platforms play a central role in this contest, providing spaces where dissenting narratives circulate beyond traditional media gatekeepers. Substack, with its long-form and minimally moderated design, has emerged as a particularly influential arena for articulating such resistance. This study critically analyses opposition to the WHO Pandemic Agreement as expressed on Substack, examining the rhetorical strategies, ideological framings, and disputes over authority that shape these narratives.

METHODS

Twenty-two purposively selected texts published between December 2021 and June 2025 were examined using Critical Discourse Analysis. The analysis explored how language and ideology intersect in constructing resistance, with attention to the ways authors perform authority and challenge the legitimacy of global health institutions.

RESULTS

The findings reveal recurring tropes and themes in opposition discourse. A heuristic typology of dissent is proposed, comprising six constructs: the Constitutional Sovereigntist, the Antiglobalist, the Christian Nationalist, the Biopolitical Libertarian, the Epistemic Dissenter, and the Conspiratorial Sceptic. Four prominent discursive strategies cut across these categories: appeals to urgency, deployment of war metaphors, invocation of religious or traditional values, and populist constructions of dichotomic narratives. These strategies collectively legitimise dissent, mobilise audiences, and dispute cognitive authority.

CONCLUSIONS

Opposition to the Pandemic Agreement extends beyond critique of technical provisions to embody wider struggles over sovereignty, globalisation, and epistemic legitimacy. The Agreement is framed symbolically as a site of sovereignty loss and moral compromise. Understanding and addressing these narratives has important implications for diplomacy, policymaking, and broader global health governance.

KEYWORDS: Global Health, International Cooperation, World Health Organization, Health Policy, Pandemic Preparedness

ABSTRACT ID: 791

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POSTER TOUR 20

Day 3 | Friday 21 November 08:30-09:15

Prevention of respiratory diseases

PRESENTER

Ahlem Fourati

ABSTRACT

Effectiveness of COVID-19 vaccine in preventing SARS-CoV-2 severe outcomes 2021-2023

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BACKGROUND

When the COVID-19 vaccination started in Tunisia, the campaign strategy prioritized high-risk groups first in order to reduce severe forms and mortality. We aimed to determine COVID-19 vaccine effectiveness (VE) in preventing SARS-CoV-2 severe forms, complications and mortality among COVID-19 patients compared to non-infected patients hospitalized for COVID-like illnesses (CLI).

METHODS

We conducted a test-negative case-control study among patients hospitalized with CLI symptoms in three hospitals between September 2021-September 2023. Cases were adults with positive laboratory/radiology-confirmed COVID-19 tests 14 days before or within 48 hours of admission, while controls had similar CLI symptoms but with negative tests within 60 days or 48 hours of admission. Cases and controls were matched by sex, age groups, and hospital. We used a structured questionnaire to collect data from hospital medical records. COVID-19 status was determined using national COVID-19 surveillance data and hospital-based databases. Vaccination status was ascertained through medical records and the national COVID-19 vaccination platform "Evax." Severity for COVID-19 followed WHO's Guidelines. VE was estimated using multivariable conditional logistic regression and calculated as $VE = (1 - \text{oddsRatio}) \times 100\%$.

RESULTS

Overall, we enrolled 1,372 individuals, 538 cases matched with controls 1:1 and 125 matched 1:2. 50.1% were females, for cases and controls and the mean age was 63.84 ± 16.58 and 61.04 ± 17.58 respectively. The final model after adjusting on tobacco use, weight status, and Charlson Comorbidity score revealed that complete Vaccination with booster dose in ≥ 6 months showed a high VE in preventing ICU admission ($VE = 72\%$; $95\%CI [49-85]$, $p < 0.001$), respiratory assistance (RA) ($VE = 70\%$; $95\%CI [46-84]$, $p < 0.001$), mechanical ventilation (MV) ($VE = 72\%$; $95\%CI [50-85]$, $p < 0.001$), complications,

(VE=64%;95%CI[40-81],p=0.001), and mortality(VE=72%;95%CI[49-85],p<0.001). Full vaccination with a booster in less than 6 months was effective only in preventing ICU admission(VE=48 %;95%CI[2-73],p=0.04). Partial/primary vaccination in less than 6months had negative VE thus higher risk regarding RA(VE=-65.8;95%CI[-155.2-7.6],p=0.022), MV (VE=-57.9;95%CI[-143.2- -2.6],p=0.038);complications (VE=-108.7 ;95%CI[-232.5- -31.5],p=0.002); and mortality(VE=-71.4 %;95%CI[-164.4- -11.1],p=0.015).

CONCLUSIONS

COVID-19 booster vaccination in ≥ 6 months was effective in preventing severe outcomes. Limited protection was observed when the booster was received prior, likely due to sample size constraints. Partial or recent primary vaccination was linked to higher risk, possibly from lower adherence to preventive measures.Strategies should consider booster timing, target high-risk groups, and promote continued preventive behaviors.

KEYWORDS: COVID-19 vaccines,COVID-19 infection,Tunisia,Vaccine Effectiveness,Matched case control studies

ABSTRACT ID: 256

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POSTER TOUR 20

Day 3 | Friday 21 November 08:30-09:15

Prevention of respiratory diseases

PRESENTER

Nathalie Nicolay

ABSTRACT

Effectiveness of vaccination programmes against serotype B invasive meningococcal disease using the screening method on surveillance data from countries in Europe

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BACKGROUND

Neisseria meningitidis serogroup B (MenB) is the principal cause of invasive meningococcal disease (IMD) in the European Union/European Economic Area (EU/EEA). We aimed to assess the effectiveness of MenB vaccination programmes in preventing IMD in Italy, Ireland, and Portugal since MenB vaccine introduction in the national immunisation programme in 2017, 2018, and 2020, respectively.

METHODS

We included cases aged ≥ 24 months reported to the EU/EEA surveillance system up to December 2023 with information on their vaccination status. A case that received at least three MenB vaccine doses was considered fully vaccinated. We obtained three-dose vaccine coverage (VC) data from public sources. We calculated median VC between year of vaccine introduction up to 2023 for each country. Vaccine effectiveness (VE) and 95% confidence intervals (95%CI) were estimated for each country using the Farrington screening method, which compares the proportion of cases vaccinated (PCV) to the population vaccination coverage (PPV) using the formula: $VE = 1 - (PCV / (1 - PCV)) / (PPV / (1 - PPV))$.

RESULTS

From the start of their respective national programme to the end of 2023, Ireland, Italy, and Portugal reported 8, 14, and 6 cases with known information on their vaccination status, of whom 4, 2 and 4 were vaccinated respectively. Median VC during each study period was 91.0% in Ireland, 69% in Italy, and 97.0% in Portugal. Estimated VE was 90.1% (95%CI: 60.5%; 97.5%) for Ireland, 92.5% (95%CI: 66.5%; 98.3%) for Italy, and 93.8% (95%CI: 66.2%; 98.9%) for Portugal.

CONCLUSIONS

Although subject to limitation inherent to the quality of the submitted surveillance data, these findings indicate high effectiveness of MenB vaccination programmes in preventing invasive MenB disease in Italy, Ireland, and Portugal. Our results need to be confirmed through observational vaccine effectiveness studies controlling for confounding factors. Meanwhile further implementation of MenB vaccination programmes should be considered across the EU/EEA.

KEYWORDS: vaccine effectiveness, *Neisseria meningitidis* serogroup B, Farrington screening method, surveillance data

ABSTRACT ID: 421

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POSTER TOUR 20

Day 3 | Friday 21 November 08:30-09:15

Prevention of respiratory diseases

PRESENTER

Magda Bucholc

ABSTRACT

Interim 2024/25 season RSV vaccine effectiveness against hospitalisation in older adults in Northern Ireland

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BACKGROUND

Respiratory syncytial virus (RSV) is a major cause of lower respiratory tract illness in older adults. In September 2024, Northern Ireland introduced a new RSV vaccination programme offering Pfizer's Abrysvo® to individuals aged 75–79 years. This interim analysis evaluates vaccine effectiveness (VE) against RSV-associated hospitalisation in this target group during the 2024-25 respiratory season.

METHODS

A test-negative case-control design was used to assess VE among individuals aged 75-79 years admitted with community-acquired respiratory infections between epidemiological weeks 40/2024 and 11/2025. Cases were patients with a positive RT-PCR test for RSV. Patients were considered vaccinated if they received an RSV vaccine at least 14 days before testing. Being unvaccinated was defined as a person having no record of receiving an RSV vaccine before the positive RT-PCR test or who had a dose administered less than 13 days before receiving a positive RT-PCR test. A logistic regression model adjusted for sex and age was used to estimate VE. To address potential small sample bias, Firth's bias-reduced logistic regression was used as a part of sensitivity analysis

RESULTS

A total of 118 patients were included, of whom 18 (15.3%) tested positive for RSV. Among RSV cases, 11.1% were vaccinated, compared to 33.0% of controls. In the primary analysis, VE against RSV-associated hospitalisation was 74.7% (95% CI: 3.0% to 96.2%). Sensitivity analysis yielded a VE of 69.1% (95% CI: -7.2% to 94.1%).

CONCLUSIONS

Preliminary findings suggest that RSV vaccination is effective in reducing RSV-related hospitalisations among adults aged 75-79 years. These results support current UK recommendations for RSV vaccination in this population.

KEYWORDS: vaccine effectiveness, RSV, vaccine, hospitalisation

ABSTRACT ID: 446

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POSTER TOUR 20

Day 3 | Friday 21 November 08:30-09:15

Prevention of respiratory diseases

PRESENTER

Elvira Marín Caba

ABSTRACT

Invasive pneumococcal disease caused by serotype 4 in Andalusia (Spain), 2022 to 2024

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BACKGROUND

Pneumococcal infections are an important cause of morbidity and mortality in Europe. In Spain in 2023, most reported cases of invasive pneumococcal disease (IPD) were caused by pneumococcal serotypes 8, 3, 22F, 4 and 19A. Almost 70.0% of the cases caused by serotype 4 in 2023 were notified in Andalusia, an autonomous region in southern Spanish, which reflected an increasing trend with respect to 2022. Serotype 4 is included in all vaccines approved to date in Andalusia. The aim of this study was to update of the epidemiological evolution of IPD in Andalusia, specifically caused by serotype 4, and to analyse the socio-demographic and clinical factors associated with the IPD cases.

METHODS

Study design: cross-sectional study. Eligible population: individuals with confirmed IPD diagnosis, reported in the RedAlerta platform of the Andalusian Epidemiological Surveillance System (SVEA) between January 2022 and December 2024. Exclusion criteria: no determination of pneumococcal serotype of IPD case. Descriptive analysis of the clinical and sociodemographic characteristics of IPD cases caused by serotype 4 and by other circulating serotypes were conducted with software R.

RESULTS

A total of 1,359 patients with serotyped IPD fulfilled inclusion criteria. Most frequent serotypes were 8 (20.1%), 3 (17.1%), 4 (10.6%), 22F (5.7%) and 15A (3.5%) within the study period, and in 2024 most frequent were 3 (23.6%), 8 (21.4%), and 4 (20.5%). Serotype 4 was predominant in patients from 45 to 64 years old (55.6%) and from 15 to 44 (27.1%), whereas patients aged 65 years or older were more frequently affected by other serotypes. Mostly sex male (79.9%), patients living in Sevilla (almost 60%) and with no previous pneumococcal vaccination (90.3%) were infected by serotype 4.

CONCLUSIONS

Andalusian surveillance has shown that serotype 4 is increasing in our medium in the last years. Factors associated with serotype 4 were sex male, younger age (<65 years), living in occidental Andalusian provinces and with no previous pneumococcal vaccination. Continuous surveillance is essential to study tendencies of emerging serotypes and public health strategies should adapt local vaccination programs in order to prevent and reduce IPD.

KEYWORDS: Pneumococcal Serotypes, Invasive Pneumococcal Disease, Vaccination Coverage, Risk factors, Surveillance

ABSTRACT ID: 646

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POSTER TOUR 20

Day 3 | Friday 21 November 08:30-09:15

Prevention of respiratory diseases

PRESENTER

Laurane De Mot

ABSTRACT

Impact of Nirsevimab on the epidemiology of pediatric RSV in Belgium in season 2024-2025

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BACKGROUND

Since 2024, new tools for preventing pediatric RSV disease have become available in Belgium: a monoclonal antibody, Nirsevimab (Beyfortus®), reimbursed since October 2024, and a vaccine for pregnant women (Abrysvo), available from January 2024 but only reimbursed from January 2025. Accordingly, the vast majority of infants eligible for prevention in our country were immunized with Beyfortus® during this first season of RSV prevention.

METHODS

In 2023, the SARI (Severe Acute Respiratory Infection) surveillance system (based on 10 sentinel hospitals) was adapted to more comprehensively include pediatric RSV cases. In parallel, the RSVPed study was launched to broaden data collection of pediatric RSV-related hospitalizations, including 20 additional hospitals. Data from both studies covering the 2023–2024 (pre-prevention) and 2024–2025 (first year of prevention) seasons were analyzed in order to assess the impact of preventive measures on a national scale.

RESULTS

Preliminary results showed a substantial reduction of at least 35% in pediatric RSV-related hospitalizations during the 2024–2025 season compared to the previous one. A significant decrease in ICU admissions was also observed. Epidemiological changes mainly concerned infants under 6 months of age—the age group targeted by prevention and eligible for Beyfortus® reimbursement due to their higher risk of complications. Moreover, based on a test-negative design analysis using preliminary SARI data, the effectiveness of Nirsevimab was estimated at over 80%, with no waning of protection over time. Finally, immunized infants who nonetheless required hospitalization due to RSV infection showed a less severe pattern of infection compared to non-immunized infants in the same age group.

CONCLUSIONS

In conclusion, introduction of Nirsevimab has already had a marked impact on the pediatric RSV burden in Belgium. Further analyses on benefits for specific subgroups (i.e., children with comorbidities) should still be carried out. Moreover, data on prevention uptake and acceptability among parents are under investigation to guide upcoming preventive campaigns.

KEYWORDS: Respiratory Syncytial Viruses, nirsevimab, immunization, hospitalization, pediatrics

ABSTRACT ID: 726

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POSTER TOUR 21

Day 3 | Friday 21 November 08:30-09:15

International health

PRESENTER

Jasna Karacic Zanetti

ABSTRACT

Patient Rights and Safety as Instruments of Health Diplomacy in Infectious Disease Preparedness and Response

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BACKGROUND

The COVID-19 pandemic highlighted weaknesses in addressing patient rights and safety during health emergencies, particularly in cross-border settings. While preparedness has focused on surveillance and logistics, less attention is paid to legal and ethical patient protection. EU instruments promote patient-centred governance, yet their application during crises is often inconsistent. Patient ombudsman structures are underused, despite their potential to improve trust and legal clarity. This study explores how embedding patient rights in health diplomacy can improve cross-border preparedness and ethical response.

METHODS

This study uses a qualitative, multi-method approach combining policy analysis, document review, and comparative case studies. A structured review of key EU instruments (Cross-Border Healthcare Directive, GDPR, HERA) was conducted, with core terms defined using WHO and EU legal sources. Case studies of selected EU member states and international actors (e.g. WHO, European Ombudsman) explored how patient rights were integrated into COVID-19 responses. Expert interviews and public reports further identified patterns in stakeholder views on patient-centred health diplomacy, focusing on trust, transparency, and cross-border coordination. This approach enabled triangulation of legal, political, and ethical aspects to assess how patient rights can be embedded in infectious disease governance.

RESULTS

The analysis revealed three key findings: inconsistent application of patient rights, limited focus on patient-centred issues, and positive role of ombudsman mechanisms. These findings indicate that integrating patient rights and safety into preparedness plans enhances both response effectiveness and public legitimacy in managing health crises.

CONCLUSIONS

This study concludes that patient rights and safety are not only ethical essentials but also undervalued strategic tools in infectious disease response. Their integration into health diplomacy can strengthen trust, transparency, and cross-border coordination. Ombudsman-type mechanisms, in particular, can help balance state duties with individual rights during crises.

KEYWORDS: health diplomacy, patient rights, patient safety, infectious disease preparedness, cross-border healthcare, ombudsman, EU health policy

ABSTRACT ID: 111

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POSTER TOUR 21

Day 3 | Friday 21 November 08:30-09:15

International health

PRESENTER

Rosie Collins

ABSTRACT

Crossing Borders: Findings from a Multinational, Foodborne Shigella sonnei Outbreak with an International Travel Signal.

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BACKGROUND

On 27 January 2025, routine national gastrointestinal surveillance detected a multidrug-resistant Shigella sonnei ST152 outbreak. As cases escalated, a multidisciplinary investigation commenced to identify the source and implement control measures.

METHODS

Laboratory referral forms indicated a signal for international travel thus, a trawling questionnaire was designed to interview cases for further information. Whole genome sequencing confirmed cases; probable cases had gastroenteritis and epidemiological links to confirmed cases. EpiPulse and International Health Regulation notifications were issued for international case finding.

RESULTS

45 confirmed and 6 probable (all co-travellers of a confirmed case) cases were identified across the UK and a Crown Dependency. Median age was 36 years (range: 5-79), 59% female. Of 38 cases with onset data, 89% fell between 7-12 January 2025, indicating a point-source outbreak. Of 32 interviewed cases, 94% reported international air travel during their incubation period – all via a singular non-European airport on their return flight. The majority (81%) travelled on 8 January 2025 (range: 7-10 January 2025). Three airlines (A-C) were reported. Where specified (n=29), 93% travelled via A (n=27); B and C were each reported by 1 case. Airlines A and B had a common food supplier. All 30 interviewed cases reporting international air-travel reportedly consumed in-flight food; multiple commonalities were observed however, the food vehicle was not identified. 69% of the 13 un-interviewed, confirmed cases also reported international travel via laboratory referral forms. A further 40 cases were identified across 7 European countries – consistent with the travel-related transmission and temporality observed in UK cases.

CONCLUSIONS

Although clinically mild and short-lived, this unique scenario, whereby a foodborne outbreak was linked to international air travel, blurs conventional distinctions between foodborne and travel-associated outbreaks. It underscores the importance of rapid, multidisciplinary investigation and international collaboration for timely source identification and mitigation of future, emerging foodborne Shigella sonnei incidents.

KEYWORDS: Shigella, Disease outbreaks, Gastrointestinal diseases, Foodborne diseases, Travel, Epidemiology

ABSTRACT ID: 212

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POSTER TOUR 21

Day 3 | Friday 21 November 08:30-09:15

International health

PRESENTER

Hanna Verweij

ABSTRACT

Characteristics of rabies exposure incidents in travellers consulting a Dutch regional health service (2014-2024)

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BACKGROUND

The public health service in the Netherlands provides post-exposure prophylaxis (PEP) for individuals with suspected rabies exposure (SRE). The increasing amount of SRE consultations mainly concern travellers returning from rabies-endemic countries. Insight in the demographics and SRE incidents of travellers aids the travel clinics in improving preventive travel advice resulting in less incidents.

METHODS

Data from electronic health records was collected retrospectively for all international travellers who reached out to the Dutch municipal health service Hollands Midden (GGDHM) after an SRE incident between 2014 and 2024. Demographic and incident data were extracted and analysed descriptively using R.

RESULTS

A total of 406 reports on travellers with SRE were included; 53.9% cases were female, median age was 28 years (IQR 22–43). Southeast Asia was most visited (39.7%). The majority of incidents involved a dog (44.8%), a cat (23.2%) or a monkey (25.1%). Over half of the incidents (61.0%) involved bite wounds and 87.7% of all wounds was located on the extremities. Of cases where the cause of the incident was reported (N=232), the incident was provoked in 64.2%; i.e., the animal was actively approached. Incidents where children and young adult travellers are involved, report actively initiating animal contact more often.

CONCLUSIONS

Travel advice is currently focused most on people in high-risk occupations, travellers to remote areas and young children. However, in travellers that reach out to the GGDHM after a SRE incident, the incident is often actively provoked by making contact with an animal, especially in young adult travellers. Travel advice could be strengthened by asking about attitude towards animals and emphasizing avoidance of any animal contact, especially when providing advice to young adult travellers.

KEYWORDS: Retrospective study, Rabies exposure, Post-exposure prophylaxis, Risk-taking, Travel medicine

ABSTRACT ID: 224

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POSTER TOUR 21

Day 3 | Friday 21 November 08:30-09:15

International health

PRESENTER

Vanessa Morton

ABSTRACT

No vacation from risk: Investigating a Salmonella Enteritidis outbreak linked to poultry and international travel

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BACKGROUND

In Canada, a single Salmonella Enteritidis (SE) cluster identified by whole genome sequencing contains about 34% of SE cases reported since 2019. Preliminary information suggested that travel to all-inclusive resorts in the Caribbean and domestic poultry exposure were risk factors. An outbreak investigation was initiated in October 2024 to understand the factors leading to illness. One objective was to develop an effective approach to subdivide this cluster based on epidemiological and laboratory data.

METHODS

An allele address system was developed to categorize isolates into progressively broader subclusters where each level reflects increasing wgMLST allele differences from identical ⁰ to closely related (≤ 10). These addresses were combined with epidemiological information collected from initial interview. Travel subclusters were defined as those where > 80% of cases report international travel, with > 90% of these cases reporting travel to the same country and without non-human isolates related to poultry.

RESULTS

Between January 1, 2019 and May 1, 2025, 4,315 human isolates and 552 non-human isolates (food, animal and environmental) were included in this cluster. A total of 138 subclusters with more than 5 isolates were identified at the 10-allele level. International travel was associated with 23 subclusters (containing 1,209 human isolates). Poultry-associated non-human isolates were grouped in 26 other subclusters (containing 2,688 human isolates). Of the remaining subclusters, 81 had not had a case since October 2024 and 8 were undetermined.

CONCLUSIONS

The allele address system enabled the examination of epidemiological data for subclusters within a highly clonal SE cluster. Use of a 10-allele threshold resulted in the identification of subclusters associated with international travel. This helped focus the epidemiological investigation on recent subclusters that were not travel associated. The next step involves examining more refined allele thresholds within these subclusters to identify potential epidemiological links and common exposures.

KEYWORDS: Salmonella Enteritidis, outbreak, poultry, whole genome sequencing

ABSTRACT ID: 405

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POSTER TOUR 21

Day 3 | Friday 21 November 08:30-09:15

International health

PRESENTER

Ahmed M Alarbi

ABSTRACT

Malaria cluster near Benina international airport, Libya: a re-emerging threat in a malaria-free country

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BACKGROUND

Although malaria was eliminated in Libya in 1973, the country remains at risk of imported cases due to increased migration from malaria-endemic countries. In November 2024, a cluster of four confirmed *Plasmodium falciparum* cases, including one death, was identified 450m from Benina Airport, Benghazi, a non-endemic area. Our investigation aimed to determine if there was potential autochthonous transmission.

METHODS

An inter-sectoral investigation was conducted around Benina Airport. Suspected cases were defined as residents of the residential area surrounding the airport within a radius of 1.5 kilometres, who developed fever, chills, sweats, headaches, nausea, vomiting during the period from November 15th to December 15th. We searched for cases by contacting healthcare facilities and through door-to-door community outreach. We interviewed suspected cases for clinical, demographic, travel, and exposure history. The Benghazi medical center laboratory tested blood samples for *Plasmodium* spp. The National Center for Disease Control carried out entomological surveillance using CDC light traps and morphologic identification of mosquitoes.

RESULTS

Four of 24 suspected cases tested positive for *Plasmodium falciparum*, with no recent travel to endemic areas. Entomological surveys found *Culex* mosquitoes, but no *Anopheles* species known as competent vectors for *Plasmodium* protozoa, ruling out local vector-borne transmission.

CONCLUSIONS

The investigations suggested likely transmission from infected mosquitoes introduced via air travel or cargo. Despite the lack of evidence of local transmission, future introductions via travels and changes in vector distributions can increase malaria transmission risk. Therefore, we recommend enhancing surveillance and introducing stricter vector control at entry points.

KEYWORDS: Airport malaria, *Plasmodium falciparum*, Libya, vector-borne diseases, autochthonous transmission

ABSTRACT ID: 649

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POSTER TOUR 22

Day 3 | Friday 21 November 08:30-09:15

Health equity and disease outbreaks

PRESENTER

Zakaria Elboukhari

ABSTRACT

Waterborne diarrheal Outbreak in a Migrant Residence Center - Tripoli, Libya, 2024

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BACKGROUND

Between October and November 2024, an outbreak of diarrheal disease occurred at a Migrant Residence Center, which hosted 240 women and children under 15 years old. Twenty residents reported diarrhea, and five required hospitalization. This was the third such outbreak in 12 months, following two prior events linked to inadequate water and sanitation (WASH) infrastructure. We investigated to identify the source, describe risk factors, and implement sustainable solutions.

METHODS

We defined a case as a resident (23/10–11/11) experiencing ≥ 3 loose stools in 24 hours. We reviewed medical records, interviewed 80 residents (cases and contacts), and collected eight stool specimens for Laboratory testing. We reviewed the history of the water supply. Also, the National Laboratory of Environmental Correction tested water samples from freshwater tanks, filtered water taps, and other taps supplying dormitories for microbial contamination.

RESULTS

We identified 41 cases (mean age 18 years SD: 11 years); 76% (32/41) resided in dormitory A. The first case had symptoms on 25/10. Cases increased between 2/11-13/11 with a peak on 6/11, suggesting a common source exposure. Of 41 cases, 29 (71%) drank unfiltered tap water and nine (22%) drank filtered tap water. While 20 (49%) reported always washing hands, only 7 (17%) had access to soap/sanitizers. Water samples were contaminated with *Escherichia coli* and *Entamoeba histolytica*. Among the eight stool samples tested, four were positive for *Entamoeba histolytica* and one was positive for *Ancylostoma* sp. eggs. Municipal reports confirmed a septic tank leakage near the main water source 17 weeks prior.

CONCLUSIONS

Recurrent outbreaks at this site were driven by systemic Water and Sanitation (WASH) failures, notably contaminated groundwater and inadequate filtration, lack of access to soap/sanitizers, and meal consumption in dormitories amplified secondary transmission risks. Post-intervention measures halted transmission, demonstrating that targeted WASH interventions and improved monitoring can disrupt disease cycles in high-risk settings.

KEYWORDS: Waterborne Outbreak ,WASH interventions,Diarrheal Disease,Migrants

ABSTRACT ID: 336

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POSTER TOUR 22

Day 3 | Friday 21 November 08:30-09:15

Health equity and disease outbreaks

PRESENTER

Aswathikutty Gireesh

ABSTRACT

Health Equity Evaluation of Public Health Interventions during Outbreak Response: The Scoping, Execution and Action (SEA) Framework

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BACKGROUND

Public health interventions (PHIs) are frequently implemented in England at a regional level in response to cases and outbreaks of infectious disease. However, evaluating the effectiveness of PHIs for disadvantaged sub-groups is not commonly undertaken due to the fast pace of health protection teams (HPTs) response work and limitations of current evaluation tools. We developed a scalable evaluation framework to facilitate equity-focused evaluation of PHIs.

METHODS

The framework was developed by evaluation, health equity and HPT stakeholders in the United Kingdom Health Security Agency (UKHSA). It was informed by findings from a systematic review of evaluation frameworks for public health interventions from which key evaluation criteria were adapted. Existing equity impact assessment tools were used to shape the equity prompts in the framework.

RESULTS

The framework comprises three stages: a) Scoping (outlining aims and objectives, stakeholder engagement, and developing a theory of change); b) Execution (identifying evaluation questions, methods, data collection and analysis); c) Action (knowledge mobilisation). Health equity prompts are embedded at each stage, including best practice in engaging equitably with disadvantaged communities. The framework includes three evaluation levels: rapid, intermediate, and comprehensive. 'Rapid' supports a feasible evaluation in a resource and time-limited outbreak response. In response to end user feedback, example evaluations are included based on potential use cases provided by HPTs (e.g. during avian influenza outbreak management).

CONCLUSIONS

The proposed framework provides a three-stage proportionate approach for responsive and rapid health equity focused evaluation of PHI by frontline HPTs. Piloting is currently underway. We anticipate this will enable the evidence base to be further developed in the context of competing priorities and limited resources. It may also support those delivering PHIs to meet the Public Sector Equality Duty and Health Inequalities Duty.

KEYWORDS: Health equity, Public health Interventions, Disease outbreaks, Evaluation methodology

ABSTRACT ID: 460

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POSTER TOUR 22

Day 3 | Friday 21 November 08:30-09:15

Health equity and disease outbreaks

PRESENTER

Caroline Russo

ABSTRACT

Adapting Wastewater-Based Epidemiology for Infectious Disease Surveillance in Remote Arctic Communities: Insights from Nunavik, Canada

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BACKGROUND

Indigenous and remote communities in Canada experience significant infectious disease burdens, compounded by challenges in timely diagnosis and clinical surveillance. In Nunavik, a region of Arctic Quebec with decentralized infrastructure and limited diagnostic coverage, traditional surveillance approaches may delay public health action. Wastewater-based epidemiology (WBE), successfully used in urban areas, offers a promising complementary tool. However, its application in low-flow, trucked wastewater systems common in Nunavik remains unexplored. This study aimed to assess the feasibility and value of adapting WBE for surveillance in this context.

METHODS

A pilot was conducted in a community in Nunavik. All samples were collected from wastewater trucks transporting effluent from household tanks to treatment lagoons. Multiple sampling techniques were tested to assess feasibility and sample quality and a dedicated sampling device, attached to the truck, has been developed. Laboratory analyses targeted SARS-CoV-2, influenza, RSV, and Tuberculosis.

RESULTS

We demonstrated that target pathogens are detectable in the trucked wastewater system. Sampling procedures and tools were refined to ensure sample quality, and we selected grab sampling of the liquid fraction at the truck outflow as the preferred approach. This method balances logistical practicality with adequate sample quality. Further standardization and validation efforts are ongoing.

CONCLUSIONS

Current work focuses on refining sampling strategies and identifying additional priority targets, including enteric viruses and antimicrobial resistance markers. A framework is under development to connect WBE data to actionable public health responses in Nunavik. These early findings offer practical insights for designing surveillance in decentralized systems and support the feasibility of implementing WBE where conventional infrastructure is lacking. Importantly, this approach may be transferable to other remote or underserved settings globally, including those with constrained diagnostic access or elevated risk of pathogen emergence. By tailoring methods to local realities, WBE can help close persistent surveillance gaps and enable earlier, more equitable outbreak detection.

KEYWORDS: Wastewater-Based Epidemiological Monitoring, Public Health Surveillance, Infectious Diseases, Arctic Regions, Tuberculosis, Indigenous Peoples

ABSTRACT ID: 495

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POSTER TOUR 22

Day 3 | Friday 21 November 08:30-09:15

Health equity and disease outbreaks

PRESENTER

Aya Hamzeh

ABSTRACT

Water Monitoring in Lebanon: Addressing Hepatitis A and Cholera through Bacteriological Testing

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BACKGROUND

Lebanon faces ongoing public health challenges from waterborne diseases, notably hepatitis A and cholera. Hepatitis A remains endemic, with outbreaks exacerbated by population displacement, inadequate sanitation, and limited access to clean water. In October 2022, Lebanon experienced its first cholera outbreak in nearly three decades, reporting more than 8,000 cases and 23 deaths by June 2023. These events underscore the urgent need for enhanced water quality monitoring and robust public health interventions.

METHODS

In response to the 2022-2023 cholera outbreak, Lebanon intensified bacteriological water quality monitoring. The initial action involved training local authorities to collaborate on water sampling, with samples collected from various sources including networks, treatment plants, springs, wells, rivers, tanks etc. Analysis was done in a network of reference water laboratories in public hospitals supported by World Health Organization. To support testing capabilities, eight portable water laboratories, provided by the Lebanese Red Cross, were allocated across provinces.

RESULTS

Between January 2023 and May 2025, 889 water samples were collected, 35.5% from wells, 17% from springs, 13.8% from the water networks, 9.2% from treatment plants and remaining percentage is from other sources. The primary triggers for testing were hepatitis A (69%) and acute watery diarrhea (19%). 93.1% were tested in public laboratories, and 6.9% using portable water laboratories, enabling rapid detection of contamination. 61% of the results were positive for bacteriological contamination with total/fecal coliforms. Results were shared with relevant partners to implement public health actions: water authorities, WASH sector and municipalities.

CONCLUSIONS

Regular bacteriological water monitoring is critical for preventing and controlling waterborne diseases in Lebanon. Ongoing training, regular source monitoring, and public awareness initiatives are recommended to strengthen water safety and public health, with the active involvement of local authorities.

KEYWORDS: Water monitoring, waterborne diseases, public health, Lebanon, bacteriological testing, fecal contamination.

ABSTRACT ID: 720

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POSTER TOUR 23

Day 3 | Friday 21 November 08:30-09:15

Tools for advances in public health

PRESENTER

Pinar Dilbaz

ABSTRACT

Who Sets the Rules? Generative AI Policies in Leading Medical Journals

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BACKGROUND

Generative AI (GAI) tools such as ChatGPT have rapidly become part of scientific authorship. However, their use introduces risks including misinformation, bias, and plagiarism. Inconsistencies in editorial policies may hinder transparency, reproducibility, and erode public trust, which is particularly concerning in medical research where patient safety is at stake.

METHODS

This study reviewed the Instructions for Authors of 998 high-impact medical journals indexed by SCImago to assess the presence and characteristics of GAI-related guidelines. Data were collected using a hybrid workflow combining automated web scraping, LLM-assisted navigation, and manual validation. Editorial features were extracted, including AI definition, model name/version disclosure, COPE referral, permitted use cases, and bias warnings. Journal metrics (SJ score, H-index, publication frequency, and gender composition) were analyzed to identify policy predictors.

RESULTS

A total of 76.5% of the 998 journals had an explicit policy on GAI use in the publication process. Yet, only 18.6% referred to COPE guidance, and just 5% defined the term “artificial intelligence.” Among journals with an AI policy, 91% required disclosure of AI use, but only 53.2% requested the model name and 27.4% its version. Only 50.9% of journals included bias or hallucination warnings. Q1 journals favored standardized locations for AI declarations (e.g., Methods), whereas Q2-Q3 journals showed greater variation. Logistic regression revealed that higher H-index, lower publication frequency, and greater female authorship were associated with stronger ethical components such as COPE referral and bias warnings. Q3 journals were significantly less likely to include any AI guidance but more permissive regarding AI-generated visuals.

CONCLUSIONS

Editorial responses to GAI remain fragmented. Despite growing recognition of its use, policy clarity and ethical alignment are lacking. The absence of standardized disclosure formats and risk warnings limits reproducibility and may contribute to an “AI-driven infodemic”. Coordinated action by publishers/research bodies is urgently needed to safeguard scientific integrity and public health.

KEYWORDS: Artificial Intelligence, Large Language Models, Natural Language Processing, Editorial Policies, Publishing/ethics, Public Health

ABSTRACT ID: 225

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POSTER TOUR 23

Day 3 | Friday 21 November 08:30-09:15

Tools for advances in public health

PRESENTER

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ABSTRACT

Calibration of an epidemiological model with intermittent sentinel hospital surveillance and wastewater data

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BACKGROUND

Mathematical modelling for infectious diseases often relies on detailed, age-stratified, continuous data from national surveillance systems to enable accurate calibration and generate long-term projections and scenarios for public health decision-making. In Belgium, such data were available for COVID-19 from 2020 to June 2023. Since then, only sentinel surveillance data on severe acute respiratory infections (SARI) have been available. While age-stratified, these data are however intermittent since, in 2022-2023, this surveillance system was only active when influenza circulation increased, complicating accurate modelling. Wastewater surveillance offers an alternative, though it lacks age-specific information and standardised scaling. This study aims to evaluate the viability of using SARI and wastewater data during the overlapping period when national surveillance data were still available.

METHODS

We used a complex age-structured compartmental model incorporating vaccination status and waning immunity. Various calibration strategies were tested for the 2022-2023 period, using Belgian hospital data as the baseline. To address gaps in SARI reporting, we normalised wastewater data using a faecal indicator (PMMoV) and estimated age-group proportions from available SARI data. We scaled both datasets using hospital admissions from national surveillance systems during the overlap period before the reporting interruption.

RESULTS

Treating SARI data as if there were no reporting issues or removing gaps resulted in inaccurate calibration. Using wastewater data helped to partially constrain the model during interruptions in SARI reporting. Applying age-specific proportions from SARI to normalised wastewater data enabled the model to better capture age-specific vulnerabilities to COVID-19.

CONCLUSIONS

Age-structured SARI data can serve as a viable alternative for calibrating complex epidemiological models, provided that appropriate rescaling is available. During intermittent reporting, wastewater data help maintain model robustness. Preserving both SARI and wastewater surveillance systems is essential for informing future public health modelling and policy.

KEYWORDS: Sentinel surveillance, COVID-19, Wastewater, Epidemiological models, Calibration, Mathematical model

ABSTRACT ID: 380

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POSTER TOUR 23

Day 3 | Friday 21 November 08:30-09:15

Tools for advances in public health

PRESENTER

Jessica Aguilar Diaz

ABSTRACT

Pandemic preparedness: potential of routine general practice data for infectious disease surveillance and early warning

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BACKGROUND

For pandemic preparedness, a key component is a well-functioning early warning system (EWS) for infectious diseases. In this proof-of-concept study we explored the potential of using electronic patient records of general practices for an EWS.

METHODS

We used data from 2014 to 2024 of 4 general practices of the Family Medicine Network (FaMe-Net) in the Netherlands. Weekly counts of registered codes related to infectious diseases were extracted from approximately 40.000 patients. We developed seven definitions for combinations of registered symptom and disease codes related to respiratory infections and gastroenteritis. Some definitions primarily focus on diseases (e.g. bronchitis), and others on symptoms (e.g. cough). The Farrington flexible algorithm was used to construct a threshold for each definition, based on 5 historical years, to generate alert signals per week. Alert signals indicated that the observed weekly count exceeded the threshold. The EWS potential was defined based on the generation of alert signals, referring to respiratory infections and gastroenteritis in 2019-2020 and 2023-2024.

RESULTS

We analysed approximately 600.000 diagnostic codes. In 153 weeks, the number of alert signals ranged from 3 to 20, depending on which combination of respiratory and gastroenteritis diagnostic codes was used. Although there was overlap, variation in alert signals was also found between the defined combinations. Within the respiratory season there were 69 alert signals and outside the respiratory season 4 alert signals (total, n=73). For gastroenteritis there were 33 alert signals within the season and 38 alert signals outside the season (total, n=71).

CONCLUSIONS

Weekly counts of registered codes related to respiratory infections and gastroenteritis from FaMe-Net general practices showed potential for an EWS because alert signals were generated but not for each week. This has to be validated with outbreak data to determine which combination of diagnostic codes performs best, ultimately providing early warning signals for timely public health action.

KEYWORDS: pandemic preparedness, public health surveillance, general practice, communicable diseases

ABSTRACT ID: 534

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POSTER TOUR 23

Day 3 | Friday 21 November 08:30-09:15

Tools for advances in public health

PRESENTER

Katja Kajikhina

ABSTRACT

Strengthening epidemiological capacities in municipal public health services: findings and perspectives from the FETP4ÖGD project

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BACKGROUND

Field Epidemiology Training Programmes (FETPs) are practice-oriented training programmes aiming to strengthen capacity of public health systems in infectious disease epidemiology. Since 1996, an advanced two-year FETP has been primarily implemented at the national and state levels in Germany. However, shorter programmes delivering specific epidemiological skills and targeted mainly at the municipal level are not yet available. We aimed to identify the content and format required for new FETPs to address the gaps in epidemiological training in public health services.

METHODS

We invited representatives from public health training academies, all 16 federal state health authorities (HA) and a purposive sample of local HA to participate in interviews and focus group discussions. The aim was to identify the requirements of a potential short FETP. Local HA were selected based on structural characteristics such as size and region (N=28). Data were analysed using qualitative content analysis.

RESULTS

The local HA showed great interest in FETPs, with a participation rate of 64% (18/28). Most municipal representatives expressed a need for a shorter FETP programme with practical content. Topics of interest included the legal basis for infection protection measures, the interpretation of laboratory reports and the application of surveillance tools. Analytical competencies including epidemiological and statistical methods were also identified as essential. Training formats combining face-to-face and online learning were favoured in order to facilitate exchange and integration into daily work. Modularity, flexibility and specific goal orientation were also highlighted as potential advantages of possible new qualification formats.

CONCLUSIONS

In addition to the established two-year training, short and modular FETPs could enable different staff groups, such as those responsible for hygiene control and outbreak management, to qualify. These programmes should focus on practical, day-to-day training. Tailored FETPs could facilitate career development and support public health authorities in securing a skilled workforce.

KEYWORDS: Education ,Infectious diseases,Workforce,Health services

ABSTRACT ID: 688

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POSTER TOUR 23

Day 3 | Friday 21 November 08:30-09:15

Tools for advances in public health

PRESENTER

Hwaraa Sweidan

ABSTRACT

Noise classification in Epidemic Intelligence from Open Sources articles using natural language processing: A random forest approach

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BACKGROUND

The Epidemic Intelligence from Open Sources (EIOS) system gathers articles using predefined keywords to support early detection of public health threats. The Epidemiological Surveillance Program at the Lebanese Ministry of Public Health screens the EIOS portal for notifiable diseases structured into boards—dashboards organized by disease. Some articles report public health events but include unrelated content due to keyword matches, creating noise and extra work. We aimed to optimize classification based on public health relevance using Natural Language Processing.

METHODS

We exported 348 articles from EIOS search results on novel influenza and cholera in February 2024. Two annotators labeled the articles as “relevant”, “irrelevant”, or “noise-found”. Relevant articles aligned with the board’s objectives. Irrelevant articles lacked clear public health events or relevant information. Noise-found articles included keywords related to the topic but discussed events that were unrelated to the board’s focus. To standardize textual data, we removed stop-words and applied automated text-cleaning techniques. We trained the Random Forest model on individual and combined boards, testing versions with and without Arabic-language articles. Data was split into 80% training and 20% testing, and evaluated by accuracy, precision, recall, and F1-score.

RESULTS

The annotators agreed on 85% (295/348) of the articles’ labeling. Two models stood out. The model excluding Arabic language articles performed best overall with accuracy 0.97 (95%CI: 0.83-0.99), precision of 0.89 recall of 0.34, and F1 score of 0.9. The model applied to all boards revealed an accuracy of 0.89 (95%CI: 0.81-0.95), precision of 0.96, recall of 0.59, and F1 score of 0.69.

CONCLUSIONS

Despite limitations in sample size and multilingual articles, our findings suggest that automated classification can streamline public health workflows by enabling personnel to focus on timely investigation of relevant signals. Exploring other models and enhancing the system with NLP can strengthen public health intelligence, for emerging threats detection.

KEYWORDS: Infectious Disease Monitoring, Media Scanning, Machine Learning in Public Health, Communicable Disease Control, Language Processing, Disease Outbreaks

ABSTRACT ID: 715

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POSTER TOUR 23

Day 3 | Friday 21 November 08:30-09:15

Tools for advances in public health

PRESENTER

Alexis Sentis

ABSTRACT

Developing a European bloodstream infection surveillance system using data from electronic health records

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BACKGROUND

Bloodstream infections (BSIs) are a major public health concern, and enhancing their surveillance by extracting data from electronic health records (EHR) is often the first target for automating the surveillance of healthcare-associated infections (HAIs). Since March 2023, EHR-based BSI surveillance has been developed across EU/EEA countries under the ECDC-funded project "Surveillance from Electronic Health Data" (SUREHD). We assessed existing BSI-surveillance systems and the progress in implementing EHR-BSI surveillance in 17 participating EU/EEA countries to guide infection control measures.

METHODS

Participating countries developed country-specific BSI-surveillance protocols based on a SUREHD-generic surveillance protocol. We summarised data on existing BSI-surveillance systems and the status of implementing EHR-BSI surveillance, collected through meetings with national representatives and review of national surveillance protocols and reports.

RESULTS

By March 2025, twelve of 17 countries lacked national BSI-surveillance systems. However, EHR-BSI surveillance is being implemented at multiple levels: nationally (n=9), in selected regions (n=2) or hospitals (n=6). Reported challenges include data standardisation (n=13), IT capacity (n=10), data linkage (n=7), system integration (n=7), and data protection (n=6). Few countries have access to structured EHR data for patient symptoms (n=1), infection origin (n=2), and catheter-related variables (n=5). Standardised controlled vocabularies for patient variables have yet to be defined in nine countries. Most countries have no data validation process yet (n=13). All countries aim to automate surveillance processes, starting with data extraction (n=17), data linkage (n=11), and BSI case/episode identification (n=11). Seven countries plan to use an ad hoc centralised data collection tool, while five explore interoperability standards to support data collection.

CONCLUSIONS

Developing a Europe-wide EHR-BSI surveillance system has facilitated experience exchange and alignment with the SUREHD protocol. Countries are developing (semi)automated systems and solutions to optimise data collection, standardisation, and validation. Future efforts will focus on harmonisation, data timeliness and quality, leveraging EHR-derived BSI data to strengthen HAI surveillance and infection control.

KEYWORDS: Healthcare associated infections, Bloodstream infection, Electronic Health Records, Public health surveillance

ABSTRACT ID: 280

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