HYBRID

ESCAIDE 20th EDITION

European Scientific Conference on
Applied Infectious Disease Epidemiology

18-20 November 2026 **Stockholm and online**



#ESCAIDE2026

ESCAIDE

ABSTRACT BOOK

ecdc
EUROPEAN CENTRE FOR DISEASE PREVENTION AND CONTROL

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

Welcome to ESCAIDE 2026.

This year marks a special milestone as we celebrate the 20th edition of the European Scientific Conference on Applied Infectious Disease Epidemiology. Over the past two decades, ESCAIDE has grown from a European forum for sharing epidemiological evidence into a global multidisciplinary conference that brings together current and future public health practitioners, policymakers and leaders to share experience and knowledge, address communicable disease threats, and translate scientific evidence into public health action. As we reflect on this journey, we can take pride in the contributions of thousands of participants who have advanced the science and practice of infectious disease prevention and control across Europe and globally.

This edition of ESCAIDE is not only an opportunity to celebrate past achievements – we also need to look ahead. The public health challenges we face today are increasingly complex, interconnected and global. Emerging pathogens, including potentially bioengineered ones; antimicrobial resistance; climate-related risks; demographic changes; international conflicts; threats to health security; and the rapid spread of mis- and disinformation all demand new approaches, stronger partnerships, innovative science and a renewed commitment to evidence-based public health action.

The ESCAIDE Scientific Committee has identified plenary and thematic sessions that reflect these challenges and how the public health community could respond. These sessions consider how innovation and engagement – including artificial intelligence, advanced analytics, data integration, laboratory infrastructure and citizen science – can strengthen threat detection and response and enhance multisectoral and multinational collaboration. Such advances could build our capacity and resilience to address emerging communicable disease threats and maintain health security.

Bridging evidence and public health action remains an ever-present focus of ESCAIDE. This is reflected in sessions that explore the evolution of integrated surveillance to improve the timeliness and accuracy of early warning systems and rapid action, as well as the important role of modelling and quantitative analysis to obtain richer insights on disease outbreaks and effectiveness of interventions. Ultimately, evidence-based approaches aim to build and maintain trust in science before, during and after health emergencies.

At the heart of ESCAIDE's three-day programme are 230 abstracts presented across 37 sessions. The broad range of timely topics is as impressive as ever, and reflects the priorities and practice of the ESCAIDE community who submit and assess abstracts. The Scientific Committee – myself included – remain indebted to all who have contributed to make this happen.

Since the founding of ESCAIDE, we have witnessed remarkable technological advances in public health – from innovations in epidemiological assessment, enhanced surveillance and data analytics, and genomic sequencing and modelling to the previously unimagined speed and effectiveness of vaccine and diagnostic development and deployment. The increasing number and impact of international health threats and multi-country outbreaks since 2006 has also prompted unprecedented international cooperation. However, the challenges ahead will require even greater ambition and collective action, and the next 20 years of infectious disease prevention and control will be defined by how successfully we can harness scientific innovation, strengthen trust in public institutions and translate scientific knowledge into action.

ESCAIDE's enduring strength lies in its ability to bring together diverse expertise, foster new partnerships, and facilitate an exchange of ideas that drives meaningful change. I invite all participants to engage fully, share experiences openly, and contribute to a common vision for the future. I hope that the discussions and relationships built during this conference will help shape the future of public health in Europe and beyond.

Piotr Kramarz
Chair, ESCAIDE Scientific Committee
Chief Scientist and Head of Unit,
Scientific Evidence and Communication, ECDC
escaide.eu

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PROGRAMME OVERVIEW

DATE	TIME *(CET)*	EVENT	LOCATION
Tuesday 17 November	13:30-17:00	*Eurosurveillance* pre-conference workshop: How to improve your chances to get published in scholarly journals	**ECDC premises** Gustav III:s Boulevard, 40 169 73 Stockholm
	15:30-17:00	ECDC pre-conference workshop: Episomer: social media threat detection	**Waterfront Congress Centre** Nils Erikson Plan 4 111 64 Stockholm
	16:00-18:00	ECDC pre-conference workshop: Misinformation Olympics	
Wednesday 18 November	08.00-21.00	**Conference Day 1**	**Waterfront Congress Centre** Nils Erikson Plan 4 111 64 Stockholm
Thursday 19 November	08.00-20.35	**Conference Day 2**	
Friday 20 November	08.00-15.45	**Conference Day 3**	

Pre-conference workshops have limited capacity and require separate registration. Please visit escaide.eu for more information.

GENERAL PROGRAMME

DAY 1 - *Wednesday 18 November 2026*

TIME (CET)	**PROGRAMME**		
08.00-09.00	**Registration and welcome coffee**		
09.00-09.30	**Opening ceremony** *Pamela Rendi-Wagner, ECDC Director,* *Piotr Kramarz, Chair ESCAIDE Scientific Committee* A1		
09.30-10.30	**Plenary session A:** Crises and challenges shaping the landscape of public health: how far we've come *Chaired by the ESCAIDE Scientific Committee members Alicia Barrasa (UKHSA/EAN, United Kingdom) and Piotr Kramarz (ECDC, Sweden)* *Speaker: Shingai Machingaidze (Coalition for Epidemic Preparedness Innovations/International Pandemic Preparedness Secretariat, United Kingdom)* A1		
10.30-11.00	Coffee break M1		
11.00-12.30	**Fireside session 1:** Respiratory viruses: evidence to practice A1	**Fireside session 2:** Food- and water-borne diseases A2	**Thematic session 1:** Towards a European One Health Data Space, *organised by European Partnership on One Health AMR (EUP OHAMR)* *Moderated by Linda van Gaalen (ZonMw, Netherlands)* *Speakers: Elina Drakvik (Sitra, Finland), Christian Giske (ECDC), Katharina Schaufler (Helmholtz Institute for One Health, Germany), Alice Aldora (World Organisation for Animal Health, France), Nichola Hawkins (Niah, UK)* A4
12.30-14.15	Lunch break M1 + Balcony	12.45-14.05 **Thematic session 2**: European Union Reference Laboratories (EURLs) in outbreak response and beyond, *organised by ECDC* *Moderated by Maximilian Riess (ECDC) and Andreas Hoefer (ECDC)* *Speakers: Klara Sondén (Public Health Agency of Sweden), Camilla Wiuff Coia (SSI, Denmark), Camille Jacqueline (Hospices Civils de Lyon, France)* A2 12.40-14.05 **EAN General Assembly** A4	
14.15-15.45	**Fireside session 3:** Antimicrobial resistance A1	**Fireside session 4:** Outbreaks of food- and water-borne diseases A2	**Fireside session 5:** Surveillance and investigation A4
15.55-16.55	**Poster tour 1:** Outbreak investigations of food-borne diseases **Poster tour 2:** One Health **Poster tour 3:** Surveillance of vaccine-preventable diseases **Poster tour 4:** Surveillance, outbreaks and high-risk populations **Poster tour 5:** Burden of respiratory diseases **Poster tour 6:** Communication and behavioural aspects **Poster tour 7:** SDG-targeted infections **Poster tour 8:** Healthcare-associated infections M1	**Thematic session 3:** From data to pandemic decisions in EU, *organised by the Norwegian Institute of Public Health (NIPH) and BE READY Partnership* *Moderated by Thomas Hofmann (ECDC)* *Speakers: Bjørn G Iversen (Norwegian Institute of Public Health), Tonje Sande Laird (Norwegian Institute of Public Health), Evelyn Depoortere (DG RTD)* A2	
16.55-17.15	Coffee break M1 + Balcony		
17.15-18.30	**Plenary session B:** The science behind EU health security, *Chaired by the ESCAIDE Scientific Committee members Bruno Ciancio (ECDC, Sweden) and Miłosz Parczewski (Pomeranian Medical University, Poland) Speakers: Annick Lenglet (Radboudumc, Netherlands), Gianfranco Spiteri (ECDC, Sweden), Helen Brown (Safinea, Ireland), and Magdalena Rosińska (National Public Health Institute, Poland)* A1		
19.00-21.00	**Networking event**, Venue: Berns Asiatiska		

GENERAL PROGRAMME

DAY 2 - *Thursday 19 November 2026*

TIME (CET)	**PROGRAMME**		
08.00-09.00	**Registration and welcome coffee**		
09.00-10.30	**Plenary session C:** Communication to (re)build trust in science *Chaired by the ESCAIDE Scientific Committee members Tyra Grove Krause (Statens Serum Institut, Denmark) and Koen Blot (Sciensano, Belgium)* *Speakers: Anders Hviid (Statens Serum Institut, Denmark), Steven van Gucht (Sciensano, Belgium), and Tina D Purnat (Harvard Chan School of public health, United States)* A1		
10.30-11.00	Coffee break M1		
11.00-12.30	**Fireside session 6:** Healthcare-associated infections A1	**Fireside session 7:** Vaccine-preventable diseases: from evidence to practice A2	**Fireside session 8:** Social determinants and actions for public health A4
12.30-14.15	Lunch break M1 + Balcony	12.40-14.10 ***Eurosurveillance* lunch seminar:** Three decades of serving infectious disease prevention and control in Europe *Moderated by Shingai Machingaidze (Coalition for Epidemic Preparedness Innovations/IPPS, UK)* *Speakers: Kevin Fenton (NHS London, UK), Ana Marušić (University of Split School of Medicine, Croatia), Roberto Croci (SSI, Denmark)* C1+C2+C3 12.40-13.10 **Refresh and recharge session:** Facilitated by Irina Ljungqvist (ECDC) Bar area floor 5	
14.15-15.45	**Fireside session 9:** SDG 3.3 -targeted diseases A1	**Fireside session 10:** Respiratory viruses: surveillance and response A2	**Fireside session 11:** Late breakers (1) A4
15.55-16.55	**Poster tour 9:** One Health and food and water-borne diseases **Poster tour 10:** Preparedness and response **Poster tour 11:** Surveillance and prevention of respiratory viruses **Poster tour 12:** Burden and prevention of vaccine-preventable diseases **Poster tour 13:** Data systems and surveillance **Poster tour 14:** Surveillance and outbreak investigations of AMR **Poster tour 15:** Artificial intelligence in public health **Poster tour 16:** Late breakers (1) M1	**Thematic session 4:** Advancing action towards SDG 3.3 among migrant populations in Europe: scaling up evidence based best practices, *organised by ECDC* *Moderated by Charlotte Deogan (ECDC)* *Speakers: Ana Requena (Barcelona Institute of Global Health, Spain), Abimbola Ajomale (Noaks Ark Mosaik, Sweden), Margarida Torres (National Health Services Portugal), Gonçalo Bento (National Health Services Portugal)* A2	
16.55-17.15	Coffee break M1 + Balcony		
17.15-18.45	**Plenary session D:** Learning from data: integrated surveillance of respiratory infections *Chaired by the ESCAIDE Scientific Committee members Angeliki Melidou (ECDC, Sweden) and Nadine Zeitlmann (Robert Koch Institute, Germany)* *Speakers: Nick Bundle (ECDC, Sweden), John Brownstein (Harvard Medical School/Boston Children's Hospital, United States), Trine Hessevik Paulsen (FHI, Norway), and Ron Fouchier (Erasmus University Medical Centre, Netherlands)* A1		
19.00-20.30	**BarCamp** Bar area floor 5		

GENERAL PROGRAMME

DAY 3 - *Friday 20 November 2026*

TIME (CET)	PROGRAMME		
08.00-09.00	**Registration and welcome coffee**		
09.00-10.30	**Plenary session E:** Modelling for better public health decisions *Chaired by the ESCAIDE Scientific Committee members Jose Canevari (ECDC, Sweden) and Hana Orlíková (National Institute of Public Health, Czech Republic)* *Speakers: Moritz Kraemer (University of Oxford, United Kingdom), Sheetal Silal (Modelling and Simulation Hub, Africa (MASHA), University of Cape Town, South Africa), and Julian Savulescu (National University of Singapore)* A1		
10.30-11.00	Coffee break M1		
11.00-12.30	**Fireside session 12:** Quantitative methods A1	**Fireside session 13:** Late breakers (2) A2	11.00-12.20 **Thematic session 5:** Can Public Health work without the "public"?, *organised by ECDC* *Moderated by Barbara Albiger (ECDC) and Cristina da Cruz (ECDC)* *Speakers: Lotta Waesterberg Tomasson (Public & Science Sweden), Sébastien Français (Luxembourg Health Directorate), Stacey Vickers (European Commission), Jörgen Lööf (ElectriCITY, Sweden)* A4
12.30-14.15	Lunch break M1 + Balcony		12.40-14.10 **Career compass:** Where can a career in epidemiology and microbiology in public health take you?, *organised by EAN* *Moderated by Natalie Fischer (Institut Pasteur Paris, France), Joaquin Baruch (WHO, Germany)* *Speakers: Amrish Baidjoe (MSF, Luxembourg), Ines Steffens (ECDC), Veronik Hutse (Sciensano, Belgium), Gianfranco Spiteri (ECDC)* A4 12.45-14.05 **Simulation exercise**: Bridging the gap between disciplines in crisis: interdisciplinary scientific advice for policy, *organised by Pandemic & Disaster Preparedness Center (PDPC)* *Moderated by Jeannette de Boer (PDPC, Netherlands)* *Facilitators: Femke Overbosch (PDPC, Netherlands), Aloïs Kessener (PDPC, Netherlands)* C4
14.15-15.15	**Poster tour 17:** Surveillance of food- and water-borne diseases **Poster tour 18:** Surveillance of COVID-19 and influenza **Poster tour 19:** Vaccine-preventable diseases: evidence to practice **Poster tour 20:** Vector-borne diseases **Poster tour 21:** Quantitative methods **Poster tour 22:** Social determinants of infectious diseases **Poster tour 23:** Evidence to practice **Poster tour 24:** Late breakers (2) M1		**Thematic session 6:** Cross-sectoral response to CBRN threats, *organised by ECDC* *Moderated by Agoritsa Baka (ECDC)* *Speakers: Arménio José Louro Liceia (Polícia de Segurança Pública, Portugal), Paul William Riley (ECDC), João Simões (Europol), Tomoya Saito (Japan Institute for Health Security)* A1
15.25-15.45	**Closing ceremony** A1		

Fireside Sessions

FIRESIDE SESSION

DAY 1 - *18 November* - 11.00-12.30 CET

Fireside session 1

Respiratory viruses: evidence to practice

moderated by Moa Rehn

11.00-12.30 CET | A1

a. Developing a respiratory swabbing tool in FluSurvey to support pandemic preparedness in England, **Hannah Wolmuth-Gordon**

b. Nirsevimab effectiveness in preventing RSV hospitalisations in children under 24 months: second season post-national immunisation implementation in Portugal (2025–2026), **Vânia Gaio**

c. Disentangling school-related and community transmission contributions to SARS-CoV-2 cases in secondary school students across pandemic phases, **Clarize de Korne**

d. Insights from implementing active surveillance for avian and swine influenza virus infections in humans in Denmark, 10 September 2024 to 7 May 2026, **Gudrun Witteveen-Freidl**

e. Impact of autumn 2023 and 2024 COVID-19 vaccination in preventing COVID-19 related hospitalisations and deaths in individuals aged ≥65 years from seven EU/EEA countries: a multicentre electronic health records-based study (VEBIS-EHR), **Baltazar Nunes**

f. Governance of Scientific Advice for Policymaking during COVID-19: Lessons from Sweden and Switzerland, **Fereshteh Kazemipour**

Fireside session 2

Food- and water-borne diseases

moderated by Anne Carroll

11.00-12.30 CET | A2

a. Setting norovirus activity level thresholds using the moving epidemic method, England, 2015-2025, **David Elliott**

b. Are Non-Contemporaneous Controls a Valid Source of Controls in Foodborne Outbreak Investigations?, **Rebecca Howarth**

c. Comparative epidemiology and seasonality of Cryptosporidium hominis and Cryptosporidium parvum in Wales, 2022 to 2024**, Craig Hogg**

d. Genomic epidemiology of clinical Listeria monocytogenes clusters in Norway, 2016–2025, **Kristian Alfsnes**

e. Vibrio and Shewanella infections in Denmark: a six-year nationwide retrospective epidemiological overview, 2020–2025, **Kristyna Faksova**

f. Ecological determinants and projections of cholera in South Kivu province, Democratic Republic of Congo, 2021–2028., **Ousmaila Bianpambe**

FIRESIDE SESSION

DAY 1 - *18 November* - 14.15-15.45 CET

Fireside session 3

Antimicrobial resistance

moderated by Arina Zanuzdana

14.15-15.45 CET | A1

a. Implementation Gaps in Antimicrobial Stewardship in Pakistan: Implications for Surveillance and Public Health Practice, **Ghania Nadeem**

b. European multi-country outbreak of NDM-5-producing Enterobacter hormaechei ST1344, March 2025–April 2026, **Amelie Friedsam**

c. From data silos to federated One Health antimicrobial surveillance: early implementation results for Estonia and Romania, **Laura- Madalina Lixandru**

d. Outbreak investigation and molecular characterization of community associated methicillin resistant Staphylococcus aureus in a secondary school in Thuringia, Germany, 2025, **Sophia Wirth**

e. Genomic virulence scores and clinical outcomes among carbapenem-resistant Klebsiella pneumoniae infections in Germany, 2023–2025, **Simon Brinkwirth**

f. From Fragmentation to Integration: Strengthening One Health AMR Surveillance Governance in Europe, **Carmela Pagano**

Fireside session 4

Outbreaks of food- and water-borne diseases

moderated by Amber Litzroth

14.15-15.45 CET | A2

a. No iron curtain for HAV: Transnational Hepatitis A outbreak shifting gears in Austria in 2025, **Miriam Van den Nest**

b. Salmonella Bochum outbreak in children caused by chocolate hazelnut spread, Germany 2026, **Hanna Buck**

c. Assessment of post-exposure vaccination campaign in control of hepatitis A outbreak in a socially vulnerable community, Czech Republic, 2025, **Eva Patrasová**

d. A foodborne hepatitis A outbreak at a manufacturing plant in Taiwan, January–February 2026, **Po-Han Huang**

e. Investigation of a cereulide-contaminated infant formula outbreak: Belgian evidence from human case confirmation, **Géraldine De Muylder**

f. Shiga toxin-producing Escherichia coli O45:H2 infections in close contacts and shedding duration during a large outbreak in Germany, 2025, **Bettina Rosner**

Fireside session 5

Surveillance and investigation

moderated by Luise Müller

14.15-15.45 CET | A4

a. Guillain-Barré syndrome cases triggered by infections: a case-control study, Denmark, 1 January 2010 to 20 April 2026, **Roberto Croci**

b. Spread of multidrug-resistant and extensively-drug resistant Shigella strains among gay, bisexual and other men who have sex with men in Europe, **Cecilia Jernberg**

c. Comparison of three Haemophilus influenzae b serotyping assays used in the Netherlands and other European countries reveals variability in assay sensitivity, **Olivia Luise Gern**

d. Environmental detection of Sabin-like poliovirus type 3 in Barcelona, Spain, 2025: investigation of asymptomatic excretors and public health response, **María Dolores Fernández García**

e. Invasive Pneumococcal Disease in Western Lisbon, 2020-2025: Surveillance Data and Public Health Implications, **Inês Félix Mendes**

f. Complementary Use of Wastewater Surveillance Indicators to Determine the Onset of Influenza and Respiratory Syncytial Virus Waves in Germany; 2023-2026, **Susan Abunijela**

FIRESIDE SESSION

DAY 2 - *19 November* - 11.00-12.30 CET

Fireside session 6

Healthcare-associated infections

moderated by Annette Jurke

11.00-12.30 CET | A1

a. Outbreak management: The Strategy for Addressing Future Epidemics in Nursing Homes (SAFE-NH) study, **Eveline Coemans**

b. Sink-drain replacement to control a carbapenemase-producing Klebsiella pneumoniae outbreak in a surgical ward, Gran Canaria, Spain, 2024–2026, **Pablo Pérez Ruiz**

c. Targeted metagenomic analysis of causes of influenza-like and respiratory illness in healthcare workers over winter, United Kingdom, 2023-2024, **Lucy Findlater**

d. Multicountry surveillance data on neonatal healthcare-associated infections from the NeoIPC Surveillance Network, **Gizem Karadağ**

e. Time-to-Antibiotics in Sepsis and Septic Shock: A Systematic Review and Meta-Analysis Accounting for Severity-of-Illness Adjustment, **Selina Ehrenzeller**

Fireside session 7

Vaccine-preventable diseases: from evidence to practice

moderated by Camelia Savulescu

11.00-12.30 CET | A2

a. An evidence-based update of recommendations for meningococcal vaccination in Germany: Introducing quadrivalent vaccination in adolescence and discontinuing meningococcal C vaccination in childhood, **Vanessa Piechotta**

b. Epidemiological impact assessment of the second winter of RSV immunisation of infants with nirsevimab, Ireland 2025/2026**, Laura Kayaert**

c. Association between influenza vaccination and severe outcomes in adults aged ≥65 years hospitalised with laboratory-confirmed influenza: a retrospective cohort study in Europe, 2015/16– 2024/25, **Angela MC Rose**

d. Reducing antibiotic eligibility from 21 to 14 days after symptom onset for cases and contacts of pertussis in England did not increase household clustering, **Eleanor Clarke**

e. Vaccine effectiveness of the influenza vaccine administered alone or concomitantly with COVID-19 vaccine against influenza A subtype hospitalisation among older adults: results from a multi-centre study, Europe, 2023/24 and 2024/25 influenza seasons, **Angela MC Rose**

f. Statistical modelling approaches for estimating vaccine effectiveness of consecutive SARS-CoV-2 variant sublineages in the absence of study-specific genetic sequencing data, **Liliana Antunes**

Fireside session 8

Social determinants and actions for public health

moderated by Jonathan Suk

11.00-12.30 CET | A4

a. An ethical roadmap for local wastewater surveillance deployment, **Maarten de Jong**

b. Addressing the data gaps: A survey of Clostridioides difficile infection practices in England, September - December 2025, **Amreet Battu**

c. From surveillance to action: One Health use of Highly pathogenic avian influenza (HPAI) data for decision making and risk communication in Norway, 2024-2026, **Tora Ziesler**

d. Association between socioeconomic deprivation and pertussis incidence in HSE Dublin and Midlands, 2024, **Christopher Murray**

e. Upsurge in congenital syphilis in the EU/EEA: time to scale up public health responses, **Otilia Mårdh**

f. Parental refusal of HPV vaccination in Morocco: prevalence and associated factors from a multicentre cross-sectional study, **Chaymae Zerrouk**

FIRESIDE SESSIONS

DAY 2 - *19 November* - 14.15-15.45 CET

Fireside session 9

SDG 3.3 - targeted diseases

moderated by Norbert Bannert

14.15-15.45 CET | A1

a. Breaking barriers to hepatitis C diagnosis among previously unreached people who inject drugs in sub-saharan Africa: A multi-country peer-driven network intervention increased HCV Diagnosis Coverage Twofold, **Chimere Nwagbo**

b. Viral Hepatitis and HIV Among People Who Use Drugs in a German Prison: Disease Prevalence and Access to Care in a Mixed-Methods Study (2025), **Antonia Genath**

c. Evaluating Türkiye's Progress Toward the WHO End TB Strategy: A Time-Series Forecasting Study of Incidence and Mortality, **Ali Kılınç**

d. Beyond Coverage: Non-use of Available Insecticide-Treated Nets and Its Implications for Malaria Risk Among Children Under Five in Zambia, **Azibadighi Walter**

e. Integrating epidemiological and entomological data to assess the risk of autochthonous dengue transmission in Spain, **Lidia Redondo Bravo**

f. Unmasking Cutaneous Leishmaniasis Outbreak in an Endemic Village, Southeast Türkiye, 2025–2026, **Hacer Demirkose**

Fireside session 10

Respiratory viruses: surveillance and response

moderated by Luisa Hallmaier-Wacker

14.15-15.45 CET | A2

a. Effectiveness and early impact of maternal RSV vaccination in Denmark, 1 November 2025 – 30 April 2026, **Ida Rask Moustsen- Helms**

b. COVID-19 vaccine effectiveness in the primary care setting among older adults in Europe in 2025/26, **Esther Kissling**

c. Early vaccine effectiveness estimates of the 2025 autumn LP.8.1-adapted COVID-19 vaccine dose against hospitalisation and death in six EU/EEA countries: VEBIS-EHR network, October 2025 to January 2026, **James Humphreys**

d. Characteristics of influenza-like illness in the community during the 2025-2026 influenza A(H3N2) subclade K dominant season, **Becki Green**

e. Vaccine effectiveness against seasonal influenza A(H1N1)pdm09 and highly drifted influenza A(H3N2) subclade K at primary care level in Europe in 2025/26, **Héloïse Lucaccioni**

f. Rapid One Health response to a zoonotic HPAI A(H5N1) outbreak involving poultry, domestic cats and occupational exposure of veterinary staff and first responders in Germany, February 2026, **Aparna Dressler**

FIRESIDE SESSION

DAY 2 - *19 November* - 14.15-15.45 CET

Fireside session 11

Late breakers (1)

moderated by Dirk Meusel

14.15-15.45 CET | A4

a. Evidence for mixed zoonotic and person-to-person transmission of Andes hantavirus outbreak during an international expedition cruise, April-June 2026, **Oda van den Berg**

b. Outbreak of Legionnaires' disease associated with a misting system in a restaurant, Chambéry, France, 2026, **Emmanuelle Vaissière**

c. Observational environmental study of possible transmission routes during an outbreak of Andes virus on the M/V Hondius expedition cruise ship, **Janko van Beek**

d. International carbapenem-resistant Acinetobacter baumannii outbreak in burn intensive care units with ongoing transmission in Germany, 2026, **Sophia Melhem**

e. Large outbreak of autochthonous West Nile virus infection in humans in the Netherlands: preliminary investigation of cases from the Utrecht province, August – September 2026, **Annelein Kuiperbak**

FIRESIDE SESSION

DAY 3 - *20 November* - 11.00-12.30 CET

Fireside session 12

Quantitative methods

moderated by Helena de Carvalho Gomes

11.00-12.30 CET | A1

a. Estimating the Presence and Abundance of Aedes albopictus in Europe Using Neural Networks, **Indaco Biazzo**

b. Reuse of unstructured hospital-based electronic health record data to enhance automated surveillance of severe acute respiratory infections in the Netherlands, **Carsten van Rossum**

c. Population-level effectiveness of long-acting monoclonal antibodies and maternal vaccination against RSV-associated hospitalisation in infants: a modelling study across 28 European countries, **Elisa Viola**

d. Climate-driven leptospirosis in Greece: predictive modeling for early warning, **Zacharoula Bogogiannidou**

e. Mpox vaccination among MSM in the EU/EEA: Estimating the uptake and modelling the impact of future campaigns, **Bastian Franklin**

Fireside session 13

Late breakers (2)

moderated by Marion Muehlen

11.00-12.30 CET | A2

a. Lower-than-expected rotavirus vaccine effectiveness in Dutch children? Preliminary findings from a test negative case–control study, **Marije Bootsma**

b. Environmental drivers of transmission in an ongoing human tularaemia outbreak in Brittany, France, 2026, **Lorenzo Arena**

c. Increasing delays across sequential tuberculosis regimen modifications and potential utility of upfront nanopore targeted next-generation sequencing in Kyrgyzstan, **Aizat Kulzhabaevad**

d. Municipal-scale dengue early warning in Colombia: prospective model performance amid the confirmed 2026 national outbreak, **Hernan Silva**

e. Investigation and population vaccination response for a multi-settingoutbreak of Hepatitis A in South Wales, December 2025 to September 2026, **Joshua Matizanadzo**

Poster Tours

POSTER TOURS

DAY 1 - *18 November*

Poster tour 1

Outbreak investigations of food-borne diseases

moderated by Patricia Margaret Garvey

15.55-16.55 CET | M1

a. Traditional Household Slaughtering Practices as Determinants of Brucellosis Risk in High Burden Areas, Armenia, 2025, **Armine Chopikyan**

b. Brucellar epididymo-orchitis in an endemic setting: clinical features, management and outcomes from a single-centre study, **Sevak Mirabyan**

c. Tip of the Iceberg Salad: Investigation of a Salmonella Typhimurium Outbreak in Denmark, November- December 2025, **Cheyenne Gumbs**

d. Outbreak of Salmonella Enteritidis Associated with Egg Based Dishes in a Restaurant in Malta, November 2025, **Gabrielle Grixti Galdes**

e. Foodborne outbreaks associated with large-volume catering: Insights from multiple Clostridium perfringens investigations in Wales, December 2024 - December 2025, **Grace King**

f. Salmonella Typhimurium (monophasic) Outbreak Investigation Utilising Loyalty Card Purchase Data, United Kingdom, January to March 2026, **Katie Bolam**

g. Integrating Whole-Genome Sequencing (WGS) to Reinforce Traditional Epidemiological Investigation of a Foodborne Salmonella Outbreak, Moldova, 2025, **Anna Punga**

Poster tour 2

One Health

moderated by Katharina Alpers

15.55-16.55 CET | M1

a. Operationalizing One Health in Emergency Preparedness and Response: Lessons Learned from Marburg Virus Disease Outbreak Response in Ethiopia, Rwanda, and Tanzania, **Tedros Fikru Teshome**

b. Avian Pathogenic Escherichia coli in Humans and Poultry in the Czech Republic, **Veronika Illíková**

c. Meteorological exposures associated with reported Legionnaires' disease incidence in Greece: a 17-year time-series analysis, **Christina Morphaki**

d. Linking food animal reservoirs to human campylobacteriosis through integrated One Health genomic surveillance in Ireland, 2017–2025, **Pedro Pinto**

e. Shared resistance plasmids in third-generation cephalosporin-resistant Escherichia coli from livestock, meat and humans in Spain, **Carlos Serna**

f. Farm-animal exposure and OXA-48-like carbapenemase-producing Enterobacterales carriage among Arab patients in northern Israel: a case-control study, **Ronza Najjar**

POSTER TOUR

DAY 1 - *18 November*

Poster tour 3

Surveillance of vaccine-preventable diseases

moderated by Esther Kissling

15.55-16.55 CET | M1

a. Maternal pertussis vaccination coverage and sociodemographic and maternal factors associated with non-uptake in Sweden: preliminary results from a nationwide cohort study, **Kévin Lasmi**

b. Spatiotemporal dynamics of measles resurgence in the EU/EEA: spatially independent outbreaks driven by national vaccination gaps, 1999–2024, **Dimitrios Kontogiannis**

c. Evaluating Measles Surveillance toward Elimination in North Rhine- Westphalia, Germany, 2024 and 2025, **Connor Moran**

d. Novel serology assay reveals large unascertained community burden of pertussis in children in North Wales, UK during the 2023-2024 epidemic., **Jennifer Howard**

e. Analysis of global mpox outbreak dynamics during the 2024-2026 Public Health Emergency, **Florence Gyembuzie Wongnaah**

f. Re-emergence of diphtheria in Germany: Differences between imported and autochthonous cases with C. diphtheriae, 2017–2025, **Lena Schneider**

g. Rapid escalation and sustained transmission of measles in an under-vaccinated community, Enfield, London, 2026, **Erjola Hani**

Poster tour 4

Surveillance, outbreaks and high-risk populations

moderated by Agoritsa Baka

15.55-16.55 CET | M1

a. Evaluation of the Cerebrospinal Meningitis surveillance system: Lessons from Sokoto State, Nigeria, **Juliet Namugenyi**

b. Outbreaks in asylum seeker accommodations in Germany, 2015-2025, **Inessa Markus**

c. Closing the Diagnostic Gap: Determinants of Timely Mpox Diagnosis and Genomic Sequencing under the 7-1-7 Framework in the Democratic Republic of the Congo, 2022–2025, **Pride Tanyi Bobga**

d. Spatial heterogeneity in RSV-SARI incidence in children at the city level: sociodemographic and epidemiological determinants of urban hotspots and coldspots, Lyon, France, 2012–2025., **Jean-Sebastien Casalegno**

e. Unrelated or linked? Integrating whole genome sequencing into epidemiological investigation to unravel a measles outbreak in Utrecht, the Netherlands, 2024, **Liza Coyer**

f. Predominance of antimicrobial-resistant serotype V Streptococcus agalactiae among colonised pregnant women in Poland, **Maksymilian Kempa**

g. Evaluation of Acute Encephalitis Syndrome (AES) Surveillance under the National Digital Disease Surveillance Platform, Assam, India, 2025, **Ashwini Yadav**

POSTER TOUR

DAY 1 - *18 November*

Poster tour 5

Burden of respiratory diseases

moderated by Johanna Young

15.55-16.55 CET | M1

a. Describing age-specific respiratory syncytial virus incidence and establishing an epidemiological baseline in Croatia (2017–2025), **Andela Vrbica**

b. Increased risk of human metapneumovirus (hMPV) infection during the first two years of life among children born <28 weeks preterm in Lyon, France, 2012–2025, **Laura Rojas-López**

c. Drivers, impact and costs of respiratory illness on the national health service (NHS) workforce over winter 2025/26 in the United Kingdom, **Sarah Foulkes**

d. COvid-19 among HEalth caRE professionals in the Nordic CountriEs (COHERENCE II), **Débora Gräf**

e. Differential Severity of Acute Respiratory Infection Outbreaks by Pathogens in Nursing Homes, **Gladys Lee**

f. Epidemiology of Respiratory Syncytial Virus and risk factors for severe outcomes among children <2 years hospitalised with respiratory infection in Skopje, Republic of North Macedonia, October 2025–April 2026, **Iris Finci**

g. Population-level burden of rhinovirus, influenza, and SARS-CoV-2 among adults: A multi-season analysis in the Netherlands, 2022–2025, **Gesa Carstens**

Poster tour 6

Communication and behavioural aspects

moderated by Ettore Amato

15.55-16.55 CET | M1

a. Awareness, attitude and practices related to brucellosis among female pastoralists of Pakistan: A one health perspective, **Olivier Sparagano**

b. Triangulated digital surveillance during a suspected cholera alert in Poland., **Maja Romanowska**

c. Comparison of vaccination determinants across seven diseases in Germany: a cross-sectional study, **Paula Dau**

d. High Awareness, Low Action: Gaps in Cervical Cancer Screening and HPV Vaccination Among Women Living with HIV in North Central Nigeria, **Oluwaseun Ojomo**

e. Measles outbreak in Antwerp, Belgium 2025: targeted response in an under-vaccinated community and lessons from an after-action review, **Aaron Devos**

f. Knowledge, attitudes and practice towards HPV vaccination among students, Kazakhstan, 2023, **Arystan Balmagambetov**

POSTER TOUR

DAY 1 - *18 November*

Poster tour 7

SDG-targeted infections

moderated by Aura Georgina Aguirre-Beltran

15.55-16.55 CET | M1

a. A pre- and post-intervention analysis of the TB surveillance system in Spain, 2018-2024, **Allegra Priya Chatterjee**

b. Performance Evaluation of Computer-Aided Detection for Triage of Chest X- Rays in Tuberculosis Screening in Ukraine, **Ludmila Kasatkina**

c. Hepatocellular carcinoma mortality following hepatitis B and C infection in Slovenia, 2016–2022: national datasets linkage study to monitor progress towards hepatitis B and C elimination, **Eva Leban**

d. Genomic epidemiology and insights on the resistance profile of Treponema pallidum in Portugal, **Diogo Ramos**

e. Increasing trends in reported gonorrhoea incidence in young adults in Slovenia, 2005-2024, **Matija Mozetič**

f. Optimising the PEP to PrEP Transition: Policy Relevant Evidence from a Structured Prevention Pathway in a Lisbon Hospital, **Bárbara Cardoso**

g. Tuberculosis among people already registered as contacts: linking tuberculosis centre, hospital and notification records in northern Portugal, 2024–2026, **Pedro Sebastiao**

Poster tour 8

Healthcare-associated infections

moderated by Vladimír Príkazský

15.55-16.55 CET | M1

a. Temporal patterns of severe Clostridioides difficile infections in Germany, 2016– 2025, **Lukas Herrmann**

b. High background noise masks transmission: whole genome sequencing as a key tool for outbreak assessment of Pseudomonas aeruginosa in a high-incidence setting, **Julia Kuhn**

c. Emergence of NDM-1 and OXA-48 producing Klebsiella pneumoniae ST395 circulating within and between hospitals with links to Ukraine, Germany, 2023- 2025, **Claudia Ruscher**

d. The association between comorbidities and recurrent urinary tract infections in Dutch long-term care residents: a longitudinal cohort study, **Charlotte de Bruijn - Onstwedder**

e. Trends in surgical site infection incidence in Piedmont, Italy, 2015–2024: findings from a regional surveillance programme, **Ilaria Long**

f. Compliance with minimum requirements for infection prevention and control programs across healthcare facilities in Nigeria, 2024, **Paul Wekunda**

g. Escalating Antimicrobial Resistance and Healthcare-Associated Infections in Greek ICUs: A Ten-Year Longitudinal Surveillance Study, **Eleni Jelastopulu**

POSTER TOUR

DAY 2 - *19 November*

Poster tour 9

One Health and food- and water-borne diseases

moderated by Joël Mossong

15.55-16.55 CET | M1

a. Environmental detection of Campylobacter spp. in soil during a childcare-associated gastroenteritis cluster, **Pedro Mendes Reis**

b. Increasing incidence of human tularaemia despite stable epidemiological patterns, Baden-Wuerttemberg, Germany, 2012–2025, **Sabrina Nothdurfter**

c. Cluster of human leptospirosis associated with environmental exposure in southern Spain, 2025/2026., **Blanca López-Villalba**

d. Cholera outbreak investigation in an urban setting: transmission dynamics and response gaps in Nairobi County, Kenya, March–April 2025, **Habiba Mohamed**

e. Unraveling Legionellosis Dynamics in the Lazio Region: Effects of Individual, Territorial and Meteorological determinants, **Martina Spaziante**

Poster tour 10

Preparedness and response

modertaed by Cristina González Pérez

15.55-16.55 CET | M1

a. Developing an evaluation framework for Epidemic Intelligence from Open Source (EIOS): a qualitative analysis of stakeholder priorities, **Imme Roewer de Porto**

b. Childhood immune imprinting and seasonal influenza-driven boosting of cross-reactive avian influenza A antibody landscapes in adults: evidence from a German population-based longitudinal cohort study, 2020-2024, **Yaw Awuku-Larbi**

c. Pooled testing for SARS-CoV-2 surveillance in schools: real-world evaluation of transmission control, testing resources, and educational disruption, **Elisabetta Colosi**

d. Characterisation of reporting interval for human cases of avian influenza A(H7N9), China, 2013–2017: a retrospective time-to-event analysis, **Chiamaka Jibuaku**

e. Risk Prioritisation of emerging infectious diseases for preparedness planning: The Belgian example, 2025-2026, **Clara Mazagatos**

f. Impact of Youth Jubilee 2025 on Emergency Department attendances in Rome: a controlled interrupted time series analysis using syndromic surveillance data, **Jasleen Singh**

g. After Action Review of the 2025 West Nile Virus Outbreak in the Lazio Region, Italy, **Ilaria Mussetto**

POSTER TOUR

DAY 2 - *19 November*

Poster tour 11

Surveillance and prevention of respiratory viruses

moderated by Kim Blom

15.55-16.55 CET | M1

a. A fine-tuned foundation model for influenza forecasting across 78 countries, benchmarked against Italy's collaborative forecasting hub, **David Hauser**

b. Vaccine effectiveness against influenza A(H3N2) infection and hospitalization in recommended target groups over four seasons: A Spanish test-negative study using surveillance data from 2022/23 to 2025/26**, Gloria Pérez Gimeno**

c. Estimating the start of the influenza season using the Moving Epidemic Method (MEM) and GLM-based outbreak detection algorithms**, Matthew Hoyle**

d. Serological evidence of substantial Respiratory Syncytial Virus infection burden among older adults residing in Swedish long-term care facilities, **Preeti Moar**

e. Impact on RSV hospitalisations among infants in Sweden following the introduction of nirsevimab, season 2025-2026, **Rakel Brodin**

f. Temporal trends and sociodemographic predictors of maternal influenza vaccination in Region Stockholm: A register-based cohort study**, Hanna Josefsson**

g. Uncovering Human Metapneumovirus Burden of Disease through the Belgian Severe Acute Respiratory Infections Surveillance Network, **Peace Mpakaniye**

Poster tour 12

Burden and prevention of vaccine-preventable diseases

moderated by Ivo Foppa

15.55-16.55 CET | M1

a. Evaluation of Nirsevimab effectiveness in preventing RSV infection in infants under one year during the first two RSV seasons following its introduction in primary and secondary care, **Annika Erdwiens**

b. Epidemiological profile and factors associated with death from meningococcal disease in the municipality of Belém, Pará State, northern Brazil, 2024–2025, **Camila Neves**

c. Coverage and timeliness for respiratory syncytial virus (RSV) immunisation and rotavirus vaccination in the National Immunisation Programme in the Netherlands, **Minke Holwerda**

d. Measles outbreak in an occupational setting in Spain: informing elimination strategies, **Esteban Aznar**

e. Rotavirus epidemiology in the Netherlands before implementation of rotavirus vaccination, 2014-2023, **Marije Bootsma**

f. RSV-related hospitalisations in infants averted by nirsevimab during the first implementation seasons in Spain and Portugal, **Sandra Campos Mena**

POSTER TOUR

DAY 2 - *19 November*

Poster tour 13

Data systems and surveillance

moderated by Edward van Straten

15.55-16.55 CET | M1

a. Nationwide epidemiology and machine learning-derived phenotypes of sepsis-associated delirium in Spain, 2017–2022, **Rosa María Cobo Zubia**

b. Data quality and reporting timeliness in Uzbekistan's infectious disease surveillance system: a baseline assessment for further strategical development, **Dariya Abzulinova**

c. From data to action: a regional epidemiological bulletin driving public health action in the Midlands region, England, **Amand Madera**

d. Completeness of laboratory surveillance for four bacterial meningitis pathogens in the Netherlands, 2015-2024, **Boas van der Putten**

e. Epidemiological trends in non-polio enterovirus infections in England, 2012–2025, **Tishya Venkatraman**

f. Extraordinary excess mortality detected by EuroMOMO during the severe heatwave affecting Europe in June-July 2026, **Sarah Kristine Nørgaard**

Poster tour 14

Surveillance and outbreak investigations of AMR

moderated by Vivian Leung

15.55-16.55 CET | M1

a. Prevalence of MRSA nasal colonisation in patients undergoing elective total joint arthroplasty: implications for targeted preoperative screening, **Nicola Sardi**

b. Investigating the effects of methodological de-duplication rules on routine bacterial antimicrobial resistance surveillance indicators in Germany 2023–2024, **Pontus Hedberg**

c. Consumption of antimicrobials relevant for multidrug-resistant infections in Piedmont, Italy, 2023–2024: regional trends and implications for antimicrobial stewardship, **Vanessa Imbriano**

d. Regional WGS surveillance identified a clinically relevant MDR Klebsiella pneumoniae ST15 cluster with possible intra-facility transmission, **Welmoed Silvis**

e. 30-day fatality of Klebsiella pneumoniae bloodstream infections in Emilia- Romagna, Italy, 2018-2025: a population-based study., **Davide Tarditi**

f. Prevalence of carbapenemase production in Enterobacterales with elevated imipenem MIC and low meropenem MIC in the Netherlands, **Rony Zoetigheid**

g. First reported outbreak of carbapenemase-producing Enterobacterales in a Belgian nursing home: investigation and management, **Hilde Vochten**

POSTER TOUR

DAY 2 - *19 November*

Poster tour 15

Artificial intelligence in public health

moderated by Angelo D'Ambroso

15.55-16.55 CET | M1

a. Scaling One Health Surveillance: AI-Driven Predictive Modeling of AMR Trends Using Municipal Wastewater in Pirkanmaa, Finland, **Saeed Ahmad**

b. Evaluating AI-assisted surveillance of healthcare-associated infections using a standard European point prevalence study in a regional hospital, the Czech Republic, 2025, **Jana Prattingerová**

c. Operationalizing LLM-based surveillance of healthcare-associated bloodstream infections: a data governance and de-identification framework, **Costanza Vicentini**

d. Artificial Intelligence for Healthcare-Associated Infection prediction in Adult Intensive Care Units: a systematic review of prognostic models, **Antonio Sciurti**

e. Are time series foundation models the new frontier for operational epidemic forecasting in Europe?, **Stefania Fiandrino**

f. All hype and no help? Assessing readiness for AI within a UK public health institute field epidemiology service, January 2026, **India Clancy**

g. Validation of locally deployed open-source LLMs for SARI detection in Spanish hospital records, **Susana Monge**

Poster tour 16

Late breakers (1)

moderated by Vasco Ricoca Peixoto

15.55-16.55 CET | M1

a. Increasing Macrolide Resistance in Invasive Group A Streptococcal Infections: A Multiregional Surveillance Study in the Netherlands, **Thera Anne Mare Peeters**

b. Moderate end-of-season influenza vaccine effectiveness in 2025/26, but measurable protection against drifted A(H3N2) in Bavaria, Germany, **Eva Martschew**

c. Hand, foot, and mouth disease remains above pre-pandemic incidence in Catalonia, Spain: paediatric primary care surveillance through August 2026, **Víctor L. de Rioja**

d. Rapid late-summer resurgence in COVID-19 notifications with accelerated reinfections and a younger case profile, Castile and León, Spain, 2026, **Morella Pierina Tello Zapata**

e. The live shingles vaccine and primary care antimicrobial prescribing in the UK: A retrospective population-based cohort study, **Rebecca Walshe**

POSTER TOUR

DAY 3 - *20 November*

Poster tour 17

Surveillance of food- and water-borne diseases

moderated by Kostas Danis

14.15-15.15 CET | M1

a. Genomic surveillance for Salmonella spp. and Shigella spp. in Belgium in the era of multiplex PCR diagnostics, **Pauline Hinnekens**

b. Drivers of Rising Legionella Notifications in Southern Finland, 2020–2025: disentangling Diagnostic, Climatic, and Seasonal Influences, **Julia Jaeger**

c. Whole-Genome Sequencing (WGS) Uncovers Multiple Concurrent Salmonella Transmission Pathways and Recognizes Greater Disease Spread Overlooked by Conventional Surveillance, Moldova, 2025, **Irina Iaroslavtev**

d. Genomic surveillance of invasive non-typhoidal Salmonella (iNTS) in Belgium, 2014-2025: Hidden danger of uncommon serovars, **Julia Steger**

e. Advancing Legionella pneumophila genomic surveillance with a high-resolution cg/wgMLST schema for outbreak detection and investigation, **Vítor Borges**

f. Evaluation of the surveillance system for campylobacteriosis, Portugal, 2020-2024: timeliness and external completeness, **Joana Vidal-Castro**

g. Cryptosporidiosis reaches unprecedented levels in France during the summer of 2026: is climate warming playing a role?, **Damien Costa**

Poster tour 18

Surveillance of COVID-19 and influenza

moderated by Margreet te Wierik

14.15-15.15 CET | M1

a. Investigating post-pandemic regime shifts in influenza epidemiological patterns: a multinational analysis, **Styliani Evaggeli**

b. Factors associated with undertaking community respiratory testing amongst symptomatic FluSurvey participants in England, 2024-2025, **Jin-Min Yuan**

c. Influenza in Malta (2017–2025): Post-Pandemic Shifts in Incidence and Seasonality, **Norman Galea**

d. Severe Acute Respiratory Infection Surveillance in North Macedonia, 2023–2025: Risk Factors for RSV Infection, Influenza Infection and ICU admission in Children, **Enkela Pollozhani**

e. Wastewater-based surveillance for SARS-CoV-2 across six European countries: system heterogeneity, country use-cases and implications for comparison, **Niamh Tiernan**

f. Influenza-like illness defined by clinical diagnostic coding: Positive predictive value for influenza and COVID-19 post-pandemic, **Robert Norrie**

g. Comparison of Belgian COVID-19 mortality between epidemiological surveillance and death certificates for the years 2020, 2021 and 2022, **Serge Nganda**

POSTER TOUR

DAY 3 - *20 November*

Poster tour 19

Vaccine-preventable diseases: evidence to practice

moderated by Zvjezdana Lovrić Makarić

14.15-15.15 CET | M1

a. Effectiveness of nirsevimab against hospitalisation with laboratory-confirmed respiratory syncytial virus in children aged <24 months, European multicentre study, September 2025—March 2026, **Lore Merdrignac**

b. Vaccine efficacy and safety of the adjuvanted herpes zoster subunit vaccine in immunocompromised adults aged 18-49 years: a systematic review to inform a German vaccination recommendation, **Sophie Hermanns**

c. Factors associated with absence of an identified epidemiological link among measles cases in an elimination setting: implications for case and contact investigation, Portugal, 2015-2025, **Raquel Eusébio**

d. Feasibility of a target trial emulation study to estimate vaccine effectiveness of the 2023 and 2024 autumn vaccine doses against hospitalisation due to COVID-19 in six EU/EEA countries: a VEBIS-EHR network study, **Alexandre Blake**

e. Determinants of vaccination intention in Romania: findings from Wave 2 of the People's Voice Survey using the 5Cs model of vaccination acceptance, **Bianca Enciu**

f. Impact of influenza vaccination in adults aged ≥65 years in Portugal: 2022/23-2024/25 seasons estimates, **Irina Kislaya**

g. Determinants of Mpox vaccine uptake in men who have sex with men and transgender persons during regular consultations at a Dutch Sexual Health Centre, **Joeri van Straalen**

Poster tour 20

Vector-borne diseases

moderated by Joana Haussig

14.15-15.15 CET | M1

a. Emerging vector-borne infectious disease risks: awareness gaps among Dutch travellers in Europe, **Iris Scholte**

b. Epidemiological Trends and Climatic Determinants of Human Leishmaniasis in Lazio Region, 2015–2025, **Francesco Vairo**

c. DENV-2 autochthonous transmission patterns in Italy: evidence from 2024 outbreaks, **Carla Molina Grané**

d. Clinical and epidemiological characteristics of West Nile Virus in Northern Cyprus: A retrospective case series (2019–2024), **Ertan Direnç**

e. Immunogenicity, clinical efficacy and safety of Malaria vaccines in children: a systematic review and meta-analysis, **Katsiaryna Bashlakova**

f. Autochthonous dengue outbreak in Tuscany, Italy: geographically dispersed cases linked to a common exposure site, August to September 2026, **Chiara Sacco**

POSTER TOUR

DAY 3 - *20 November*

Poster tour 21

Quantitative methods

moderated by Javier del Águila Mejía

14.15-15.15 CET | M1

a. Cost-effectiveness of MenB vaccination to control the spread of gonorrhoea in the UK, **Soeren Metelmann**

b. A hidden Markov model reveals environmental persistence and inter-department transfers as key drivers of drug-resistant Citrobacter spp. in a hospital, **Taeyong Lee**

c. Decrease in prevalence of sexually transmitted chlamydia infection among 15–29 years old individuals during 2009–2024 in Sweden: a mathematical modelling study, **Inga Velicko**

d. Cost-Effectiveness and Uncertainty Analysis of Ebola Vaccination Strategies in Children and Adolescents, **Marianna Zarro**

e. Economic evaluation of a bivalent respiratory syncytial virus prefusion F vaccine for older adults in Sweden: cost-effectiveness and budget impact, **Andreas Palmborg**

f. Optimal epidemic control: a nonlinear programming approach, **Sandra Montes-Olivas**

Poster tour 22

Social determinants of infectious diseases

moderated by TBC

14.15-15.15 CET | M1

a. Ethnic inequalities in respiratory virus epidemics in England: a mathematical modelling study, **Alexis Robert**

b. Barriers to mpox vaccination among rural residents in Manitoba and Alberta, Canada, **Mikayla Hunter**

c. Socioeconomic and demographic disparities in HPV awareness and cervical cancer prevention in rural Romania: findings from a large population-based survey, **Florina Ionete**

d. Screening and attitudes towards hepatitis C among marginalised populations in high-risk districts of southern Slovakia: results from 2024–2025, **Zuzana Jányová**

e. Correlates of Seroconversion among HIV-exposed Infants in Three High-burden Counties in Kenya, **Lucy Munyeki**

f. Epidemiological Analysis for Sexually Transmitted Infections in migrant population in Catalonia using multimodal healthcare data, **Nikolaos Karanikolaou**

POSTER TOUR

DAY 3 - *20 November*

Poster tour 23

Evidence to practice

moderated by XXX

14.15-15.15 CET | M1

a. Declining effectiveness of contact tracing during the emergence of the SARS-CoV-2 Omicron variant in Östergötland, Sweden, November 2021 – February 2022, **Marie Jansson Mörk**

b. Systematic review of effectiveness of wide-spread population-based laboratory testing strategies during the COVID-19 pandemic, **Eeva Broberg**

c. Evaluating usage and impact of English AMR & HCAI surveillance outputs to inform future improvements, **Kathrin Loosli**

d. Sporadic community-acquired Legionnaires' disease by distance to cooling towers; To what extent does distance matter?, **Kevin Wassing**

e. The use of a multi-stream evidence synthesis to revise national Shiga toxin-producing Escherichia coli (STEC) infection guidelines on microbiological clearance in Norway, 2026 , **Liz Ertzeid Ødeskaug**

f. Mind the gap: Rebound of post-pandemic respiratory infections in children born during the COVID-19 pandemic, **Henrik Mellström Dahlgren**

g. Strengths, weaknesses, opportunities and threats (SWOT) of national surveillance systems for infectious diseases in Germany, **Paulina vom Felde genannt Imbusch**

Poster tour 24

Late breakers (2)

moderated by Howard Needham

14.15-15.15 CET | M1

a. Epidemiological and Molecular Investigation of Enteroviral Meningitis in the West Midlands, England, 2026, **Georgia Davidson**

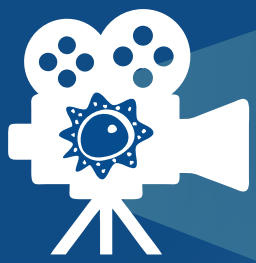
b. Monitoring of tendinitis and tendon rupture after ciprofloxacin use during the meningococcal B outbreak in Kent, 2026, **Julia Stowe**

c. Persistent environmental contamination in a food premises linked to two neonatal listeriosis cases in England, 2026, **Juliette Cavaye**

d. Severe Shiga toxin-producing Escherichia coli (STEC) outbreak among young children linked to a petting farm, Belgium, 2026, **Valeska Laisnez**

e. Time to population access for new immunisations across Europe: a 30-country analysis, **Anna Vicere**

f. From guidance to practice: contact management across European countries during an international Andes virus infection outbreak on a cruise ship, May-June 2026, **Esteban Aznar**



CineSCAIDE

DAY 1

10:30 (51 mins)
Mind the gap: advancing trustworthy AI in public health

12:00 (92 mins)
The hand hygiene paradox: why a simple solution remains so hard to implement

13:45 (41 mins)
Rapid Risk Assessment in action in public health emergencies

15:00 (95 mins)
CNN documentary: "Unseen Enemy"
Film screening (Radboudumc license, purchased by Alma Tostmann, Radboud University, Netherlands)

DAY 2

08:00 (51 mins)
Mind the gap: advancing trustworthy AI in public health

10:30 (41 mins)
Rapid Risk Assessment in action in public health emergencies

12:00–15:00
Break

15:00 (95 mins)
CNN documentary: "Unseen Enemy"
Film screening (Radboudumc license, purchased by Alma Tostmann, Radboud University, Netherlands)

16:30 (30 mins)
Discussion and reflections on "Unseen Enemy",
moderated by Alma Tostmann, Radboud University, Netherlands

DAY 3

08:00 (95 mins)
CNN documentary: "Unseen Enemy"
Film screening (Radboudumc license, purchased by Alma Tostmann, Radboud University, Netherlands)

10:30 (41 mins)
Rapid Risk Assessment in action in public health emergencies

12:00 (51 mins)
Mind the gap: advancing trustworthy AI in public health

13:45 (92 mins)
The hand hygiene paradox: why a simple solution remains so hard to implement



Sessions & Speakers

The hand hygiene paradox: why a simple solution remains so hard to implement

MODERATOR

Christian Giske, Head of Section Antimicrobial Resistance and Healthcare-Associated Infections, ECDC

SPEAKERS

Birgitta Lytsy, Medical specialist Infection Prevention and Control, Public Health Agency of Sweden

Ana Paula Coutinho Rehse, Technical Officer, WHO Regional Office for Europe, Denmark

Theoklis Zaoutis, Department Chair and Professor, National and Kapodistrian University of Athens, Greece

Ermira Tartari, Infection Prevention and Control Professional, Senior Lecturer, Faculty of Health Sciences, Mater Dei Hospital, Malta

Katerina Mougkou, Expert in Antimicrobial Resistance and Healthcare-Associated Infections, ECDC

Mind the gap: advancing trustworthy AI in public health

Anca Moruzov, Group Leader Artificial Intelligence, Data and Information Management, ECDC

Angelo D'Ambrosio, Expert Healthcare-Associated Infections, ECDC

Quim Berenguer Jornet, Chair of the EUAN Working Group on AI Lead of AI Implementation & Digital Strategy Solutions, EMA

Rapid Risk Assessment in action in public health emergencies

Agoritsa Baka, Principal expert, Emergency Preparedness and Response, ECDC

Jorgen Stassijns, Head of Service Crisis Preparedness & Response, Sciensano, Coordinator, Belgian Risk Assessment Group, Belgium

Bernard Bottex, Crisis coordinator, EFSA

Rukshanda Ahmad, Director and Medical Advisor, Risk Assessment Hub, Public Health Agency of Canada

Savina Stoitsova, Epidemiologist, WHO Health Emergencies Programme

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 2026 will feature five plenary sessions, chaired by the ESCAIDE Scientific Committee.

Scientific Committee



PIOTR KRAMARZ

ECDC

Chief Scientist & Head of Unit Scientific Evidence and Communication | Chair of ESCAIDE Scientific Committee

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.



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.



ANGELIKI MELIDOU

ECDC

Principal Expert Respiratory Viruses | Directly transmitted and Vaccine-preventable Diseases Unit

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.



BRUNO CIANCIO

ECDC

Head of Unit | Directly transmitted and Vaccine-preventable Diseases Unit

Bruno Ciancio 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 focussed 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 Ciancio has authored about fifty scientific articles in peer-reviewed journals and a book chapter on influenza surveillance.



HANA ORLÍKOVÁ

Czech Republic

Senior epidemiologist | Department of Infectious Disease Epidemiology of the Center for Epidemiology and Microbiology |National Institute of Public Health

Hana Orlíková is a medical epidemiologist. As a senior epidemiologist, she specializes primarily in vector-borne diseases, surveillance, outbreak investigation, training in epidemiology and public health, One Health, and vaccinology. She participates in European projects focused on research of vector-borne diseases and surveillance. She cooperates with the ECDC as the National Focal Points. Since 2011, she has been nominated as the National Coordinator of the Coordinating Competent Body.

She is a medical doctor and, after graduating in 1991, worked as a field epidemiologist and public health specialist at the Regional Public Health Authority of the Moravian-Silesian Region in the Czech Republic until 2008. From 2008 to 2011, she worked at the National Institute of Public Health – National Institute of Hygiene in Warsaw, Poland, where she completed the ECDC European Programme for Intervention Epidemiology Training (EPIET) in 2010. Since 2011, she has been working at the Department of Infectious Disease Epidemiology of the Center for Epidemiology and Microbiology of the National Institute of Public Health in Prague, Czechia. Since 2023, she has been an external lecturer at the Third Faculty of Medicine of Charles University in Prague, at the Department of Epidemiology and Biostatistics.



JOSÉ CANEVARI

ECDC

Principal Expert Mathematical Modelling | Scientific Evidence and Communication Unit

José Canevari is a veterinary epidemiologist with a PhD in mathematical modelling and quantitative analytical methods. He is currently a Principal Expert in Mathematical Modelling at the European Centre for Disease Prevention and Control (ECDC) where he works on the application of statistical and mathematical models to support public health decision-making. Prior to joining ECDC, he held senior roles at the Victorian Department of Health in Australia where he led modelling and analytical epidemiology activities during the COVID-19 pandemic, including vaccine effectiveness studies, scenario modelling, and network-based analyses. He has also worked as a consultant at the World Health Organization Regional Office for Europe and as an operational epidemiologist in national emergency response programmes in New Zealand and Argentina. His research interests include infectious disease modelling, vaccine-preventable diseases, outbreak preparedness, and the burden of communicable diseases.



KOEN BLOT

BELGIUM

Head of Infectious Diseases Epidemiology | Sciensano

Koen Blot is a medical doctor specialised in general internal medicine (2020). He obtained his PhD degree in epidemiology and prevention of infectious diseases (2021) at the University of Ghent, Belgium.

He made the transition from clinical to public health work after the first COVID-19 pandemic wave in 2020, coordinating the epidemiological surveillance of hospitalised COVID-19 patients. In 2021 he took the position as Head of Infectious Diseases Epidemiology at Belgium's National Public Health Institute (Sciensano).

From 2021 onwards he has developed and been implementing an operational plan for reinforcing Belgium's capacity for infectious diseases surveillance during crisis and peacetime expanding from not only COVID-19 but other relevant pathogens for public health. This includes transversal domains such as digitalisation and integration of surveillance systems, preparedness and risk evaluation, and academic collaboration across the surveillance pillars at the level of sentinel laboratories, general physicians, hospitals and wastewater-based epidemiology.



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.



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'.



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 (HERA).



CARLOS DAS NEVES

EFSA

Chief Scientist | Executive Director Office

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.

Plenary speakers



PLENARY A

Crises and challenges shaping the landscape of public health: how far we've come

SHINGAI MACHINGAIDZE

UNITED KINGDOM

Head of Africa Strategy and Engagement / Co-Chair STEG | Coalition for Epidemic Preparedness Innovations (CEPI) / International Pandemic Preparedness Secretariat (IPPS)

Shingai Machingaidze is the Head of Africa Strategy and Engagement at the Coalition for Epidemic Preparedness Innovations (CEPI). She is an epidemiologist and public health specialist with over a decade of experience building the capacity of Africa-based scientists and institutions. She previously served as Acting Chief Science Officer for Africa Centres for Disease Control and Prevention (Africa CDC) and led the Conference on Public Health in Africa (CPHIA) Secretariat, following earlier roles at the European & Developing Countries Clinical Trials Partnership (EDCTP), South Africa's Medical Research Council, and the University of Cape Town. She has authored many publications in leading medical journals and serves on several global health advisory boards, including a role as Co-Chair of the International Pandemic Preparedness Secretariat's Science and Technology Expert Group. Her expertise includes strategic engagement, planning and support of large public health programmes, and the management of strategic partnerships and engagements with national, regional and international agencies.



PLENARY B

The science behind EU health security

GIANFRANCO SPITERI

ECDC

Principal Expert/Group Leader Epidemic Intelligence | European Centre for Disease Prevention and Control (ECDC)

Gianfranco Spiteri is the Head of the Global Epidemic Intelligence and Health Security Section at the European Centre for Disease Prevention and Control (ECDC). Originally from Malta, he graduated as a medical doctor in 2003 and trained as an EPIET fellow before returning home to work in infectious disease surveillance and control. He joined ECDC in 2010, going on to coordinate surveillance of sexually transmitted infections (STI) for eight years while also supporting emergency responses to outbreaks including Zika, Ebola, COVID-19 and hantavirus. Gianfranco later became Group Lead of the Epidemic Intelligence team at ECDC, before stepping into his current role in 2025.



HELEN BROWN

IRELAND

Director | Safinea

Helen Brown is the Director of Safinea and a highly experienced researcher, specialising in the use of AI methods in political decision-making, with a focus on accounting for uncertainty, reducing bias, and ensuring representation. Between 2017 and 2023, she worked as a mathematical modeller at ECDC and the European Commission, advising decision-makers on pandemic policy including social distancing, border closures and vaccine strategy. An applied mathematician, she has advanced the use of Bayesian methods for inferring the causes of health outcomes and is committed to promoting understanding of non-linearity and dynamic systems in policy decisions. She holds degrees in Physics and Biomolecular Science from Imperial College London and in the Control of Infectious Diseases from the London School of Hygiene & Tropical Medicine.



MAGDALENA ROSIŃSKA

POLAND

Professor | National Public Health Institute of Poland

Magdalena Rosińska is a Professor at the National Institute of Public Health (NIH) – National Research Institute of Poland in Warsaw, where she has worked since 2002. She is a physician and epidemiologist specialising in public health data analysis, with research focused on HIV and viral hepatitis. Drawing on an interdisciplinary background in medicine, biostatistics and mathematics, she combines classical epidemiological approaches with modern statistical techniques, such as missing data imputation, reporting delay analysis, and Bayesian modelling. She collaborates with international institutions including ECDC, the World Health Organization (WHO), and the Medical Research Council (MRC) Cambridge on projects involving big data and digital tools for public health decision-making, making her one of the leading figures in data-driven epidemiology in Poland.



ANNICK LENGLET

NETHERLANDS

Senior Researcher | Radboudumc, Nijmegen

Annick Lenglet is an infectious disease field epidemiologist with over 25 years' experience working on the design, implementation and evaluation of surveillance systems, largescale emergency and outbreak response efforts, operational research related to hepatitis A and E, cholera, noma, antimicrobial resistance, mental health, and non-communicable diseases. She holds a masters degree from the London School of Hygiene and Tropical Medicine and the Spanish National School of Public Health and a PhD in Medical Sciences from Radboudumc. She completed the European Programme for Intervention Epidemiology Training (EPIET) in 2006. Annick currently works as a Senior Researcher for Radboudumc focusing on improving antimicrobial use and infection prevention and control in communities and health facilities globally. She is a senior consultant for the International Centre for AMR Solutions (ICARS). She has previously worked for Médecins Sans Frontières, the European Centre for Disease Prevention and Control (ECDC) and the World Health Organization.

PLENARY C

Communication to (re)build trust in science



TINA D PURNAT

UNITED STATES

Doctoral researcher | Harvard Chan School of public health

A Harvard DrPH (Doctor of Public Health) candidate (2027) and global health leader with two decades of experience at WHO and ECDC, Tina D. Purnat specialises in the intersection of technology, policy, and public health systems innovation. During the COVID-19 pandemic, she led the development of WHO's global approach to infodemic management and health misinformation response, work which has been adopted by health authorities worldwide. Her doctoral research extends this work to the local level, examining how the NYC Department of Health and Mental Hygiene can systematically learn from what its frontline community health workers observe about community trust, information gaps, and service barriers.

Tina is Vice President of the European Public Health Association (EUPHA) Global Health Section and co-chair of the Global Health Equity and Digital Transformation working group of the World Federation of Public Health Associations.

She is Associate Editor of JMIR Infodemiology, editorial advisor for Health Promotion International, and a Fellow of the Australasian Institute of Digital Health.

She holds affiliated visiting researcher appointments at the WHO Collaborating Centre for Health Literacy at the Technical University of Munich and at the Laboratory for Infodemiology and Infodemic Management at the University of Belgrade School of Medicine.



STEVEN VAN GUCHT

BELGIUM

Scientific Director | Sciensano

Steven Van Gucht is scientific director at the Belgian national public health institute, Sciensano, where he leads multidisciplinary activities in public health surveillance, microbiology and virology, with a strong focus on emerging infectious diseases and pandemic preparedness. His work is grounded in the One Health approach and translating science into actionable public health advice and communication. D, he served as a government advisor and national spokesperson and at present, he is the Belgian National Microbiology Focal Point for ECDC and a Visiting Professor at Ghent University, Belgium.



ANDERS HVIID

DENMARK

Head of Department | Statens Serum Institut

Anders Hviid is Head of the Department of Data Science and AI in Health at Statens Serum Institut and an affiliated professor at the PandemiX Center at Roskilde University in Denmark. He is an epidemiologist with a background in mathematics and physics. He has used Denmark's nationwide health registers to answer questions about the safety and effectiveness of vaccines. Many of his large population-based vaccine safety studies are internationally recognised, and many of them have shaped public debate. In 2019, he led a nationwide cohort study of 657 461 children that found no increased risk of autism associated with MMR vaccination. In 2025, he led a study of 1.2 million children that found no increased risk of autoimmune, allergic or neurodevelopmental conditions associated with aluminium-adsorbed childhood vaccines.

Hviid is also an active public communicator on social and in traditional media. Here he promotes solid scientific evidence on vaccines and infectious diseases. He has engaged directly with controversies surrounding vaccines in the United States, including responding publicly to criticism of his group's aluminium-in-vaccines study from the U.S. Health Secretary Robert F. Kennedy Jr. He values scientific rigour, transparency and open engagement to help protect and rebuild public trust in science.



PLENARY D

Learning from data: integrated surveillance of respiratory infections

NICK BUNDLE

ECDC

Principal Expert Respiratory Viruses

Nick Bundle completed specialty training in public health and a field epidemiology training programme in London and South-East England. In 2018, he moved to Stockholm to take up a position at ECDC, where he has focused primarily on vaccine-preventable diseases and respiratory viruses. From early 2020, he was assigned full-time to the COVID-19 response and developed many of ECDC's COVID-19 surveillance outputs. As a Principal Expert in ECDC's Respiratory Viruses section, he coordinates weekly EU-level surveillance of acute respiratory infections, working closely with experts from 30 European Union/European Economic Area (EU/EEA) Member States and WHO's Regional Office for Europe. He serves as the ECDC project manager for the European mortality monitoring activity, EuroMOMO, co-developed the joint European Respiratory Virus Surveillance Summary and has recently led the production of updated respiratory virus surveillance technical guidance for the EU/EEA.



JOHN BROWNSTEIN

UNITED STATES

Professor | Harvard Medical School, Boston Children's Hospital

John Brownstein, Ph.D is a Professor of Pediatrics at Harvard Medical School as well as Senior Vice-President and Chief Innovation Officer of Boston Children's Hospital. He directs both the Computational Epidemiology Laboratory and the Innovation and Digital Health Accelerator. Trained as an epidemiologist at Yale University, his research has been instrumental in facilitating the control and prevention of disease, improving public health practice, and engaging the public in health issues. As a pioneer in computational epidemiology, Dr. Brownstein's research is recognised for its translational impact, particularly through the development and application of Artificial Intelligence (AI), data mining, and citizen science. His innovative platforms, such as Vaccines.gov, Global.health, and HealthMap, serve millions annually and have received recognition from the National Library of Congress and the Smithsonian Institute in the US. His research was pivotal in the early detection and response to major disease outbreaks, including H1N1 in 2009, Ebola in 2014, Zika in 2015 and COVID in 2019.

Dr. Brownstein's contributions extend beyond academia into advisory roles for agencies including the US Department of Health and Human Sciences (HHS), the Demographic and Health Surveys Program (DHS), the US Food and Drug Administration (FDA), the US Department of Defense (DOD), the US Centers for Disease Control and Prevention (US CDC), WHO, and the White House. As Chief Innovation Officer, his efforts have catalysed the launch of dozens of new start-ups and unique partnerships with companies such as Google, Amazon, Apple, Uber, Instacart, Microsoft, and OpenAI. He also plays a leading role in shaping the hospital's comprehensive digital strategy, including the integration of AI to improve patient care.

Dr Brownstein has been honoured with the Presidential Early Career Award for Scientists and Engineers, the highest honour bestowed on outstanding scientists by the US government, the Lagrange Prize for international achievements in complexity sciences and an Emmy for his contributions to medical reporting for ABC News during the COVID-19 pandemic. Dr. Brownstein is co-founder of digital health companies Epidemico and Circulation and an ABC Medical News contributor. He has authored over 300 peer-reviewed articles on epidemiology and public health.



TRINE HESSEVIK PAULSEN

NORWAY

Senior Medical Adviser | Norwegian Institute of Public Health

Trine is a medical doctor and specialist in public health medicine who has been working as a Senior Medical Adviser at the Norwegian Institute of Public Health (NIPH) since 2018.

In the last few years, she has worked with a wide range of respiratory infection surveillance systems across the disease pyramid, using different data sources, more recently with a particular focus on health register data. She serves as public health lead for several respiratory infections and frequently contributes to public health communication as a media spokesperson and editor of NIHP's respiratory disease bulletin.

She currently coordinates the epidemiological surveillance of respiratory infections in Norway and serves as the ECDC National Focal Point for Viral Respiratory Diseases and Operational Contact Point for influenza. She will enter ECDC's EPIET Fellowship Programme in autumn 2026.



RON FOUCHIER

NETHERLANDS

Professor | Erasmus University Medical Centre

Ron Fouchier (1966) is professor of Molecular Virology at the Viroscience Department of Erasmus University Medical Centre, Rotterdam. He obtained a PhD in 1995 for HIV/AIDS research at the University of Amsterdam and then continued HIV work at the Howard Hughes Medical Institute, University of Pennsylvania School of Medicine in the US. In 1998, he started a molecular virology research line on respiratory viruses, in particular influenza, at the Erasmus University Medical Centre. His team contributed substantially to the identification and characterisation of various 'new' viruses, such as human metapneumovirus, human coronavirus NL63, SARS coronavirus, MERS coronavirus, and influenza A virus subtype H16. His current research is focused on respiratory viruses in humans and animals, antigenic drift, and influenza virus zoonoses, transmission and pandemics. Ron is an elected member of the Royal Dutch Academy of Sciences (KNAW) and the Royal Holland Society of Sciences and Humanities (KHMW). In 2006, he received the Heine-Medin award of the European Society for Clinical Virology, in 2013, the Huibregtsen award for top innovative science with societal impact, and in 2023, the KNAW Beijerinck Virology Prize. Fouchier coordinates the consortium that will act as the EU Reference Laboratory in Public Health in the field of Respiratory Viruses that is expected to commence operations s in 2027.

PLENARY E

Modelling for better public health decisions



MORITZ KRAEMER

UNITED KINGDOM

Professor of Epidemiology & Data Science | University of Oxford

Moritz Kraemer is a Professor of Epidemiology and Data Science at the University of Oxford, co-director of Pandemic Genomics at the Oxford Martin School, and co-founder of Global.health, an open-access platform for outbreak data and analytics. His interdisciplinary lab combines mathematical modelling, AI and machine learning, and phylodynamics for the study of infectious disease dynamics, focusing on climate-sensitive diseases such as dengue and Zika, as well as SARS-CoV-2, mpox and Ebola outbreaks. He frequently advises governments and organisations on disease surveillance, outbreak response, and biosecurity, and has been recognised with awards including a Branco Weiss Fellowship. Prior to taking up his position at Oxford, he held a fellowship in biomedical informatics at Harvard Medical School. He also holds a DPhil in Statistical Epidemiology from the University of Oxford.



JULIAN SAVULESCU

SINGAPORE

Professor in Medical Ethics | National University of Singapore

Professor Julian Savulescu is the Chen Su Lan Centennial Professor in Medical Ethics and Head of the Centre for Biomedical Ethics at the Yong Loo Lin School of Medicine, National University of Singapore (NUS). He is an award-winning ethicist and moral philosopher, trained in neuroscience, medicine, and philosophy and has held the Uehiro Chair in Practical Ethics at the University of Oxford since 2002.

He is a Visiting Professorial Fellow in Biomedical Ethics at Murdoch Children's Research Institute and Distinguished International Visiting Professor in Law at the University of Melbourne where he leads the Biomedical Ethics Research Group. Professor Savulescu is a Fellow of the Australian Academy of Health and Medical Sciences, a Fellow of the Australian Academy of the Humanities, and has received an honorary doctorate from the University of Bucharest. In 2026, he was elected as a Fellow of the Academy of Medical Sciences.



SHEETAL SILAL

SOUTH AFRICA

Director, Professor | Modelling and Simulation Hub, Africa (MASHA), University of Cape Town

Professor Sheetal Silal is an internationally recognised leader in the field of infectious disease modelling, with a particular focus on vector-borne and vaccine-preventable diseases and pandemic preparedness in Africa and globally. She is Director of the Modelling and Simulation Hub, Africa (MASHA) at the University of Cape Town and an Honorary Visiting Research Fellow in Tropical Disease Modelling at Oxford University. Her research focuses on developing and applying mathematical transmission models to understand disease dynamics, assess public health interventions, and support evidence-based decision-making. Her work spans African and global contexts, with a strong emphasis on translating complex modelling outputs into actionable insights for public health decision-making. She chairs WHO's Immunization and Vaccines-related Implementation Research Advisory Committee and is a Gates Foundation Calestous Juma Science Leadership Fellow. Through these roles, she contributes to global immunisation strategy and advances the use of modelling to inform health system planning, endemic disease control, and pandemic preparedness efforts. Professor Silal is deeply committed to building capacity in Africa by training the next generation of African modellers, fostering interdisciplinary collaboration, and strengthening networks across the continent to ensure that African countries are equipped to respond to both endemic diseases and emerging public health threats.

Plenary summaries

Plenary A

Crises and challenges shaping the landscape of public health: how far we've come

Day 1 - Wednesday 18 November, 9:30-10:30

Global public health leadership is becoming more distributed. Alongside WHO, regional institutions such as Africa CDC and ECDC are taking on greater responsibility for preparedness, surveillance, and outbreak response, raising pressing questions about how cooperation, equity, and evidence-driven decision-making can be sustained as influence spreads across regions.

Drawing on her experience in vaccinology, innovation, and international coordination, Shingai Machingaidze will reflect on the opportunities this shift brings, while taking into account geopolitical tensions' effects on data sharing and resources and the potential for deeper collaboration between bodies like Africa CDC and ECDC. The session invites the audience to consider how Europe and global partners can work effectively in a public health landscape shaped by several regional leadership centres, rather than one.

Plenary B

The science behind EU health security

Day 1 - Wednesday 18 November, 17:15-18:30

Health security in Europe rests on a scientific foundation, including epidemic intelligence, field epidemiology, modelling, and genomic surveillance, that must be embedded within coordination mechanisms before a cross-border threat emerges. When this infrastructure is in place, evidence can shape how quickly a threat is contained; when it isn't, response stalls.

This session examines the conditions under which science can do this work effectively. Geopolitical instability, disinformation, conflict, and fragile supply chains are placing new pressures on Europe's health security systems, while uneven laboratory capacity, workforce shortages, and investment gaps expose persistent weaknesses in preparedness. Drawing on lessons from recent outbreaks, speakers will explore how innovative surveillance, AI, and new analytical tools can support faster, more coordinated decision-making, and what it will take to close capacity gaps and strengthen collaboration without losing strategic leadership when crises hit.

Plenary C

Communication to (re)build trust in science

Day 2 - Thursday 19 November, 9:00-10:30

Trust in science is increasingly tested during epidemics and pandemics, where misinformation and disinformation spread alongside the outbreak itself. Effective risk communication depends not only on the accuracy of the message, but on how well it is tailored to different audiences and embedded within broader preparedness efforts from the outset, rather than added as an afterthought once a crisis is underway.

This session brings together experts from academia, public health, and health policy to share their experiences navigating mistrust in science and communicating under pressure. A panel discussion will follow, exploring how risk communication can be integrated into preparedness planning, tailored to different audiences, and adapted to today's digitalised media landscape, along with the tools and approaches best suited to different settings.

Plenary D

Learning from data: integrated surveillance of respiratory infections

Day 2 - Thursday 19 November, 17:15-18:45

The COVID-19 pandemic exposed the limits of siloed disease surveillance and accelerated efforts to build something more integrated. Since then, the EU/EEA has made significant progress in strengthening respiratory virus surveillance, moving toward systems that are harmonised, scalable, and sustainable across influenza, RSV, and SARS-CoV-2, rather than treating each threat in isolation.

This plenary will present ECDC's new operational framework and the key improvements it brings to respiratory surveillance across Europe. Experts will showcase advances in multi-source data integration, early threat detection, e-health and electronic health records, and the role of enhanced laboratory networks, including the European Union Reference Laboratories. Drawing on country experiences and practical challenges, the session will offer a forward-looking vision for an integrated, future-ready respiratory surveillance system, along with concrete recommendations for EU/EEA countries.

Plenary E

Modelling for better public health decisions

Day 3 - Friday 20 November, 9:00-10:30

Modelling of infectious diseases has become a cornerstone of public health decision-making. Yet using it in a meaningful and responsible way demands more than technical skill alone: it calls for methodological rigour, a grasp of the real-world contexts in which decisions unfold, and careful attention to the ethical implications of how models are built, interpreted, and applied.

This plenary brings together perspectives on innovation, implementation, and ethics to explore what responsible modelling looks like in practice. The session will begin with recent advances in infectious disease modelling, including the growing role of AI and data-intensive approaches, before turning to the realities of applying models in public health decision-making. It will close with a critical look at trust, transparency, and responsibility, identifying practical principles to strengthen the impact and integrity of modelling going forward.

ABSTRACT PRESENTATIONS

Abstract presentations are a key part of the ESCAIDE scientific programme. This year, we received a remarkable number of nearly 800 abstract submissions, encompassing both standard call and late breaker abstracts. Out of these, around 230 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 mins) and a moderator-led discussion and questions from the audience (5 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 8 minutes to discuss their work, which includes a short presentation by the speaker (~4 min), a moderator-led discussion with the audience (~4 min).

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Fireside Sessions

FIRESIDE SESSION 1

Respiratory viruses: evidence to practice

Developing a respiratory swabbing tool in FluSurvey to support pandemic preparedness in England

ABSTRACT ID: 687

Hannah Wolmuth-Gordon [1], ***Richard Pebody*** [1], ***Gayatri Amirthalingam*** [1], ***Becki Green*** [2], ***Gavin Dabrera*** [1]

1. *UK Health Security Agency,* ***2.*** *UKHSA*

Background

Participatory surveillance systems can supplement near real-time monitoring of community respiratory illness, including those not attending healthcare. FluSurvey is a UK participatory surveillance system, established in 2009, through which participants report weekly respiratory symptoms, healthcare use and social contacts. To support rapid public health assessment and monitoring of emerging respiratory viruses, we developed a respiratory self-swabbing feature. We aimed to assess the feasibility of FluSurvey swabbing to monitor community respiratory virus infections.

Methods

FluSurvey self-swabbing was deployed in England between January-March 2026. Adults reporting a recent sudden onset of Acute Respiratory Infection symptoms were eligible for a postal self-swabbing Covid-19, RSV and Influenza PCR test. We described swabbing timeliness and participant demographics to aid insight into willing participants. We evaluated participant feedback to understand their experiences and improve the process.

Results

40.3%(107/265) eligible participants requested test kits and 93.4%(100/107) were returned. Of these, 97.0%(97/199) had valid results; the median age was 61.1years (IQR:47.4-67.4), 67.0%(67/100) were female and 90.0%(90/100) were of white ethnicity. All nine regions in England were represented. The median time between requesting and doing the swab was 1.5days (IQR:1.2-2.5), from symptom onset to doing the swab was 4.0days (IQR:3.0-5.0) and from requesting a swab and us receiving results was 9.5days (IQR:1.2-2.5). Of participants completing feedback surveys, 93.1%(67/72) that requested a swab kit found it easy and 96.7%(59/61) that received results would consider participating in self-swabbing again.

Conclusions

We developed a tool to test individuals, often not presenting to healthcare, for respiratory viruses. This tool can be rapidly deployed and adapted according to public health need, such as for emerging respiratory pathogens or in a pandemic, to inform situational awareness of community respiratory illness. The short time intervals between reporting symptoms and completing the test, high return rate and positive feedback suggests continued engagement of the FluSurvey cohort in respiratory virus swabbing.

FIRESIDE SESSION 1

Respiratory viruses: evidence to practice

Nirsevimab effectiveness in preventing RSV hospitalisations in children under 24 months: second season post-national immunisation implementation in Portugal (2025–2026)

ABSTRACT ID: 708

Vânia Gaio [1], ***Raquel Guiomar*** [2], ***Teresa Fernandes*** [3], ***Camila Henriques*** [2], ***Licínia Gomes*** [2], ***Ausenda Machado*** [4], ***Ana Paula Rodrigues*** [1]

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Background

RSV is a major cause of severe respiratory disease, particularly among infants in the first months of life. The 2025–26 season, initiated in September 2025, marks the second national routine nirsevimab immunisation season in Portugal. We conducted a test-negative case–control study using the national hospital-based RSV surveillance network to estimate the effectiveness of nirsevimab (NE).

Methods

This study included children eligible for the intervention: under 24 months, hospitalised with severe acute respiratory infection, across 15 hospitals. Cases were defined as children testing positive for RSV by RT-PCR or rapid antigen test, while controls tested negative. Immunisation status was obtained from national electronic medical records. NE was estimated using logistic regression as (1 – adjusted odds ratio) × 100, with adjustment for age group, sex, month of symptom onset, low birth weight, prematurity, and chronic conditions.

Results

Between weeks 39/2025 and 16/2026, 107 cases and 180 controls were included. The median age in both groups was 2 months (IQR:1–5). The median time from immunisation to symptom onset was longer among cases than controls (71.5 days [IQR:25.5–106.6] vs 51.0 days [IQR:45.5–108.8], respectively). Among RSV-positive infants, 72.9% had received nirsevimab at least 2 days before symptom onset, compared with 82.2% of RSV-negative controls. NE against RSV-associated hospitalisation was 67.5% (95%CI: 31.2–85.3). Sensitivity analysis restricted to RT-PCR-confirmed cases yielded a similar, though higher estimate (74.3%, 95%CI: 28.5–91.4).

Conclusions

During the second post-implementation season in mainland Portugal, nirsevimab reduced severe RSV cases by approximately two-thirds in young children. A lower NE compared with the first season (78.5%) was observed, consistent with findings from other countries such as Spain, although the underlying reasons remain unclear and may relate to potential limitations of the test-negative design in this context. Continuous monitoring of nirsevimab's effectiveness is warranted, given the potential changing RSV epidemiology.

FIRESIDE SESSION 1

Respiratory viruses: evidence to practice

Disentangling school-related and community transmission contributions to SARS-CoV-2 cases in secondary school students across pandemic phases

ABSTRACT ID: 741

Clarize de Korne [1], ***Patricia Bruijning-Verhagen*** [1]

1. UMC Utrecht

Background

During the COVID-19 pandemic, repeated school closures were implemented to reduce SARS-CoV-2 transmission, despite substantial educational and societal costs. Evidence-based decision-making requires insight into the contribution of school-related transmission and the impact of school-specific mitigation measures. We address this using an endemic-epidemic modelling framework that disentangled school-related and community transmission across pandemic phases.

Methods

We used confirmed SARS-CoV-2 infection records from Dutch Municipal Health Services during Jun-2020 to Dec- 2021. Records were individually linked to secondary education data to generate daily infection time series per student stratified by educational track, grade and school (7869 subgroups across 929 schools). Next, time series were decomposed in an endemic-epidemic model into infections attributable to community or school-related transmission, based on relative clustering of cases within and between student subgroups. Model estimates during the summer holiday period were used to define infections attributable to transmission within and between student subgroups, but not related to school attendance. Model parameters were estimated separately for seven predefined pandemic phases with distinct mitigation policies.

Results

In total 171k confirmed SARS-CoV-2 infections were recorded among students, with daily infection rates ranging from 22 to 130 cases per 100,000 students across pandemic phases. The endemic-epidemic model closely reproduced observed trends. The percentage of student infections attributed to school-independent within-and between subgroup transmission was 23% (within: 14.5%, IQR: 12.9-16.1%; between: 8.3, IQR: 5.8-10.7%). The percentage of infections attributable to school-related transmission differed markedly by pandemic phase, from 5% during partial lockdown to 22-36% during phases with fully open schools and limited mitigation measures.

Conclusions

This endemic-epidemic modelling approach to disentangle the relative contribution of school-related transmission to SARS-CoV-2 infections in secondary school students allows for a targeted evaluation of school mitigation policies. This supports informed decision-making on the trade-off between transmission control and educational continuity.

FIRESIDE SESSION 1

Respiratory viruses: evidence to practice

Impact of autumn 2023 and 2024 COVID-19 vaccination in preventing COVID-19 related hospitalisations and deaths in individuals aged ≥65 years from seven EU/EEA countries: a multicentre electronic health records-based study (VEBIS-EHR)

ABSTRACT ID: 493

Yohann Mansiaux [1], Alexandre Blake [1], Nathalie Nicolay [2], James HUMPHREYS [1], Toon Braeye [3], Izaak Van Evercooren [4], Christian Holm Hansen [5], Ida Rask Moustsen-Helms [5], Daniele Petrone [6], Alberto Mateo Urdiales [6], Iván Martínez-Baz [7], Jesús Castilla [8], Ausenda Machado [9], Patricia Soares [9], Rickard Ljung [10], Nicklas Pihlstrom [10], Hinta Meijerink [11], Anthony Nardone [1], Esther Kissling [1], Susana Monge [12], Sabrina Bacci [2], Baltazar NUNES [1]

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Background

Within the VEBIS-EHR project, monthly COVID-19 vaccine effectiveness (VE) is routinely estimated across EU/EEA. While VE quantifies direct protection, it does not capture the overall population benefit of vaccination in terms of events prevented. We estimated the impact of the 2023 and 2024 autumn COVID-19 vaccination campaigns in individuals aged ≥65 years by quantifying averted COVID-19-related hospital admissions and deaths during the 12 months following each campaign.

Methods

We conducted a retrospective cohort study using EHR data from Belgium, Denmark, Italy, Navarre (Spain), Portugal, Norway and Sweden. Cox regression with calendar time as the underlying time scale was used to estimate monthly (8-week rolling periods starting on day 1 of each month) confounder-adjusted hazard ratios (aHR) for vaccination against hospitalisations and deaths, at study site level. Pooled VE estimates were obtained by random-effects meta-analysis. Weekly numbers of averted events (NAE) were estimated using observed COVID- 19-related hospitalisations and deaths, vaccine coverage (VC) and weekly interpolated VE from the monthly estimates. Yearly estimates were obtained by summing weekly NAE. Prevented fraction (PF) was estimated as NAE/(NAE+observed events).

Results

Across participating sites, among adults ≥65 years, the 2023 autumn vaccination campaign averted 6,200 COVID- 19-related hospitalisations (PF=10%) and 2,200 (PF=12%) in 2024. Among those ≥80 years, the number of averted COVID-19-related deaths was 811 (PF=13%) for the 2023 campaign and 156 (PF=12%) for 2024. Impact varied across countries and weeks, being higher when maximum VC was achieved before the incidence peak and before VE start to decline

Conclusions

Although with similar PF, the 2023 and 2024 autumn vaccination campaigns resulted in substantially different numbers of averted COVID-19-related hospitalisations and deaths among older adults, with fewer events averted in 2024. These findings highlight that the impact of vaccination programmes depends not only on VC and VE but also on alignment between vaccination timing and periods of increased incidence.

FIRESIDE SESSION 1

Respiratory viruses: evidence to practice

Governance of Scientific Advice for Policymaking during COVID-19: Lessons from Sweden and Switzerland

ABSTRACT ID: 447

Fereshteh Kazemipour [1], ***Miriam Saso*** [2], ***Eveline Cleynen*** [2], ***Nienke Schutte*** [2]

1. Maastricht University; Sciensano, 2. Sciensano

Background

During the COVID-19 pandemic, countries implemented widely varying structures to govern scientific advice for policymaking. These governance choices proved critical, shaping the legitimacy, timing, and nature of public health measures. Sweden and Switzerland represented contrasting governance models during COVID-19. This study reviews academic literature on scientific advice governance in Sweden and Switzerland during the COVID-19 pandemic, aiming to identify lessons for future health crises.

Methods

A systematic literature review was conducted following PRISMA criteria using the Medline, Web of Science, and SCOPUS databases. Only papers published in English from 2020 onwards were included and screened by two reviewers. Data were extracted using the Belgian Pandemic Intelligence Network (BE-PIN) analytical framework developed from prior research on evidence-based policymaking, defining three key dimensions: legal, organisational, and collaborative aspects.

Results

A total of 591 papers were identified, of which 36 remained after removing duplicates and screening (20 for Sweden, 16 for Switzerland). In Sweden, the legal aspect was robust: the public health agency held a strong institutional mandate and operated with high independence from political interference. However, the collaborative dimension revealed some gaps. The range of expertise feeding into advisory processes was limited to biomedical fields, lacking input from social sciences and ethics. In Switzerland, the scientific advisory body lacked a formal mandate. On the collaborative side, it was more diverse than Sweden's and most other countries. However, due to its ad hoc nature, there was no existing articulation with authorities, making collaboration with policymakers and administrative bodies challenging.

Conclusions

For effective crisis management, policymakers should establish clear structures, selection criteria, and responsibilities for scientific advisory committees in peacetime. This prevents politicization of evidence and enables timely decision-making when crises arise. Diverse expertise, a clear division of roles between scientists and policymakers, and transparent public communication are also essential for maintaining trust and legitimacy.

FIRESIDE SESSION 1

Respiratory viruses: evidence to practice

Insights from implementing active surveillance for avian and swine influenza virus infections in humans in Denmark, 10 September 2024 to 7 May 2026

ABSTRACT ID: 298

Charlotte Kristiane Hjulsager [1], Pia Ryt-Hansen [2], Sophie Agger [3], Amanda Bolt Botnen [1], Amalie Ehlers Bedsted [1], Lars Erik Larsen [2], Stine Kjær Lefèvre [4], Stefanie Pöhl Nielsen [1], Anne Christine Mariager Nordholm Breschel [5], Sofie Skovmand [1], Ramona Trebbien [1], Tinna Ravnholt Urth [5], Lasse Skafte Vestergaard [5], Gudrun Witteveen-Freidl [3]

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Background

Avian and swine influenza A viruses (AIV, swIAV) are among the top ten cross-border pathogens prioritized for coordinated surveillance. In Denmark, dedicated surveillance for AIV in humans is passive and absent for swIAV. Therefore, the objective was to assess the feasibility of implementing active surveillance for AIV and swIAV among individuals exposed to birds or pigs.

Methods

Participants self-collected combined nasal and throat swabs using project-specific sampling kits and completed a questionnaire to characterize exposure. For AIV, we included individuals with mild or no symptoms 1–2 days after exposure to domestic or wild birds, with or without confirmed AIV infection, respectively. Persons exposed to laboratory-confirmed AIV-positive birds performed a second sampling 2–3 days later. For swIAV, we enrolled symptomatic and asymptomatic swine veterinarians with exposure to pigs in private practice or slaughterhouses within the previous 7 days. Samples were returned via pre-paid envelopes for PCR testing.

Results

The project comprised two periods. In the first (10 September 2024–15 May 2025), sampling uptake was low with 8 AIV- and 13 swIAV-associated samples; all tested negative. To identify barriers and improve the setup, we conducted a stakeholder workshop in June 2025. Feedback included, among others, clearer communication about consequences of positive results and offering the option of delayed testing. After incorporating this feedback, we collected 79 AIV- and 15 swIAV-associated samples in the second period (25 September 2025–7 May 2026), coinciding with high AIV infection pressure in birds. All samples were negative, except for one swine veterinarian in private practice, who tested positive for human seasonal A(H3N2).

Conclusions

Although close animal contact was reported for >90% of the samples, we found no evidence of zoonotic influenza transmissions. Despite some remaining barriers, the active surveillance setup proved feasible and may complement existing systems by enhancing early detection and supporting timely risk assessment.

FIRESIDE SESSION 2

Food- and water-borne diseases

Setting norovirus activity level thresholds using the moving epidemic method, England, 2015-2025

ABSTRACT ID: 773

David Elliott [1], ***Magali Collonnaz*** [1], ***Danielle Hearn*** [1], ***Gauri Godbole*** [1], ***Cristina C Celma*** [1], ***Stuart Beard*** [1], ***Amy Douglas*** [1]

1. *United Kingdom Health Security Agency*

Background

Incidence of norovirus, one of the most common causes of gastroenteritis in England, increases in winter, though the timing and intensity of the annual increase vary. Timely characterisation of norovirus activity can support planning and risk assessment across the health and social care system. We tested the suitability of the Moving Epidemic Method (MEM), a threshold setting method developed for respiratory virus surveillance, for norovirus surveillance.

Methods

Using positive norovirus laboratory reports from English laboratories to the national surveillance system, we calculated weekly national incidence rates for the 2015/2016 to 2018/2019 and 2022/2023 to 2024/2025 seasons (starting week 27 and ending week 26), excluding the intervening seasons due to COVID-19 impacts. Thresholds for epidemic, low, medium and high activity were calculated using the MEM with the pre-2024/2025 rates (n = 43,356 laboratory reports) and applied to the 2024/2025 rates. Model performance metrics were calculated for threshold parameter values between 1 and 3 (main analysis = 2).

Results

In the main analysis, the epidemic period had a mean length of 22 weeks (range 18-25) with a mean start of week 48. The epidemic threshold rate was 0.26 norovirus positive samples per 100,000 people, and activity threshold rates ranged from 0.48 (low) to 0.79 (high). The sensitivity of the model was 74% and the specificity was 78%. The 2024/2025 season saw very high activity, including 13 weeks above the high activity threshold.

Conclusions

The MEM provided valid estimates of the epidemic and activity thresholds, providing evidence that a threshold setting method developed for respiratory viruses may be appropriately used for norovirus. Thresholds may support improved situational awareness and public health communication of norovirus activity levels. Further work is required to calibrate the sensitivity and specificity of the model and to validate outputs.

FIRESIDE SESSION 2

Food- and water-borne diseases

Are Non-Contemporaneous Controls a Valid Source of Controls in Foodborne Outbreak Investigations?

ABSTRACT ID: 412

Rebecca Howarth [1], ***Clare Sawyer*** [2], ***Ann Hoban*** [2], ***Nicola Love*** [2], ***Lesley Larkin*** [2], ***Lynda Browning*** [3], ***Andrew Nelson*** [4], ***Sooria Balasegaram*** [2]

1. *Field Epidemiology Training Program, United Kingdom Health Security Agency,* ***2.*** *United Kingdom Health Security Agency,* ***3.*** *Public Health Scotland,* ***4.*** *Public Health Wales*

Background

During foodborne outbreak investigations, contemporaneous controls can be difficult to recruit rapidly. Controls recruited outside the outbreak period (non-contemporaneous), matched by seasonality, age and geography have been used; however, this methodology has not been formally validated. Using UK national outbreak case–control studies, we assessed whether non-contemporaneous controls yielded comparable epidemiological conclusions to original control sources.

Methods

We examined a Hepatitis A (HAV) outbreak (January-April 2021), which used contemporaneous HAV case-controls and non-contemporaneous *Salmonella* case-controls from Autumn 2019. HAV cases were asked about exposures eight weeks prior to symptom onset. For a *Salmonella* Enteritidis outbreak (May-September 2020), analyses were previously conducted with non-contemporaneous controls recruited in late summer/early autumn 2019 and 2020 but was restricted to adults due to data availability. Re-analysis used age frequency-matched market panel controls recruited in July-August 2024. Univariable and multivariable regression outputs were compared between control sources.

Results

HAV outbreak analyses found consistent epidemiological conclusions of an association with consumption of dates, using both contemporaneous (aOR 47.4, 95% CI 1.8-1256.1) and non-contemporaneous controls (aOR 58.9, 95% CI 4.7-734.5). Original *S.* Enteritidis analyses found an association between consumption of reformed chicken products (nuggets, poppers, goujons, and balls) from identified retailers (aOR 76.4, 95% CI 8.6-680.9). Re-analysis using all age groups found a consistent association (aOR 9.1, 95% CI 3.8-21.5). Availability of a control group with all age groups enabled narrowing the signal to products that aligned with original microbiological findings (poppers: aOR 14.7, 95% CI 4.7-46.0 and nuggets: aOR 8.1, 95% CI 3.0-21.5); these individual products were not significant in the original analysis.

Conclusions

Non-contemporaneous controls provide a valid alternative to accelerate outbreak investigations. Contemporaneous controls may elucidate specific exposures; however, this may not always be necessary to commence public health responses. Further work will compare additional examples with non-contemporaneous controls and explore the impacts of non-seasonal matching.

FIRESIDE SESSION 2

Food- and water-borne diseases

Genomic epidemiology of clinical Listeria monocytogenes clusters in Norway, 2016–2025

ABSTRACT ID: 525

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Background

Listeria monocytogenes (*Lm*) causes listeriosis, a severe foodborne illness with high case fatality, affecting immunocompromised individuals, pregnant women, and the elderly. In recent years, an increase of listeriosis cases has been reported in Norway and Europe. We aimed to characterise the genomic population structure of clinical *Lm* isolates in Norway and to explore transmission dynamics.

Methods

We retrospectively analysed WGS data from 261 clinical isolates including socio-demographic characteristics from patients between 2016 and 2025. We identified lineages and core genome alignment, masked recombination blocks, and constructed maximum-likelihood phylogenies. Strains were classified as outbreak clusters (≥5 isolates, ‹10 SNPs or cgMLST ‹5 AD, ‹3 years), persistent (≥5 isolates, ≤25 SNPs or ≤10 AD, spanning ≥3 years), emerging (rising incidence ≥2 consecutive years), or replacing (≥50% decline or absent for ≥3 years). Patient characteristics were compared using Mann–Whitney U or Fisher's exact tests. Agreement between cgMLST and SNP-based cluster assignments was evaluated using Cohen's kappa. Analyses used R (v4.5.1).

Results

Of 261 isolates, 33% (n=85) belonged to Lineage I and 67% (n=176) to Lineage II. The cgMLST and SNP-based methods were concordant (κ›0.81). Ten clusters were detected (three in Lineage I and seven in Lineage II): six persistent (CC1, CC6, CC7, CC9, CC37, CC121), two emerging (CC4 and CC11/ST451 since 2023), one replacing (CC20), and one outbreak (CC90). No socio-demographic differences were observed between clusters (p›0.05).

Conclusions

Clinical *L. monocytogenes* in Norway comprises genomically distinct lineages with fundamentally different transmission dynamics. Lineage I is dominated by smaller clusters, while Lineage II included larger, longer-running clusters consistent with environmental persistence. The reported increase in Norwegian listeriosis cases reflects ongoing Lineage II persistence and emerging clonal expansion since 2023. We recommend integrating recombination-aware, lineage-stratified WGS surveillance with explicit outbreak criteria to improve detection and public health response.

FIRESIDE SESSION 2

Food- and water-borne diseases

Vibrio and Shewanella infections in Denmark: a six-year nationwide retrospective epidemiological overview, 2020–2025

ABSTRACT ID: 73

Kristyna Faksova [1], ***Aoife Ronayne*** [1], ***Maarten Nauta*** [1], ***Steen Ethelberg*** [1]

1. Department of Data Science and AI in Health, Statens Serum Institut, Copenhagen, Denmark; ECDC Fellowship Programme, Field Epidemiology path (EPIET), European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden

Background

Non-cholera *Vibrio* and *Shewanella spp.* are marine bacteria causing gastrointestinal, wound, ear, and invasive infections after exposure to brackish seawater. Climate change-driven heatwaves are expected to increase infection incidence in Northern Europe. We provide a retrospective nationwide epidemiological overview of marine bacteria cases in Denmark to support seasonal preparedness and provide a baseline for upcoming routine surveillance from spring 2026.

Methods

Laboratory-confirmed *Vibrio* and *Shewanella* episodes from the nationwide Danish Microbiology Database were analysed from 1 January 2020 to 31 December 2025. Repeated positive tests with the same pathogen within 6 months were grouped into episodes. Specimen type (blood, wound, soft tissue, respiratory mucus, faeces) was used as a proxy for infection type. Travel-related episodes were excluded. Residential municipality was assigned using patient-linked coordinates; cumulative incidence per 100,000 population was calculated using Statistics Denmark denominators.

Results

Of 1,021 episodes, 87 (9%) were travel-related. Annual counts ranged from 129 to 185. *Vibrio* accounted for 524/934 (56%) episodes and *Shewanella* for 410/934 (44%). Episodes were rare in winter months and peaked in July–August (54% of episodes). Cumulative 2020-2025 incidence was highest in coastal municipalities, particularly on Fyn (138.6 per 100,000 for both genera combined); most municipalities recorded ‹20 per 100,000. Episodes mainly regarded adults aged 65-79 years and were more common in males (58%). Wound/soft tissue episodes comprised 724/934 (78%); gastrointestinal 64/934 (7%); invasive 42/934 (5%) and deep soft tissue infection 41/934 (4%). *Shewanella algae* caused 267 episodes including 23 invasive; *Vibrio vulnificus* caused 28, including 8 invasive/deep soft tissue.

Conclusions

Marine bacterial infections are a recurrent summer public health concern in Denmark, with coastal clustering and occasional severe cases. Targeted warm-season risk communication and increased clinical awareness, especially for wound and invasive infections in older adults, may prevent severe outcomes. Planned laboratory-based surveillance from 2026 will support standardized monitoring and strengthen public health response.

FIRESIDE SESSION 2

Food- and water-borne diseases

Title: Ecological determinants and projections of cholera in South Kivu province, Democratic Republic of Congo, 2021–2028.

ABSTRACT ID: 604

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Background

Cholera remains a major public health problem in the Democratic Republic of Congo. Despite ongoing multisectoral elimination efforts, the endemic province of South Kivu reports the highest caseload. We assessed ecological factors associated with rising cases from 2021 to 2025 and predicted future burden (2026–2028).

Methods

An ecological study was conducted using monthly health-zone-level cholera surveillance data from 2021 to 2025. A negative binomial generalized linear mixed model with a random intercept for health zone and log-population offset was fitted. Covariates included lake area, river, conflicts, cumulative monthly rainfall, monthly precipitation anomalies, internal population displacement, and humanitarian presence. Adjusted incidence rate ratio and 95% confidence interval were calculated. Future projections were generated under two contrasting scenarios: the low-incidence year 2021 (best scenario) and the peak-incidence year 2025 (worst scenario).

Results

From 2021 to 2025, 34,825 suspected cases and 267 deaths were reported across 79% of health zones. The hotspots health zones were situated near Lakes Kivu and Tanganyika. A significant rising trend was observed (slope = 0.64, $p < 0.001$), accentuated during the rainy seasons. Ecological factors associated with higher case counts were lake area (aIRR 23.37; 95% CI 2.67–204.81), internal population displacement (aIRR 1.06; 95% CI 1.01–1.12), and precipitation anomalies (aIRR 1.17; 95% CI 1.05–1.31). The worst-case scenario projected 23,695 cases (95% CI 9,503–59,344) in 2026, nearly double the number observed in 2025, and a cumulative total of 98,134 cases for the entire 2026–2028 period.

Conclusions

Overall, Cholera cases in South Kivu rose significantly, marked in the rainy season, driven by proximity to the lake and population dynamics, and are predicted to escalate sharply. Urgent strengthening of collaborative surveillance across the Great Lakes region, in addition to sustainable investments in safe water, sanitation, and hygiene, is needed to meet the 2030 cholera elimination agenda.

FIRESIDE SESSION 2

Food- and water-borne diseases

Comparative epidemiology and seasonality of Cryptosporidium hominis and Cryptosporidium parvum in Wales, 2022 to 2024

ABSTRACT ID: 756

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Background

Cryptosporidiosis is a gastrointestinal illness characterised by prolonged, watery diarrhoea, and can cause long-term sequelae. The leading causative species are *Cryptosporidium parvum* and *Cryptosporidium hominis*. We aimed to describe how seasonality is influenced by the comparative epidemiology of the two species in Wales.

Methods

We conducted a case-case study using surveillance data and exposure questionnaires for cases resident in Wales between 01/01/2022 and 31/012/2024. Species was derived via PCR. Species other than *C. parvum* or *C. hominis* were excluded. We used univariable and multivariable logistic regression (including seasonal harmonics) to compare case characteristics and reported exposures between species, and between seasonal peaks within species. A generalised additive model (GAM) was used to examine the contribution of exposures to differences in seasonality.

Results

C. parvum (n=808) was more common than *C. hominis* (n=427). C. parvum had a primary spring peak and secondary autumn peak. *C. hominis* displayed a single autumn peak. *C. hominis* cases were more likely to report anthroponotic exposures e.g. household GI illness (aOR:2.73, 95%CI:1.63-4.64) whilst *C. parvum* cases were more likely to report environmental exposures e.g. soil or water courses (aOR: 3.13, 95%CI:1.85-5.56). GAM analysis demonstrated a 19 percentage point reduction in explained deviance in seasonality differences after adjustment for significant exposures from MVA. Within-species analysis highlighted seasonal exposure variation, for example autumn *C. parvum* cases were less likely to have visited animal premises compared to spring cases (aOR:0.18, 95%CI:0.09-0.34). Similarly, autumn *C. hominis* cases had increased odds of reporting travel abroad compared to non-peak cases (aOR:2.05, 95%CI:1.12-3.79).

Conclusions

We provide evidence that comparative exposure differences drive species specific seasonality. This analysis highlights opportunities for seasonal interventions targeting specific exposures e.g. targeted animal premises handwashing advice during spring. Findings underscore the importance of speciation in *Cryptosporidium* surveillance. Our novel approach to analysing comparative seasonality could be applied to other pathogens.

FIRESIDE SESSION 3

Antimicrobial resistance

Implementation Gaps in Antimicrobial Stewardship in Pakistan: Implications for Surveillance and Public Health Practice

ABSTRACT ID: 889

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Background

Antimicrobial resistance (AMR) represents a growing public health threat, particularly in low- and middle-income countries where healthcare systems face resource and surveillance limitations. In Pakistan, antimicrobial stewardship programs (ASPs) have increasingly been introduced to improve antibiotic use; however, implementation remains inconsistent across healthcare settings. This scoping review aimed to identify major implementation gaps affecting ASP effectiveness and sustainability in Pakistan and explore implications for public health practice and AMR surveillance.

Methods

A scoping review was conducted using Arksey and O'Malley's methodological framework and reported according to PRISMA-ScR guidance. Six electronic databases were searched for empirical studies published between 2021 and 2025 evaluating ASP implementation in Pakistan. Eligible studies included hospital-based, community-based, and multidisciplinary stewardship interventions. Data were extracted and thematically synthesised to identify recurring implementation barriers and system-level challenges.

Results

Thirty-five studies met the inclusion criteria. While several studies demonstrated improvements in antibiotic prescribing practices and awareness, substantial implementation gaps were identified. Key barriers included inadequate microbiological diagnostic capacity, fragmented AMR surveillance systems, lack of formal stewardship governance structures, limited workforce training, inconsistent adherence to prescribing guidelines, and resource constraints. ASP implementation was predominantly concentrated in tertiary healthcare facilities, with limited integration into primary and secondary care settings.

Conclusions

ASPs in Pakistan demonstrate promising effectiveness but remain constrained by systemic implementation challenges. Strengthening diagnostic infrastructure, integrating surveillance systems, improving workforce capacity, and enhancing institutional stewardship governance are essential for sustainable AMR control. These findings highlight the need for context-specific stewardship strategies to support effective public health responses in comparable resource-limited settings.

FIRESIDE SESSION 3

Antimicrobial resistance

European multi-country outbreak of NDM-5-producing Enterobacter hormaechei ST1344, March 2025–April 2026

ABSTRACT ID: 620

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Background

Enterobacter hormaechei producing New Delhi metallo-β-lactamase-5 (NDM-5) poses a critical public health threat, as this carbapenemase confers resistance to nearly all β-lactam antibiotics, severely limiting therapeutic options. In September 2025, genomic surveillance across several EU/EEA countries first identified a distinct genetic cluster of NDM-5-producing *E. hormaechei* sequence type (ST) 1344. This signal, suggesting a multi-country outbreak, prompted a joint investigation to identify a common source and guide infection control measures.

Methods

Cases were defined as individuals infected/colonised with *E. hormaechei* ST1344 carrying *bla* , confirmed via NDM-5 whole genome sequencing (WGS) of isolates as belonging to the specific core-genome multilocus sequence typing (cgMLST) cluster within ≤4 allelic differences. Epidemiological data of cases on demographics, healthcare exposures, use of medication and medical/care products, and travel history were collected using a standardised questionnaire and analysed descriptively.

Results

Between March 2025 and April 2026, 57 cases were identified in Germany (n=19), the Netherlands (n=16), Denmark (n=15), Ireland (n=3), Austria (n=2), Norway (n=1), and Luxembourg (n=1). Median age of cases was 73 years (range 37–94) and 51% were female. Of 52 cases with information available, 45 (87%) were inpatients and 7 (13%) outpatients. For 4 outpatient cases, a previous hospitalisation within 12 months was explicitly excluded. Isolates were predominantly identified from clinical samples, including urine (38%), wound/soft tissue (14%), and blood (9%). No common travel history was identified. Danish cases concentrated in two hospitals, while most other cases were geographically dispersed. Investigations into shared exposures have not yet identified a common source.

Conclusions

The simultaneous emergence of genetically highly related NDM-5-producing *E. hormaechei* ST1344 across several countries suggests a common source. The outbreak is considered to be ongoing. Investigations continue with a particular focus on medications and medical/care products. We recommend prompt WGS of all carbapenem-resistant *E. hormaechei* isolates to aid identification of new cases and the source.

FIRESIDE SESSION 3

Antimicrobial resistance

From data silos to federated One Health antimicrobial surveillance: early implementation results for Estonia and Romania

ABSTRACT ID: 614

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Background

Antimicrobial resistance (AMR) surveillance requires a One Health approach, yet integrated surveillance is facing challenges due to data protection constraints, protocol diversity, human factors, and limited interoperability across human, animal and environmental data streams. Federated learning (FL) enables multi-site analytics without raw data transfer but dataset heterogeneity and ethical hurdles stall most ongoing efforts in clinical and veterinary medicine. Robust harmonization is the prerequisite for any federated analytics framework and remains an open methodological gap.

Methods

We deployed an initial two-node FL prototype across two EU nodes. The Estonian node contributed 250 companion and production animal isolates (dogs, cats, horses and dairy cows) characterized through bacteriology, MALDI-TOF and antimicrobial susceptibility testing (AST) using the Kirby-Bauer disk diffusion method. The Romanian node contributed 250 dog and cat isolates characterized by Analytical Profile Index kits, MALDI-TOF and Kirby Bauer AST. We mapped schema heterogeneity across both nodes and built a harmonization framework covering species taxonomy, AST encoding under CLSI and EUCAST v13.0, antimicrobial panel reconciliation, and host and temporo-spatial metadata.

Results

The framework exposed three classes of heterogeneity: identification-method-dependent species labels, divergent AST interpretive thresholds, and inconsistent metadata granularity for host and location attributes. Reconciliation rules were implemented as a shared ontology, with agreed canonical terminology across the two nodes. A comparative analysis of protocols (SOPs) was carried out across participating laboratories, outlining antibiotic regime differences correlated with local AMR surveillance data. The federated architecture executed end-to-end across both nodes with raw data remaining on-site, and resistome profile mapping characterizing resistance distribution across the two nodes.

Conclusions

The harmonization framework provides a reusable, GDPR-compliant baseline for cross-border veterinary AMR surveillance and a transferable scaffold for near-real time data reporting across nodes, preparing the FRL architecture for expansion to nodes in Sri Lanka and Colombia.

FIRESIDE SESSION 3

Antimicrobial resistance

Outbreak investigation and molecular characterization of community associated methicillin resistant Staphylococcus aureus in a secondary school in Thuringia, Germany, 2025

ABSTRACT ID: 375

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Background

Community-associated methicillin-resistant *Staphylococcus aureus* (CA-MRSA) carrying the Panton-Valentine leukocidin (PVL) gene can cause skin and soft tissue infections (SSTIs) and, rarely, systemic infections including necrotizing pneumonia. In October 2025, 3 PVL-positive CA-MRSA cases among students at a secondary school in Thuringia, Germany, were reported to the local health authority. We investigated the outbreak and conducted contact tracing to identify further cases, describe transmission pathways, and implement control measures.

Methods

Confirmed cases were those with PVL-positive MRSA isolates from February-December 2025 and ≤10 allelic differences in core genome-multilocus sequence-typing and probable those with PVL-positive MRSA isolates since February linked to confirmed cases. We interviewed cases using structured questionnaires to obtain clinical and epidemiological information. We screened cases' contacts (family members, classmates, teachers) and children and staff in two kindergartens exposed during a case's internship, for nasal colonization. Isolates were confirmed as PVL-positive MRSA by PCR for *mecA* and PVL genes and typed by whole genome sequencing (WGS).

Results

Overall, 13 cases (median age 17 years [IQR: 15–43]; 62% female) were detected. Screening identified 10 cases among contacts (7 family members, 2 classmates, 1 teacher); no cases were detected in the kindergartens. Seven (54%) cases had SSTI; one previously healthy adolescent developed fatal necrotizing pneumonia following influenza superinfection. All isolates available for WGS (n=12) were sequence type ST1153 with spa types t903 (n=10) and t22505 (n=2), indicating clonal spread. Interviews suggested transmission via close person-to-person contact among adolescents (6/9; 67%), and shared clothing or make-up use (3/9; 33%). All cases were offered treatment with mupirocin and remediation.

Conclusions

Our investigation identified a PVL-positive CA-MRSA outbreak in a secondary school with person-to-person transmission and subsequent household spread. We recommend contact tracing and screening of contacts when infections are identified in community settings. Treatment and remediation can reduce infection risk and interrupt transmission chains.

FIRESIDE SESSION 3

Antimicrobial resistance

Genomic virulence scores and clinical outcomes among carbapenem-resistant Klebsiella pneumoniae infections in Germany, 2023–2025

ABSTRACT ID: 224

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Background

Carbapenem-resistant hypervirulent *Klebsiella pneumoniae* are a rising public health concern, combining antimicrobial resistance with enhanced virulence. Genomic virulence scores have been proposed to detect potentially hypervirulent strains; however, their association with clinical outcomes remains unclear. We assessed the association between genomic virulence scores and severe clinical outcomes using national surveillance data.

Methods

We conducted a retrospective study using data from the German Integrated Genomic Surveillance. The analysis included carbapenem-resistant *Klebsiella pneumoniae* isolates with sequencing data matched to mandatory infection notifications reported in January 2023–August 2025. Virulence scores were assigned using Kleborate (v2.3.2) and a marker set by Russo et al. Severe clinical outcome comprised invasive infection (blood or cerebrospinal fluid), ICU admission, or death. Associations were assessed using adjusted logistic regression, including age, sex, and acquisition setting (aORs).

Results

Among 845 matched cases, the median age was 68 years and 568 (67%) were male. Overall, 302 (36%) met the definition of severe clinical outcome. Invasive infection was reported in 160 (19%), ICU admission in 131 (16%), and death in 74 (9%). Kleborate scores of 5 and 4 were observed in 6 (0.7%) and 232 (27%), respectively; no isolate had a Russo score of 5, while 42 (5%) had 4. Neither Kleborate (aOR 1.02 per point, 95% CI 0.92–1.12) nor Russo (aOR 1.04 per point, 95% CI 0.91–1.20) was associated with severe clinical outcome. No significant associations were observed for invasive infection, ICU admission, or death analysed separately.

Conclusions

In our surveillance, genomic virulence scores were not significantly associated with severe clinical outcomes among carbapenem-resistant *Klebsiella pneumoniae* infections. This may reflect limited predictive value of current genomic markers for routinely captured clinical outcomes but may also be influenced by the low number of high-scoring isolates. Better integration of genomic and clinical data is needed to refine interpretation of virulence markers for public health surveillance.

FIRESIDE SESSION 3

Antimicrobial resistance

From Fragmentation to Integration: Strengthening One Health AMR Surveillance Governance in Europe

ABSTRACT ID: 141

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Background

Effective public health surveillance is essential to detect, assess, and respond to antimicrobial resistance (AMR) threats. In Europe, surveillance systems operate across human, animal, and environmental sectors under a One Health framework. However, despite the availability of EU-level surveillance infrastructures, fragmentation in governance and regulatory design continues to limit data integration, comparability, and timely public health action across sectors.

Methods

A qualitative policy and surveillance systems analysis was conducted, combining a systematic review of relevant European policy and strategic frameworks on antimicrobial resistance and One Health with a comparative assessment of eight national AMR action plans across EU Member States representing diverse governance models. The analysis focused on key surveillance performance dimensions, including legal mandates for data sharing, interoperability mechanisms, coordination structures, and integration of environmental monitoring.

Results

Three major governance barriers impacting surveillance effectiveness were identified. First, only three of eight countries included explicit legal provisions enabling cross-sectoral data sharing, limiting interoperability between human, veterinary, and environmental surveillance systems. Second, environmental AMR surveillance remains insufficiently integrated, with no binding requirements and heterogeneous data collection practices across countries. Third, fragmented institutional responsibilities across sectors lead to delays in data exchange, reduced data comparability, and limited capacity for coordinated response. While countries with formal One Health coordination platforms showed improved integration, the absence of enforceable standards hindered consistent implementation. These gaps reduce the completeness, timeliness, and usability of surveillance data, despite existing EU-level infrastructures.

Conclusions

Strengthening AMR surveillance in Europe requires governance reforms that directly address system performance. Establishing binding data-sharing mechanisms, integrating environmental surveillance into regulatory frameworks, and reinforcing cross-sectoral coordination are critical to improve data quality, comparability, and timeliness. Aligning legal and institutional frameworks with surveillance objectives is essential to enhance early warning capacity and support effective and timely public health responses to AMR.

FIRESIDE SESSION 4

Outbreaks of food- and water-borne diseases

No iron curtain for HAV: Transnational Hepatitis A outbreak shifting gears in Austria in 2025

ABSTRACT ID: 847

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Background

Hungary, Slovakia and Czechia experienced major hepatitis A outbreaks primarily in Roma communities between 2022 and 2024. In Austria, a marked increase in 2025, representing the largest rise in the past decades, was noted. We initiated an outbreak investigation to inform infection control strategies by improved understanding of personal risk factors and affected populations.

Methods

Cases were defined as laboratory-confirmed hepatitis-A-Virus (HAV) genotype cluster A (reference strain from Hungary) or cluster B (reference strain from Slovakia) according to the HAV-Net protocol by the National Reference Laboratory. Cases were investigated by public health authorities using physician reports, registry data and -in Vienna- standardized interviews, inquiring about potential exposures and risk factors. We descriptively analyzed surveillance and questionnaire data of outbreak cases.

Results

In 2025, 171 (69%) of 248 notified HAV-cases in Austria were genotyped (45 cluster A, 84 cluster B), resulting in 129 outbreak-related cases, of which 101 (76%) were reported in Vienna. Additionally, one case from 2023 (associated with homelessness, cluster B) and two cases from 2024 (Hungarian citizen, cluster A; patient of a Slovakian 24-hour-caregiver, cluster B), were retrospectively linked. Overall, 55 cases were hospitalized, and five deceased. Cases were predominantly male (77%), with a median age of 37 (IQR: 31-47), interviews (n=74) indicated heterogeneous potential risk factors, including homelessness (n=31), recent travel (n=19), close contact with cases (n=19) and intravenous drug use (n=13); no cases were identified among Roma populations. In Vienna, control measures were tailored toward high-risk groups.

Conclusions

This outbreak investigation highlights cross-border HAV transmission as starting point, with a shift in Austria towards different marginalized populations with spillover into the broader community, in contrast to other involved countries. Limited access to affected groups for targeted measures made outbreak response challenging. Establishing stronger transnational partnerships, and building up long-term trust in vulnerable communities will be critical for future events.

FIRESIDE SESSION 4

Outbreaks of food- and water-borne diseases

Salmonella Bochum outbreak in children caused by chocolate hazelnut spread, Germany 2026

ABSTRACT ID: 780

Hanna Buck [1], ***Michael Pietsch*** [2], ***Clara Spieker*** [3], ***Sandra Simon*** [2], ***Jennie Fischer*** [4], ***Marina Lamparter*** [4], ***Bettina Rosner*** [5], ***Anika Meinen*** [3]

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Background

In February 2026, the Robert Koch Institute (RKI) identified an outbreak among children in Germany caused by the rare *Salmonella* (*S.*) *enterica* subspecies *enterica* serovar Bochum.

Methods

We used descriptive epidemiology and exploratory patient interviews to develop a hypothesis. To test this hypothesis, the RKI compared outbreak cases (n = 12) and participants from the RKI panel "Health in Germany" aged 2–15 years (n = 197) regarding consumption of chocolate hazelnut spreads in the three days before symptom onset or completing the questionnaire. Findings were shared with food safety authorities, prompting onsite inspections and food sample analyses.

Results

The outbreak involved 40 cases, predominantly in eastern Germany. Three cases were identified in other EU countries (1x France, 2x Austria). Children aged 2–15 years accounted for 75 % of cases (30/40). More males than females were affected (62 % vs. 38 %). The National Reference Center assigned all isolates with sequence data (n=18) to the same genomic cluster by cgMLST analysis. In exploratory patient interviews 12 of 14 interviewed cases (86 %) stated consumption of a specific brand of chocolate hazelnut spread in the three days before symptom onset. The case-control study indicated a strong association with being a case (odds ratio: 93 [95% confidence interval: 21-663]). Genome comparison confirmed S. Bochum strains isolated from the product in the genomic outbreak cluster by cgMLST. In April 2026, the implicated product was recalled after the outbreak strain was detected in certain batches.

Conclusions

The hypothesis that consumption of a specific brand of chocolate hazelnut spread caused an outbreak mainly among children in Germany was confirmed by our case-control study. Trustful collaboration and rapid communication of findings between infection control and food safety authorities enabled fast detection of the infection vehicle and outbreak control measures such as the recall of the product from the market.

FIRESIDE SESSION 4

Outbreaks of food- and water-borne diseases

Assessment of post-exposure vaccination campaign in control of hepatitis A outbreak in a socially vulnerable community, Czech Republic, 2025

ABSTRACT ID: 455

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Background

Since 2023, a European multi-country hepatitis A (HA) outbreak involving IB genotype affecting mainly socially vulnerable populations has been ongoing. In 2025, a genetically linked community outbreak occurred in Ústí nad Labem, Czechia. Following notification of a case in a four-year-old on 04/03/2025, an investigation was initiated to assess transmission and implement control measures, including post-exposure vaccination (PEP). Vaccine effectiveness (VE) of PEP was evaluated.

Methods

Laboratory-confirmed HA cases (anti-HAV IgM positive) identified between 24/02/2025-04/09/2025 residing in affected community or directly exposed to a confirmed case were included. Close contacts were defined as individuals sharing household or sanitary facilities during the infectious period. Susceptible contacts were offered PEP within 14 days of their last exposure. Accounting for repeated exposures, a retrospective cohort study among susceptible contacts at exposure-episode level was conducted to estimate relative risk (RR) of infection and VE of PEP. A ring vaccination campaign targeting susceptible pupils and staff of affected school was implemented (no VE analysed).

Results

A total of 26 cases (median age: 5 years, IQR: 4–7) were identified, predominantly among community residents (92%) and (pre)school children (62%). Among 214 contacts, 151 were susceptible, with 10 secondary cases identified (secondary attack rate: 6.0%). A total of 194 exposure episodes were analysed: no cases occurred among 67 episodes with PEP (0/67), compared with 8/127 without. Estimated RR was 0.11 (95%CI: 0.01–1.89), corresponding to VE of 89%. Following the ring vaccination of 240 individuals, no further cases were reported.

Conclusions

Person-to-person transmission of HA in a socially vulnerable community in Czechia was driven by schoolattending children. Rapid investigation, contact tracing, and timely PEP were essential for outbreak control. Our findings support targeted reactive (ring) vaccination as a key component of outbreak response in similar settings, complemented by preventive vaccination and health education among at-risk populations to reduce future outbreaks.

FIRESIDE SESSION 4

Outbreaks of food- and water-borne diseases

A foodborne hepatitis A outbreak at a manufacturing plant in Taiwan, January–February 2026

ABSTRACT ID: 374

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Background

In Taiwan, hepatitis A typically occurs among international travellers or men who have sex with men (MSM). From January to February 2026, four hepatitis A cases were reported among employees at a 2,000-worker manufacturing plant. The cases were not MSM, reported no international travel, and had worked in different departments with no prior contact. We investigated the outbreak to identify the source of hepatitis A virus (HAV) infection.

Methods

We conducted a case-control study. A case was defined as illness in an employee with acute onset of fever, abdominal pain, or jaundice, combined with positive anti-HAV IgM, or who had detectable serum HAV RNA, from 18 January to 25 February 2026. Controls were randomly selected, non-case employees, frequency-matched 1:10 by age group and sex. We collected demographic, clinical, and food exposure data via an online questionnaire. Risk factors were analysed using Firth-penalised logistic regression. We investigated food preparation process and compared available HAV sequences.

Results

We identified 12 cases and enrolled 114 controls. Among the cases, 11 (92%) were symptomatic, and four (33%) required hospitalisation. Univariable analysis identified porridge, bread, and boxed lunches sold at the privately managed plant cafeteria as potential risk factors. Multivariable analysis identified boxed lunches as the sole significant risk factor (adjusted odds ratio = 15.8; 95% confidence interval: 3.8–66.6). These boxed lunches were prepared entirely by one food handler. Although asymptomatic and vaccinated with one dose of the hepatitis A vaccine seven years prior, the food handler tested positive for HAV RNA. Phylogenetic analysis revealed that HAV RNA sequences from the food handler and 10 tested cases exhibited 100% sequence identity.

Conclusions

Boxed lunches contaminated by an infected food handler caused this HAV outbreak. While strict hand hygiene remains essential, we recommend that all food handlers without HAV immunity complete a full course of hepatitis A vaccination.

FIRESIDE SESSION 4

Outbreaks of food- and water-borne diseases

Investigation of a cereulide-contaminated infant formula outbreak: Belgian evidence from human case confirmation

ABSTRACT ID: 299

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Background

In December 2025, a multi-country food safety incident involving infant formula contaminated with cereulide triggered large-scale recalls across Europe. Cereulide, a thermostable emetic toxin produced by *Bacillus cereus,* causes rapid-onset vomiting and gastrointestinal symptoms, but laboratory confirmation and toxin detection is rarely included in routine clinical diagnostics . The objective of this study was to investigate the link between symptomatic cases and consumed infant formula in Belgium to inform public health actions and prevent further exposure.

Methods

A multisectoral outbreak investigation team, involving the regional health authorities, the food safety agency and the Belgian institute for health, carried out epidemiological and laboratory investigations. Testing strategy shifted from confirmation of cereulide intoxication in human cases towards the detection of contaminated and previously unidentified infant formula batches. Toxin quantification in human and food samples was performed using liquid chromatography–tandem mass spectrometry based on the ISO18465 method.

Results

A total of 74 infant formula samples were tested in January and February 2026, of which nine tested positive for cereulide, with concentrations ranging from 0,98 ug/kg to 10,04 ug/kg. One sample corresponded to a non-recalled batch that was subsequently recalled. In the same timeframe, clinical samples were analysed for 19 suspected cases, of which eight tested positive for cereulide (concentrations ranged from 0,1 ug/kg to 12,9 ug/kg). For four cases, the cereulide toxin was detected in both a clinical sample and a consumed infant formula sample. For the remaining four positive cases, a formula sample was not tested. None of the cases were hospitalized and all recovered after stopping formula consumption.

Conclusions

In Belgium, laboratory testing demonstrated the presence of cereulide in both consumed infant formula and clinical samples, suggesting a link between illness and contaminated products. The Belgian testing capacity also contributed to risk assessment and public health decision-making at national and European level.

FIRESIDE SESSION 4

Outbreaks of food- and water-borne diseases

Shiga toxin-producing Escherichia coli O45:H2 infections in close contacts and shedding duration during a large outbreak in Germany, 2025

ABSTRACT ID: 117

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Background

In 2025, Germany experienced a large outbreak of Shiga toxin–producing *Escherichia coli* (STEC) O45:H2 infections, predominantly affecting young children. Evidence on person-to-person transmission for this rare serotype is limited. We aimed to estimate the frequency of STEC infection among cases' close contacts and describe the stool shedding duration to inform future outbreak management.

Methods

We collected existing data from 76 local health authorities on laboratory-confirmed STEC O45:H2 outbreak cases and their close contacts (as defined by each authority based on their guidelines) using a standardized form, including demographics, symptoms, and stool test results with dates. We calculated infection frequency among close contacts, median and interquartile range (IQR) of days between case and contact symptom onset, and shedding duration (period from first positive to first negative stool test). Differences by symptom status and age (<18 vs. ≥18 years) were assessed using Wilcoxon's rank-sum test.

Results

Contact tracing and testing was conducted for 81/150 cases (54%), identifying 196 close contacts (83% household members). Overall, 40/196 (20%) contacts tested positive for STEC O45, with the highest proportion among contacts aged <5 years (13/28, 46%). Among infected contacts, 65% (26/40) were asymptomatic, 85% (34/40) were household members including 52% (21/40) being cases' siblings. Median interval between symptom onset in cases and symptomatic contacts was 3.0 days (IQR 2.0–7.8). Median shedding duration was 15 days (IQR 7.0– 23) and statistically significantly longer in symptomatic than in asymptomatic individuals (17 vs. 7.0 days; $p = 0.002$); no difference was observed between individuals aged <18 and ≥18 years.

Conclusions

A substantial proportion of close contacts tested positive for STEC O45, with frequent asymptomatic infections, particularly among young children in household settings. Some infections were likely primary. Prolonged shedding indicates potential for sustained transmission. These findings underscore the importance of contact testing and hygiene measures as key components of STEC outbreak control.

FIRESIDE SESSION 5

Surveillance and investigation

Guillain-Barré syndrome cases triggered by infections: a case-control study, Denmark, 1 January 2010 to 20 April 2026

ABSTRACT ID: 60

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Background

Guillain-Barré syndrome causes acute flaccid paralysis. Several infections can trigger it, but, to our knowledge, no large study has investigated multiple culprits. We bridge the gap: we quantify the role of preceding infections through a case-control study and report population attributable fraction (PAF) estimates.

Methods

We linked individual-level data deterministically across nationwide Danish registries. We extracted incident cases (01-01-2010/20-04-2026) using International Classification of Diseases-10 codes previously validated in Denmark. We retrieved infections during the 60 days before diagnosis, confirmed by Polymerase-Chain Reaction (PCR) for Cytomegalovirus, influenza virus, *H.influenzae*, *M.pneumoniae*, Respiratory Syncytial Virus (RSV) and SARS-CoV-2 and PCR or culture for Campylobacter spp. We conducted a case-control study, randomly selecting ten controls per case matched individually on sex, municipality of residence, and age (5-year bands). Controls' exposure period was the same calendar period as cases. We estimated per-pathogen matched odds ratios (mOR) using conditional logistic regression and the pooled unadjusted PAF with Bruzzi's formula, alongside 95% confidence intervals (CI). For *Campylobacter*, influenza, SARS-CoV-2 and RSV, we applied published correction factors for under-ascertainment and recalculated the point estimate and range for their combined PAF.

Results

We identified 2,062 cases; median age was 56 years (interquartile range 35-69), 1,204 (58%) were males. In the case-control study including 2,047 cases (99%) with municipality information and 20,470 matched controls, mORs were 150 (95% CI 37-650) for *Campylobacter spp*., 50 (5.8-430) for Cytomegalovirus, 16 (5.8-44) for influenza, 20 (5-80) for *M.pneumoniae*, 14 (7.8-27) for SARS-CoV-2, incalculable for *H.influenzae* and RSV. The pooled PAF was 3.6% (2.8-4.6). After correcting for under-ascertainment, the combined PAF was 16% (range 11-20) for the four preventable triggers.

Conclusions

Recorded infections trigger one in twenty Guillain-Barré syndrome cases in Denmark. Our estimates show that up to one in five could be prevented by increasing vaccination coverage for respiratory viruses and stricter Campylobacter control measures.

FIRESIDE SESSION 5

Surveillance and investigation

Spread of multidrug-resistant and extensively-drug resistant Shigella strains among gay, bisexual and other men who have sex with men in Europe

ABSTRACT ID: 380

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Background

In recent years, transmission routes for Shigella infection reported by countries to ECDC have shifted from predominantly food- and water-borne to sexual transmission, particularly among gay, bisexual, and other men who have sex with men (gbMSM). Emergence and circulation of multidrug-resistant (MDR) and extensively drug-resistant (XDR) Shigella strains warrant additional descriptive and genomic cluster analysis to raise awareness, to improve coordinated surveillance, and to inform treatment and control options.

Methods

Shigellosis event-based surveillance data including whole genome sequencing data reported to ECDC were analysed. By using ECDC's allele address, a stepwise cluster code that group isolates by increasing genetic similarity thresholds, core genome MLST based single linkage clusters were identified where country reports indicated a link to gbMSM.

Results

Seven genetically distinct MDR/ XDR clusters of *S. sonnei* and *S. flexneri,* predominantly affecting gbMSM, were identified to be associated with over 2,300 infections since 2023 across 12 countries (Belgium, Denmark, France, Germany, Ireland, Luxembourg, the Netherlands, Norway, Spain, Sweden the United Kingdom and the United States). Several clusters carried resistance determinants to all major antimicrobial classes used for shigellosis treatment (macrolides, fluoroquinolones, third-generation cephalosporins, sulfonamides and trimethoprim, and aminopenicillins) in addition to resistance markers to other antibiotics and disinfectants. The XDR strains specifically, carried CTX-M-15 or CTX-M-27 genes (third-generation cephalosporins), which are often carried on mobile genetic elements with other antibiotic resistance markers, severely limiting oral antibiotic options.

Conclusions

The spread of MDR/XDR Shigella strains in Europe reflects changing transmission dynamics and increasing antimicrobial resistance. Frequent antimicrobial use for treatment or for prophylaxis of other bacterial STIs, particularly among gbMSM with high STI burden, can create indirect selective pressure driving resistance in Shigella, contributing to wider antimicrobial-resistance spread. Sustained transmission within sexual networks and limited treatment options underscore the need for strengthened surveillance, increased awareness, targeted prevention, and prudent antimicrobial use.

FIRESIDE SESSION 5

Surveillance and investigation

Comparison of three Haemophilus influenzae b serotyping assays used in the Netherlands and other European countries reveals variability in assay sensitivity

ABSTRACT ID: 601

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Background

Haemophilus influenzae (Hi) serotype b (Hib) is a vaccine-preventable cause of severe disease in young children. Accurate surveillance data are essential for monitoring vaccine impact and guiding public health policy. Despite similar vaccination rates, the Netherlands consistently reports the highest Hib incidence in Europe, accounting for about 30% of cases reported to ECDC since 2010. The objective was to assess whether differences in Hib agglutination tests on cultured material used by reference laboratories across Europe contribute to these variations.

Methods

To compare agglutination tests for invasive Hi surveillance, we surveyed 20 European reference laboratories on their Hi serotyping methods. Two commercial assays and one Dutch in-house assay were selected and applied blindly to 163 Dutch invasive Hi isolates (68 b, 95 non-b). Sensitivity and specificity were calculated using PCR-based capsular typing as reference. Results from the in-house assay were compared to the two commercial assays using McNemar's Chi-squared test.

Results

Eleven of 14 participating European laboratories (78.6%) reported use of agglutination assays for serotyping. Nine out of the eleven laboratories (81.8%) complement agglutination with PCR. Testing the 95 non-b Hi isolates with the three agglutination assays yielded no false positives (100% specificity). The Dutch in-house assay showed 100% sensitivity (detected 68/68 Hib isolates), compared to 98.5% (67/68 Hib isolates, p=1.0) and 90.7% (60/68 Hib isolates, p=0.013) for the two commercial assays respectively.

Conclusions

Relying solely on agglutination for serotyping can lead to misclassification and underestimation of Hib incidences depending on the diagnostic assay used. Minor differences in assay sensitivity on cultures may only partly explain the higher incidence in the Netherlands versus other European countries. Harmonising laboratory techniques by using well-performing agglutination assays and combining phenotypic with molecular approaches can improve comparability of surveillance data. Phylogenetic analyses, comparing population Hib immunity and evaluating reported surveillance data completeness could identify additional factors affecting incidences.

FIRESIDE SESSION 5

Surveillance and investigation

Environmental detection of Sabin-like poliovirus type 3 in Barcelona, Spain, 2025: investigation of asymptomatic excretors and public health response

ABSTRACT ID: 729

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Background

Environmental surveillance is a key component of poliovirus (PV) detection in polio-free countries, where most infections are asymptomatic. In September 2025, PV was detected in wastewater in metropolitan Barcelona (Catalonia, Spain), triggering a coordinated multi-level public health response under the *National Polio Eradication Plan (NPEP)*

Methods

Wastewater samples from treatment plants (WWTPs) and upstream collectors were analyzed between August-December 2025. Viral characterization was performed through VP1 sequencing. Clinical surveillance included stool sampling from suspected carriers and contacts, analyzed by WHO-accredited methods. Contact tracing and reinforced acute flaccid paralysis (AFP) surveillance were implemented. Coordination was ensured through the NPEP-established multi-agency *Technical Support Group*.

Results

Of 55 wastewater samples analyzed, 28 tested positive for Sabin-like poliovirus type-3 (PVSL3), showing <1% divergence from the vaccine strain. Following upstream wastewater detection, epidemiological investigation identified one asymptomatic 4-month-old excretor vaccinated with oral polio vaccine (OPV) in Catalonia. Contact tracing of 67 individuals identified two additional asymptomatic paediatric excretors in the Balearic-Islands, both from OPV-using countries; all other contacts tested negative. Genetic analysis showed several nucleotide differences between isolates, with distinct but partially overlapping patterns, suggesting multiple independent excretion events rather than person-to-person transmission. Reinforced AFP surveillance identified no poliomyelitis cases. Public health measures included excretor isolation, vaccination of close contacts, targeted catch-up vaccination with public and professional outreach in affected health areas, and intensified surveillance.

Conclusions

The identification of multiple PVSL3 variants supports near-simultaneous importations, likely linked to exposure in OPV-using countries. No evidence of transmission was found, and transmission risk was assessed as extremely low. WHO highlighted the Spanish surveillance system's high sensitivity, noted that Sabin-like PV1/3 detection is not considered a public health event under Global Polio Eradication Initiative guidance, and recommended de-escalating to routine environmental surveillance at selected WWTPs. These findings support adapting public health actions under the NPEP to transmission risk and international guidance.

FIRESIDE SESSION 5

Surveillance and investigation

Invasive Pneumococcal Disease in Western Lisbon, 2020-2025: Surveillance Data and Public Health Implications

ABSTRACT ID: 830

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Background

Invasive pneumococcal disease (IPD) remains a major cause of morbidity, disproportionately affecting children under five years of age and older adults. In Portugal, despite sustained high paediatric vaccination coverage and risk-based guidelines for adults, the burden of IPD caused by non-vaccine serotypes has increased. This epidemiological shift prompted the recent transition to the 20-valent vaccine (Pn20). This study assesses the epidemiology of IPD in the Western Lisbon Local Health Unit (WLLHU).

Methods

Case definitions followed EU surveillance criteria. All confirmed IPD cases notified through the national surveillance system (SINAVE) between 2020 and 2025 were included. Descriptive analyses were performed by year and age groups to assess temporal trends and patterns. Temporal trends were evaluated using Poisson regression models.

Results

We identified 167 confirmed IPD cases (median age 66 years, IQR 54-77; 58.1% male). Adults aged ≥65 years accounted for 53.3% of cases. The overall notification rate (NR) was lowest in 2020 (2.7/100,000) and peaked in 2024 (9.3/100,000) (IRR: 1.24/year, 95% CI: 1.14-1.37, p<0.001). Bacteraemic pneumonia (73.1%) or meningitis (12.6%) were the primary clinical presentations. Hospitalization was required for 97.6% of cases (case fatality rate: 4.2%). Among cases with available information on institutionalisation (n=91), 12.1% lived in long-term care facilities (LTCF). Serotyping data were available for 5.4% of cases (n=9), identifying seven non-PCV13 serotypes, including serotypes 3 (n=5) and 8 (n=2).

Conclusions

IPD NR in Western Lisbon increased 3.4-fold between 2020 and 2024. Older adults accounted for more than half of all cases. Limited routine serotyping hinders detection of serotype replacement and weakens local surveillance. Improving serotype reporting and increasing adult vaccine uptake are key public health priorities to assess the value of emerging higher-valency pneumococcal vaccines.

FIRESIDE SESSION 5

Surveillance and investigation

Complementary Use of Wastewater Surveillance Indicators to Determine the Onset of Influenza and Respiratory Syncytial Virus Waves in Germany; 2023-2026

ABSTRACT ID: 331

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Background

Accurate description and timely detection of influenza and respiratory syncytial virus (RSV) waves is essential for public health response, such as campaigning for “last-minute” vaccinations. Wastewater surveillance offers a complementary population-level approach. We evaluated wastewater-derived indicators to identify the waves´ onset and compared them with established case-based surveillance systems in Germany.

Methods

We conducted a national time-series study using influenza data from 1 October 2023 to 10 May 2026 and RSV data from 1 October 2024 to 10 May 2026. We evaluated two wastewater indicators: the proportion of wastewater treatment plants with samples above the limit of quantification (WW-LOQ-P) and viral load (WW-VL). We compared these with three case-based indicators: hospital sentinel incidence, primary care virological sentinel positivity (VS-P; proportion of positive samples), and notification incidence. WW-LOQ-P and VS-P were proportion-based indicators, while the others were based on absolute counts. We assessed seasonal dynamics using visual inspection and cross-correlation analysis and determined waves’ onset using the first step of the Moving Epidemic Method, a threshold-based approach applied to identify the start of epidemic periods.

Results

Influenza and RSV showed similar seasonal dynamics across wastewater and case-based surveillance systems. The two proportion-based indicators consistently showed earlier increases and later declines compared with absolute-count indicators. Cross-correlation analyses indicated largely synchronous dynamics between wastewater and case-based data. Season onset analysis showed that WW-LOQ-P detected waves´ onset earliest and most consistently, followed by VS-P and other case-based indicators, while WW-VL detected onset latest.

Conclusions

Wastewater surveillance showed good agreement with case-based surveillance systems. The proportional wastewater indicator WW-LOQ-P detected waves´ onset most consistently and at the earliest time points, indicating its suitability for timely seasonal monitoring. These findings support integrating wastewater surveillance into routine respiratory virus surveillance to support timely public health response, particularly in countries with limited or delayed case-based surveillance.

FIRESIDE SESSION 6

Healthcare-associated infections

Outbreak management: The Strategy for Addressing Future Epidemics in Nursing Homes (SAFE-NH) study

ABSTRACT ID: 592

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Background

Infectious disease outbreaks remain challenging in nursing homes (NHs), with far-reaching consequences for residents, staff and organisational functioning. These include higher morbidity and & mortality rates, fear of infection, workload, and increased costs. Compared with hospitals, NHs have limited infection prevention and control (IPC) resources, which may affect preparedness and outbreak response. The Strategy for Addressing Future Epidemics in Nursing Homes (SAFE-NH) study aims to identify determinants influencing outbreak management effectiveness in NHs.

Methods

A sequential mixed-method study (initiated November 2024) comprised a cross-sectional survey administered via Qualtrics XM® (n=40) and semi-structured interviews with NH-staff responsible for outbreak management (n=4), experts from the Infectious Disease and Control team of the Government of Flanders (IDCGF) (n=2), and a physician responsible for coordinating care in NHs (PCC) (n=1). Additionally, two focus groups were conducted with 1) IDCGF experts (n=3), and 2) PCCs (n=6).

Results

Survey results (response rate 60.6%; 40/66 NHs) showed that 87.5% of NHs had experienced an outbreak. An outbreak management procedure was available in 84.6% of NHs. Isolation cards were used during outbreaks in 72.5% of facilities. Insufficient outbreak management training during initial professional education was reported by 41% of NHs. Awareness and clarity regarding mandatory outbreak reporting were reported by 77.5% of NHs. Qualitative thematic analysis identified 30 determinants influencing effective outbreak management, which were organised into 7 overarching themes: 1) leadership style, 2) organisational context, 3) policy, 4) collaboration and network integration, 5) communication & information dynamics, 6) IPC and implementation knowledge & skills, and 7) behavioural and psychological influences.

Conclusions

The identified determinants indicate the need for targeted multi-level health actions, including pro-active plan-ning, context-specific IPC training, supportive leadership, and enhanced collaboration and communication. Together, these findings highlight that effective outbreak management requires a coordinated, system-wide approach. Addressing these determinants may strengthen outbreak management and support safe care.

FIRESIDE SESSION 6

Healthcare-associated infections

Sink-drain replacement to control a carbapenemase-producing Klebsiella pneumoniae outbreak in a surgical ward, Gran Canaria, Spain, 2024–2026

ABSTRACT ID: 551

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Background

Carbapenemase-producing Klebsiella pneumoniae is a major healthcare-associated threat. Surgical wards are particularly vulnerable because wounds, surgical drains, catheters and frequent invasive care may facilitate progression from colonization to infection. We investigated a prolonged outbreak in a general surgery ward at a 800-bed acute-care hospital in Spain where environmental source control was required.

Methods

A case was defined as carbapenemase-producing K. pneumoniae infection in a clinical sample from a patient who had stayed in the ward ≥48 hours in the ward during the preceding three months. Cases from 1 January 2024 to 10 March 2026 were reviewed.

Results

Baseline incidence density (ID) was 1.26 per 1,000 patient-days (95% CI: 0.67–2.15). Between December 2024–January 2025, ID increased to 3.09 (95% CI: 1.13–6.73) when six cases were detected. Initial measures, including admission and weekly screening, patient relocation and cohorting in contact-precautions, cleaning reinforcement and staff feedback, achieved temporary negative screens but 11 cases were detected and ID remained 3.09 (95% CI: 1.54–5.53). During subsequent surveillance (June-November 2025), 23 cases were detected and ID increased to 4.03 (95% CI: 2.55–6.04). Molecular characterisation revealed a polyclonal outbreak with six sequence types (ST13, ST15, ST147, ST152, ST307, ST115) and multiple carbapenemases (OXA-48, NDM, OXA-48+NDM), excluding clonal transmission as the primary mechanism. Room-level mapping suggested spatial clustering consistent with an initial environmental reservoir and subsequent wider ward dissemination. Environmental sampling identified contaminated wastewater outlets, including sink-drains. The second-level intervention included replacement of sink drainage systems and faucet aerators, terminal cleaning of all rooms and intensified audit-feedback. After this intervention (December 2025-March 2026), the number of clinical cases decreased to 5 and ID fell to 1.62 per 1,000 patient-days (95% CI: 0.53–3.78)

Conclusions

Prolonged carbapenemase-producing K. pneumoniae outbreaks may evolve hidden reservoirs. Drainage-system replacement interrupt transmission in a high-risk surgical ward.

FIRESIDE SESSION 6

Healthcare-associated infections

Multicountry surveillance data on neonatal healthcare-associated infections from the NeoIPC Surveillance Network

ABSTRACT ID: 467

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Background

Healthcare-associated infections (HAIs) remain a major cause of mortality and morbidity among high-risk neonates, while harmonised multicountry surveillance data remain limited. The NeoIPC Surveillance Network was established to collect standardised surveillance data on neonatal HAIs, antimicrobial exposure and resistance, and infection prevention and control (IPC) practices across participating neonatal departments.

Methods

The surveillance framework integrates prospective patient-level surveillance into daily IPC practice across participating departments. This analysis included surveillance data recorded between January 2024 and May 2026 from 30 neonatal departments in Europe and South Africa. Eligible neonates included infants with birth weight ‹1500 g and/or gestational age ‹32 weeks admitted within the first 120 days of life. Surveillance used harmonised case definitions and daily recording of HAIs, device exposure, antimicrobial use and protective care practices. Incidence densities, exposure-days and antimicrobial resistance indicators were calculated.

Results

Thirty neonatal departments contributed 2,489 patient records representing 99,876 patient-days. Overall, 939 infections were recorded, including 745 primary sepsis/bloodstream infection (BSI) corresponding to 7.5 infections per 1,000 patient-days. The incidence density of central venous catheter-associated sepsis/BSI was 11.1 per 1,000 device-days. Infectious agents were identified in 42.8% of infections. Coagulase-negative staphylococci predominated among detected microorganisms, while Enterobacterales accounted for a substantial proportion of Gram-negative isolates. Third-generation cephalosporin-resistant Enterobacterales, particularly *Klebsiella pneumoniae*, represented the most frequently reported multidrug-resistant organisms. Non-invasive ventilation was the most frequently recorded device exposure, accounting for 49.9 days per 100 patient-days, while reserve-group antibiotics accounted for 0.7 days per 100 patient-days. Neonates received 66.8 days of exclusive human milk feeding per 100 patient-days.

Conclusions

The NeoIPC Surveillance Network demonstrates the feasibility of harmonised multicountry neonatal HAI surveillance across diverse healthcare settings. The surveillance framework provides comparable epidemiological data and enables benchmarking to support IPC activities, antimicrobial stewardship, and continuous surveillance-informed improvement in neonatal care.

FIRESIDE SESSION 6

Healthcare-associated infections

Time-to-Antibiotics in Sepsis and Septic Shock: A Systematic Review and Meta-Analysis Accounting for Severity-of-Illness Adjustment

ABSTRACT ID: 579

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Background

Surviving Sepsis Campaign guidelines for timely antibiotics (‹1h for septic shock, ‹3h for sepsis without shock) are based on meta-analyses that did not find significant signals for recommended intervals, perhaps because they combined sepsis and septic shock and included studies that varied widely in their rigor of risk adjustment.

Methods

We searched PubMed, Embase, Cochrane Register, and Scopus for randomized trials and observational studies reporting associations between antibiotic timing and mortality in adults with sepsis or septic shock, that differentiated between sepsis with and without shock, and that adjusted at minimum for severity-of-illness. We compared administration ›1h vs ‹1h, ›3h vs ‹3h, ›6h vs ‹6h and estimated effects per hour amongst studies that pooled together antibiotic intervals up to a maximum of 6h and with broad risk adjustment.

Results

We identified 40 eligible studies with 688,399 patients. In septic shock, antibiotic administration after ›1h vs ‹1h was associated with increased mortality (aOR 1.16; 95% CI 1.01-1.33). In sepsis without shock, there was no significant association for antibiotics ›1h vs ‹1h (aOR 1.05, 95% CI 0.93-1.17), nor for ›3h vs ‹3h (aOR 1.11, 95% CI 0.95-1.31), but increased mortality with ›6h vs ‹6h (aOR 1.22, 95% CI 1.03-1.44). Across studies that pooled together antibiotic intervals up to a maximum of 6h and with broad risk adjustment, each additional hour until antibiotics was associated with increased mortality in septic shock (aOR 1.12, 95% CI 1.04–1.21) but not in sepsis without shock (aOR 1.03; 95% CI 0.98-1.09).

Conclusions

In summary, delays of ›1h were associated with increased mortality in septic shock and delays of ›6h were associated with increased mortality in sepsis without shock. Our results strengthen the evidence underlying current Surviving Sepsis Campaign time-to-antibiotic goals for septic shock but suggest longer intervals may be safe for patients without shock.

FIRESIDE SESSION 6

Healthcare-associated infections

Targeted metagenomic analysis of causes of influenza-like and respiratory illness in healthcare workers over winter, United Kingdom, 2023-2024

ABSTRACT ID: 529

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Background

Healthcare workers (HCWs) have an increased risk of infection with respiratory viruses, leading to a burden on healthcare services over winter. We used targeted metagenomic sequencing, rather than PCR-based diagnostics, to understand the full range of viruses associated with respiratory illness in HCWs in winter 2023.

Methods

SIREN is a UK-wide cohort study of HCWs, who completed fortnightly questionnaires and provided nasopharyngeal swabs for SARS-CoV-2, influenza, and respiratory syncytial virus (RSV) PCR testing over winter 2023-24. Based on participant symptoms, we selected PCR-negative swabs taken in November-December 2023 for bait capture metagenomic sequencing targeting 29 respiratory viruses and strains.

Results

We sequenced 1321 PCR-negative samples from November-December 2023. Respiratory viruses were detected in 29% (49/170) of influenza-like illness (ILI) samples and 32% (272/858) of respiratory illness without fever (RWF) samples. The most common viruses in both groups were rhinovirus (16%), seasonal coronavirus (8%), and human metapneumovirus (3%). Only 3% (3/106) of non-respiratory illness without fever (NWF) samples and 5% (10/187) of asymptomatic samples had a virus detected. All viral species could be detected up to 3 days before onset of first symptom. 19% of PCR-negative individuals with a metagenomically-detected virus took time off work for their symptoms, for a median of 2 days.

Conclusions

We show that many non-vaccine-preventable viruses are implicated in respiratory illness in HCWs over winter and contribute to time off work. We detected all species pre-symptomatically and in participants without fever. Interventions targeting a broader range of respiratory pathogens are required to reduce winter pressures on healthcare systems.

FIRESIDE SESSION 7

Vaccine-preventable diseases: from evidence to practice

An evidence-based update of recommendations for meningococcal vaccination in Germany: Introducing quadrivalent vaccination in adolescence and discontinuing meningococcal C vaccination in childhood

ABSTRACT ID: 123

Vanessa Piechotta [1], ***Felix Guenther*** [2], ***Madita Fahrenwald*** [2], ***Julia Wilhelm*** [2], ***Frank Sandmann*** [2], ***Heike Claus*** [3], ***Reinhard Berner*** [4], ***Thomas Gruenewald*** [5], ***Marianne Roebl-Mathieu*** [6], ***Christian Schoenfeld*** [7], ***Julia Tabatabai*** [8], ***Robin Schaefer*** [2], ***Alexander Dalpke*** [9]

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Background

In Germany, the Standing Committee on Vaccination (STIKO) issues evidence-based vaccination recommendations. Routine vaccination for infants/young children against *Neisseria meningitidis* serogroup C (MenC) was introduced in 2006 and against MenB in 2024. In 2025, STIKO evaluated MenACWY vaccines considering epidemiological developments to adapt recommendations to further reduce invasive meningococcal disease (IMD).

Methods

We reviewed IMD surveillance data and epidemiological trends in Germany, conducted a systematic review on efficacy/effectiveness and safety of MenACWY vaccines, developed a mathematical model evaluating effectiveness and efficiency of different MenACWY vaccination strategies, and performed a survey on vaccination practices and acceptance among vaccinating physicians. Evidence was evaluated using the GRADE evidence-todecision framework incorporating considerations of equity, acceptability and feasibility.

Results

In 2025, MenB (~0.15 cases/100,000) and MenY (~0.13 cases/100,000) were the most prevalent serogroups causing IMD in Germany; MenC and other serogroups were rare (‹0.01 cases/100,000). MenB primarily affected young children, and MenY mainly adolescents and older adults. The systematic review showed a vaccine effectiveness of ›90% against MenACWY-IMD (3 studies), with very low risk of serious adverse events, comparable to other age-appropriate vaccinations (RR 0.86, 95%-CI 0.60-1.23, 13 studies). GRADE certainty of evidence was low. Mathematical modelling yielded a number-needed-to-vaccinate (NNV) to prevent one IMD case of 51,000 (95%- CI 45,000-59,000) for adolescents, 81,000 (71,000-91,000) for combined vaccination of children and adolescents, and 120,000 (98,000-140,000) for children, indicating adolescent vaccination as the most efficient strategy.

Surveyed physicians (n=386, of those 86% pediatricians) reported high acceptance of MenACWY vaccination (95% for children, 94% for adolescents). Frequency of healthcare visits differed by age, indicating best access to vaccinate adolescents from 10-‹14 years of age.

Conclusions

STIKO now recommends routine MenACWY vaccination for 12–14-year-olds to ensure protection against IMD before rising MenY incidence in late adolescence. Routine MenC vaccination in childhood is discontinued due to the rarity of MenACWY-IMD in young children.

FIRESIDE SESSION 7

Vaccine-preventable diseases: from evidence to practice

Epidemiological impact assessment of the second winter of RSV immunisation of infants with nirsevimab, Ireland 2025/2026

ABSTRACT ID: 256

Laura Kayaert [1], ***Lisa Domegan*** [2], ***Margaret Fitzgerald*** [2], ***Carina Brehony*** [2], ***Katie O'Brien*** [2], ***Kevin Brown*** [3], ***Piaras O'Lorcain*** [2], ***Michael Carton*** [2], ***Lois O'Connor*** [4], ***Augustine Pereira*** [4], ***Victor Aiyedun*** [2], ***Éamonn O'Moore*** [4]

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Background

Infant immunisation with nirsevimab reduces the risk of severe respiratory syncytial virus (RSV) disease. During winter 2025/2026, Ireland implemented at birth immunisation for infants born September 2025-February 2026 (birth cohort) and for the first time catch-up immunisation for infants born March-August 2025 (catch-up cohort). This study aimed to assess the impact of nirsevimab immunisation in Ireland on RSV-related infant morbidity.

Methods

All notified Irish RSV cases (1 September 2025-31 March 2026) among infants born March 2025-February 2026 were included. Using immunisation uptake data and effectiveness estimates, we estimated averted events and number needed to immunise to prevent events (cases, emergency department (ED), hospital, and intensive care unit (ICU) admissions) for birth and catch-up cohorts.

Results

During winter 2025/2026, immunisation uptake was 87% for birth and 52% for catch-up cohorts. There were 403 and 695 RSV cases among the birth and catch-up cohorts, respectively, compared to 1154 (-65%) and 1341 (-49%) in the same age groups in 2023/2024. At birth immunisation averted 966 (95%CI: 956-977) cases, 442 (95%CI: 436-447) ED presentations, 364 (95%CI: 360-368) hospitalisations, and 35 (95%CI: 34-36) ICU admissions. The number needed to immunise was 25 (95%CI: 23-26) to prevent one case, 54 (95%CI: 50-58) for ED presentation, 65 (95%CI: 60-71) for hospitalisation, and 675 (95%CI: 494-857) for ICU admission. Catch-up immunisation averted 477 (95%CI: 472-483) cases, 240 (95%CI: 237-243) ED presentations, 155 (95%CI: 153-156) hospitalisations, and 7 (95%CI: 7-7) ICU admissions. The number needed to immunise was 29 (95%CI: 27-31) for preventing one case, 58 (95%CI: 53-63) for ED presentation, 88 (95%CI: 80-97) for hospitalisation, and 2026 (95%CI: 1086-2966) for ICU admission.

Conclusions

Immunising infants during winter 2025/2026 reduced RSV-related infant morbidity in Ireland. To maintain optimal protection, it is recommended that annual immunisation continues to include both groups, with sustained efforts to increase uptake among the catch-up cohort.

FIRESIDE SESSION 7

Vaccine-preventable diseases: from evidence to practice

Association between influenza vaccination and severe outcomes in adults aged ≥65 years hospitalised with laboratory-confirmed influenza: a retrospective cohort study in Europe, 2015/16–2024/25

ABSTRACT ID: 296

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Background

Older adults face an increased risk of influenza-related severe outcomes, including intensive care unit (ICU) admission and in-hospital death (IHD). Although influenza vaccination reduces risk of hospitalisation, its effect on disease severity among already hospitalised patients remains uncertain. We estimated the association between influenza vaccination and severe outcomes (ICU and IHD) among adults aged ≥65 years hospitalised with laboratory-confirmed influenza.

Methods

We conducted a retrospective cohort study using European multi-centre hospital network data across multiple seasons (2015/16–2024/25). RT-PCR-confirmed influenza patients entered the cohort at hospital admission and were followed until ICU admission, IHD or discharge. Vaccination was defined as vaccine receipt ≥14 days before symptom onset. We estimated pooled-season confounder-adjusted vaccine risk ratios (aRR) using modified Poisson regression. We calculated relative risk reduction (RRR) as (1 – aRR) × 100 and assessed vaccine effect modification by age group (65–79, ≥80 years).

Results

After exclusions, we included 4,257 patients from five study sites across six seasons (2016/17–2018/19 and 2022/23–2024/25). ICU admission occurred in 3% (81/2,490) of vaccinated and 5% (89/1,767) of unvaccinated patients. IHD occurred in 5% of both vaccinated (119/2,490) and unvaccinated (96/1,767) patients. The RRR against ICU admission was 11% (95% CI: -21–34): -4% (95% CI: -46–25) among 65–79-year-olds and 44% (95% CI: -11–72) among ≥80-year-olds (p-value-interaction = 0.03). The RRR against IHD was 26% (95% CI: 3–43): 17% (95% CI: -38–50) among 65–79-year-olds and 29% (95% CI: 4–48) among ≥80-year-olds (p-value-interaction = 0.79).

Conclusions

Although we observed effect modification by age, associations with ICU admission were not statistically significant. However, influenza vaccination was associated with a 26% reduction in IHD among older adults hospitalised with influenza, reinforcing vaccination benefits beyond preventing hospitalisation. Multicentre hospital studies pooled across seasons provide the necessary sample size to evaluate these rare severe outcomes.

FIRESIDE SESSION 7

Vaccine-preventable diseases: from evidence to practice

Reducing antibiotic eligibility from 21 to 14 days after symptom onset for cases and contacts of pertussis in England did not increase household clustering

ABSTRACT ID: 371

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Background

Exceptionally high pertussis activity in England necessitated urgent revisions to public health (PH) recommendations in June 2024. An important change was the reduction in timeframe for advising antibiotic therapy for cases without high-risk contacts and eligible contacts from 21 to 14 days from symptom onset. We investigated whether this reduction was associated with increased household transmission compared to earlier periods.

Methods

We analysed data on all notified cases in England between January 2018 and February 2026 from case management system, excluding 2020-2023 due to extremely low transmission. Clusters were defined as two or more cases with symptom onset within 90 days of another case at the same at the same residential address (Unique Property Reference Number, England). Cases and clusters were categorised into four time periods according to the level of pertussis activity (high or endemic) and PH recommendations (21-day or 14-day). We compared the proportion of clustered cases with 95% confidence intervals and examined differences in age, sex and deprivation distribution across the four periods.

Results

In total, 7,960 out of 55,123 (14.4%) cases were clustered, with 3,603 clusters identified. During high transmission, 17.6% (17.0-18.1%) of cases were clustered in the 21-day recommendation period and 12.2% (11.7-12.7%) in the 14-day recommendation period. The corresponding proportions during endemic transmission were 15.6% (14.9-16.2%) and 8.2% (7.6-8.9%). Clustered and non-clustered cases showed similar distributions of age, sex and deprivation across all four periods.

Conclusions

Despite very high community transmission, reducing the antibiotic eligibility timeframe from 21 to 14 days was not associated with increased household clustering. While interpretation is limited by the lack of detailed individual-level data, these findings offer cautious reassurance that the 2024 guidance did not adversely affect household transmission. Further studies using enhanced epidemiological data are needed to confirm this novel observation and inform refinements to PH management guidance.

Vaccine-preventable diseases: from evidence to practice

Vaccine effectiveness of the influenza vaccine administered alone or concomitantly with COVID-19 vaccine against influenza A subtype hospitalisation among older adults: results from a multi-centre study, Europe, 2023/24 and 2024/25 influenza seasons

ABSTRACT ID: 403

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Background

Concomitant influenza and COVID-19 vaccination have been widely implemented in Europe, but evidence on its impact on influenza vaccine effectiveness (IVE) is limited. We compared IVE of concomitant versus influenza-only vaccination against influenza A subtypes during the 2023/24 and 2024/25 seasons among adults aged ≥65 years, through a European multi-centre hospital-based study.

Methods

We used the test-negative design, recruiting cases and controls from hospitalised severe acute respiratory infection (SARI) patients eligible for influenza and COVID-19 vaccination. We defined cases as SARI patients testing RT-PCR-positive for each influenza subtype; controls tested negative for all influenza viruses. We defined "concomitant" as those receiving both vaccines the same day; "influenza-only" patients received only influenza vaccine that season; "unvaccinated" received neither vaccine that season (those receiving different-day vaccinations were excluded).

We estimated IVE for each subtype and season from confounder-adjusted odds ratios (aORs) for vaccination using logistic regression, expressed as (1–aOR)×100, and compared differences between vaccination groups.

Results

We included 647 influenza A(H1N1)pdm09 cases and 6150 controls, 298 A(H3N2) cases and 6012 controls in 2023/24; 746 and 7363, and 473 and 6740 in 2024/25, respectively. In 2023/24, IVE against A(H1N1)pdm09 was higher for concomitant vaccination than influenza vaccination alone (difference: 23%; 95%CI: 3–44), while IVE was similar against A(H3N2) (difference: 5%; 95%CI: -25–34). In 2024/25, IVE for concomitant vaccination was higher for both subtypes (difference: 11%; 95%CI: -4–25 against A(H1N1)pdm09; 11%; 95%CI: -8–30 against A(H3N2)), although differences were not statistically significant.

Conclusions

We observed a signal of higher IVE among individuals receiving concomitant COVID-19 and influenza vaccination compared with influenza-only vaccination alone across two seasons with predominant A(H1N1)pdm09 circulation. Although other elements need to be considered, our findings align with evidence supporting co-vaccination. Ongoing research aims to incorporate additional determinants of IVE (e.g. virus clade, vaccine type) in current and subsequent seasons.

FIRESIDE SESSION 7

Vaccine-preventable diseases: from evidence to practice

Statistical modelling approaches for estimating vaccine effectiveness of consecutive SARS-CoV-2 variant sublineages in the absence of study-specific genetic sequencing data

ABSTRACT ID: 425

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Background

Genetic changes in COVID-19 variants/sublineages (VSLs) can reduce vaccine effectiveness (VE). Timely VSL-specific VE estimates are essential, but virus classification using whole genome sequencing (gold standard) is resource-intensive. Alternatively, restricting the study to the VSL predominant periods (PP) using external sequencing data is commonly used. We propose novel methods to estimate and formally compare VSL-specific VE in test-negative design studies during variant transitions.

Methods

We developed the variant category model (VCM) and the variant proportion model (VPM), incorporating VSL and vaccination*VSL interaction terms in logistic regression models. In the VCM, VSL is a binary variable representing the most likely underlying VSL; in the VPM, VSL is a continuous variable reflecting the weekly proportion of the emerging VSL; both can be derived from publicly available sequencing data. Formal comparison of VSL-specific VE was assessed using the ratio of odds ratios (ROR), which can be derived from the interaction term. The proposed methods were applied to data from a European hospital-based multicentre study, during the transition from XBB to BA.2.86 (2023/24), among adults ≥65 years, and compared with study-specific sequencing data (SD) and PP methods.

Results

Overall, at 14–59 days post-vaccination, VE against XBB was 68% (95%CI:38–86) and 71% (95%CI:50–83) using VCM and VPM, respectively, consistent with the PP method (67%; 95%CI:1–92). Validation using SD was not possible due to absence of vaccinated XBB cases. Against BA.2.86, VE was 41% (95%CI:23–54) and 48% (95%CI:35–59), using VCM and VPM, respectively, with lower VE results from SD (34%; 95%CI: -14–64) but equivalent results from the PP (42%; 95%CI:25–56). VE was lower against BA.2.86 when compared with XBB (ROR = 1.8; 95%CI:1.1–2.9).

Conclusions

The proposed models yield VE estimates consistent with established methods, enabling formal comparison of VE across variants. The novel methods could also provide VE estimates when standard techniques are limited by low sample size.

FIRESIDE SESSION 8

Social determinants and actions for public health

An ethical roadmap for local wastewater surveillance deployment

ABSTRACT ID: 414

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Background

Wastewater surveillance tracks infectious diseases by detecting pathogen signals, offering early warnings and population-level insights. It guides public health actions like vaccinations or isolation but relatively lacks deployment frameworks which might lead to field questions. Dutch public health authorities have developed an ethical roadmap to address potential challenges.

Methods

The roadmap was developed by applying multiple methods. First, a literature review was conducted to identify the key ethical and legal principles regarding wastewater surveillance. This was followed by a moral deliberation session in which 15 professionals from communicable disease control, law, and academia participated. The purpose of the moral deliberation was to explore which questions need to be asked to determine the necessary ethical considerations regarding the deployment of wastewater surveillance in a specific (outbreak) setting. The moral deliberation was facilitated by an ethicist using a value-based reflection tool. During workshops with public health professionals and a tabletop exercise with medical doctors and nurses focused on communicable disease control, the concept roadmap was tested and refined.

Results

The roadmap outlines key principles for ethical decision-making:

• Public health benefit and relevance: considering disease severity and contagiousness • Proportionality: balancing measures with outbreak severity and alternatives • Societal impact: addressing privacy, stigmatization and community concerns • Transparency, accountability and stakeholder engagement: ensuring clear communication about data use to build public trust • Legal and institutional responsibility: defining mandates and accountability

Conclusions

The ethical decision-support roadmap for wastewater surveillance provides a structured framework to balance public health benefits with societal concerns, ensuring proportional, transparent, and accountable use of wastewater data. By addressing legal gaps and fostering stakeholder trust, this roadmap empowers outbreak response teams to leverage wastewater surveillance effectively while safeguarding community privacy and ethical standards. Its iterative development and practical focus make it a valuable tool for guiding future public health actions.

FIRESIDE SESSION 8

Social determinants and actions for public health

Addressing the data gaps: A survey of Clostridioides difficile infection practices in England, September - December 2025

ABSTRACT ID: 875

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Background

Clostridioides difficile infection (CDI) incidence increased in England from 2021–2025, with variation between hospital trusts. Previous analyses identified system-wide data gaps in infection prevention and control (IPC), environmental cleaning, care in non-standard settings (e.g. corridors), and testing practices. This study aimed to characterise these factors and assess their association with CDI incidence.

Methods

A survey was conducted across all acute NHS trusts in England covering IPC, laboratory, staffing, and clinical practice information for 2019, 2023 and 2024. It was open for ten weeks and completed by relevant hospital specialists. Associations between hospital-acquired CDI incidence in 2023/24 and isolation times and corridor care in 2024 were assessed using negative binomial regression with bed-day offsets, adjusting for trust type and region. Free-text responses were analysed thematically.

Results

The response rate was 76% (102/134 trusts). Trusts not always isolating diarrhoeal patients within four hours had higher median CDI rates than those always isolating within four hours (25.6 [IQR 19.7–32.2] vs 16.1 [10.4–23.6] per 100,000 bed-days). CDI incidence in these trusts was 27% higher in multivariable analysis (95% CI 1.05–1.54, p=0.014). Trusts reporting >10% corridor care had higher CDI rates than those reporting none (median 34.7 [30.9–38.8] vs 18.1 [7.6–25.7]). Corridor care of >10% was associated with a 53% higher CDI incidence in multivariable analysis (95% CI 1.15–2.05, p = 0.004). No other variables investigated were significantly associated with higher CDI incidence. Qualitative analysis identified operational pressures, estate constraints, resource limitations, and inconsistent clinical engagement as barriers to IPC implementation, reflecting system-level challenges.

Conclusions

Corridor care and delayed isolation were strongly associated with higher CDI incidence, and qualitative findings suggest these reflect deeper estate and capacity constraints that limit timely cleaning and room turnaround. Addressing these upstream constraints may be essential for improving CDI prevention.

FIRESIDE SESSION 8

Social determinants and actions for public health

From surveillance to action: One Health use of Highly pathogenic avian influenza (HPAI) data for decision making and risk communication in Norway, 2024-2026

ABSTRACT ID: 777

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Background

HPAI has emerged as a One Health threat with pandemic potential, requiring integrated surveillance that not only detect virus circulation in animals, but directly inform public health action.

Methods

As part of the OH4Surveillance project (EU4Health), we expanded and strengthened One Health surveillance system for HPAI in Norway (2024-2026). The system combined passive and targeted active surveillance for HPAI virus (HPAIV) in wildlife, serological investigations in wild birds and mammals, and whole-genome sequencing (WGS). The study area included mainland Norway, Svalbard in the Arctic and Queen Maud Land in Antarctica. Surveillance planning, data sharing and interpretation were integrated into the existing collaboration between the Norwegian Veterinary Institute and the Norwegian Institute of Public Health.

Results

HPAIVs (H5 clade 2.3.4.4b), including H5N1 and H5N5, were mostly detected in wild birds, with occasional spillover to wild mammals (>300 samples were analysed). Surveillance outputs directly informed public health actions: detections triggered targeted infection prevention advice for volunteers and professionals handling sick or dead wild birds. WGS data shared via GISAID EpiFlu were incorporated into national risk assessments, strengthening evaluation of zoonotic potential and guiding preparedness. Serological investigations in seabirds and mammalian sentinels (e.g. polar bears and Arctic foxes) provided complementary evidence of virus exposure in ecosystems relevant to specific risk groups such as hunters and wildlife professionals.

Conclusions

OH4Surveillance outputs have been actively used in Norway to enhance situational awareness, risk assessment, and risk communication. By integrating data on virus detection, WGS and serology, the system has supported timely assessment of spillover risk and informed infection control guidance. The project demonstrates how coordinated One Health surveillance can move beyond data generation to provide decision support. This approach illustrates how wildlife surveillance can be translated into actionable public health measures, strengthening preparedness for HPAI and serving as a model for responding to emerging zoonotic threats.

FIRESIDE SESSION 8

Social determinants and actions for public health

Association between socioeconomic deprivation and pertussis incidence in HSE Dublin and Midlands, 2024

ABSTRACT ID: 641

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Background

Pertussis notifications increased substantially in Ireland during 2024, with incidence greatly exceeding previous seasonal peaks, consistent with international trends. This study examined the association between area-level socioeconomic deprivation and pertussis incidence in the HSE Dublin and Midlands region to assess inequalities in disease burden and inform public health interventions.

Methods

All 121 laboratory-confirmed pertussis cases notified to the regional Department of Public Health during 2024 were included. Demographic, clinical, and vaccination data were recorded for each case. Cases were geocoded to residential Small Areas and assigned deprivation scores using the Pobal HP Deprivation Index. Population denominator data from Health Atlas Ireland (2022 Census) were used to calculate cumulative incidence rates. Associations between deprivation and incidence were analysed using Poisson regression with population offset terms. Sensitivity analyses using negative binomial regression and robust standard errors were also performed.

Results

A clear socioeconomic gradient in pertussis incidence was identified. Using four-band deprivation categorisation, cumulative incidence increased from 1.2 per 100,000 population in the most affluent areas to 15.4 per 100,000 in the most deprived areas. When deprivation was analysed ordinally using the full eight-category deprivation index, each one-category increase in deprivation was associated with a 16% higher pertussis incidence rate (IRR 1.16, 95% CI 1.03–1.31; p=0.016). Compared with the most affluent areas, incidence in more deprived communities was between nine- and thirteen-fold higher.

Conclusions

These findings demonstrate substantial socioeconomic inequalities in pertussis burden during the 2024 outbreak and highlight the importance of targeted vaccination strategies, strengthened maternal immunisation uptake, and equity-focused public health interventions in deprived communities.

FIRESIDE SESSION 8

Social determinants and actions for public health

Upsurge in congenital syphilis in the EU/EEA: time to scale up public health responses

ABSTRACT ID: 445

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Background

Congenital syphilis (CS) is under routine surveillance in the EU/EEA. In 2024, CS notifications reached their highest level in the past decade, coinciding with increasing syphilis notifications among women. This study describes CS cases in 2024, analyses 2015-2024 trends, examines associations between syphilis among women of reproductive age and CS rates, and highlights public health implications.

Methods

Confirmed CS cases and syphilis notifications among women aged 15-44 years reported by EU/EEA countries for 2015–2024 were extracted from European Surveillance Portal for Infectious Diseases. For CS cases reported in 2024, key demographics and clinical outcomes (alive/deceased) were described. Country-specific CS and syphilis rates per 100,000 were calculated using Eurostat denominators. Associations between syphilis in women and CS were assessed using quasi-Poisson regression adjusting for population size and year.

Results

In 2024, 140 confirmed CS cases were reported by 28 EU/EEA countries (4.7 per 100,000 live births). Bulgaria, Hungary and Portugal accounted for 62% (87/140) of cases. Most cases were diagnosed neonatally (86/99; 87%), and 19% (11/58) of cases with known outcomes were reported as deceased. During 2015–2024, in 23 countries with consistent reporting, the EU/EEA CS rate increased from 1.3 to 5.2 per 100,000 live births. After a gradual rise to 2019 and a decline in 2020–2021, the rate nearly doubled between 2022 and 2024. Over the same period, syphilis notification rates among women increased by 183%, from 1.9 to 5.3 per 100,000 population. Significant positive associations between syphilis rates and CS rates were observed in Germany (incidence rate ratio [IRR] 2.48, 95% CI 1.36–4.52) and Hungary (IRR 1.10, 95% CI 1.01–1.21). CS increases in Romania and Slovakia were independent of syphilis rates among women.

Conclusions

The CS upsurge highlights prevention gaps across the EU/EEA. Strengthened surveillance, national audits of antenatal screening pathways, and testing policies adapted to evolving epidemiology are warranted.

FIRESIDE SESSION 8

Social determinants and actions for public health

Parental refusal of HPV vaccination in Morocco: prevalence and associated factors from a multicentre cross-sectional study

ABSTRACT ID: 356

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Background

Vaccination against the human papillomavirus (HPV) is an effective way to prevent cervical cancer. Nonetheless, acceptance rates in Morocco are low. The objective of this study was to measure the prevalence of parental refusal of the HPV vaccine and the associated risk factors.

Methods

A multicenter cross-sectional survey was conducted among Moroccan parents of girls aged 11 to 14 who visited health facilities from March 3 to September 30, 2025. The study looked at sociodemographic factors, awareness of HPV and cervical cancer, and attitudes toward vaccination. Multivariate logistic regression analysis was used to identify risk factors associated with vaccine rejection. We used Epi-Info version-7 for analysis data.

Results

The study included 1,444 participants, with a mean age of 37.7±6.6 years. Among them, 415 (28.7%) refused HPV vaccination for their daughters. This refusal was significantly associated with higher education levels (Adjustedodds-ratio (AOR)=3.88; [1.67-9.05]), lower income (AOR=2.26; [1.21-4.24]), less trust in the healthcare system (AOR=28.4; [15.59-51.7]), limited knowledge about cervical cancer (AOR=2.75; [1.58-4.78]), and insufficient information about the vaccine (AOR=2.03; [1.21-3.41]). Refusal was also correlated with a poor understanding of the severity of the infection (AOR=2.43; [1.37-4.30]), concerns about vaccinating girls (AOR=3.98; [2.45-6.46]), failure to adhere to previous vaccination schedules (AOR=3.86; [2.05-7.28]), difficulties accessing health centers (AOR=6.49; [2.32-18.17]), and a lack of support from healthcare professionals (AOR=7.39; [2.24-24.3]).

Conclusions

Parental refusal of the HPV vaccine remains a major barrier to cervical cancer prevention. Improving vaccine acceptance in Morocco requires effective communication strategies, increased public awareness, and stronger involvement of healthcare professionals.

FIRESIDE SESSION 9

SDG 3.3 - targeted diseases

Breaking barriers to hepatitis C diagnosis among previously unreached people who inject drugs in sub-saharan Africa: A multi-country peer-driven network intervention increased HCV Diagnosis Coverage Twofold

ABSTRACT ID: 668

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Background

In sub-Saharan Africa, the seroprevalence of Hepatitis C Virus (HCV) among Persons Who Inject Drugs (PWID) ranges from 12% to 50%; however, criminalisation and social exclusion remain persistent barriers to diagnosis and care. Baseline HCV diagnosis coverage in Kaduna (Nigeria), Ashaiman (Ghana), and Monrovia (Liberia) was 39%, 31%, and 36%, respectively, well below the WHO 90% target. To bridge these gaps, we deployed a peer-driven network recruitment strategy adapted from Respondent-Driven Sampling to increase HCV diagnosis coverage.

Methods

From March 2024 to February 2026, 35 PWID (15 females, 20 males; 16 in Kaduna, 9 in Ashaiman, 10 in Monrovia) were engaged as community consultants. They were provided with uniquely coded recruitment coupons (target: 2 PWID/consultant/month) to distribute within their social networks. Eligible participants were PWID aged ≥18 years residing in the target cities who had not previously participated. HCV screening was offered to clients, and those with confirmed HCV RNA-positive infections initiated treatment. Data from standardised testing registers and intake forms were analysed using Bayesian hierarchical modelling to account for site-level clustering.

Results

The pre-post implementation study linked to HCV testing services, 1,668(1668/1680=99.3% achievement) previously unreached PWID (mean age: 30.9±5.2 years); 566(33.9%) females and 1102(66.1%) males. By location, 787 in Kaduna, 404 in Ashaiman and 477 in Monrovia, of whom 1413(84.7%) were seropositive, and 585 (41.4%) confirmed positive were placed on treatment. Integrated HIV testing identified 219 (13.1%) positive clients. HCV diagnosis coverage increased to 73%, 67% and 71% in Kaduna, Ashaiman and Monrovia respectively. Bayesian hierarchical analyses showed strong posterior evidence of increased diagnosis coverage across sites: Kaduna (aRR=1.86, 95% CrI: 1.46-2.09), Ashaiman (aRR=2.14, 95% CrI: 1.82-2.61), and Monrovia (aRR=1.96, 95% CrI: 1.54- 2.18). The pooled effect showed 35.opp increase in diagnosis coverage; pooled aRR=1.99 (95% CrI: 1.61-2.55; P(aRR›1)›0.999).

Conclusions

Peer-driven network recruitment can substantially improve HCV diagnosis coverage among previously unreached PWID.

FIRESIDE SESSION 9

SDG 3.3 - targeted diseases

Viral Hepatitis and HIV Among People Who Use Drugs in a German Prison: Disease Prevalence and Access to Care in a Mixed-Methods Study (2025)

ABSTRACT ID: 312

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Background

People in prison (PIP), particularly those who use drugs (PWUD), are disproportionately affected by viral hepatitis (HBV, HCV) and HIV. Therefore, prisons are important settings for testing and treatment, yet healthcare access often remains limited despite the principle of equivalence of care. We assessed HBV, HCV, and HIV prevalence and barriers to healthcare access among PWUD in a German prison.

Methods

We conducted a mixed-methods study in June 2025. The investigated prison houses ~700 individuals (≤100 females, ≤70 adolescents) across all detention types. The quantitative component was a cross-sectional survey among adult PIP with current or past drug use, including laboratory testing for HBV, HCV, and HIV and interviewer-assisted questionnaires on sociodemographics, substance use, risk behaviours, and testing and treatment experiences. The qualitative component comprised semi-structured interviews with medical and custodial prison staff on healthcare access, barriers and improvement opportunities. Quantitative data were analysed descriptively; interviews were analysed using qualitative content analysis.

Results

Among 159 participants (median age 36 years; 91% male), current infection was detected in 3.7% for HBV (5/136), 18.5% for HCV (29/157), and 3.2% for HIV (5/157). Testing during current incarceration was low (8.6% HBV, 21.3% HCV, 19.4% HIV). During current incarceration, 4/5 participants with HIV and 4/29 with current HCV received treatment. Qualitative interviews (n=8) identified structural barriers to testing and treatment, including staff shortages, bureaucratic hurdles, and long waiting times for medical appointments. HCV treatment was conditional on sentence length, compliance, and drug abstinence. Limited disease-specific knowledge and the absence of harm reduction were also highlighted.

Conclusions

PWUD in the investigated prison carried a high burden of viral hepatitis and HIV, while access to testing and treatment remained limited, highlighting gaps between need and care. Offering opt-out screening, health education, and staff training, as well as removing prerequisites to treatment, are essential to address the identified gaps.

FIRESIDE SESSION 9

SDG 3.3 - targeted diseases

Evaluating Türkiye's Progress Toward the WHO End TB Strategy: A Time-Series Forecasting Study of Incidence and Mortality

ABSTRACT ID: 675

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Background

The WHO European Region identifies Türkiye as one of 18 high-priority countries for tuberculosis (TB) control. In alignment with the WHO End TB Strategy, Türkiye has implemented significant control measures to meet the 2030 and 2035 targets. While global research has assessed progress toward WHO goals, no such forecasting study currently exists for Türkiye.

Methods

This study utilized annual incidence rates per 100,000, death counts, and case fatality ratios (CFR) from 2004 to 2023, sourced from the Ministry of Health Tuberculosis Department. Exponential Smoothing (ETS), Autoregressive Integrated Moving Average (ARIMA), and Linear Trend models were compared. Model selection was based on Root Mean Square Error (RMSE), Mean Absolute Percentage Error (MAPE), and Mean Absolute Scaled Error (MASE). Analysis was conducted using R-4.6.0.

Results

For incidence rates, ETS was the superior model (RMSE: 0.713, MAPE: 3.49%, MASE: 0.477). Projections indicate incidence will decrease from 15.9 per 100,000 in 2015 to 7.84 by 2030 and 6.36 by 2035. The ARIMA model provided the best fit for death counts (RMSE: 77.1, MAPE: 7.76%, MASE: 0.950) and CFR (RMSE: 0.386, MAPE: 6.58%, MASE: 0.748). Compared to 2015 baselines of 723 deaths and a 5.7% CFR, death counts are projected to reach 972 in 2030 and 999 in 2035, while CFR is predicted to rise to 12.8% and 14.9%, respectively.

Conclusions

The results suggest that Türkiye's progress has yet to reach the anticipated pace toward meeting the WHO End TB targets for both incidence and mortality. Although the incidence is declining, it is estimated that the rate of decline will not be sufficient to achieve the targeted 90% and 95% reductions. Furthermore, the surging death counts and CFR values, which are potentially linked to an aging population necessitate robust public health interventions. Future research is required to explore the underlying drivers of this increasing mortality trend.

FIRESIDE SESSION 9

SDG 3.3 - targeted diseases

Beyond Coverage: Non-use of Available Insecticide-Treated Nets and Its Implications for Malaria Risk Among Children Under Five in Zambia

ABSTRACT ID: 649

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Background

Despite high household ownership of insecticide-treated nets (ITNs) in Zambia, many children under five years do not consistently use available ITNs, potentially undermining malaria prevention efforts. However, the extent to which this ownership–utilisation gap contributes to malaria risk remains unclear. We assessed the prevalence, determinants, and malaria-related implications of non-use of available ITNs among children under five in Zambia.

Methods

We conducted a secondary data analysis of the 2024 Zambia Malaria Indicator Survey among 2,550 children under five years. Analyses were restricted to children residing in households with at least one ITN. Survey-weighted descriptive statistics and logistic regression analyses accounting for clustering, stratification, and sampling weights were performed. The primary outcome was non-use of an available ITN the night preceding the survey. Malaria infection was defined using rapid diagnostic test positivity.

Results

Although household ITN ownership was high (83.8%), 15.3% (95% CI: 12.5–18.5) of children with household ITN access did not sleep under an ITN. Non-use was higher among children aged 2–4 years (18.0%), children residing in urban areas (23.9%), and children from high socioeconomic households (21.1%). In adjusted analysis, older age (aOR: 1.81; 95% CI: 1.31–2.50) and urban residence (aOR: 1.55; 95% CI: 1.10–2.18) remained independently associated with ITN non-use. Overall malaria prevalence among under-five children was 29.6% (95% CI: 25.2– 34.5). However, ITN non-use was not independently associated with malaria infection after adjustment for age, residence, socioeconomic status, and IRS exposure (aOR: 0.97; 95% CI: 0.65–1.45).

Conclusions

High household ITN ownership in Zambia does not necessarily translate into consistent utilization among children under five years. Socioeconomic, and geographic inequalities in ITN utilization and malaria risk persist beyond ITN use alone, suggesting that malaria control programs may need to shift focus beyond ITN coverage toward community-based interventions that promote consistent utilization of available nets among vulnerable populations.

FIRESIDE SESSION 9

SDG 3.3 - targeted diseases

Integrating epidemiological and entomological data to assess the risk of autochthonous dengue transmission in Spain

ABSTRACT ID: 743

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1. *HM hospitals*

Background

Autochthonous dengue transmission requires both viral introduction and vector presence. However, integrated approaches combining these components are limited in non-endemic settings. We developed a composite index to assess regional transmission risk in Spain.

Methods

We combined post-pandemic dengue-related hospitalisation incidence (proxy for viral introduction) with *Aedes albopictus* occurrence data from the Global Biodiversity Information Facility. Vector data were log-transformed and normalised to account for reporting heterogeneity. A multiplicative index was constructed and rescaled from 0 to 1 at the autonomous community level.

Results

Substantial geographic heterogeneity was observed. Highest risk levels were identified in Catalonia (index=1.00), Madrid (0.71), and the Basque Country (0.70), where high incidence overlapped with vector presence. Moderate risk was observed in Aragón, Balearic Islands, and Valencian Community. Regions without vector presence showed null risk despite reported hospitalisations. The multiplicative structure prioritised areas where both components coexist.

Conclusions

This composite index provides a practical tool to identify areas at higher risk of autochthonous dengue transmission. Integrating epidemiological and entomological data can support targeted surveillance and preparedness strategies in non-endemic settings.

FIRESIDE SESSION 9

SDG 3.3 - targeted diseases

Unmasking Cutaneous Leishmaniasis Outbreak in an Endemic Village, Southeast Türkiye, 2025–2026

ABSTRACT ID: 707

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Background

In January 2026, health authorities in southeast Türkiye reported an unusual cluster of cutaneous leishmaniasis (CL) in a rural endemic village following one sporadic case in December 2025. Because endemicity can mask outbreaks, we conducted a village-wide investigation to define transmission dynamics, identify modifiable risk factors, confirm the causative agent, and guide control measures.

Methods

We undertook a retrospective cohort study using the entire village population as the sampling frame (n=722). Structured household interviews were completed for 631 residents (87.4%) in 84 households. A case was any resident with one or more lesions compatible with CL identified during fieldwork. Individual and household exposures related to sandfly contact and breeding/resting sites were assessed. Relative risks (RR) with 95% confidence intervals were calculated. Samples were sent microscopy, culture and PCR; surveillance data were reviewed through the national surveillance system.

Results

Ninety-six cases were identified (crude attack rate: 13%), indicating transmission where initial cases were treated as a sporadic outbreak. Median age was 24.5 (1-72) years; 60.4% were female. Lesions mainly involved arms and legs (84.4%); most cases had fewer than five lesions (median=2). Outdoor sleeping increased risk (RR 1.7, 95% CI 1.2–2.6). Strong household-level associations were found for proximity to agricultural areas (RR 8.0, 95% CI 4.0–16.0), animal shelters (RR 4.7, 95% CI 2.9–7.7), open waste (RR 2.3, 95% CI 1.4–3.8) and roof/terrace sleeping (RR 2.2, 95% CI 1.3–3.7). Laboratory testing confirmed *Leishmania major.*

Conclusions

The investigation transformed an apparent endemic occurrence into a documented outbreak with actionable environmental drivers. Response included active case-finding, treatment, referral, healthcare-worker training, community awareness and municipal commitments on waste and vector control. These findings show that outbreak analytics in endemic CL setting can reveal preventable transmission clusters and support integrated surveillance, vector-exposure reduction and environmental control.

FIRESIDE SESSION 10

Respiratory viruses: surveillance and response

Effectiveness and early impact of maternal RSV vaccination in Denmark, 1 November 2025 – 30 April 2026

ABSTRACT ID: 757

Ida Rask Moustsen-Helms [1], ***Hanne-Dorthe Emborg*** [1], ***Sarah Kristine Nørgaard*** [2], ***Karina Lauenborg Møller*** [3], ***Niels Bindslev*** [3], ***Palle Valentiner-branth*** [1], ***Steen Ethelberg*** [1], ***Lone Graff Steensballe*** [4], ***HeleneKildegaard*** [4], ***Bolette Soborg*** [5], ***Christian Holm Hansen*** [1]

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Background

Denmark introduced maternal RSVpreF vaccination in October 2025. Despite reported 66–82% effectiveness against infant RSV hospitalisation, evidence beyond 3 months and population-level impact remains limited. We assessed effectiveness through age 6 months, vaccination timing and early population impact using nationwide registers.

Methods

We conducted a retrospective cohort study linking national registers. Infants born between Nov 1, 2025, and Mar 31, 2026 were followed until Apr 30, 2026. The outcome was PCR-confirmed RSV hospitalisation. VE was estimated using Cox regression with calendar time as the underlying time adjusted for confounders, overall and by infant age (0–3 and 4–6 months). We also examined the effect of maternal vaccination timing through an interaction with days between vaccination and birth. The proportion of RSV-associated hospitalisations prevented was estimated based on VE and vaccine coverage in the study population.

Results

Among 22,593 infants (48·3% female), 72.7% were born to vaccinated mothers. Median maternal age was 31.7 years (IQR 28·9–34·9). Median follow-up was 113 vs 101 days, and RSV hospitalisation rates were 4.73 vs 1.20 per 1,000 person-months among infants of unvaccinated vs vaccinated mothers. Overall adjusted VE against RSV hospitalisation was 76.0% (95% CI 67.2–82.5), while age-stratified VE was 79.4% (95% CI 70.4–85.7) at 0–3 months and 63.6% (95% CI 33.5–80.1) at 4–6 months. Further, VE tended to increase with longer time between maternal vaccination and birth (p for trend = 0.079).
The proportion of RSV-associated hospitalisations prevented in the study population was 55.2% (95% CI 48.9-60.0) based on observed coverage and VE.

Conclusions

The maternal RSVpreF vaccination campaign achieved high coverage and substantially reduced the number of RSV hospitalisations in infants. The reduction appeared most pronounced during the first three months of life. Earlier maternal vaccination may be associated with greater protection. Continued RSV circulation after January 2026 suggests that extending the vaccination period could enhance population-level impact.

Respiratory viruses: surveillance and response

Early vaccine effectiveness estimates of the 2025 autumn LP.8.1-adapted COVID-19 vaccine dose against hospitalisation and death in six EU/EEA countries: VEBIS-EHR network, October 2025 to January 2026

ABSTRACT ID: 511

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Background

SARS-CoV-2 circulation has declined globally, though periodic surges, shifting lineages, and waning protection support recommending an autumn vaccine dose to reduce severe disease. In Europe, LP.8.1-adapted COVID-19 vaccines were recommended for the 2025 autumn campaigns, optimising COVID-19 vaccine effectiveness (CVE) against the predominant XFG lineage in EU/EEA countries through late 2025. We provide early estimates of CVE against hospitalisation due to COVID-19 and against COVID-19-related death to inform vaccination strategy.

Methods

We constructed a retrospective cohort using linked electronic health records (EHR) from October 2025 to January 2026 in six EU/EEA countries: Denmark, Italy, Spain-Navarre, Norway, Portugal, and Sweden. Eligible individuals aged ≥75 years were included in the study when the 2025 autumn vaccination campaign started in each country. We estimated hazard ratios (HRs) using Cox proportional hazards models –with vaccination as a time-dependent exposure–adjusted for age, sex, comorbidities, and previous vaccination. We pooled site-specific aHR estimates using a random-effects meta-analysis, with fixed-effect models as a sensitivity analysis. We estimated CVE as (1–pooled aHR) by time since vaccination.

Results

During the follow-up of 4.4 million unvaccinated and 1.2 million vaccinated individuals (99.3% with LP.8.1-adapted vaccines), there were 2,880 and 469 hospitalisations, and 404 and 102 deaths, respectively. CVE against hospitalisation was 54% (95% confidence interval: 42–63) at 14–59 days and 48% (20–66) at 60–119 days post-vaccination. Against death, CVE was 49% (17–69) and 64% (24–83), respectively. CVE estimates showed moderate heterogeneity across sites (I 2 ranging 43–66%). Sensitivity analyses produced similar point estimates (varying 0.3–2.1%).

Conclusions

The 2025 autumn LP.8.1-adapted CVE against hospitalisation and death was approximately 50% in individuals aged ≥75 years during the first 4 months post-vaccination, with no waning of protection. Our estimates are consistent with early estimates reported in previous autumn campaigns for individuals aged ≥65 years by the VEBIS-EHR network.

FIRESIDE SESSION 10

Respiratory viruses: surveillance and response

Characteristics of influenza-like illness in the community during the 2025-2026 influenza A(H3N2) subclade K dominant season

ABSTRACT ID: 490

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Background

In winter 2025/26, a drifted influenza A(H3N2) lineage “subclade K” circulated across Europe leading to early increases in activity. Due to partial antigenic mismatch to the seasonal influenza vaccine, concerns were raised about outcome severity and vaccine effectiveness. Characteristics of milder infections and impacts outside of medical settings were also unclear; therefore, we aimed to characterise influenza-like illness (ILI) during the 2025/26 season using a community cohort in England.

Methods

We used data from FluSurvey – a surveillance tool used to monitor community respiratory illness through weekly symptoms surveys. We included data reported by England participants during the 2025/26 and 2024/25 seasons. Using weekly surveys, we derived ILI (ECDC case definition) and subsequent illness behaviours. In each season, we estimated i) weekly ILI rates per 1000 participants, ii) ILI episodes and the proportion report-ing use of healthcare services, medication, and impact on daily life. We compared peak ILI activity, vaccine uptake and ILI episode characteristics by season.

Results

There were 3385 participants in 2025/26 (female=67% mean age=58.4y; influenza vaccination=72%) and 2005 ; in 2024/25 (female=64%, mean age=60.4y; influenza vaccination=71.6%). Weekly ILI rates peaked earlier in the 2025/26 season with similar intensity (71.6 per 1000 in week 50 2025, compared with 73.3 per 1000 in week 52 2024). Vaccine uptake, symptom profiles and illness characteristics were comparable. A minority of ILI episodes contacted healthcare services in both seasons (15%), with similar patterns by healthcare type. Approximately ¾ reported impact on daily life (2025/26=73%; 2024/25=76%) and the majority reported medication use (2025/26=91%; 2024/25=89%).

Conclusions

Consistent with other surveillance data, we observed earlier ILI activity in the 2025/26 season, with no clear deviations in severity or illness characteristics. Our findings provide insights on the broader impact of the 2025/26 influenza A(H3N2) subclade K dominant season in the community, including reassurance the majority do not contact healthcare services.

FIRESIDE SESSION 10

Respiratory viruses: surveillance and response

Rapid One Health response to a zoonotic HPAI A(H5N1) outbreak involving poultry, domestic cats and occupational exposure of veterinary staff and first responders in Germany, February 2026

ABSTRACT ID: 200

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Background

High pathogenicity avian influenza (HPAI) A(H5N1) continues to pose a zoonotic threat in Europe, with increasing reports of mammalian infections. We describe a One Health investigation of an outbreak involving poultry and cats in Sigmaringen, Baden-Wuerttemberg, Germany, in February 2026, and assess zoonotic transmission risk.

Methods

A coordinated investigation involving veterinary and public health authorities was conducted. Epidemiological data on exposed individuals and affected animals were collected. HPAI A(H5N1) infection was confirmed by RT-qPCR in poultry and cats. Serum samples from all surviving cats were analysed by a commercial ELISA. Contact tracing, risk stratification, symptom monitoring, and serological testing of veterinary staff and first responders were implemented. Sera from 11 of 17 exposed individuals were analysed using a haemagglutination inhibition assay (HI).

Results

The outbreak occurred in a backyard poultry holding with limited biosecurity and involved 21 chickens and nine free-roaming cats. HPAI A(H5N1) was confirmed by RT-qPCR in four chickens and three cats, with high viral loads (quantification cycle values 16.5–24.3 in cat brain tissue). Cats presented with neurological and respiratory symptoms; all surviving cats (n = 6) became seropositive for H5-specific antibodies, indicating widespread infection. A total of 17 individuals were identified as exposed, mainly through occupational or direct animal contact; several had unprotected exposure during early response activities. One exposed veterinarian developed respiratory symptoms but tested negative for HPAI A(H5N1) (human coronavirus OC43 was detected). Serologic testing of exposed individuals showed no evidence of HPAI A(H5N1) infection. Rapid implementation of control measures, included culling of poultry, isolation of cats, personal protective equipment (PPE) use, and monitoring of exposed individuals.

Conclusions

This outbreak demonstrates the importance of rapid One Health coordination, early risk assessment, and appropriate use of PPE. Infection in domestic cats underscores cross-species transmission risk and highlights the need for integrated surveillance across animal and human health sectors.

FIRESIDE SESSION 10

Respiratory viruses: surveillance and response

COVID-19 vaccine effectiveness in the primary care setting among older adults in Europe in 2025/26

ABSTRACT ID: 367

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Background

Limited evidence exists on the effectiveness of COVID-19 vaccines administered during the 2025/26 season, during which the XFG lineage predominated. Older adults are a key vaccination target group, with age-specific recommendations varying by country. We estimated autumnal COVID-19 vaccine effectiveness (VE) against primary care attended SARS-CoV-2 infection among older adults in Europe (September 2025–March 2026).

Methods

The multi-country VEBIS primary care study used a test-negative design, recruiting participants across seven European sites. We included patients from the older target group (i.e. aged ≥60, ≥65 or ≥70 years, depending on country) with acute respiratory infection presenting to primary care physicians ≥14 days after the 2025/26 autumnal vaccination campaign started in their country. We defined cases and controls as patients testing RT-PCR-positive and -negative for SARS-CoV-2, respectively. Vaccinated patients had received a 2025/26 COVID-19 vaccine dose ≥14 days before symptom onset; unvaccinated patients had received none. We used logistic regression to estimate VE (1 – odds ratio of vaccination among cases and controls x 100), overall and by time since vaccination, adjusting for a priori confounders.

Results

We included 177 (5%) cases and 3,493 (95%) controls, of median age 73 years (IQR: 66–79). Six percent (11/177) of cases were vaccinated, vs. 20% (702/3,493) of controls. Median time since vaccination was 49 days (IQR: 34–58) among cases, 58 (IQR: 33–88) among controls. All 247/713 (35%) vaccinees with known vaccine valency received LP.8.1-adapted mRNA vaccines. Vaccine effectiveness was 51% (95% CI: 10–76) overall; 60% (95% CI: 7–86) and 40% (95% CI: -40–79) at 14–41 and 42–83 days post vaccination, respectively.

Conclusions

Vaccination reduced the risk of primary care attended COVID-19 by half among vaccinated older adults in Europe. Information about COVID-19 VE in key populations can guide the development and timing of future vaccination campaigns.

FIRESIDE SESSION 10

Respiratory viruses: surveillance and response

Vaccine effectiveness against seasonal influenza A(H1N1)pdm09 and highly drifted influenza A(H3N2) subclade K at primary care level in Europe in 2025/26

ABSTRACT ID: 747

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Background

Seasonal influenza vaccine effectiveness (VE) varies by vaccine composition, antigenic properties of circulating viruses, and population characteristics. In mid-2025, the highly drifted influenza A(H3N2) subclade K emerged. Results from antigenic studies showing diminished reactivity of subclade K with post-infection ferret sera raised against 2025/26 vaccine strain prompted concerns about reduced VE in the 2025/26 season. We estimated the effectiveness of 2025/26 vaccines against primary care-attended influenza A(H1N1)pdm09 and A(H3N2) in Europe by age group (all-age, 0–17, 18–64, ≥65 years).

FIRESIDE SESSION 11

Late breakers (1)

Evidence for mixed zoonotic and person-to-person transmission of Andes hantavirus outbreak during an international expedition cruise, April-June 2026

ABSTRACT ID: 993

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Background

Andes hantavirus (ANDV), which has a rodent reservoir, is the only hantavirus with documented person-toperson transmission. In May 2026, a cluster of severe respiratory illness was identified on a Dutch-flagged expedition cruise ship. We investigated modes of transmission and risk factors for ANDV infection.

Methods

We conducted a retrospective cohort study among passengers and crew who stayed overnight on the m/v *Hondius* during 1 April-18 May 2026 (data collection: 9 May-5 August 2026). Participants completed a standardised questionnaire on pre-boarding exposures, cabin-sharing, contacts and activities. Cases were laboratoryconfirmed or probable ANDV infections. We reconstructed case exposure windows using a 4-42-day incubation period. We compared secondary attack rates and estimated crude risk ratios (RRs) with 95% confidence intervals (CIs) in univariable analyses.

Results

Thirteen cases (12 confirmed, one probable), including three fatalities (case-fatality 23%), were identified among 182 individuals of whom 118 completed the questionnaire. Attack rates were 8% (10/120) among passengers and overall 5% (3/62) among crew, with 22% (2/9) among expedition guides. Median case age was 66 years; nine were men. At contact screening on 7 May, excluding known cases, 15 contacts reported symptoms, three (20%) of whom became cases. Cabin-sharing participants had a higher attack rate than those without a cabinlink (44.4% vs 8.3%; RR 5.4, 95% CI 2.1-14.1). One case was classified as infected pre-boarding, eight as either pre-boarding or onboard, and four as onboard.

Conclusions

Findings are most consistent with a zoonotic introduction before boarding followed by person-to-person transmission onboard. The higher attack rate among cabin-linked participants suggests that close, prolonged contact contributed to onboard transmission, although for some cases, no close contact on board the ship could be identified. Severe respiratory illness clusters among travellers warrant prompt diagnostic assessment, and timely notification of potential travel-associated infections through national and International Health Regulations channels for coordinated cross-border response.

FIRESIDE SESSION 11

Late breakers (1)

Outbreak of Legionnaires' disease associated with a misting system in a restaurant, Chambéry, France, 2026

ABSTRACT ID: 984

Emmanuelle Vaissière [1], ***Florence Culoma*** [2], ***Mathilde Ballet*** [3], ***Camille Jacqueline*** [4], ***Emmanuel Forestier*** [5], ***Garance Terpant*** [1], ***Anne Thuez*** [3], ***Monika Wolska*** [3], ***Christelle Nolibos*** [2], ***Guillaume Spaccaferri*** [1], ***Sophie Jarraud*** [4], ***Sophie Vaux*** [6], ***Jean-Marc Yvon*** [1]

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Background

In July 2026, local health authorities observed an increase in the number of Legionnaires' disease (LD) cases in Savoie, France.

Methods

Case definition included laboratory-confirmed cases of LD, with symptom onset from 1 June 2026 and who resided in or had visited Savoie during their 14-day exposure period. Cases were interviewed using a standardized questionnaire to identify potential sources of exposure. Environmental investigations consisted in sampling water systems, both at the cases' homes and at facilities frequented by at least two cases, to be analyzed by qPCR or culture. Microbiological investigations used molecular typing techniques on respiratory specimens or strains.

Results

A total of 51 LD cases were investigated, with symptoms onset between 8 June and 14 August. Among these cases, 34 (66%) visited the same restaurant with a fresh-food display misting system showing favorable conditions for *Legionella* growth: outlet water temperature at 30°C, long small-bore pipes and intermittent operation. The median interval between visiting the restaurant and symptoms onset was 7 days, consistent with the published incubation. *Legionella pneumophila* (*Lp*) serogroup 1 strains, isolated from 4 restaurant-exposed cases, belonged to sequence type 20 and differed by only 1–3 alleles using 2,009-loci scheme, supporting a common source of contamination. No new cases have been reported among the restaurant's customers since the misting system shutdown on 5 August. Water samples collected from the device, on 7 August, were negative for *Lp* by qPCR and culture but positive for *Legionella* spp. by qPCR.

Conclusions

For the first time, we describe a fresh-food display misting system in a restaurant as the source of a large LD outbreak. Another outbreak, involving the same type of device, occurred in southwest of France this summer. Elevated water temperatures in distribution networks, more frequently observed as a result of global warming, could be a contributing factor.

FIRESIDE SESSION 11

Late breakers (1)

International carbapenem-resistant Acinetobacter baumannii outbreak in burn intensive care units with ongoing transmission in Germany, 2026

ABSTRACT ID: 973

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Background

Following patient transfer after a mass-casualty incident in Switzerland, carbapenem-resistant *Acinetobacter baumannii* (CRAb) were detected in three German burn intensive care units (ICU), clustering with a Swiss index patient. We investigated the outbreak on the most affected ICU A to elucidate transmission and inform targeted control measures.

Methods

In collaboration with Swiss colleagues, we informed via EpiPulse. We reviewed patient records and conducted an ICU A site visit. Cases were defined as patients with CRAb detected at this ICU from 3rd January 2026 onwards and with isolates belonging to the outbreak cluster by whole-genome sequencing. We conducted a retrospective cohort study among patients admitted for ›24hours to the ICU A from 3rd January to 27th April 2026 (ward closure) analysing data as of 25 June 2026 to identify risk factors. Significance was tested using Wilcoxon ranksum and Fisher's exact test.

Results

We found 20 cases in Germany with transmission in one Swiss and three German ICUs. The cohort in ICU A among 70 patients, comprised 11 cases excluding the primary case transferred from Switzerland. Median age of cases was 54 years (range: 18–73); 82% were male. Nine of 27 burn patients (33%) acquired CRAb; cases had a higher median total body surface area burned than non-cases (35% vs 11%; p=0.01). Burn-bath exposure among burn and plastic surgery patients was associated with CRAb detection (RR: 5.5, 95%CI: 1.4–22.3; p‹0.01). Only adapted environmental sampling detected the outbreak strain in the ICU A environment. No other European country reported associated cases.

Conclusions

This prolonged cross-border CRAb outbreak led to two ward closures. Severely burned patients should be screened upon transfer, irrespective of country-level prevalence. Shared facilities such as burn bath require particular attention. Environmental sampling should use sensitive methods. Early detection, international communication, and rapid interdisciplinary response reduce transmission and preserve specialised burn-care capacity.

FIRESIDE SESSION 11

Late breakers (1)

Observational environmental study of possible transmission routes during an outbreak of Andes virus on the M/V Hondius expedition cruise ship

ABSTRACT ID: 902

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Background

Between April and June 2026, 13 Andes virus (ANDV) cases, including 3 fatalities, occurred on the Dutch-flagged expedition cruise ship M/V Hondius. Primary ANDV transmission occurs via rodent exposure. Human-tohuman transmission is recognised but less common. We studied possible transmission routes and viral RNA presence in the environment aboard the ship.

Methods

A visual onboard inspection for rodent traces was performed, and swabs of high-risk areas were analysed by vertebrate environmental DNA (eDNA) metabarcoding to assess possible zoonotic exposure. Surface swabs, wastewater, HEPA filters from portable air purifiers, ventilation inlets, and towels and bedding specimens were systematically collected from cabins of cases and adjacent cabins. All specimens were collected on 18-19 May 2026. Environmental specimens were tested by pan-orthohantavirus and ANDV-specific RT-qPCRs. PCR positive specimens were sequenced using amplicon-based whole genome sequencing.

Results

No evidence of rodents was found by visual inspection or in eDNA from 15 environmental specimens, making on-board zoonotic transmission unlikely. Among 10 sampled cabins with cases, ANDV RNA was confirmed in 3 out of 80 surface specimens, 2 out of 8 HEPA filters from portable air purifiers, and 3 out of 6 bed linen and towel specimens. ANDV RNA was not detected in the sampled ventilation inlets or 5 adjacent cabins; hence no evidence was found for cabin-to-cabin virus transmission via the central ventilation system. ANDV RNA was not detected in wastewater. ANDV RNA was detected in the environment up to 24 days after the cases last occupied the cabin. In four cabins, environmental and human-case sequences showed an identical mutation profile.

Conclusions

The environmental findings, sequence data, and available data on symptom onsets exceeding the maximum reported ANDV incubation period support onboard human-to-human transmission via direct contact, and/or transmission via the air, and/or fomites. Environmental sequencing can be added to the toolbox for virus transmission studies.

FIRESIDE SESSION 11

Late breakers (1)

Large outbreak of autochthonous West Nile virus infection in humans in the Netherlands: preliminary investigation of cases from the Utrecht province, August – September 2026

ABSTRACT ID: 999

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Background

The Netherlands recorded its only previous autochthonous West Nile virus (WNV) outbreak in humans in 2020. From July 2026, WNV was detected in a juvenile song thrush and dead corvids in the Utrecht province. In August, Sanquin Research initiated prospective RT-PCR monitoring of whole blood donations in areas with previous zoonotic detections. On 12 August, Sanquin notified the season's first autochthonous human WNV infection to the Public Health Service of Utrecht (PHSoU). We describe the outbreak and public health response in the Utrecht province.

Methods

We defined outbreak cases as residents of the Utrecht province with WNV nucleic acid in blood or cerebrospinal fluid (CSF), or a WNV-specific antibody response in CSF, or a significant WNV-specific serum antibody response with compatible clinical symptoms, in 2026, without travel outside the Netherlands in the two weeks before symptom onset or sampling. Sanquin initiated screening of all blood donations intended for transfusion products in the affected area, and medical specialists were alerted to WNV circulation. PHSoU conducted source investigations using interviewer-administered questionnaires among cases and issued press releases in affected municipalities. Urbanity was classified by 4-digit postcode (1=very urban, 5=very rural).

Results

By 23 September 2026, ten cases had been notified (23% of cases nationally; province accounts for 8% of population). Eight were male and median age was 71 years (range: 40 – 90). Nine had neuroinvasive disease and were hospitalised; two died. One case was detected through donor screening. Cases were identified across eight municipalities; nine lived in moderate (score 3) to very urban areas (1).

Conclusions

This is the first time autochthonous human WNV cases are reported during the height of mosquito season in the Netherlands. The high proportion of neuroinvasive disease reflects severity-based testing and underascertainment of PHSoU cases. Continuation of One Health surveillance is essential to track transmission patterns in coming years.

FIRESIDE SESSION 12

Quantitative methods

Estimating the Presence and Abundance of Aedes albopictus in Europe Using Neural Networks

ABSTRACT ID: 784

indaco biazzo [1], ***Lia Orfei*** [1], ***Ioannis Kioutsioukis*** [2], ***Lea Schuh*** [1], ***Celine Gossner*** [3], ***Olivier Briet*** [3], ***Peter Markov*** [1]

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Background

Aedes albopictus, an invasive mosquito vector of dengue, chikungunya and Zika viruses, is rapidly expanding across Europe, increasing the risk of local arbovirus transmission. Accurate prediction of mosquito presence and abundance is important for surveillance, preparedness and targeted vector control. Existing mechanistic and statistical approaches may struggle to capture the complex non-linear relationships between environmental variables and mosquito dynamics.

Methods

We developed AIedes, a neural-network framework to estimate both the spatial presence and weekly abundance of *Ae. albopictus* across Europe using climatic variables. Presence prediction was trained on harmonised ECDC/EFSA VectorNet distribution data projected onto a 12.5 km European grid and paired with Copernicus climate projections. Abundance prediction was trained using harmonised AIMSurv ovitrap egg-count data from 24 European countries combined with ERA5-Land climate reanalysis variables. Feed-forward neural networks were trained and evaluated using independent test datasets.

Results

For presence prediction, the best-performing model achieved high predictive performance on the test dataset (accuracy 0.988; sensitivity 0.983; specificity 0.991; critical success index 0.974), substantially outperforming logistic regression approaches. For abundance prediction, the best model achieved $R^2 = 0.63$ on unseen test data while correctly distinguishing zero from non-zero egg counts with approximately 92% accuracy. Predictions reproduced both large-scale spatial patterns and local seasonal egg-laying dynamics across multiple European regions.

Conclusions

AIedes demonstrates that neural-network approaches can effectively model the climatic drivers of invasive mosquito dynamics at continental scale. The framework, together with harmonised datasets and code, provides a reproducible benchmark for future vector modelling studies and may support public health authorities in surveillance planning and vector-borne disease preparedness.

FIRESIDE SESSION 12

Quantitative methods

Population-level effectiveness of long-acting monoclonal antibodies and maternal vaccination against RSV-associated hospitalisation in infants: a modelling study across 28 European countries

ABSTRACT ID: 407

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Background

Respiratory syncytial virus (RSV) is the leading cause of acute lower respiratory infection in infants under 12 months. The recent licensure of long-acting monoclonal antibodies and a maternal vaccine in the European Union has opened the way to universal infant prevention. Mathematical models of infectious diseases can be used to explore the population-level impact of immunisation strategies via alternative scenarios. Whereas exist-ing modelling assessments focus on national or sub-national settings, we quantify the impact of these products across 28 EU/EEA countries.

Methods

We developed an age-stratified, stochastic compartmental model of RSV transmission. The model combines literature-based clinical and product efficacy parameters with country-specific demographic and contact patterns. After calibration against age- and country-specific RSV-associated hospitalisation estimates in absence of interventions, we run scenarios for each product at four coverage levels. We additionally explored the impact of catch-up for infants under six months at season onset. We then evaluated each scenario against the no-immunisation baseline, computing averted hospitalisations as paired simulation-level differences.

Results

At 95% coverage, the cross-country median reduction in RSV-associated hospitalisations in infants under 12 months is 29.9% for monoclonal antibodies (country range: 27.7–33.9%) and 22.4% for maternal vaccination (20.0–25.6%), scaling linearly with coverage. Out of all averted hospitalisations, 78.2% (90% CI: [67.3, 82.9]%) occur in infants aged 0-2 months for monoclonal antibodies and 72.6% (90% CI: [61.4, 8.6]%) for maternal vaccination. A catch-up campaign nearly doubles the overall reduction for both products.

Conclusions

Despite country-specific differences in the model, immunisation effects are comparable across settings and concentrated in the immunised age group. This suggests that impact depends primarily on product efficacy rather than country-specific factors and that herd-immunity effects are negligible. These findings support harmonised European guidelines on coverage targets for RSV prevention in infants. Seasonal catch-up campaigns emerge as a particularly effective lever to maximise the impact of immunisation programmes.

FIRESIDE SESSION 12

Quantitative methods

Climate-driven leptospirosis in Greece: predictive modeling for early warning

ABSTRACT ID: 378

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Background

Extreme weather events and shifting hydroclimatic conditions favor *Leptospira* spp. transmission, yet predictive tools remain limited. We aimed to examine the association between climatic factors and leptospirosis incidence in Greece and evaluate climate-based indicators for short-term risk prediction to inform leptospirosis prevention strategies.

Methods

We analysed monthly notified cases across 13 NUTS2 Greek regions (2004–2024), together with monthly air temperature, dew-point temperature, and precipitation data. Observations related to extreme flooding events were excluded. We employed Generalized Linear Mixed Models with negative binomial distribution and region-level random effects, including longitude as a geographic covariate, to estimate incidence rate ratios (IRRs), at 0–2-month lags (up to two months prior to symptom onset). For early warning, we developed a predictive ensemble model combining logistic regression, random forest, and gradient boosting with predicted probabilities pooled using non-negative least squares weighting. Models were trained on 2004-2019 and evaluated on 2020-2024 data, using area under the curve (AUC), sensitivity, specificity and negative predictive value (NPV).

Results

Overall, 518 cases were included, with substantial regional heterogeneity (random effect σ=0.57). Disease occurrence was associated with dew point temperature at 1-month lag (IRR=1.13 per 1°C, 95%CI:1.06–1.21) and precipitation at 2-month lag (IRR=1.005 per mm, 95%CI:1.002-1.009). A west-to-east gradient was identified, with higher incidence in western regions (IRR=0.69 per degree longitude, 95%CI:0.56-0.85). The predictive model achieved AUC=0.59, sensitivity=26%, specificity=80%, and NPV=0.89.

Conclusions

Higher dew point temperature and precipitation were associated with increased leptospirosis risk at 1–2-month lags, exceeding the leptospirosis incubation period, permitting early warning and implementation of preventive measures. A west-to-east gradient in incidence was observed, with rates steadily declining toward the east, suggesting that regional hydroclimatic differences may independently influence transmission risk. Although predictive performance was modest, the relatively high NPV suggests that climate-based models may help identify lower-risk periods and support targeted surveillance and prevention efforts.

FIRESIDE SESSION 12

Quantitative methods

Mpox vaccination among MSM in the EU/EEA: Estimating the uptake and modelling the impact of future campaigns

ABSTRACT ID: 185

Bastian Franklin [1], ***Disa Hansson*** [1], ***Liana Aphami*** [2], ***Kai J. Jonas*** [2], ***Jordi Borrell Pique*** [1], ***Xanthi Andrianou*** [1], ***Anastasia Pharris*** [1], ***Diamantis Plachouras*** [1], ***Axel J. Schmidt*** [3], ***Lina Nerlander*** [1]

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Background

In October 2025, monkeypox virus (MPXV) clade I cases were detected among men who have sex with men (MSM) in the EU/EEA, suggesting ongoing local transmission. Considering the large MPXV clade II outbreak among MSM in 2022, clade I poses a potential public health risk for the EU/EEA. This work assesses the potential of further vaccination campaigns to prevent mpox outbreaks (either clade) among MSM.

Methods

For 28 EU/EEA countries (given too few responses for two countries), we fit Bayesian mixed-effects models to data from the European MSM and Trans Persons Internet Survey 2024 to obtain: The current mpox vaccine uptake among MSM; the proportion of unvaccinated MSM who would like to get vaccinated; and the proportion of recovered MSM. The models describe the vaccine/recovery status on individual level depending on the number of sexual partners and country. Using a susceptible-infectious-recovered mathematical model on a sexual contact network, we estimate the reduction of the effective reproduction number if vaccines are provided to MSM who are willing to get vaccinated.

Results

The estimated vaccine uptake among MSM ranges from 1.0-31.4% (posterior medians, PM) depending on the country, with a median of 13.6% across countries. Population-level natural immunity varies from 0.75-3.07% (PM), with a median of 1.25% across countries. Vaccinating MSM who are willing to get vaccinated given a rapid increase of mpox cases in their community yields an estimated uptake of 59.3-84.0% (PM) with a median of 75.0% across countries, reducing the effective reproduction by an estimated 37.6-74.8% (PM) and a median of 57.1% across countries.

Conclusions

Our results suggest a considerable willingness for further mpox vaccination among MSM in the EU/EEA if cases increase, and a resulting large potential to reduce transmission. Therefore, countries should consider implementing vaccination strategies with focus on pre-exposure vaccination and maintain active risk communication and community engagement.

FIRESIDE SESSION 12

Quantitative methods

Reuse of unstructured hospital-based electronic health record data to enhance automated surveillance of severe acute respiratory infections in the Netherlands.

ABSTRACT ID: 762

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Background

National surveillance of severe acute respiratory infections (SARI) is essential for public health response and pandemic preparedness. Accuracy is often challenging when using hospital admission data. We compared the performance of automated SARI surveillance incorporating unstructured text data from electronic health records (EHR) using machine learning techniques with surveillance using structured EHR data only.

Methods

Data from patients with acute clinical admissions between January 2022 and June 2026 were extracted from the EHR of a Dutch university medical centre. Admissions were categorised as SARI/non-SARI using SARI-related ICD-10 diagnosis codes as gold standard. Transformer-based natural language processing (NLP) models (MedRoBERTa.nl and mmBERT with context windows of 512 and 2048 tokens) were finetuned on training (62.6%), validation (25.5%) and testing (12.0%) datasets. SARI surveillance using structured data was based on SARI-related financial diagnosis treatment codes and laboratory test requests. Performance (sensitivity, positive predictive value [PPV], accuracy and F1-score) and timeliness (F1-score at 2, 5 and 7 days after admission) were calculated for different NLP models and the structured-data algorithm.

Results

Of 9,598 acute hospital admissions (7,629 patients), 10% were classified as “SARI” according to ICD-10. The structured-data algorithm yielded a PPV of 72.5%, sensitivity of 35.2%, F1-score of 47.4% and accuracy of 92.2%. In comparison, the best performing NLP model was mmBERT-2048 (PPV: 57.7%, sensitivity: 83.9%, F1: 68.4%, accuracy: 92.2%). Regarding timeliness, mmBERT-2048 outperformed the structured-data algorithm, even when restricting analysis to data available at two, five and seven days after admission (F1: 62.6%/66.2%/67.5%, respectively).

Conclusions

Incorporating free text from unstructured hospital EHR notes in SARI surveillance enhances performance, without compromising timeliness. Robust and reliable SARI surveillance can strengthen public health intelligence, and inform infectious disease outbreak response, policy and resource allocation. Future research involves further optimisation and validation, discrepancy analysis, and assessing the feasibility of implementation across diverse healthcare settings.

FIRESIDE SESSION 13

Late breakers (2)

Increasing delays across sequential tuberculosis regimen modifications and potential utility of upfront nanopore targeted next-generation sequencing in Kyrgyzstan

ABSTRACT ID: 1013

Aizat Kulzhabaeva [1], ***Ainur Soorombaeva*** [1], ***Atyrkul Toktogonova*** [2], ***Altyn Iskakova*** [2], ***Muratbek Ahmatov*** [1], ***Bakyt Myrzaliev*** [1], ***Andrii Slyzkyi*** [3], ***Meerim Sydykova*** [2], ***Urmatbek Borzhiev*** [2], ***Abdullaat Kadyrov*** [2], ***Edine Tiemersma*** [3], ***Kristin Kremer*** [3]

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Background

WHO surveillance data reported 72.8% treatment success in the 2021 rifampicin-resistant/multidrug-resistant tuberculosis (RR/MDR-TB) cohort; ›50% received 18–20-month regimens in 2024. We assessed regimen modifications and nanopore targeted next-generation sequencing (tNGS).

Methods

Adults with Xpert MTB/RIF Ultra-positive pulmonary tuberculosis were enrolled January 2024–February 2025 and followed through September 2026. Regimens came from clinical records and drug-susceptibility testing (DST) from laboratory records. Treatment-change appropriateness was assessed using contemporaneous DST/clinical information, with expert review for complex cases. Resistance-related delay was measured from the earliest actionable result. tNGS results were unavailable to clinicians. Unsuccessful RR/MDR-TB outcomes were analysed by multivariable logistic regression.

Results

Among 1,007 patients, 356 (35.4%) had a first, 142 (14.1%) a second and 31 (3.1%) a third modification. Of 528 modification events, 225 (42.6%) were resistance-related. The proportion classified as appropriate declined from 81.7% to 67.6% and 61.3%, while median intervals to successive changes increased from 28 days (IQR 12– 62) to 71 (30–175) and 104 (28–180). For resistance-related changes, median delay was 6 days (2–13) after the first actionable result versus 28 (15–49) after the second; 76% of second changes occurred ›14 days after the result became available. Baseline tNGS contained a matching resistance signal for 120/225 (53.3%) resistancerelated events. Of 228 RR/MDR-TB patients, 216 (94.7%) had outcomes; 160/216 (74.1%) achieved treatment success. Unsuccessful outcome was associated with older age (aOR 1.72 per decade, 95% CI 1.33–2.22) and each additional substance-related risk factor (aOR 2.08, 1.23–3.51).

Conclusions

Increasing delays and declining appropriateness across successive regimen modifications highlight a programmatic gap in translating resistance information into timely treatment decisions. Earlier consolidation of resistance information, potentially through upfront tNGS, together with faster clinical review and targeted patient support, could simplify treatment pathways and reduce the burden of prolonged, repeatedly modified treatment.

FIRESIDE SESSION 13

Late breakers (2)

Municipal-scale dengue early warning in Colombia: prospective model performance amid the confirmed 2026 national outbreak

ABSTRACT ID: 1012

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Background

Dengue remains a major public health challenge in Colombia, marked by pronounced spatial and temporal heterogeneity. Since epidemiological week 24 of 2026, the Instituto Nacional de Salud has classified the country in outbreak status, coinciding with the confirmed 2026 El Niño climate event. By epidemiological week 33, Guaviare and Magdalena departments exceeded expected dengue thresholds, including the municipalities of El Retorno and Fundación.

Methods

We previously developed municipal-scale early warning models (logistic regression and XGBoost) for three highincidence municipalities (Valencia, Fundación, El Retorno), trained on 2007–2019 epidemiological, demographic and climatic data and evaluated on 2020–2024. Here, these validated models were applied prospectively to July– August 2026 conditions in Fundación and El Retorno, combining satellite-derived climate variables with recent case counts estimated from official departmental surveillance trends, in the absence of finalised municipal-level 2026 case data.

Results

Retrospectively, XGBoost achieved precision/recall of 0.84/0.93 in Valencia and 0.81/0.85 in Fundación, outperforming a national baseline model (precision 0.43); performance was weaker in El Retorno (0.50/0.57), below a simple historical-count baseline. Prospectively, both XGBoost and logistic models classified Fundación as high risk for August 2026 (probability 0.99 and 0.88, respectively), consistent with a sustained rise in recent case counts. El Retorno was classified as low risk (0.04 and 0.05), reflecting a declining recent trend despite an earlier departmental peak; this result warrants caution given the model's weaker historical performance in that municipality.

Conclusions

Municipal-scale early warning models retain operational value during the ongoing 2026 outbreak, although prospective performance is heterogeneous across territories. Prospective validation with finalised surveillance data, and hybrid approaches for municipalities with unstable signals, are needed before operational deployment.

FIRESIDE SESSION 13

Late breakers (2)

Investigation and population vaccination response for a multi-setting outbreak of Hepatitis A in South Wales, December 2025 to September 2026.

ABSTRACT ID: 997

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Background

Hepatitis A is uncommon in Wales and is usually associated with international travel; however, sustained local transmission can occur. Between December 2025 and September 2026, we investigated a hepatitis A outbreak in Barry, Wales. We described the epidemiology, transmission pathways, recommended and evaluated control measures.

Methods

Cases were identified through clinical notifications and laboratory testing and investigated by the local health protection team. Demographic and exposure information was collected through questionnaires, and links explored using network analysis. Viral genomes were sequenced to assess genetic relatedness. Interventions included contact tracing, targeted vaccination and media communications. Between 17/8/2026 and 15/9/2026, community-wide vaccinations targeting children aged 1-5 years living or attending childcare settings in Barry were delivered.

Results

During this period, 13 cases were identified across six households, with no history of international travel. The median age was 10 years (range: 3-46); seven cases were aged under 11 years. Three cases, all aged under five years, were asymptomatic. Network analysis identified four possible transmission links between household clusters through two nurseries, one primary school, and one sports club. Over half of linked cases were aged 3-4-years and all were under 10 years. No evidence of onward community transmission was identified among adolescents or adults. All confirmed cases shared an identical genotype IA sequence, with a difference of three single-nucleotide polymorphisms across four sequenced households. This strain had not been detected elsewhere in the United Kingdom since May 2025. Over 500 people were vaccinated in case-associated households, primary schools and nurseries, and over 1000 through community-wide vaccinations.

Conclusions

This outbreak involved sustained hepatitis A transmission amongst children attending community settings, with spread across multiple households. Asymptomatic infection in children suggests transmission from unascertained cases. These findings supported the targeted vaccination, an intervention which should be considered when hepatitis A outbreaks involve child community networks.

FIRESIDE SESSION 13

Late breakers (2)

Lower-than-expected rotavirus vaccine effectiveness in Dutch children? Preliminary findings from a test negative case–control study

ABSTRACT ID: 995

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Background

Since 2006, rotavirus vaccines have been introduced into national immunization programmes worldwide and shown high vaccine effectiveness (VE) against severe disease in low- mortality countries (›80%). In the Netherlands, universal rotavirus vaccination, using a monovalent vaccine, was implemented in 2024. We aimed to estimate the effectiveness of rotavirus vaccination against severe rotavirus gastroenteritis in the Netherlands.

Methods

We conducted a test- negative case–control study in 11 hospitals across the Netherlands. Eligible children were ‹2 years of age, born on or after 01-01-2024, and presented at the hospital with severe gastroenteritis during the rotavirus seasons (January-June) of 2025 or 2026. Stool samples were tested by RT-PCR for rotavirus and other viral pathogens. Detected rotaviruses were genotyped. Cases were children with rotavirus as the primary causative pathogen. Controls were rotavirus-negative, or rotavirus-positive with another virus as causative pathogen. Vaccination status was obtained via parent questionnaires and the national vaccination register. VE of 2 versus 0 doses was estimated using logistic regression, adjusting for age at symptom onset and presence of medical risk conditions.

Results

We included 90 infants (32 cases, 58 controls). The median age at symptom onset was 9 months (interquartile range 6-13 months); 46% were female. Among cases, 53% had received 2 doses of rotavirus vaccination and 69% among controls. The adjusted VE was 67% (95% CI: 11%-89%). The most prevalent rotavirus genotypes were G9P[8] (n=12) and G3P[8] (n=9); G1P[8] was detected in one case.

Conclusions

Results indicate a somewhat lower rotavirus VE in the Netherlands than expected from evidence from other lowmortality countries, although the estimate is uncertain given the small sample size. Recent genotype shifts may have affected the observed VE. Inclusions will continue in the 2027 season to refine VE estimates. Continued monitoring of rotavirus VE, including in countries with longer-standing rotavirus vaccination, is essential to understand the role of genotype shifts.

FIRESIDE SESSION 13

Late breakers (2)

Environmental drivers of transmission in an ongoing human tularaemia outbreak in Brittany, France, 2026

ABSTRACT ID: 909

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Background

Tularaemia is a rare, highly-infectious, zoonotic disease often diagnosed late due to low awareness. It is transmitted by wild animals, contaminated environments, or arthropod bites, causing severe infections with clinical forms varying by entry route. In Brittany, France, an increase in tularaemia was identified, with 93 cases reported from January to June 2026, versus a yearly-average of 33 (2016-2025). We aimed to describe notified cases and identify environmental transmission drivers to implement control measures.

Methods

We described all notified tularaemia cases in Brittany (January–June 2026), classified as confirmed (PCRpositive/seroconversion/4-fold antibody titre increase) or probable (single high titre). We performed a timeseries analysis (January 2016–June 2026) of weekly cases using mixed-effects Poisson regression with seasonality, population, precipitation, temperature, and relative humidity as fixed effects, and postal-code as random effect. Spatial regression using Bayesian Conditional Autoregressive model assessed associations with water body density, mean normalised difference vegetation index (NDVI), and population. Regressions results are presented as rate ratios (RR) with 95% confidence intervals (95%CI).

Results

Of the 93 notified cases (59% confirmed), most occurred in February (38%) and March (28%). The median age was 59 years (IQR: 43-69), male-to-female ratio 3:1. Respiratory form was most common (70%). Outdoor activities (57%) and soil contact (55%) were frequent risk activities. Cases increased significantly with precipitation (RR=1.35, 95%CI: 1.23–1.49) after 4-week lag, unlike temperature (RR=0.99, 95%CI: 0.96–1.02) or relative humidity (RR=1.06, 95%CI: 0.82–1.38). No association was found with water body density (RR=1.03, 95%CI: 0.87–1.18) or NDVI (RR=1.09, 95%CI: 0.69–1.79).

Conclusions

Risk activities and respiratory forms suggest inhalation of contaminated environmental airborne particles as likely transmission mode. Precipitation was a significant transmission driver. Ecological studies of animal reservoirs and transmission cycles are critical to identify ways to diminish environmental contamination and human transmission. We recommend awareness campaigns among clinicians to improve reporting.

Poster Tours

POSTER TOUR 1

Outbreak investigations of food-borne diseases

Traditional Household Slaughtering Practices as Determinants of Brucellosis Risk in High Burden Areas, Armenia, 2025

ABSTRACT ID: 853

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Background

Human brucellosis incidence in Armenia increased between 2018 and 2025. However, unclear etiologic exposures have limited targeted prevention strategies. This study aimed to identify risk factors associated with brucellosis in Armenia.

Methods

We conducted a matched case–control study in two high-incidence regions. Laboratory-confirmed brucellosis cases reported to the national surveillance system between January and May 2025 were enrolled. Controls were selected from the same household or neighborhood as cases, matched by age and sex and having negative test results by the standard agglutination test and enzyme-linked immunosorbent assay. Risk factor data were collected using a standardized questionnaire. Conditional logistic regression was used to estimate both crude and adjusted odds ratios (OR, aOR) with 95% confidence intervals (CI) for all exposures. Separate multivariable models were run for each exposure of interest and adjusted for education, occupation, and travel history.

Results

A total of 32 cases and 69 matched controls were enrolled. Backyard animal slaughtering was significantly associated with brucellosis (OR=3.83, CI:1.34–10.94); aOR=7.1, CI:1.42–35.45), particularly sheep slaughtering (OR=3.64, CI:1.38–9.64; aOR=5.2, CI:1.26–21.53). Furthermore, 12 of the 32 affected individuals reported selling meat to others, an activity prohibited under current regulations. In contrast, consumption of unpasteurized dairy products was not significantly associated with brucellosis in this study (OR=1.40, CI:0.38–5.12; aOR=1.54, CI:0.42–5.67).

Conclusions

Findings from high-incidence regions of Armenia suggest that brucellosis transmission may be more strongly associated with backyard sheep slaughtering than consumption of unpasteurized dairy products, highlighting the need to enhance public education on safe animal slaughtering practices. Strengthening enforcement of existing regulations that prohibit the sale of meat from backyard slaughter is crucial to reducing the risk of brucellosis transmission.

Outbreak investigations of food-borne diseases

Brucellar epididymo-orchitis in an endemic setting: clinical features, management and outcomes from a single-centre study

ABSTRACT ID: 252

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Background

Brucellosis remains a significant zoonotic disease in endemic regions, with focal complications posing diagnostic and therapeutic challenges. Brucellar epididymo-orchitis (BEO) is an uncommon but important genitourinary manifestation that may mimic other causes of acute scrotum. This study aimed to describe the clinical presentation, risk factors, diagnostic approach, and treatment outcomes of BEO cases in an endemic setting.

Methods

We conducted a one-year retrospective analysis of patients diagnosed with BEO at a tertiary care centre. Diagnosis was based on compatible clinical findings (scrotal pain and swelling), epidemiological exposure, positive serology (Wright–Hedleston agglutination test and/or elevated Brucella-specific IgM/IgG), and ultrasonographic confirmation. Demographic, clinical, laboratory, treatment, and outcome data were analysed descriptively.

Results

Ten patients were included, with a mean age of 41 years (range: 29–63). Symptom duration was ‹2 weeks in 80% and ›6 weeks in 20% of cases. Epidemiological risk factors included animal husbandry (80%) and consumption of unpasteurised dairy products (20%). BEO was unilateral in 80% and bilateral in 20% of patients. The most common symptom was testicular pain, while scrotal swelling was the most frequent clinical finding. Elevated C-reactive protein was the predominant laboratory abnormality. Diagnosis was confirmed by Wright–Hedleston agglutination in 90% of cases and positive Brucella serology in all patients. Initial treatment regimens included combinations of gentamicin with levofloxacin or co-trimoxazole, alongside corticosteroids. Following hospitalisation (approximately two weeks), all patients completed oral therapy with doxycycline and rifampicin for at least six weeks; treatment was extended to eight weeks in three cases. Clinical recovery was achieved in all but one patient, who required orchiectomy due to delayed presentation.

Conclusions

BEO should be considered in the differential diagnosis of epididymo-orchitis in endemic regions, particularly in patients with relevant exposure history. Early recognition and appropriate combination antimicrobial therapy lead to favourable outcomes and can prevent complications and unnecessary surgical intervention.

POSTER TOUR 1

Outbreak investigations of food-borne diseases

Tip of the Iceberg Salad: Investigation of a Salmonella Typhimurium Outbreak in Denmark, November- December 2025

ABSTRACT ID: 395

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Background

On 27 November 2025, Danish national surveillance detected a cluster of nine cases of *Salmonella* Typhimurium sequence type 19 (ST19). We investigated the source and evaluated use of the case-case method.

Methods

We defined cases as laboratory confirmed *S.* Typhimurium ST19, clustered within 0–3 allelic differences by core genome multilocus sequence typing (Enterobase scheme), with sample dates between 8 November and 28 December 2025. Investigation included trawling questionnaires, consumer purchase data, and a matched case-control study. Controls were selected from the Danish population registry and matched on sex, age, and municipality, then interviewed by phone regarding food history. We used conditional logistic regression to calculate odds ratios (OR) with 95% confidence intervals (95% CI). We also conducted a case-case study, comparing early cases in this outbreak (n=11) with a concurrent *Salmonella* Strathcona outbreak (n=21) associated with tomato exposure.

Results

We identified 49 cases (55% female; median age 30 years; range 7-88), of which 18 were eligible and compared with 44 population registry controls. Compared to controls, cases were more likely to have consumed lettuce (OR 2.92, 95% CI 1.02-8.30). Of the nine cases providing consumer purchase data, seven (78%) had bought salads and traceback pointed to a common wholesaler. In the case-case study, outbreak cases were less likely than comparator cases to have shopped at grocery store A (OR 0.10, 95%CI 0.01-0.58) or consumed tomatoes (OR 0.03 95% CI 0.00-0.24) compared to cases in the concurrent outbreak.

Conclusions

Findings implicate iceberg lettuce as the possible outbreak source. The case-case study did not provide useful re-sults, likely because the comparator outbreak was dominated by a single exposure. Case-case methodology may be more informative when comparator cases have a broad range of exposures. Establishing a digital database of exposures all *Salmonella* cases could facilitate use of case-case methodology in future investigations.

POSTER TOUR 1

Outbreak investigations of food-borne diseases

Outbreak of Salmonella Enteritidis Associated with Egg Based Dishes in a Restaurant in Malta, November 2025

ABSTRACT ID: 538

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Background

Salmonellosis remains a leading cause of foodborne outbreaks in Europe, commonly linked to egg and poultry products. In November 2025, gastroenteritis cases associated with a restaurant in Malta prompted an outbreak investigation to identify the source and halt further transmission.

Methods

Cases were identified through enhanced surveillance and contact tracing. A confirmed case was defined as an individual with gastroenteritis and laboratory confirmed Salmonella infection following consumption of food from the implicated establishment from 1 November 2025. Epidemiological data were collected via telephone interviews. Environmental inspections and food sampling were conducted at the establishment. Veterinary investigations assessed the egg supply chain and implicated farm. Stool samples from cases and food-handlers, together with food and environmental samples, were analysed using RT-PCR and culture. Whole genome sequencing (WGS) was conducted on all positive Salmonella samples from humans, food and environment.

Results

Ten cases were identified until 13 November, with 6 confirmed positive for *Salmonella Enteritidis*. The median age was 27.5 years, 7 were female and 4 required hospitalisation. All cases reported consumption of egg-based dishes, mostly containing Hollandaise sauce. Multiple food safety breaches were identified in the restaurant, including improper in-house pasteurisation methods and storage of fresh Hollandaise sauce at room temperature. *Salmonella Enteritidis* was isolated from Hollandaise sauce samples. *Salmonella Livingstone* was isolated from environmental farm samples. Human and food isolates were genetically identical, whilst a farm sample positive for *Salmonella Enteritidis (*collected in July 2025 as part of annual routine surveillance) was within 8 single-nucleotide polymorphisms.

Conclusions

Use and improper storage of unpasteurized egg products was the likely cause of this outbreak. Post-investigation, the establishment updated their food safety procedures, using pasteurised eggs and control measures were instituted at the farm. This investigation evidences the importance of WGS and One Health collaboration in solving outbreak investigations.

Outbreak investigations of food-borne diseases

Foodborne outbreaks associated with large-volume catering: Insights from multiple Clostridium perfringens investigations in Wales, December 2024 - December 2025

ABSTRACT ID: 483

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Background

Clostridium perfringens continues to cause foodborne outbreaks particularly in large-volume catering settings where suboptimal temperature controls create high-risk conditions. We describe three *C. perfringens* food-borne outbreaks reported by Local Authority Environmental Health Teams to Public Health Wales, linked to restaurants and pubs during the autumn-winter period.

Methods

Retrospective cohort studies were conducted for all outbreaks, incorporating descriptive and analytical epidemiology. Online questionnaires and Firth logistic regression were used to assess exposures. Stool samples were collected for microbiological testing, and environmental health officers visited venues to assess food-hygiene practices.

Results

All outbreaks occurred during peak weekend services, when high demand may compromise food-handling practices. Settings included a buffet-style venue, a plated meal service, and a Christmas set-menu event; each served a limited menu typical of a traditional British roast dinner (roast meat, potatoes, vegetables and gravy). Cohort investigations identified 23, 44 and 30 cases respectively, representing small but significant clusters of illness. Attack rates ranged from 46–71% (median: 69%), with incubation periods of 12–14 hours. Analytical epidemiology consistently implicated roast beef as the likely vehicle (Outbreak A: OR 12.7, 95%CI 3.5–45.9, p<0.001; Outbreak B: OR 4.0, 95%CI 1.2–13.3, p=0.022; Outbreak C: aOR 6.9, 95%CI 1.4–34.2, p=0.013). Environmental health investigations identified temperature control failures in all outbreaks, and detection of the *cpe* enterotoxin gene confirmed the potential for *C. perfringens*-mediated diarrhoeal illness.

Conclusions

Roast beef was identified as the most likely vehicle for infection across all three outbreaks, and the high attack rates and short incubation periods were consistent with *C. perfringens* infection. These findings highlight the critical importance of effective hot holding and temperature control during the cooling of cooked meat products, as failures in implementation can lead to outbreaks. Ensuring adherence to established food safety guidelines is the most effective way to prevent future *C. perfringens* outbreaks.

Outbreak investigations of food-borne diseases

Salmonella Typhimurium (monophasic) Outbreak Investigation Utilising Loyalty Card Purchase Data , United Kingdom, January to March 2026

ABSTRACT ID: 199

Katie Bolam [1], ***Ann Hoban*** [1], ***Rebecca Howarth*** [2], ***Clare Sawyer*** [1], ***Frieda Jorgensen*** [1], ***Rob Johnston*** [1], ***David R Greig*** [1], ***Anais Painset*** [1], ***Amina Ismail Ahmed*** [1], ***Paul Crook*** [1], ***Ellen Heinsbroek*** [1], ***Georgia Beckett-Hill*** [1], ***Eleanor Clarke*** [1], ***Isobel Todd*** [1], ***Amreet Battu*** [2], ***Motolani Awokoya*** [1], ***William Stonebanks*** [3], ***Jacquelyn McCormick*** [3], ***Andrew Nelson*** [4], ***Lesley Larkin*** [5], ***Lynda Browning*** [5], ***Catriona Dobosz*** [5], ***Caoimhe McKerr*** [5], ***Andrew Robb*** [6], ***Patrick McAleavey*** [7], ***Danielle McMichael*** [7], ***Gauri Godbole*** [1], ***Hannah Charles*** [1]

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Background

Following routine whole genome sequence (WGS) cluster assessment in the UK, a 5-single nucleotide polymorphism (SNP) cluster of *Salmonella* Typhimurium (monophasic) (eBG1 1.1.1.124.6054.10393.%, HC5:274986) was identified and investigated between January and March 2026. Investigations utilised food chain traceback, microbiological testing and supermarket loyalty card (LC) data.

Methods

Cases were confirmed via WGS. International sequence comparisons were conducted through EpiPulse. LC data were obtained to identify exposures. Food chain and microbiological investigations included testing of products retained by cases and supplier testing. A case-case analyses (case-controls: yersiniosis cases) and case-control study (controls: market research panel) were undertaken to generate and test hypotheses.

Results

94 cases (50 male; median age 33.5 years) were reported in the UK (England: 76, Wales: 10, Scotland: 6, Northern Ireland: 2) with sample dates between 07 January and 12 March 2026. One additional genomically linked case was identified outside the UK via EpiPulse. Trawling questionnaires generated an early hypothesis of a saucisson product (11 cases) and high exposure to a national retailer, confirmed by case-case results (aOR 11.2, 95% CI 1.53–138). LC enabled the saucisson product to be specified and detected 4 additional cases who had purchased it within the incubation period but had not reported it during interviews. Food chain traceback identified an imported saucisson product. Multivariable case-control analyses also highlighted saucisson [[aOR 23.98, 95% CI 5.52-106.13]. Microbiological testing isolated the outbreak strain from product samples at a case's home. Testing of product samples by the business identified two mST positive samples, one was sequenced and matched the outbreak strain. The implicated batch of saucisson was withdrawn and recalled.

Conclusions

Evidence derived from multi-agency investigations highlighted the likely food vehicle as a cured pork product. LC purchase data was essential in identifying a specific saucisson product, facilitating food traceback and microbiological investigations, enabling the rapid implementation of control measures.

Outbreak investigations of food-borne diseases

Integrating Whole-Genome Sequencing (WGS) to Reinforce Traditional Epidemiological Investigation of a Foodborne Salmonella Outbreak, Moldova, 2025

ABSTRACT ID: 582

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Background

Integrating whole-genome sequencing (WGS) enhances foodborne outbreak investigations by linking human and food isolates, and delineating outbreak-related cases without reported connections. In August 2025, routine surveillance in Moldova identified 31 patients with suspected gastroenteritis who reported ordering food from the same food delivery company in Chisinau. We aimed to better define linkages between cases and food using WGS.

Methods

Patient interviews assessed food consumption and common-event exposures. During the outbreak, stool samples collected from patients and the company's kitchen staff, and ready-made and frozen foods obtained from the kitchen were cultured. Positive *Salmonella* cultures were tested by WGS. High-quality single nucleotide polymorphism (hqSNP) analysis was performed at the genomic laboratory in September 2025.

Results

Of 31 suspected patients and 15 kitchen staff who were tested, *S. enterica* was identified from 17 stool samples (14 patients, 3 kitchen staff). One omelette sample also yielded *S. enterica*; sushi samples tested negative. WGS confirmed that *S. enteritidis* from all 17 human isolates and the omelette were genetically related within 1 SNP, suggesting a common source. Although patients had not reported consuming omelette in initial interviews, interviews with food handlers confirmed it was included with the sushi meal. A single isolate from one epidemiologically-linked case was not related genetically to the outbreak strain, while two cases with no connection to this outbreak were genetically linked, suggesting broader or unrecognized exposure.

Conclusions

WGS enhanced the outbreak investigation by providing higher-resolution characterization for outbreak cases, supporting source attribution and identifying genetically-linked cases that were not epidemiologically recognized to be related to reveal the broader scale of outbreak. In outbreak investigations, genomic results must be interpreted alongside epidemiological evidence. A combined genomic and epidemiological evidence is essential for accurate source attribution and effective outbreak response.

POSTER TOUR 2

One Health

Operationalizing One Health in Emergency Preparedness and Response: Lessons Learned from Marburg Virus Disease Outbreak Response in Ethiopia, Rwanda, and Tanzania

ABSTRACT ID: 148

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Background

Recent Marburg virus disease outbreaks in Rwanda, Tanzania, and Ethiopia (2024–2025) highlighted differences in outbreak response approaches and persistent gaps in the operationalisation of the One Health approach during real-time public health emergencies. This narrative review assessed how One Health was applied during outbreak response and identified barriers to multisectoral implementation.

Methods

A structured narrative review was conducted using WHO outbreak situation reports, national Ministry of Health updates, and peer-reviewed literature published between 2024 and 2025. Evidence was synthesized to assess the operationalization of One Health across surveillance, laboratory systems, outbreak investigation, risk assessment, and coordination structures linking human, animal, and environmental health sectors.

Results

Across all three countries, outbreak response activities were predominantly led by the human health sector, including surveillance strengthening, contact tracing, infection prevention and control, laboratory confirmation, and community engagement. Operational implementation of One Health was largely limited to ad hoc coordination meetings and technical briefings, with minimal real-time integration of animal health surveillance, environmental risk assessment, or joint human–animal outbreak investigations. Coordination mechanisms were activated primarily in response to outbreaks and were not institutionalized as sustained One Health platforms. Interoperable cross-sector surveillance systems and routine data sharing across sectors were also limited. Key systemic barriers included fragmented surveillance architectures, weak interoperability between human and animal health information systems, delayed cross-sector information exchange, and the absence of formalised joint outbreak investigation mechanisms.

Conclusions

These findings indicate that although the One Health approach is widely endorsed, its operationalization during Marburg virus disease outbreaks remains inconsistent. Strengthening preparedness requires institutionalized One Health coordination platforms, interoperable surveillance and laboratory systems, and formal joint outbreak investigation protocols to enable timely and coordinated multisectoral response to emerging zoonotic threats.

POSTER TOUR 2

One Health

Avian Pathogenic Escherichia coli in Humans and Poultry in the Czech Republic

ABSTRACT ID: 752

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Background

Avian pathogenic *E. coli* (APEC) are opportunistic pathogens causing secondary infections in poultry. Their zoonotic relevance is associated with similarities between human and avian strains in terms of phylogenetic background, virulence and antimicrobial resistance determinants. This study investigates the molecular epidemiology of APEC strains isolated from humans and poultry to determine whether these populations share common genetic characteristics.

Methods

A collection of human isolates from urine and stool samples and veterinary isolates from poultry was established. Human isolates were collected in clinical laboratories as cefotaxime-susceptible and cefotaxime-resistant isolates. Veterinary isolates were selected on MacConkey agar without antibiotics and, in parallel, on plates supplemented with cefotaxime (2 mg/L) to detect cephalosporin resistance. Both, human and poultry isolates were tested using multiplex PCR targeting five genes associated with APEC pathotype.

Results

The study cohort comprised 1546 human isolates, of which 23% were identified as APEC, and 686 poultry isolates, of which 54% were identified as APEC. In total, 465 APEC isolates were analysed by whole-genome sequencing. Both collections showed high rates of phenotypic resistance to narrow-spectrum β-lactams (55%), ciprofloxacin (39%) and tetracycline (35%). Genotypic analysis confirmed the presence of genes associated with resistance to narrow-spectrum β-lactams, particularly *bla* (31%). ESBL genes occurred less frequently: TEM-1B *bla* was found mainly in poultry isolates, whereas *bla* and *bla* were predominated among CTX-M-1 CTX-M-15 CTX-M-27 human isolates. Both populations showed substantial sequence type diversity. Human isolates were most frequently assigned to ST95 and ST73, while poultry isolates were dominated by ST162 and ST1011. Despite this diversity, ST95, ST162 and ST73 were detected in both datasets.

Conclusions

These findings demonstrate that APEC represent an epidemiologically important group of *E. coli* with shared lineages occurring in both human and veterinary sectors, supporting the need for comprehensive One Health surveillance. The study was funded by the Czech Health Research Agency (project NW24-09-00510)

One Health

Meteorological exposures associated with reported Legionnaires' disease incidence in Greece: a 17-year time-series analysis

ABSTRACT ID: 297

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Background

The reported Legionnaires' disease (LD) incidence has been increasing globally, and meteorological conditions have been proposed as important contributors. Evidence from Greece remains limited. We aimed to investigate the associations of meteorological exposures with LD incidence at national and sub-national level.

Methods

We included sporadic LD cases with a known region of exposure within Greece between 2008 and 2024, recorded through the National Mandatory and the European Legionnaires' disease surveillance systems. We obtained temperature, precipitation, relative humidity and wind speed data from the Multi-Source Weather dataset and population data from the Hellenic Statistical Authority. We grouped regions with similar climatic characteristics into four climatic zones. We conducted a weekly time-series analysis at the national and sub-national levels using negative binomial regression models, presenting results as adjusted incidence rate ratios (aIRR) with 95% confidence intervals (95%CI). A population denominator, accounting for tourist inflows, was included as an offset in all models.

Results

The analysis included 1,180 cases. LD incidence increased significantly over time and exhibited strong summer seasonality. Nationally, adjusted for trend, seasonality and autocorrelation, each 1-mm increase in precipitation was associated with increased LD incidence (aIRR=1.10, 95%CI:1.04–1.15). A significant temperature-humidity interaction was observed (aIRR=1.005, 95%CI:1.003–1.007), with the strongest association at moderate humidity levels (65–73%) and temperatures >16.4°C. Wind speed was not associated with LD incidence (aIRR=0.86, 95%CI:0.73–1.01). Sub-nationally, the temperature-humidity interaction effect was stronger in the West and South zones than in the North.

Conclusions

Rainfall and specific temperature-humidity combinations were associated with increased LD incidence in Greece, with geographical variation in the temperature-humidity effects. These findings highlight the value of sub-national analyses and can inform targeted prevention, including enhanced monitoring and maintenance of water systems during high-risk periods and increased diagnostic vigilance in summer. In the context of climate change, weather-informed early warning systems warrant further investigation.

POSTER TOUR 2

One Health

Linking food animal reservoirs to human campylobacteriosis through integrated One Health genomic surveillance in Ireland, 2017–2025

ABSTRACT ID: 239

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Background

Campylobacter is the most frequently reported foodborne pathogen in Europe, with transmission predominantly driven by contaminated poultry and ruminant products. Despite a national notification rate of 72.6 per 100,000 exceeding EU averages, the food animal sources driving Ireland's elevated incidence remain uncharacterised, with limited integration between human and agricultural genomic surveillance. This study aimed to genomically link human campylobacteriosis to food animal reservoirs within Ireland's first integrated One Health whole genome sequencing (WGS) framework.

Methods

This study was conducted by the Public Health Laboratory (PHL) Dublin in collaboration with the Department of Agriculture, Food and the Marine (DAFM), integrating 1,356 human clinical isolates (2019–2025) with 241 food animal isolates (2017–2024) from poultry, sheep, pork, and beef, within a shared core genome multilocus sequence typing (cgMLST) scheme using Ridom SeqSphere+. Clusters were defined as ≥2 isolates within ≤5 allele differences; human–animal clusters required ≥1 isolate from each source. Antimicrobial resistance (AMR) determinants were identified from WGS assemblies using AMRFinderPlus.

Results

cgMLST identified 32 human–animal clusters, linking 14.6% of human (198/1,356) and 34.4% of animal isolates (83/241). Poultry (23 clusters, 79.5%) and sheep (seven clusters, 19.3%) were the predominant reservoirs linked to human cases. Five large clusters (≥20 isolates) spanned 5–8 years; six intermediate clusters (10–19 isolates) spanned 2–7 years while 21 smaller clusters (≤9 isolates) typically spanned one to two years. *C. jejuni* AMR profiling revealed preserved macrolide susceptibility (0.2%) and fluoroquinolone resistance below the EU average (33.1% vs. 72.0%).

Conclusions

This PHL–DAFM study provides the first genomic evidence of both persistent and sporadic poultry-to-human and sheep-to-human *Campylobacter* transmission in Ireland. Linkage rates substantially exceeded a prior Irish retrospective analysis using non-overlapping datasets (human: 0.5%; animal: 3.8%), underscoring the importance of contemporaneous cross-sectoral sampling. These findings can inform food chain-targeted interventions and AMR monitoring across human and animal transmission chains.

One Health

Shared resistance plasmids in third-generation cephalosporin-resistant Escherichia coli from livestock, meat and humans in Spain

ABSTRACT ID: 699

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Background

Third-generation cephalosporin-resistant *Escherichia coli* (3GC-R *E. coli*) is a major One Health concern, but the source of human infection remains under discussion. It is unclear whether dissemination of 3GC-R *E. coli* is driven by transmission of successful lineages or mobile resistance plasmids circulating between niches. We compared 3GC-R *E. coli* from livestock, meat and humans to quantify sharing of lineages, resistance genes and plasmids.

Methods

We analysed 408 Spanish 3GC-R *E. coli* genomes from livestock (n=163), meat (n=52) and humans (168 healthcare-associated, 25 community), collected in 2014-2023. Animal and meat isolates were sequenced using Illumina. Human genomes were selected from 22 public BioProjects based on ESBL/AmpC genotype. We inferred sequence types, phylogroups, resistance determinants and plasmid replicons. Resistance-gene profiles were compared by source using Jaccard PERMANOVA and ESBL-gene location was predicted with MOB-recon and rfplasmid. *bla* -carrying IncI1 plasmids were compared using plasmid MLST and Mash networks. SHV-12

Results

The collection comprised 120 sequence types. ST131 was mainly healthcare-associated, whereas ST10 and phylogroups A/B1 were detected across niches. ESBL genes were detected in 83% of isolates, acquired *AmpC* genes in 11% and *AmpC* promoter mutations in 8%. *bla* was the most frequent ESBL gene (24%), mainly detected SHV-12 in livestock and meat, but also present in healthcare-associated isolates. *bla* and *bla* were mainly CTX-M-15 CTX-M-14 human-associated. Resistance-gene profiles differed by source (PERMANOVA R^2=0.058; p=0.001). *bla* was SHV-12 predicted to be plasmid-borne in 89% of positive isolates (n=96); 59% carried IncI1-alpha replicons, mainly CC- 3/pST3-like or CC-2/pST26-like plasmids. Both IncI1 groups were found in livestock, meat and human isolates, and frequently co-carried tetracyclines, aminoglycosides, phenicols and sulphonamides resistance genes.

Conclusions

Preliminary findings suggest limited sharing of *E. coli* lineages between food-animal sources and healthcare-associated human isolates, but recurrent cross-compartment circulation of *bla* IncI1 plasmids. One Health SHV-12 surveillance should include plasmid-level monitoring to detect resistance elements shared between animals, food and humans.

POSTER TOUR 3

Surveillance of vaccine-preventable diseases

Maternal pertussis vaccination coverage and sociodemographic and maternal factors associated with non-uptake in Sweden: preliminary results from a nationwide cohort study

ABSTRACT ID: 129

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Background

Maternal pertussis vaccination (MPV) provides effective protection for newborns during their first months of life. In August 2022, Sweden introduced a national recommendation for MPV. However, MPV is not captured in the National Vaccination Register, posing challenges for surveillance and research. Using alternative registers, this study aims to provide updated MPV coverage in Sweden and to identify factors associated with non-uptake.

Methods

We conducted a population-based cohort study using data from the Swedish Pregnancy Register, covering 99.9% of births in Sweden, including self-reported vaccination information, supplemented with information from the Region Stockholm vaccination database. Deliveries between 1 July 2024 and 30 June 2025 were included. Coverage was calculated nationally and by region. Factors associated with non-uptake were assessed using Poisson regression with a log link and robust standard errors to estimate risk ratios (RR) with 95% confidence intervals (CIs).

Results

Among 95,619 deliveries, vaccination status was available for 79,465 (83.1%). National vaccination coverage (complete-case analysis) was 73.9%, ranging from 64.3% in Region Skåne to 90.1% in Region Gotland. Younger women had lower uptake (20–24 years: RR 0.80; 95% CI 0.77–0.83; reference 30–34). In age-adjusted results, lower uptake was associated with lower education (RR 0.82; 95% CI 0.81–0.84; reference post-secondary), being a job seeker (RR 0.67; 95% CI 0.63–0.70, reference employed), and multiparous (≥2 births: RR 0.68; 95% CI 0.66– 0.70, reference nulliparous). Compared with Nordic-born, uptake was significantly lower among women born in African, non-EU European, and Eastern Mediterranean regions (RR range 0.45 – 0.58), but also among women born in non-Nordic EU countries (RR 0.76; 95% CI 0.73–0.80).

Conclusions

MPV coverage in Sweden is similar to levels observed in other high-income and EU countries but could be improved. Heterogeneity across regions and population groups highlights inequities in uptake and the need for improved surveillance data and targeted interventions to ensure equitable infant protection.

POSTER TOUR 3

Surveillance of vaccine-preventable diseases

Spatiotemporal dynamics of measles resurgence in the EU/EEA: spatially independent outbreaks driven by national vaccination gaps, 1999–2024

ABSTRACT ID: 132

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Background

Measles resurgence has accelerated across Europe since 2017, with further concern following COVID-19-related disruptions to immunisation programmes. Simultaneous outbreaks in multiple countries have raised questions about whether transmission reflects cross-border spatial diffusion or independent national dynamics — a distinction with direct implications for response strategy.

Methods

We analysed annual measles notification rates and second-dose measles-containing vaccine (MCV2) coverage for 26 EU/EEA countries with sufficient surveillance data from 1999 to 2024, using ECDC Surveillance Atlas data. Outbreak years were defined as annual notification rates exceeding 10 cases per million, a threshold applied in published European measles assessments; sensitivity analyses at 5 and 20 per million yielded consistent re-sults.Spatial autocorrelation was quantified annually using Global Moran's I under two complementary weight specifications with 999 permutation-based inference. Local Moran's I identified spatial clusters in years with the highest number of affected countries.Spearman correlation assessed associations between MCV2 coverage and notification rates at lags of 0–3 years.

Results

We identified 129 outbreak country-years,peaking in 2019(16 countries).Significant global spatial autocorrelation was detected in only 3 of 24 years(2000,2008, and 2020 — the latter attributable to near-universal suppression of transmission; $p<0.05$ under both specifications).Local Moran's I revealed no high-high clusters during the major outbreak wave of 2017–2019. MCV2 coverage showed a consistent inverse association with notification rates across all lags(Spearman $\rho = -0.31$ to -0.37, all $p<0.001$). Mean MCV2 declined from 90.1% pre-COVID (2017–2019) to 88.1% post-COVID (2022–2023), persistently below the WHO 95% target.

Conclusions

Across a 25-year observation period, measles outbreaks in the EU/EEA were spatially unstructured and driven by within-country vaccination deficits rather than geographic diffusion. This suggests that national, rather than regionally coordinated, immunisation strategies are the primary lever for outbreak prevention. Countries failing to achieve the WHO 95% MCV2 target represent priority targets for catch-up programmes.

POSTER TOUR 3

Surveillance of vaccine-preventable diseases

Evaluating Measles Surveillance toward Elimination in North Rhine-Westphalia, Germany, 2024 and 2025

ABSTRACT ID: 815

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Background
Measles elimination requires ≥95% population immunity, supported by sensitive surveillance from local health authorities (LHAs). As Germany's most populous state, North Rhine-Westphalia (NRW) is pivotal for identifying surveillance gaps for elimination verification. In 2024, NRW introduced an origin-of-infection classification. We evaluated NRW's measles surveillance in 2024 and 2025 to guide state and national elimination efforts.

Methods
We conducted a retrospective evaluation of NRW measles notification data from 2024 and 2025. We described diagnostic delay (symptom onset to clinical or laboratory diagnosis) and measured performance against WHO targets (≥80%) using four indicators: timeliness of notification (diagnosis to notification ≤48 hours); viral detection for sporadic cases (PCR or sequencing in an accredited laboratory); viral detection in chains of transmission (≥2 epidemiologically linked cases: ≥1 PCR-confirmed case); and completeness of origin of infection ("imported", "import-related" or "endemic"). Cases with insufficient information were classified as "sporadic" or "unknown". Medians, interquartile ranges (IQR) and proportions were calculated using R (v4.5.1).

Results
Median diagnostic delay was 5 days (IQR:2–7) in 2024 and 4 days (IQR:3–7) in 2025. Timeliness of notification (≤48 hours) increased from 70.2% in 2024 to 80.0% in 2025. Viral detection for sporadic cases decreased from 34.1% (14/41) in 2024 to 13.0% (6/46) in 2025. Among chains of transmission, 76.5% (13/17) in 2024 and 75.0% (6/8) in 2025 had ≥1 PCR-confirmed case. Origin of infection was recorded in 61.6% (196/318) in 2024 and 39.7% (29/73) in 2025.

Conclusions
NRW achieved the WHO target for reporting timeliness in 2025 and virus detection was available for most chains of transmission. However, gaps remain in molecular confirmation of sporadic cases, as standard diagnostic workflows rely on serological testing, which aligns with clinical guidance but limits the viral genotyping required for WHO elimination verification. We recommend improving LHA awareness of elimination surveillance indicators through standardised questionnaires and targeted workshops.

POSTER TOUR 3

Surveillance of vaccine-preventable diseases

Novel serology assay reveals large unascertained community burden of pertussis in children in North Wales, UK during the 2023-2024 epidemic.

ABSTRACT ID: 319

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Background

During 2023-2024, Wales experienced a year-long pertussis epidemic. Due to under-ascertainment, the real burden of pertussis is unknown. Anti-pertussis toxin (PT) serum IgG measurement is well established for serodiagnosis but doesn't distinguish recent vaccination from infection. A novel assay measures antibodies binding a *Bordetella pertussis* (Bp)-mutant lacking the four antigens present in UK pertussis vaccines (BP-4aP-KO), enabling detection of infection only. We used this assay to better understand community burden of pertussis among children ≤17-years-old during the epidemic.

Methods

We collected residual paediatric blood samples from pathology tests in three hospitals in North Wales (April- July 2024). We measured serum PT-IgG and Bp-4aP-KO-IgG and defined preliminary concentration thresholds to identify recent Bp infection. We linked sample data to pertussis vaccination status (Welsh immunisation service) and regional pertussis notifications from the surveillance system (August 2023-July 2024). We calculated proportions of children with recent Bp infection by age, sex, vaccination and notification status.

Results

There were 330 suspected pertussis notifications among children in the region (median age: 8-years, 47.6% female). Of the 1,380 residual blood samples collected, only one had a lab-confirmed pertussis notification, despite 175 (12.6%) and 190 (13.8%) showing evidence of recent Bp infection by PT-IgG and Bp-4aP-KO-IgG positivity respectfully. 84.3% of sampled children had received all 4 recommended pertussis vaccine doses and 90.1% at least one dose. Older age groups had higher prevalence of serology detected infection than younger: 16.1% of samples from 12-17-year-olds had above threshold levels of Bp-4ap-KO-IgG vs 11.3% from 7-11 and 2.6% from 0-6-year-olds.

Conclusions

Bp-4aP-KO serology analysis of pertussis infection in children after the 2023-2024 epidemic indicates for every 1 notification there were 189 undetected cases. Notifications captured fewer older children than serology, indicating under-detection in this age-group. This data supports the hypothesis that pertussis epidemics are driven by infections among older children, possibly due to waning immunity.

POSTER TOUR 3

Surveillance of vaccine-preventable diseases

Analysis of global mpox outbreak dynamics during the 2024-2026 Public Health Emergency

ABSTRACT ID: 321

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Background

The second WHO Public Health Emergency of International Concern (PHEIC) for mpox was declared on 14 August 2024 following clade Ib MPXV emergence in the Democratic Republic of the Congo (DRC) and rapid regional and international spread. The PHEIC ended on 5 September 2025; the Africa CDC Public Health Emergency of Continental Security was lifted on 22 January 2026. To characterise global and Africa-specific mpox epidemiology across the full second PHEIC cycle and immediate post-emergency period, January 2024 to February 2026.

Methods

A retrospective surveillance analysis was conducted using the WHO Global Mpox Trends dashboard, supplemented by WHO situation reports S32-S64 and international and national surveillance reports. Analyses included negative binomial segmented regression, network analysis, event-study comparisons, and descriptive statistics. Models used reported case counts with log population offsets; incidence rate ratios compare reported case rates.

Results

Between January 2024 and February 2026, 82,738 cases and 306 deaths (CFR 0.37%) were reported globally. The PHEIC period accounted for 74.0% of cases, peaking at 7,405 in May 2025. In total, 163 clade-specific importation or travel-linked events were reported across 41 countries; onward transmission occurred in 25 (15.3%) across 16 countries. Within DRC, 200 health zones recorded 144,035 cases (CFR 1.42%), with 45.4% of burden in the top 20 zones. Transmission decelerated after PHEIC termination but persisted.

Conclusions

Emergency termination marked an administrative transition, not the end of mpox transmission. The post-emergency period requires sustained surveillance, maintained diagnostic capacity, targeted response in persistent transmission settings, and equitable access to vaccines and countermeasures.

POSTER TOUR 3

Surveillance of vaccine-preventable diseases

Re-emergence of diphtheria in Germany: Differences between imported and autochthonous cases with C. diphtheriae, 2017–2025

ABSTRACT ID: 537

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Background

Diphtheria is very rare in Germany. Since 2022, *Corynebacterium (C.) diphtheriae* case numbers have increased following an outbreak among newly-arriving migrants. We describe epidemiological trends and differences between imported and autochthonous *C. diphtheriae* cases.

Methods

We included all laboratory-confirmed (toxigenic or *tox* gene-positive) *C. diphtheriae* cases and cases epidemiologically linked to a laboratory-confirmed case in Germany between 2017 and 2025. We conducted a time series analysis and fitted a Poisson regression model to quantify trends regarding autochthonous transmission. We compared case characteristics (manifestation, age, sex and hospitalization) using Chi-squared and Fisher's exact test to assess differences between autochthonous (no reported travel or migration history in 21 days prior to detection) and imported cases.

Results

Overall, 346 diphtheria cases were reported (average annual incidence: 0.045 per 100,000 population) including 306 (88%) with cutaneous, 22 (6%) respiratory, and 18 (5%) double manifestation. Three respiratory cases died, all reported since 2024, with one unvaccinated and two individuals with unknown vaccination status affected. Acquisition of *C. diphtheriae* shifted from predominantly migration-associated (232/261; 89%) in 2022-2023 to autochthonous transmission (35/54; 65%) in 2024-2025. We observed an increasing trend in autochthonous *C. diphtheriae* cases (incidence rate ratio per quarter 1.19, 95% CI 1.14–1.27; p=<0.001). Compared to imported cases, autochthonous cases were older (25/45 vs. 19/283 being >45 years old, p=<0.001) and more frequently female (12/45 vs. 16/283, p=<0.001). Respiratory manifestations (10/45 vs. 30/283, p=<0.05) and hospitalizations were more common among autochthonous cases (36/45 vs. 83/283, p=<0.001).

Conclusions

Diphtheria is re-emerging in Germany with a shift from predominantly imported to increasingly autochthonous transmission. Given the surprisingly frequent occurrence of double manifestations, systematic reporting may help to further clarify transmission chains. To prevent severe cases and deaths, immunisation gaps should be closed, particularly among vulnerable groups. Clinicians should refamiliarize themselves with the disease to facilitate prompt diagnosis and treatment.

POSTER TOUR 3

Surveillance of vaccine-preventable diseases

Rapid escalation and sustained transmission of measles in an under-vaccinated community, Enfield, London, 2026

ABSTRACT ID: 1034

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Background

England has experienced a resurgence of measles since 2023, leading to loss of UK elimination status. Outbreaks have shifted geographically, with London dominating transmission; areas of highest deprivation and low vaccine uptake have been most affected. National incidents and MMR catch-up campaigns have been stood up in response, but pockets of under-vaccinated communities remain. We describe the evolution and severity of a rapidly escalating outbreak in Enfield, London, which started in January 2026.

Methods

The UK Health Security Agency (UKHSA) conducts enhanced surveillance of suspected measles cases in England. A national measles linelist is established by linking laboratory, contextual, demographic and vaccination data. Laboratory-confirmed cases, defined by serology or PCR, between 1 January and 30 April 2026 were included. Severity was assessed through linkage to hospitalisation data from the Emergency Care Data Set and Secondary Uses Service.

Results

London accounted for over half of national cases (312/543, 58%), with Enfield contributing almost one third (100/312, 32%). Almost all cases (97/100) were unvaccinated. Under-10-year-olds represented 83% (83/100) of cases. 90% (90/100) resided in the two most deprived quintiles. 72% (72/100) of cases were genotyped as b3 and all sequenced as DSID 6418, consistent with ongoing community transmission from a single introduction. The outbreak effected 15 schools and 23 families. Almost all cases attended emergency care (95%, 95/100); 45% went on to be admitted (43/95). Admission was most frequent amongst under-1-year-olds (80%, 8/10). Median length of stay was 3 days.

Conclusions

MMR uptake in Enfield is below the England average, at 78% for dose 1 and 62% for dose 2 at age five. This outbreak demonstrates how measles introduction into an under-vaccinated community can drive sustained transmission, particularly where unvaccinated children attend shared schools. High incidence among young children in deprived areas highlights inequalities in disease burden and the need to restore ≥95% MMR coverage.

POSTER TOUR 4

Surveillance, outbreaks and high-risk populations

Evaluation of the Cerebrospinal Meningitis surveillance system: Lessons from Sokoto State, Nigeria

ABSTRACT ID: 872

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Background

Cerebrospinal meningitis (CSM) is endemic in Nigeria, with seasonal outbreaks in northern states causing substantial morbidity and mortality. Sokoto State reported 800 suspected cases and 72 deaths during the February to May 2025 outbreak. Effective surveillance during outbreaks is essential for timely action and reducing preventable outcomes. We evaluated the Sokoto State CSM surveillance system to determine its performance during and immediately after the 2025 outbreak.

Methods

We conducted a retrospective evaluation of the surveillance system from January to September 2025 using the CDC guidelines for evaluating public health surveillance systems. We assessed reporting timeliness and data quality, through a review of line lists, laboratory reports, and case investigation forms (CIF). System attributes; simplicity, acceptability, representativeness, usefulness, and coverage were evaluated through structured interviews with 160 purposively selected surveillance officers across all 23 Local Government Areas (LGAs), and key informant interviews (KIIs) with five state level stakeholders. Quantitative data were analyzed descriptively in R, and qualitative results summarized thematically.

Results

Overall, of 845 suspected cases, 80% were reported from LGA to state level within 24 hours of facility notification, 37% had complete CIF data, and 98% had consistent demographic and clinical information across reporting tools. Only 113 (13.3%) of the 800 suspected cases during the outbreak, had specimens collected for laboratory confirmation. Most (93%, 96%, and 90%) officers were motivated, found reporting tools easy to use, and reported use of surveillance data to guide response activities respectively. However, only 70% reported full coverage of their assigned areas. KIIs showed insecurity in multiple communities and a substantial workforce turnover that resulted in many newly deployed, undertrained surveillance officers.

Conclusions

The system demonstrated good timeliness, accuracy, and usefulness but low completeness and coverage. Continous training for new officers and improving security will be essential for maintaining a robust CSM surveillance in Sokoto State.

POSTER TOUR 4

Surveillance, outbreaks and high-risk populations

Outbreaks in asylum seeker accommodations in Germany, 2015-2025

ABSTRACT ID: 688

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Background

Due to crowded living conditions, shared facilities and vulnerable populations, settings such as asylum seeker accommodations (ASA) are prone to infectious diseases outbreaks. In Germany, the notification of outbreaks of infection diseases in such congregate settings is mandatory by law. We describe notified outbreaks in ASA to guide outbreak management and prevention efforts.

Methods

The data from the statutory surveillance system from 2015-2025 on outbreaks with outbreak setting ASA was analysed. We describe case number, diseases and characteristics of cases, as well as number and size of outbreaks. Outbreaks were defined as two or more cases with an epidemiological link.

Results

In total, 11,856 cases with the exposure place ASA were reported between 2015 and 2025. Cases ranged in age between 0 and 86 years (mean age: 17 years), with a higher proportion being male (60% vs. 34%). Scabies, chickenpox, head lice, norovirus gastroenteritis and influenza were the most reported diseases (45%, 20%, 8,4%, 5,6%, 4,0% respectively). In total, 11,755 cases were part of 2,079 outbreaks (median: 4 cases, range 2-126) with scabies, chickenpox, head lice, norovirus gastroenteritis and influenza being most common ones (892, 453, 159, 99, 79 outbreaks). High number of outbreaks were observed in 2015 (288) and 2016 (147) following influx of migrants, declined during the COVID-19 pandemic and reached the highest number observed in 2023 (343) and 2024 (337). Of all cases, 9% (1,026/11,856) were hospitalized most due to infection with Rotavirus (140), Influenzavirus (127) and Norovirus (112).

Conclusions

Outbreaks with ectoparasites such as scabies and head lice are likely due to crowded living conditions or could be acquired during migration and are preventable by hygiene measures. The high burden of chickenpox and hospitalisation due to Influenza indicates the need for more focus on vaccine program efforts in these settings.

POSTER TOUR 4

Surveillance, outbreaks and high-risk populations

Closing the Diagnostic Gap: Determinants of Timely Mpox Diagnosis and Genomic Sequencing under the 7-1-7 Framework in the Democratic Republic of the Congo, 2022–2025

ABSTRACT ID: 607

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Background

Mpox remains a global public health concern with laboratory diagnosis being a critical component for effective outbreak detection and response under the 7-1-7 framework. In the Democratic Republic of Congo (DRC), diagnostic delays weaken surveillance. This study evaluated the proportion and operational factors associated with achieving mpox diagnosis within 7 days of symptom onset.

Methods

We conducted a retrospective observational study using exhaustive sampling of suspected mpox cases recorded in the national DHIS2 tracker surveillance and laboratory database between 2022 and 2025 in the DRC. Timeliness was defined as time from symptom onset to diagnosis (≤7 days versus >7 days). Variables assessed included demographics, sample type, investigator category, and surveillance-laboratory intervals, including symptom-to-alert, alert-to-sample collection, collection-to-expedition, laboratory reception-to-analysis, symptom-to-Mpox result, and Mpox result-to-sequencing. Logistic regression was performed to estimate crude and adjusted odds ratios (COR and AOR) with 95% confidence intervals (CI).

Results

Results

A total of 30,784 alerts were recorded; 11,771 (38.2%) were validated; 9,139 (77.6%) samples collected; and 2,829 tested by PCR, yielding an mpox positivity rate of 33.6% (951/2,829), with 50.6% diagnosed within 7 days. Only 386 (40.58%) samples underwent sequencing, and 53.9% were sequenced within 7 days. Faster symptom-toalert intervals were associated with achieving ≤7 Mpox diagnosis 3–4 days (AOR=2.85; 95% CI:1.90–4.28), 24– 48h (AOR=4.10; 95% CI:2.80–6.01), and ≤24h (AOR=5.20; 95% CI:3.40–7.90), all $p<0.001$. Alert-to-sample collection within ≤24h significantly improved timeliness (AOR=4.79; 95% CI:2.49–7.51). Laboratory reception-to-analysis within 24–48h (AOR=2.75; 95% CI:1.85–4.10) and ≤24h (AOR=3.40; 95% CI:2.20–5.10) were also significant pre-dictors. Symptom-to-Mpox result ≤7 days (AOR=6.90; 95% CI:4.20–10.50) and Mpox result-to-sequencing ≤24h (AOR=3.85; 95% CI:1.70–8.50) independently increased the likelihood of achieving timely sequencing.

Conclusions

Timely diagnosis of Mpox remains sub-optimal affected by operational determinants in DRC. Sequencing proportion meets Africa CDC and WHO requirements. Strengthening surveillance decentralizing diagnostic capacity are critical for enhancing outbreak preparedness and response performance in DRC.

POSTER TOUR 4

Surveillance, outbreaks and high-risk populations

Spatial heterogeneity in RSV-SARI incidence in children at the city level: sociodemographic and epidemiological determinants of urban hotspots and coldspots, Lyon, France, 2012–2025.

ABSTRACT ID: 595

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Background

RSV is a leading cause of severe acute respiratory infections (SARI) in young infants. Substantial spatial heterogeneity is observed at country and regional levels. Still urban-level RSV-SARI patterns remain poorly understood. We sought to identify sociodemographic, epidemiological, and urban determinants distinguishing RSV-SARI hotspots from coldspots at the city level.

Methods

We performed a retrospective study of PCR-confirmed RSV hospitalizations among children under 2 years of age born at Lyon University Hospitals (2012–2025), estimating age-specific incidence rates by postal code. Hotspots and coldspots were defined as areas exceeding or falling below one standard deviation from the mean city incidence rate. Socioeconomic data were sourced from the French census 2020; prematurity and multiparity from the birth cohort.

Results

Among 114,110 linked children, 1,974 RSV hospitalizations were identified. Mean annual incidence was 9.2/1,000 person-years (95%CI 8.8–9.6), with marked spatial heterogeneity: 13.0 (95%CI 11.8–14.3) in hotspots, 9.0 (95%CI 8.6–9.5) in intermediate areas, and 5.9 (95%CI 5.1–6.9) in coldspots. Hotspots clustered in eastern suburbs, coldspots in centre-western suburbs. Peak incidence occurred earlier in hotspots (0–1 month of age; 58.3/1,000 person-years, 95%CI 45.8–70.8) than in intermediate and coldspot areas (1–2 months of age; 45.1, 95%CI 39.9–50.3 and 32.5, 95%CI 22.5–42.4, respectively). Hotspots compared to intermediate areas and coldspots showed higher crude birth rates (15.3 vs 13.8 vs 11.5 annual births /1,000 inhabitants), younger populations (25.2% vs 21.1% vs 19.8% aged ‹18 years), greater poverty (24.1% vs 19.4% vs 13.0%), higher prematurity (10.2% vs 9.0% vs 7.4%), and higher multiparity (58% vs 54% vs 51%).

Conclusions

Hotspot infants face both earlier RSV exposure and heightened vulnerability, underscoring the need for city-level targeted prevention. Systematic passive immunization at birth, taking into account the risk of prematurity, should be prioritized in these high-risk areas.

POSTER TOUR 4

Surveillance, outbreaks and high-risk populations

Unrelated or linked? Integrating whole genome sequencing into epidemiological investigation to unravel a measles outbreak in Utrecht, the Netherlands, 2024

ABSTRACT ID: 426

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Background

In November–December 2024, three apparently unrelated measles cases were reported in the Utrecht region of the Netherlands, all unvaccinated young children. Epidemiological investigation initially found no clear links between these cases. We describe how integrating epidemiological data and whole genome sequencing (WGS) clarified transmission routes and supported outbreak control.

Methods

Following the first notification in November 2024, the Public Health Service of Utrecht conducted source and contact tracing. A related measles case was defined as a clinically compatible illness with an epidemiological link to a confirmed case. High-risk contacts – those with insufficient immunity and close or prolonged (>15 minutes) contact in the same space – were offered post-exposure prophylaxis (PEP): MMR vaccination or immunoglobulins. WGS was performed on available PCR-positive samples; resulting sequences were used for phylogenetic analysis to assess transmission clusters and relationships between cases.

Results

In total, 57 contacts were identified, 31 of whom were high-risk; 11 accepted PEP. The outbreak comprised three subclusters with 21 secondary cases, predominantly unvaccinated young children. Epidemiological investigation initially suggested the three cases were unrelated. However, WGS data from 15 cases (including all three initial cases) indicated that all sequences were part of a single molecular cluster, distinct from sequences from other Dutch regions, suggesting a single introduction. Detailed case review then revealed that all three initial cases had been present at the same location during the first case's infectious period. WGS also identified an additional case belonging to the same cluster, with an inconclusive epidemiological link to the outbreak.

Conclusions

This outbreak illustrates the added value of WGS in complex measles outbreak investigations. The combination of epidemiological investigation and WGS revealed transmission dynamics not apparent from epidemiological data alone and helped exclude multiple independent introductions. The outbreak findings were translated into a case study for WGS-based outbreak investigation training, available on request.

POSTER TOUR 4

Surveillance, outbreaks and high-risk populations

Predominance of antimicrobial-resistant serotype V Streptococcus agalactiae among colonised pregnant women in Poland

ABSTRACT ID: 302

Milena Kwidzinska [1], Alicja Grabicka [1], Maksymilian Kempa [1], Sebastian Borzyszkowski [1], Konrad Wiśniewski [1], Dominik Jarosz [1], Marta Katkowska [1], Alina Gębska [1], Bartosz Rybak [2], Katarzyna Garbacz [1]

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Background

Group B streptococci (GBS) remain a significant aetiological factor of neonate infections in Poland. The emerging antimicrobial resistance mechanisms pose a major challenge to effective intrapartum antibiotic prophylaxis, particularly in patients allergic to β-lactams. We aimed to assess the distribution of GBS serotypes among colonised pregnant women in a Polish clinical hospital setting and their potential association with antimicrobial resistance patterns.

Methods

A total of 59 clinical strains of *S. agalactiae*, isolated between 5 June 2025 and 20 October 2025 from pregnant women, were evaluated. Only one isolate from each patient was included in the study. The strains were isolated and identified using routine microbiological diagnostic methods. Antibiotic susceptibility testing was performed by disc diffusion, according to EUCAST guidelines. PCR was used for serotyping the strains and for detecting selected drug resistance genes.

Results

Serotypes Ia, II and V were the most prevalent, accounting for 25.4%, 20.3% and 25.4% of all strains, respectively. Notably, six strains appeared to be nontypeable. All examined strains were susceptible to penicillin, trimethoprim/sulfamethoxazole and vancomycin. The percentage of strains resistant to erythromycin and clindamycin was 44.1% each. Remarkably, serotype V strains showed the highest resistance rate to both erythromycin and clindamycin (80.0%), as opposed to 6.7% of serotype Ia strains and 33.3% of serotype II strains. The association between the strains belonging to serotype V and resistance to both erythromycin and clindamycin was statistically significant (p-value ‹ 0.001).

Conclusions

Streptococcus agalactiae serotype V showed higher rates of resistance to erythromycin and clindamycin than other serotypes, potentially limiting the use of perinatal prophylaxis and highlighting the need for surveillance in patients allergic to β-lactams. Our results might also prove useful in the future design of a polyvalent vaccine and its implementation in our region.

Surveillance, outbreaks and high-risk populations

Evaluation of Acute Encephalitis Syndrome (AES) Surveillance under the National Digital Disease Surveillance Platform, Assam, India, 2025

ABSTRACT ID: 809

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Background

Acute Encephalitis Syndrome (AES) is a public health concern with 4.80 million related disability adjusted life years (DALYs) estimated globally. In India, the incidence rate is 0.42 per 100,000 population and for Assam it was 21 per 100, 000 population (2022-2025). We described and evaluated the AES surveillance system under the national digital disease surveillance platform in Assam.

Methods

We conducted a mixed-methods cross-sectional evaluation of AES surveillance system in Assam. It was evaluated for simplicity, stability, acceptability and data quality attributes based on the standardized evaluation guideline. We interviewed the stakeholders using the semi-structured interview guide. We reviewed the records and noted field observations. We analysed AES case data reported from 2022 to October 2025 for diagnostic outcomes. We calculated frequencies, rates and proportions for quantitative data. Attributes were summarized using the average of all the indicators. Thematic analysis was done for qualitative responses.

Results

We visited 13 health facilities (HFs) and interviewed 68 stakeholders. AES surveillance in Assam was carried out through sentinel surveillance sites and other HFs. Electronic reporting was done on digital surveillance platform. The platform was interlinked for JE case details and details of laboratory confirmed cases for non- JE AES etiologies needed to be added separately. The surveillance attribute score was simplicity- 50% (11/22), stability-83%, acceptability-62%, representativeness- 5% (9/177) and data quality 42%. Confirmed diagnosis were available for 10% of the AES cases. Key informant interviews highlighted diagnostic challenges due to constraints in human resources and laboratory capacity for enhanced AES surveillance.

Conclusions

The AES surveillance was functional and stable in Assam. However, low representativeness, average data quality, varied reporting practices and limited diagnostic capacity were affecting the early detection and timely response. We recommended strengthening AES surveillance by increasing workforce trainings, engaging private sector, diagnostic strengthening and integrated data system for One Health aligned surveillance.

Burden of respiratory diseases

Describing age-specific respiratory syncytial virus incidence and establishing an epidemiological baseline in Croatia (2017–2025)

ABSTRACT ID: 186

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Background

Respiratory syncytial virus (RSV) causes high global morbidity, but comprehensive, national-level data on its incidence and seasonality in Croatia hasn't been described. Early detection of RSV activity is important for public health resource planning and hospital preparedness. This study aims to describe yearly RSV incidences by age group, and to establish the first national baseline for early epidemic detection.

Methods

This retrospective study analysed routine primary care records from the Croatian Central Health Information System during 2017–2025. We identified ICD-10 coded RSV-associated episodes (J20.5,J21,J12.1,B97.4). We calculated age-specific annual incidences (per 100,000 and Interquartile Range (IQR)) and analysed sex distribution. The moving epidemic method (MEM) was used to identify the epidemiological baseline, season timing and intensity across seven seasons (excluding 2020/2021 due to COVID-19).

Results

Among 27,382 RSV-associated episodes, gender distribution revealed statistically significant age-related inversion ($p < 0.001$): males predominated in the 0–4 (57.2%) and 5–14 (60.5%) age groups, while females accounted for most cases over 15 years, peaking at 68.3% among individuals ≥80. Children 0–4 exhibited the highest incidence (median 1126.45/100,000; IQR: 948.68-1442.07/100,000). Adults 15-29 and ≥80 had the lowest incidence (medians 9.29/100,000 and 11.65/100,000). The MEM-established baseline threshold was 77 weekly cases. Epidemics started in ISO week 44 (95% Confidence Interval: 36–48) and lasted 27 weeks. The 2023/2024 and 2024/2025 seasons reached very high and high intensities (peak: 365 and 329 weekly cases, respectively).

Conclusions

This study provides the first description of age-specific RSV incidence in Croatia, highlighting peak burden in young children (0–4 years) and differing gender distribution by age. In addition to serving as actionable thresholds for early detection, the established baselines provide a benchmark for evaluating the impact of RSV vaccination if introduced into the national immunization program. The observed post-pandemic shift toward higher-intensity epidemics aligns well with global trends.

POSTER TOUR 5

Burden of respiratory diseases

Increased risk of human metapneumovirus (hMPV) infection during the first two years of life among children born <28 weeks preterm in Lyon, France, 2012–2025

ABSTRACT ID: 834

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Background

Although severe hMPV disease is more frequent in the first months of life and among vulnerable groups such as preterm infants, European incidence data on preterm infants remain limited. To date, no hMPV vaccines have been licensed, although candidate vaccines are under development. We aimed to estimate the incidence of hMPV in young children and preterm infants to identify high-risk groups and inform prevention strategies and future vaccine policies.

Methods

We conducted a retrospective cohort study including all children born at Lyon University Hospitals during 2012– 2025. We linked birth records with hospital laboratory data containing laboratory-confirmed hMPV cases using unique anonymized patient identifiers. Cases were defined as children ≤2 years with a positive PCR result for hMPV. We estimated age-specific annual incidence rates using person-years, overall and by period (pre-, during- , and post-COVID-19) or gestational age. We used Poisson regression models to estimate incidence rate ratios (IRRs).

Results

After linkage of 127,261 children, 386 hMPV cases were identified. Mean annual incidence was 19.5 per 1000 person-years (95%CI:17.6–21.6). Incidence was highest at 1 month of age (5.31/1000 person-years) and declined with age (IRR=0.92; 95%CI:0.905-0.934). Preterm infants had 15 (IRR=15.0, 95%CI:10.0–21.6) times higher incidence of hMPV infection than full term infants. Incidence varied by birth cohort, with higher rates observed after the COVID-19 pandemic (IRR= 2.26, 95%CI:1.81–2.81), but not during the pandemic period (IRR=1.09, 95%CI:0.81–1.44) compared with the pre-pandemic period.

Conclusions

hMPV incidence increased with decreasing age and was significantly higher among preterm infants. Prematurity was a strong independent determinant, supporting the need for targeted prevention strategies for high-risk infants early in life.

POSTER TOUR 5

Burden of respiratory diseases

Drivers, impact and costs of respiratory illness on the national health service (NHS) workforce over winter 2025/26 in the United Kingdom

ABSTRACT ID: 550

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Background

Healthcare systems experience additional pressure during winter, due to increased admissions and staff absence from respiratory illness. Healthcare workers (HCW) are highly exposed and critical to health system resilience. We aimed to characterise drivers (circulating respiratory viruses), impact (respiratory illness and associated staff absence), and costs (economic impact) of respiratory illness among HCW.

Methods

A United Kingdom HCW cohort study collected fortnightly data (October-March 2025/26) on respiratory symptoms, sickness absence, and influenza vaccination via linkage to national databases. A subset provided weekly nasopharyngeal swabs (December-January), for metagenomic viral sequencing. Influenza-like illness (ILI) and sickness absence were analysed by vaccination status. The cost of respiratory illness absence was estimated using occupation, wage band, and absence duration. Viral detection rates and virus types were described. The association between viral detection and demographic and occupational characteristics were estimated using logistic regression.

Results

3,328 participants were included; 84% were female, median age 55 years, 67% in clinical roles and 79% influenza vaccinated. 47% of participants reported at least one ILI episode (59% unvaccinated vs 43% vaccinated, p<0.001). 18% took sick leave due to ILI (23% unvaccinated vs 15% vaccinated, p<0.001). The estimated cost of cohort sickness absence was £709,975. Viral detection rate was 33% (208/640) for symptomatic samples, with 11 viruses identified - most commonly rhinovirus (24%), respiratory syncytial virus (16%), and influenza A (15%). Only age was associated with viral detection (>55years: OR 1.4; 95%CI 0.99-1.9; p=0.050). Influenza (2.2; 0.98–4.9; p=0.055) and RSV (2.9; 1.4–6.4; p=0.005) were linked to higher odds of sick leave compared with virus-negative samples.

Conclusions

Respiratory illness significantly impacts HCWs, with half reporting ILI and one in five taking sick leave. While vaccination can help, many viruses are not vaccine preventable, highlighting the need for other pathogen-agnostic interventions (e.g. the built-environment). Researching their effectiveness in real-world healthcare settings is a priority.

POSTER TOUR 5

Burden of respiratory diseases

COvid-19 among HEalth caRE professionals in the Nordic CountriEs (COHERENCE II)

ABSTRACT ID: 418

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Background

During the COVID-19 pandemic, healthcare professionals (HCPs) faced elevated occupational exposure to SARS- CoV-2. Although previous research indicates higher infection rates among HCPs, uncertainties remain regarding disease severity, differences across countries, and how risks evolved alongside pandemic waves. This study aims to compare the incidence of COVID-19 between HCPs and other occupations across three Nordic countries, investigating temporal trends and the possible impact of preventive policies.

Methods

We conducted a population-based cohort study using national registers from Denmark, Sweden, and Norway including the active workforce aged 20–65 from February 1, 2020, to September 30, 2022. The primary exposure was occupation (HCPs versus non-HCPs), and the primary outcomes were COVID-19 infection (PCR/antigen tests) and hospitalization. To evaluate how risks evolved over time, we stratified the analyses across four specific pandemic periods. We used Cox proportional hazards models for time-to-first-event analyses, adjusting for sociodemographic characteristics and baseline comorbidities.

Results

Preliminary analyses from Denmark included an active workforce cohort of approximately 3 million individuals. During follow-up, 1,922,577 COVID-19 infections and 11,591 hospitalizations occurred. The overall incidence rate of positive tests was 347 per 1,000 person-years among HCPs compared to 259 in non-HCPs, and 1.4 versus 1.3 hospitalizations per 1,000 person-years in each group. During the first period (February 2020-June 2021), HCPs had a significantly higher risk of infections (adjusted HR: 1.55; 95% CI: 1.53-1.57) and hospitalizations due to COVID-19 (adjusted HR: 1.47; 95% CI: 1.33-1.63) when compared to other active workforce professionals. Hospitalization risk peaked in the first period and decreased subsequently, while infection risk showed a U-shaped pattern. Data analysis for Norway and Sweden remains ongoing.

Conclusions

HCPs experienced disproportionately higher rates of COVID-19 infection and severe disease compared to other active workers, particularly in the first part of the pandemic. The risk varied across analytical periods and outcomes.

POSTER TOUR 5

Burden of respiratory diseases

Differential Severity of Acute Respiratory Infection Outbreaks by Pathogens in Nursing Homes

ABSTRACT ID: 128

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Background

Understanding pathogen-specific differences in acute respiratory infection (ARI) outbreak severity may inform risk-based response strategies. We aimed to characterise outbreak severity using attack rate, hospitalisation rate, mortality, and outbreak duration.

Methods

We conducted a descriptive analysis of ARI outbreaks in nursing homes using routine surveillance data in 2024 and 2025. A pathogen was considered associated with an outbreak if identified in at least one case; outbreaks could be associated with more than one pathogen. Outbreak severity was summarised by associated pathogen using resident and staff attack rates (AR), resident hospitalisation rate (HR), resident mortality, and outbreak duration (defined as the number of calendar days between onset of the first and last case).

Results

Between 2024 and 2025, 68 ARI outbreaks were reported. SARS-CoV-2 was associated with 50 outbreaks, followed by rhinovirus/enterovirus (RV/EV) (18), influenza (13), respiratory syncytial virus (RSV) (10), other coronaviruses (7), human metapneumovirus (hMPV) (5), and parainfluenza virus (4). RSV showed the highest median resident AR at 21.5% (IQR: 12.6-35.8) and staff AR at 11.0% (IQR: 5.2-15.8). Influenza demonstrated the highest HR at 31.6% (IQR: 18.9-39.6), followed by RSV at 29.7% (IQR: 16.5-39.5). SARS-CoV-2 had the lowest HR at 14.1% (IQR: 8.2-25.1) despite being most common. Mortality was highest in influenza outbreaks but rare in RV/EV and parainfluenza outbreaks. Other coronaviruses and hMPV had the longest median outbreak durations at 48 days (IQR: 19-52) and 44 days (IQR: 11.5-50.5) respectively, whilst SARS-CoV-2 had the shortest at 18 days (IQR:12-22.3).

Conclusions

Respiratory pathogens exhibit distinct outbreak patterns in nursing homes. RSV and hMPV demonstrated high resident attack rates and prolonged transmission respectively, whilst influenza showed the greatest hospitalisation and mortality risk. These findings support pathogen-specific outbreak preparedness strategies and highlight the importance of comprehensive diagnostic testing to identify co-infections that may complicate outbreak management and increase mortality risks among vulnerable populations.

POSTER TOUR 5

Burden of respiratory diseases

Epidemiology of Respiratory Syncytial Virus and risk factors for severe outcomes among children <2 years hospitalised with respiratory infection in Skopje, Republic of North Macedonia, October 2025–April 2026

ABSTRACT ID: 766

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Background

Respiratory syncytial virus (RSV) is the leading cause of lower respiratory tract infections worldwide among children <2 years. Maternal RSV vaccination and monoclonal antibodies significantly reduce RSV burden in infants. In countries where these products have not yet been introduced, local data on RSV epidemiology and severity can help guide decisions about their use. We aimed to identify factors associated with severe outcomes among children <2 years hospitalised with respiratory infection in Skopje, R.N. Macedonia.

Methods

From October 2025 to April 2026, we enrolled children <2 years hospitalised in two tertiary hospitals in Skopje who met the WHO extended severe acute respiratory infection (eSARI) case definition. Children were systematically tested for RSV, influenza, and SARS-CoV-2 by RT-PCR. We used descriptive statistics to describe patient characteristics and multivariable Poisson regression with robust standard errors to calculate adjusted risk ratios (aRR) associated with severity (a composite outcome of use of supplemental oxygen, mechanical ventilation, ICU admission or death).

Results

Of 224 children meeting the eSARI definition, 193 (86%) were tested, 104 (54%) were RSV-positive, 13 (7%) influenza-positive and 9 (5%) SARS-CoV-2-positive. Overall, 121 (54%) children were male; 117 (52%) were aged <6 months, and RSV positivity was highest in this age group (74/117, 63%). Severe outcomes occurred in 63 (33%) children, with no deaths reported. Severe outcomes occurred in 46% of RSV-positive compared with 22% of RSV-negative children. In multivariable analysis adjusted for age and comorbidities, RSV positivity (aRR 2.1, 95%CI 1.2–3.8) and male sex (aRR 1.9, 95%CI 1.1–3.3) were independently associated with severe outcomes.

Conclusions

Among hospitalized children <2 years, RSV infection and male sex were independently associated with severe outcomes. RSV positivity was highest among children aged <6 months, the primary target group for new RSV immunisation products. Our findings provide local evidence to inform RSV immunisation policy in R.N. Macedonia.

POSTER TOUR 5

Burden of respiratory diseases

Population-level burden of rhinovirus, influenza, and SARS-CoV-2 among adults: A multi-season analysis in the Netherlands, 2022–2025

ABSTRACT ID: 400

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Background

Rhinoviruses circulate year-round, typically causing mild illness, whereas influenza viruses and SARS-CoV-2 are associated with more severe disease but distinct peaks. How these differences translate into overall population-level burden remains unclear. We aimed to compare the community-level burden of rhinovirus, influenza, and SARS-CoV-2 infections among adults in the Netherlands in the lower level of the surveillance pyramid.

Methods

We used data from Infectieradar, a community-based surveillance system (2022-2025, ~10,000 weekly participants). Weekly incidence of self-reported acute respiratory infections (ARI) of adults (aged 15-75) was estimated and weighted to represent the Dutch population. Each week, a random subset of ARI cases (~170) provided swabs for multiplex PCR testing. For each pathogen, we estimated weekly positivity and the proportion of infections with ≥6 symptoms including fever, defined as high-burden infections. Annual population burden was calculated as the product of ARI incidence, pathogen-specific positivity, and the proportion of high-burden infections per pathogen, aggregated by year (October–October). Associations with healthcare determinants were assessed using regression models adjusted for age, sex, and comorbidities.

Results

We analyzed data from 2,2 million reports and 26,000 samples. Preliminary estimates indicate rhinoviruses had the highest annual incidence (1–1,1 per person), compared with SARS-CoV-2 (0.4–0.6) and influenza (0.1– 0.2), while the annual incidence of high-burden infections was relatively similar across pathogens ([0.07-0.08 vs 0.12-0.13 vs 0.06-0.1 per person, respectively]). Infections with SARS-CoV-2 and influenza were associated with increased general practitioner visits, sick leave, and medication use compared with rhinovirus infections.

Conclusions

This large, year-round, survey showed that despite having a lower individual-level burden, the high number of rhinovirus infections contribute substantially to the community-level burden among adults through sustained year-round transmission. These findings demonstrate that population-level burden is shaped by both severity and frequency, and that rhinovirus can rival influenza and SARS-CoV-2 in their public health impact.

POSTER TOUR 6

Communication and behavioural aspects

Awareness, attitude and practices related to brucellosis among female pastoralists of Pakistan: A one health perspective

ABSTRACT ID: 865

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Background

Brucellosis, a globally prevalent zoonotic disease, poses significant health challenges, especially in developing countries. Several studies from brucellosis-endemic countries have assessed livestock farmers' knowledge and attitudes toward the disease. However, no such study has been conducted in Pakistan to access awareness of female livestock workers. This study aimed to assess the awareness, attitudes, and practices (AAPs) of female livestock farmers in Pakistan

Methods

A community-based cross-sectional study was conducted in Sindh and other regions of Pakistan, focusing on participation from female livestock workers. A structured questionnaire, comprising of 70 questions, was used to collect data on demographics, AAPs related to brucellosis. Statistical analysis, including Chi-square tests, was performed using SPSS, with a P-value ‹ 0.05 considered significant

Results

Out of 210 female participants, the majority were housewives (67.1%), resided in rural areas (75.2%), and had no formal education (53.3%). Knowledge about brucellosis was limited, with most participants unaware of its zoonotic nature or health implications. Despite consuming raw or boiled milk, 91.9% of respondents reported using no protective measures during milking. Practices such as disposing of aborted fetuses improperly and assisting animals during parturition without gloves were common. While 78.1% believed in animal vaccination, only 6.2% had vaccinated their animals against brucellosis. Regional differences in consulting veterinarians for aborted animals were significant, highlighting varying levels of awareness and preventive practices.

Conclusions

The study revealed a critical gap in awareness and preventive practices regarding brucellosis among female livestock handlers, particularly in rural regions. Limited knowledge of its zoonotic transmission and the widespread neglect of protective measures during livestock handling pose significant public health concerns. These findings emphasize the urgent need for targeted educational initiatives, community awareness programs, and enhanced veterinary services to effectively address the risks of brucellosis in vulnerable communities of Pakistan.

POSTER TOUR 6

Communication and behavioural aspects

Triangulated digital surveillance during a suspected cholera alert in Poland.

ABSTRACT ID: 506

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Background

Acute health events test the preparedness and communication capacity of public health (PH) systems in real time. Poor coordination and premature pathogen naming can drive information overload, prolonged public uncertainty, and erosion of trust - even for clinically limited events. Existing tools detect volume quickly but lack the narrative classification and PH interpretive logic needed for acute event surveillance. We piloted a multi-stream digital surveillance workflow during a Vibrio cholerae alert in Poland in July–August 2025.

Methods

Four data streams were combined: a custom component using Polish-adapted small language models (HerBERT/XLM-RoBERTa-class) classified approximately 700 relevant X posts against an analyst-guided narrative taxonomy; Brand24 captured 7,542 mentions across social media, news portals and forums; Google Trends assessed search interest; and qualitative review identified recurring narrative patterns. Official communication was scored against the WHO Emergency Response Framework 2024 across four domains: listening, understanding and promoting, building resistance, and community engagement.

Results

Both patients had detected vibrio cholerae genetic material, later confirmed as non-toxigenic vibriosis. The first official statement used the term cholera before toxin confirmation and was followed by rapid amplification. Search interest peaked on day one. Brand24 recorded 1,882 same-day mentions with an estimated reach of 33 million. Sentiment varied substantially by sampling frame: 65% of all X mentions were negative, compared with 37% of thematically filtered posts and 43% across the full dataset. Discussion continued for two weeks despite corrective statements. WHO ERF scores were low across listening, resistance-building and community engagement domains.

Conclusions

Multi-stream digital surveillance documented a poorly coordinated PH communication response, with sustained information overload disproportionate to the clinical threat. Premature pathogen naming, low WHO ERF scores, and prolonged public uncertainty point to structural gaps in acute event preparedness. Preparedness plans should include explicit pathogen-naming criteria, communication protocols aligned with international frameworks, and digital surveillance integrated into acute response planning.

Communication and behavioural aspects

Comparison of vaccination determinants across seven diseases in Germany: a cross-sectional study

ABSTRACT ID: 233

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Background

Research on determinants of vaccination intention is extensive but has largely focused on single diseases, e.g. COVID-19. It remains unclear whether psychological predictors generalise across diseases with different exposure contexts. This study aimed to compare predictors of vaccination intention across seven diseases to inform public health communication.

Methods

A cross-sectional online survey was conducted in a representative sample of the German general population (N = 2,138). Vaccination intention was assessed for seven diseases: influenza, COVID-19, tick-borne encephalitis (TBE), polio, yellow fever, dengue fever, and human papillomavirus (HPV). Measures included risk perceptions, knowledge, trust in information sources, conspiracy mentality, and perceived barriers. Hierarchical linear regression models were computed for each disease.

Results

Perceived likelihood of infection and disease-related concerns were the strongest predictors of vaccination intention across all diseases. The effect of perceived likelihood of infection was strongest for yellow fever (β = .41, $p \leq .001$) and weakest for COVID-19 (β = .12, $p \leq .001$). Disease-related concerns were highest for influenza (β = .36, $p \leq .001$) and lowest for yellow fever (β = .11, $p \leq .001$). Perceived vaccine effectiveness was relevant for influenza (β = .18, $p \leq .001$) and COVID-19 (β = .14, $p \leq .001$), while vaccine safety only mattered for COVID-19 (β = .14, $p \leq .001$) and HPV (β = .13, $p \leq .001$). Effects for conspiracy mentality and perceived barriers were not significant for vaccination intention for any disease. Trust in personalized and interactive information sources was positively associated with vaccination intention for five diseases; trust in institutional expert sources was only linked to TBE.

Conclusions

Perceived likelihood of infection appears to be the most generalisable predictor of vaccination intention across diseases. Conspiracy mentality and safety concerns seem to be context-specific and relevant only for selected diseases. This highlights the need for disease-specific communication strategies.

POSTER TOUR 6

Communication and behavioural aspects

High Awareness, Low Action: Gaps in Cervical Cancer Screening and HPV Vaccination Among Women Living with HIV in North Central Nigeria

ABSTRACT ID: 212

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Background

Women living with HIV (WLHIV) face a disproportionately high risk of cervical cancer, yet uptake of preventive measures remains critically low in many high-burden settings. Understanding modifiable barriers is essential for designing effective public health interventions. This study aimed to assess knowledge, practices, barriers, and risk perception related to cervical cancer screening and HPV vaccination among WLHIV in North Central Nigeria, to inform evidence-based programmatic action.

Methods

A facility-based cross-sectional study was conducted among 991 WLHIV of reproductive age (15–49 years) attending ART clinics in Kwara and Niger States, North Central Nigeria. A multi-stage sampling technique was used, with participants systematically selected. Data were collected using a 77-item semi-structured questionnaire. Outcome measures included lifetime cervical cancer screening, HPV vaccination uptake, comprehensive knowledge (scored >66%), and barriers. Descriptive statistics, chi-square tests, and binary logistic regression were applied (α=0.05).

Results

Although 76.2% had heard of cervical cancer, only 34.6% demonstrated comprehensive knowledge. Alarmingly, 61.5% had never been screened for cervical cancer, and 96.3% had never received HPV vaccination. Key barriers included fear of pain (59.7%), fear of positive results (71.0% in Niger), lack of awareness of screening services (63.3% in Kwara), limited access to facilities (60.9%), cost (61.7%), and cultural concerns (fear of male screeners: 67.5% in Niger). Higher education and urban residence were associated with better knowledge ($p<0.001$). Married women had significantly higher screening uptake than unmarried women (Kwara: OR=17.19, 95% CI:2.34– 126.01). High barrier levels reduced screening odds by over 55% (OR=0.43–0.44, $p<0.001$). Risk perception did not differ significantly between screened and unscreened women.

Conclusions

Awareness of cervical cancer is high, yet screening and vaccination uptake are critically low. Major programmatic barriers persist within HIV care settings. Key findings urge integration of screening and vaccination into routine HIV services, community-based delivery, male engagement, and targeted communication to address fear, access, cost, and cultural obstacles.

POSTER TOUR 6

Communication and behavioural aspects

Measles outbreak in Antwerp, Belgium 2025: targeted response in an under-vaccinated community and lessons from an after-action review

ABSTRACT ID: 521

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Background

MMR vaccination coverage in Flanders is high though suboptimal (first dose 96%; second dose 89%) but immunity gaps exist. In 2025, an outbreak occurred in the city of Antwerp, mostly affecting a population group with lower vaccination uptake. We describe the outbreak and evaluate response strategies.

Methods

We conducted a descriptive epidemiological analysis of notified measles cases from March to June 2025. An after-action review (AAR) was performed, including stakeholder surveys, to assess governance, surveillance, communication and vaccination.

Results

A total of 73 patients were identified within a geographically and a socially connected cluster, largely concentrated in a single postal code (80%), predominantly affecting children (86% aged 0 – 9 years) and unvaccinated persons (79%). The hospitalisation rate was 50.6%, with 6.9% requiring intensive care. In total, 118 cases were reported citywide, indicating potential spillover beyond the initial cluster. Two genotypes (B3 and D8) were identified, suggesting multiple introductions. Control measures included rapid establishment of an outbreak management team, enhanced diagnostic coordination, and targeted communication via general practitioners, paediatricians, and key community figures. A centrally organised vaccination point achieved limited uptake, whereas a 10.5-fold increased vaccination activity was observed through primary care with 847 vaccinations administered during a period of 4 months, compared to an average of 81 vaccination during this period in the last three years. The AAR identified strengths including rapid coordination and effective engagement of trusted community actors. Challenges included unclear roles and responsibilities, limited real-time data access, and suboptimal reach of centralised vaccination strategies. Outreach approaches embedded in community networks were more effective than stand-alone interventions.

Conclusions

The outbreak demonstrates that measles can spread quickly through pockets with undervaccinated individuals. Targeted, trust-based interventions integrated within community structures, combined with improved coordination and real-time surveillance, are critical to address heterogeneity and strengthen outbreak preparedness.

POSTER TOUR 6

Communication and behavioural aspects

Knowledge, attitudes and practice towards HPV vaccination among students, Kazakhstan, 2023

ABSTRACT ID: 544

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Background

Medical students and future healthcare workers play an important role in improving vaccine confidence and increasing immunisation coverage. In Kazakhstan, declining childhood vaccination coverage and increasing vaccine hesitancy have raised concerns regarding the preparedness of future healthcare professionals to promote vaccination. This study aimed to assess knowledge, attitudes and practices (KAP) related to HPV vaccination among senior medical students in Kazakhstan.

Methods

A cross-sectional study was conducted among senior medical students from three universities in Astana, Almaty and Karaganda between March and May 2023. Logistic regression analysis was used to identify factors associated with inadequate KAP. Students scoring ›70% on knowledge questions were considered to have adequate knowledge. Odds ratios (OR) and 95% confidence intervals (CI) were calculated.

Results

A total of 3,956 students participated, including 1,716 (43%) from Astana, 1,313 (33%) from Almaty and 927 (24%) from Karaganda. Overall, 74% were female and 65% were aged 21–23 years. Most participants studied general medicine (89%), followed by pediatrics (8%) and public health (3%). Only 38% reported receiving vaccination-related training. Adequate knowledge was identified in 1,291 (33%) students, positive attitudes in 951 (24%) and good practices in 2,311 (58%). More than half (53%) were neutral regarding HPV vaccine safety, while 48% were neutral towards the statement that HPV vaccines are more dangerous than HPV infection. Inadequate knowledge was associated with male sex (OR: 1.52; 95% CI: 1.27–1.82), Islamic religion (OR: 1.49; 95% CI: 1.23– 1.80), negative attitudes (OR: 3.41; 95% CI: 2.87–4.04) and inadequate practices (OR: 2.56; 95% CI: 2.17–3.04).

Conclusions

The study identified insufficient knowledge and unfavourable attitudes towards HPV vaccination among medical students in Kazakhstan. Strengthening vaccine education within undergraduate medical curricula may improve vaccine confidence and support future immunisation programmes.

POSTER TOUR 7

SDG-targeted infections

A pre- and post-intervention analysis of the TB surveillance system in Spain, 2018-2024

ABSTRACT ID: 826

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Background

In Spain, tuberculosis (TB) surveillance is decentralised across nineteen regions, leading to heterogeneity in data quality. The National Centre for Epidemiology has circulated annual regional feedback reports applying to data from 2021 onwards. We quantified changes in TB surveillance internal completeness following introduction of feedback reports and assessed their acceptability and perceived usefulness.

Methods

We estimated internal completeness of 40 TB variables on reported cases from 2018-2023 in two periods: before implementation of feedback reports (2018–2020) and after (2021–2023). We compared mean completeness of each period using the paired t-test or the Wilcoxon signed-rank test. We circulated results to regional focal points, and an online survey to assess acceptability, perceived usefulness of feedback reports, and barriers to data completeness.

Results

Between 2018 and 2023, 25,299 cases were reported. Nationally, mean completeness increased from 66% in 2018–2020 to 76% in 2021–2023 (+10%, p<0.001). Improvements were greatest for laboratory-related (+14%, p=0.001) and illness-related variables (+13%, p<0.001), while patient-related variables had minimal change (+2.4%, p=0.48) as many started near 100% completeness at baseline. Of the 19 regions, 84% had improved completeness in period 2, though substantial variation persisted. Amongst the 18 regional respondents, 61% (11/18) were satisfied with both the current surveillance system, and the completeness of data reported by their region. All respondents considered feedback reports useful. Challenges highlighted included limited system interoperability between laboratory and surveillance, resource constraints, and patient follow-up particularly for patients moving between regions.

Conclusions

Following introduction of annual feedback reports, which were well accepted by regions, Spain saw significant improvements in TB data completeness. Annual reports will continue to be updated according to regional feedback as part of a continuous improvement cycle. Sustained feedback mechanisms, streamlined report-ing requirements, continued integration between surveillance laboratory systems, and improved protocols for follow-up are key to strengthening TB surveillance.

POSTER TOUR 7

SDG-targeted infections

Performance Evaluation of Computer-Aided Detection for Triage of Chest X-Rays in Tuberculosis Screening in Ukraine

ABSTRACT ID: 99

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Background

In this study, we determined the optimal thresholds for two computer-aided detection (CAD) systems to improve tuberculosis screening efficiency and coverage in Ukraine's war-affected, resource-limited regions.

Methods

Analysis used a dichotomous classification of 3,156 de-identified chest X-rays with existing radiologist reports. CAD system scores were assessed at the default threshold (0.5), at the WHO-recommended sensitivity ≥0.91, and at the Youden index-derived threshold. With GeneXpert molecular test as the gold standard, we evaluated sensitivity, specificity, and Cohen's kappa coefficient to indicate the level of agreement between CAD and GeneXpert results.

Results

Raising the CAD score threshold to the Youden index (0.668 for qXR, 0.558 for CAD4TB) increased specificity (0.821 vs 0.716 for qXR, and 0.895 vs 0.821 for CAD4TB) without notably reducing sensitivity. Cohen's kappa for the two models was 0.75, indicating strong agreement. The analysis demonstrated a fair discriminatory ability of CAD systems, with an area under the curve for both systems of 0.79. Specificity observed at a sensitivity of ≥0.91 (0.328 for qXR and 0.343 for CAD4TB) is consistent with previously reported ranges from three independent evaluations of CE-marked technologies conducted by January 2020, namely CAD4TB v6 (Delft Imaging), Lunit Insight CXR (Lunit), and qXR v2 (Qure.ai), evaluated across diverse populations and clinical settings, for both screening and triage.

Conclusions

CAD systems calibration using locally obtained data improved specificity, reducing false-positive findings and optimizing the use of bacteriological testing. While Youden's index is mathematically justified, it assumes equal weighting of sensitivity and specificity, which may not reflect real-world clinical needs. In high tuberculosis-burden settings, prioritizing sensitivity may minimize missed cases, whereas in low-resource contexts, higher specificity reduces unnecessary follow-up and prevent system overload. Thresholds based on Youden's index and the WHO-recommended sensitivity benchmark can improve tuberculosis screening efficiency in Ukraine while maintaining consistency with prior evaluations and supporting the real-world CAD use.

SDG-targeted infections

Hepatocellular carcinoma mortality following hepatitis B and C infection in Slovenia, 2016–2022: national datasets linkage study to monitor progress towards hepatitis B and C elimination

ABSTRACT ID: 430

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Background
The WHO strategy to eliminate viral hepatitis as public health threat by 2030 recommends monitoring viral hepatitis B and C mortality. We aimed to estimate annual hepatocellular carcinoma (HCC) mortality following hepatitis B virus (HBV) and/or hepatitis C virus (HCV) infection in Slovenia for 2016–2022.

Methods
We conducted a linkage study using the Slovenian Cancer Registry, the National Hospital Health Care Statistics Database and the Communicable Disease Registry. HCC deaths had a C22.0 International Classification of Diseases-10 code recorded as underlying cause of disease and previous HCC diagnosis registered. We linked all three datasets using personal identification number or name, surname and date of birth. Information about previous HBV and HCV infection was obtained from the National Hospital Health Care Statistics Database for 2001–2022 and from the Communicable Disease Registry for 1990–2022.

Results
Among 926 HCC deaths during 2016–2022, 91 (10%) occurred following HBV and/or HCV infection; 41/91 (45%) followed HBV infection, 43/91 (47%) followed HCV infection, 2/91 (2%) followed HBV and HCV coinfection and 5/91 (5%) followed an unknown type of viral hepatitis. Overall HCC mortality ranged from 5.9/100,000 population in 2016, to 7.1/100,000 in 2020, and declined to 6.0/100,000 in 2022 (median=6.2/100,000). HBV-related mortality ranged from 0.3/100,000 in 2016 and 2017, to 0.5/100,000 in 2018 and declined to 0.1 in 2022 (median=0.3/100,000), and HCV-related mortality ranged from 0.6/100,000 in 2016 to 0.1/100,000 in 2021 and 2022 (median=0.2/100,000).

Conclusions
Our estimates were lower compared with previous Slovenian estimates using different methods and suggest that up to 10% of HCC deaths might have been prevented, if HBV and/or HCV had been eliminated. Linking national data was feasible. We recommend establishing routine monitoring of HCC mortality following HBV and HCV infection, linking data from existing national datasets, to monitor progress towards hepatitis B and C elimination.

POSTER TOUR 7

SDG-targeted infections

Genomic epidemiology and insights on the resistance profile of Treponema pallidum in Portugal

ABSTRACT ID: 496

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Background

Syphilis, a sexually/vertically transmitted infection, remains a public health concern, with a significant resurgence in developed countries across Western Europe and the Americas. Notably, Portugal presents one of the highest notification rates within the EU/EEA. Management of the infection is challenged by the diagnostic complexity, asymptomatic cases, the absence of a vaccine, and the spread of antibiotic-resistant (AMR) strains. Syphilis genomic epidemiology still remains poorly explored, due to *Treponema pallidum* subsp. *pallidum in vitro* culture limitations.

Methods

We present a *T. pallidum* genomic dataset generated from 174 clinical specimens, collected in Portugal from 2004 to 2026, from the Reference Laboratory for Sexually Transmitted Infections at INSA, using target enrichment capture followed whole-genome sequencing. Clustering analysis was performed on SNP informative sites, integrated with ›1000 *T. pallidum* publicly available genomes. AMR mutations were screened in *16SrRNA*, *23SrRNA*, *mrcA* (PBP3), and *pbp2* genes. Inter and intra-patient variability targeting the variable regions of *T. pallidum*'s major antigen TprK was also assessed.

Results

Our results show the co-circulation of strains from both SS14 and Nichols lineages in Portugal, at least since 2016 (previously, only SS14 was detected), integrated into multi-country clusters. The A2058G mutation in *23SrRNA*, responsible for high-levels of resistance to azithromycin, was present in ›93% of strains. Additional mutations were detected, namely the A1873G (›47%) and the G2122A (›62%) in *mrcA*, with suggested association to reduced susceptibility to penicillin. Intra- and inter-patient *tprK* variability remains rampant across its variable regions associated with antigenic potential.

Conclusions

These findings highlight the need for routine surveillance of syphilis towards informing clinicians and public health authorities, preventing the spread of AMR strains. This constitutes the largest *T. pallidum* genomic study in Portugal, serving as the starting point to develop a cost-effective surveillance strategy to be routinely implemented at the laboratory, focused on the key adaptive drivers of *T. pallidum*.

SDG-targeted infections

Increasing trends in reported gonorrhoea incidence in young adults in Slovenia, 2005-2024

ABSTRACT ID: 534

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Background

Gonorrhoea incidence has recently increased in many European countries, particularly among young adults of both sexes and among men who have sex with men (MSM). We described gonorrhoea cases and temporal trends in Slovenia, to determine whether similar patterns occurred and to inform targeted preventive measures.

Methods

We included pseudonymised gonococcal infection cases notified during 2005-2024. We calculated annual incidence per 100,000 population overall and by sex and age group, and described MSM cases by year and age group. We described monthly incidence trends using negative binomial regression.

Results

During 2005-2024, 2,201 cases were reported, 1,888 in men and 313 in women. Annual incidence ranged from 1.2/100,000 in 2011 to 13.9/100,000 in 2022 (median=3.25/100,000). After the COVID-19 pandemic decrease, incidence rose markedly in 2021-2022, and decreased slightly in 2023 (11.7/100,000) and 2024 (9.51/100,000). Negative binomial regression indicated that monthly incidence increased by 1.1% (95% CI: 1.0-1.2; p<0.001). Increases occurred in all age groups aged ≥15 years, with the highest incidence among young adults, particularly men aged 25-29 years (median annual incidence 22.2/100,000, ranging from 5.0/100,000 in 2006 to 80.1/100,000 in 2022) and women aged 20-24 years (median annual incidence 3.7/100,000, ranging from 0/100,000 in 2008 to 31.4/100,000 in 2022). Among men, MSM accounted for 48% of cases, with the number of cases peaking among 35-44 year-olds in 2023 (n=28).

Conclusions

Reported gonorrhoea incidence in Slovenia increased significantly during 2005-2024, with the highest age-sex-specific incidence observed among young adults of both sexes and a substantial proportion of reported male cases occurring among MSM. These findings are broadly consistent with trends reported across Europe and underscore the need for sexual-health awareness, safe-sex promotion, early healthcare-seeking for sexually transmitted infection signs and symptoms, and targeted interventions for MSM.

POSTER TOUR 7

SDG-targeted infections

Optimising the PEP to PrEP Transition: Policy Relevant Evidence from a Structured Prevention Pathway in a Lisbon Hospital

ABSTRACT ID: 646

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Background

The transition from post-exposure prophylaxis (PEP) to pre-exposure prophylaxis (PrEP) is recognized by World Health Organization as a critical “sentinel moment” for HIV prevention. In this clinical setting, most individuals initiate PEP through the emergency department and are promptly referred to a PEP appointment. When ongoing risk is identified, clinicians systematically offer PrEP, enabling immediate transition without waiting lists or administrative barriers. However, uptake remains dependent on user acceptance, creating a behavioural and policy relevant gap in the prevention cascade.

Methods

A retrospective analysis was conducted of all PEP consultations from 1 January to 31 December 2025. Extracted variables included sex assigned at birth, age, nationality, previous PEP episodes, PEP regimen, and subsequent attendance at both PEP and PrEP specialty appointments. A successful transition was defined as attending one appointment in each specialty within the study period.

Results

A total of 286 PEP users were identified. The cohort was 74.2% male and 25.8% female, with a median age of 32 years (IQR 25–44). Most users were Portuguese (58.4%), followed by Brazilian (21.3%). First time PEP use accounted for 78.4% of cases, while 21.6% had 1–4 previous episodes, indicating repeated exposures and missed opportunities for earlier PrEP initiation. The standard regimen was FTC/TDF + DTG (96.2%). Overall, 65 individuals (22.7%) transitioned directly from PEP to PrEP; among them, 23.1% had a history of prior PEP episodes.

Conclusions

This structured emergency-to-PEP-to-PrEP pathway enables rapid linkage to sustained HIV prevention and re-duces structural barriers. However, the 22.7% transition rate and the prevalence of repeated PEP use highlight that acceptance at the sentinel moment remains a primary bottleneck. These findings suggest a need for strengthened counselling, automatic referral protocols, and targeted follow-up for those initially decline PrEP to inform national HIV prevention policies and support progress toward SDG Goal 3.

POSTER TOUR 7

SDG-targeted infections

Tuberculosis among people already registered as contacts: linking tuberculosis centre, hospital and notification records in northern Portugal, 2024–2026

ABSTRACT ID: 1043

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Background

Preventing tuberculosis in contacts is central to elimination, but disease among registered contacts is rarely measured. In Portugal, outpatient tuberculosis centres record contact follow-up separately from case notifications. We measured it in a northern local health unit (20.8 cases per 100,000 in 2024).

Methods

Using national health numbers, we linked confirmed cases notified January 2024–June 2026 (extracted 1 July 2026) to same-period activity listings of the unit's four tuberculosis centres (obtained July 2026) and to hospital records reviewed 31 July–23 September 2026. Registered contacts had at least one nursing appointment or visit coded as contact follow-up. Cases diagnosed within 90 days of first registration were co-prevalent, later ones incident. We estimated incidence among registered contacts from day 91.

Results

Of 213 linkable cases, 20 (9.4%) had been registered as contacts before diagnosis (9.3% of those diagnosed from 2025): 12 co-prevalent and eight incident (4–16 months after registration). Among 4,592 registered contacts, incidence after 90 days was 168 per 100,000 person-years (95% confidence interval 72–331), eight times the unit's rate, or 84 excluding four incident cases from one cluster. Of the incident cases, four were smear-positive and four hospitalised (112 bed-days); notifications documented preventive treatment for three (two completed isoniazid regimens, one incomplete). In that cluster (nine cases, the unit's largest), a contact registered in April 2024 was diagnosed with smear-positive cavitary tuberculosis in September 2025; within six months his wife, daughter and seven-year-old nephew were diagnosed.

Conclusions

Nearly one in ten people with tuberculosis were already registered as contacts, and eight were diagnosed months after registration, two despite completed preventive treatment. Existing records sufficed to show this. We recommend reviewing every case in a registered contact as a sentinel event, following contacts after preventive treatment, and tracking this proportion as a programme indicator.

Healthcare-associated infections

Temporal patterns of severe Clostridioides difficile infections in Germany, 2016–2025

ABSTRACT ID: 801

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Background

Clostridioides difficile infections (CDI) remain a major cause of healthcare-associated morbidity. Severe CDI cases (sCDI) are mandatorily notifiable in Germany and initial data suggest a recent increase in reported sCDI. We therefore aimed to quantify variation in reported sCDI in Germany within and across years between 2016 and 2025.

Methods

We analysed monthly sCDI from 2016-2025 using nationwide statutory surveillance data. To account for potential changes in healthcare utilization and infection control practices we stratified by COVID-19 periods defined as: pre-pandemic; pandemic (2020-2022); and post-pandemic. We compared COVID-19 periods based on the relative difference in mean monthly case counts between periods. For assessing within-year variation, we used negative binomial regression models, with predictors including COVID-19 period, time, month of the year, and their interaction. Model estimates are presented as monthly incidence rate ratios (IRRs) with corresponding p-values.

Results

In total, 20,763 sCDI were reported between 2016-2025. Mean monthly sCDI counts declined from 216 in the pre-pandemic period to 125 during the pandemic (-42%), followed by an increase to 163 in the post-pandemic period (+30%). Negative binomial regression modeling showed variation in reported monthly cases with high case counts observed in January (reference), significantly lower counts in February (IRR=0.87, p=0.033), and April (IRR=0.85, p=0.014), highest counts in August (IRR=1.03, p=0.61), and significantly lower counts from October to December (IRRs=0.77-0.85, all p<0.05).

Conclusions

After an initial decline during the pandemic, sCDI increased thereafter, emphasizing the importance of continued surveillance, prevention efforts, and further investigation of potential drivers such as health care utilization, antibiotic consumption and geographical distribution in Germany. Reported sCDI showed within-year variation, including unexpected higher case counts during summer (August). Increasing case numbers should be interpreted in the context of both changes over time and within-year variation, particularly as notification data may be influenced by reporting behavior.

POSTER TOUR 8

Healthcare-associated infections

High background noise masks transmission: whole genome sequencing as a key tool for outbreak assessment of Pseudomonas aeruginosa in a high-incidence setting

ABSTRACT ID: 785

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Background

In a supra-regional neurological rehabilitation hospital with frequent direct inter-hospital ICU transfers, high baseline *Pseudomonas aeruginosa* incidence often obscures transmission. During a suspected outbreak (June– August 2025), 42/64 patients tested positive. Persistent detection of *Pseudomonas aeruginosa* in the water suggested a large-scale event. We used epidemiological and genomic approaches to distinguish waterborne clusters, patient-to-patient transmission, and independent introductions.

Methods

We analysed 42 patients (Jan–Sept 2025) for spatiotemporal overlaps via room-occupancy and transfer histories. Whole-genome sequencing (WGS) of 64 isolates (49 human isolates from 25 patients and 15 environmental isolates, comprising 7 surface swabs and 8 water samples) was performed on using core-genome multilocus sequence typing (cgMLST, 3,867 targets) and sequence typing (ST). Clusters were defined by ‹12 allelic differences. Intra-individual diversity was captured by sequencing multiple isolates per patient.

Results

Genomic analysis revealed a multifactorial scenario without a common source, contradicting the initial outbreak hypothesis. Since sampling was indicative, early cases were likely underreported. Six genetic clusters (2–4 patients each) involved 52% of the 25 sequenced patient isolates (13/25), including the international emerging clones ST253, ST395 and ST207. These included both patient-to-patient and joint-patient-water clusters. However, 48% of patients (12/25) were singletons and the water isolates exhibited substantial genetic diversity. Intra-individual diversity was identified in a patient initially carrying ST1621 but subsequently acquired a water-linked cluster strain (ST207). Overall, 74% of all 42 cases (31/42) were colonisation.

Conclusions

In high-incidence settings, WGS is essential for distinguishing coincidental clusters from true transmission. It proves that already colonized patients can still acquire outbreak strains, a risk that conventional surveillance often dismisses as background noise. Our findings demonstrate that early WGS implementation is crucial for deciphering multifactorial scenarios, ensuring that Water Safety Plans and hygiene audits are strictly maintained to guarantee clinical compliance.

POSTER TOUR 8

Healthcare-associated infections

Emergence of NDM-1 and OXA-48 producing Klebsiella pneumoniae ST395 circulating within and between hospitals with links to Ukraine, Germany, 2023-2025

ABSTRACT ID: 704

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Background

Carbapenemase producing *Klebsiella pneumoniae* (KP) is a significant public health concern, causing nosocomial infections with severely limited therapeutic options. Sequence Type (ST)395 is an internationally disseminated high-risk clone. In September 2023, a genetic cluster of ST395 cases across three hospitals in Berlin was identified through integrated genomic surveillance. We conducted an outbreak investigation to identify cases and trace potential transmission chains.

Methods

Outbreak cases were defined as patients diagnosed with KP ST395 infection or colonization between 2022 and 2025 who belonged to the outbreak cluster. Case information on clinical course, hospitalizations, exposures abroad, as well as the date, location and site of pathogen detection were systematically collected by hospital staff and local health authorities. Isolates underwent carbapenemase detection, phenotypic resistance testing, and cgMLST. Clusters were defined using a cut-off of ≤ 7 allelic differences.

Results

Between May 2022 and December 2025, 68 outbreak cases colonized (56%) or infected (44%) with NDM-1 and OXA-48-producing KP ST395 belonging to the same genomic cluster were identified. Prior exposure in Ukraine was reported for 14 patients; four of them were identified as index patients of different nosocomial transmission chains comprising a total of 17 cases. Ten patients with exposure in Ukraine, as well as two patients without exposure in Ukraine, emerged independently at different German hospitals. The largest transmission chain involved 39 cases across four hospitals in Berlin without known links to Ukraine or between the hospitals.

Conclusions

A genomic cluster of KP ST395 caused nosocomial transmission chains in several German hospitals over a span of several years, driven by hospitalisations of patients exposed in Ukraine. Despite admission screening, several local transmission chains were identified. Timely surveillance integrating genomic and epidemiological information is crucial for tracing and detecting supra-regional outbreaks of highly resistant *KP.* Risk-adapted admission screening needs to precede strict hygiene measures to prevent onward transmission.

POSTER TOUR 8

Healthcare-associated infections

The association between comorbidities and recurrent urinary tract infections in Dutch long-term care residents: a longitudinal cohort study

ABSTRACT ID: 686

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Background

Little is known about the relationship between comorbidities and recurrent urinary tract infections (UTIs) among residents of long-term care facilities (LTCFs). Gaining insight into this association could help identify high-risk individuals, improve targeted infection prevention strategies, and ultimately enhance the quality of care. We aim to determine whether common comorbidities are associated with recurrent UTIs.

Methods

We conducted a longitudinal cohort study within the Dutch sentinel Surveillance Network Infectious Diseases in Nursing Homes (SNIV), as part of ECDC's Healthcare-associated infections and Antimicrobial use in LTCFs (HALT) project. Data were collected using questionnaires. Each UTI occurrence was reported during a 12-month follow-up period (January – December 2022). Recurrent UTIs were defined as the presence of UTI-related symptoms more than eight weeks after the initial infection had resolved. Comorbidities commonly associated with UTIs (dementia, diabetes, kidney- and urinary disorders) were recorded at baseline. We used survival analysis, adjusted for potential confounders, with multiple imputation and accounting for the competing risk of death, to assess the association between comorbidities and recurrent UTIs.

Results

In total, 275 predominantly female, incontinent residents with a median age of 85 years (IQR 77-91) were included, of whom 52 acquired a UTI during follow-up. 11 residents (21%) experienced at least one recurrent UTI, of which 27% had dementia, diabetes, kidney- and/or urinary disorders. The preliminary hazard ratios show no significant association between dementia (1.6, 95%CI 0.2-17.4), diabetes (0.8, 95%CI 0.2-3.8) or urinary disorders (1.4, 95%CI 0.2-12.1) and UTI recurrence. The association for kidney disorders (19.7, 95%CI 2.6-150.0) was significant.

Conclusions

Based on our small sample study, we found no statistical significant evidence of an association between documented comorbidities and UTI recurrence, except for kidney disorders. Larger multi-country longitudinal cohort studies may help to further determine the association between comorbidities and UTI recurrence in order to optimise infection prevention measures in LTCFs.

POSTER TOUR 8

Healthcare-associated infections

Trends in surgical site infection incidence in Piedmont, Italy, 2015–2024: findings from a regional surveillance programme

ABSTRACT ID: 630

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Background

Surgical site infections (SSIs) represent a critical public health challenge due to their substantial impact on patient morbidity, mortality, and healthcare expenditures. Active surveillance programs have proven highly effective in mitigating SSI rates. This study evaluates the longitudinal trends of SSI incidence in the Piedmont region over a ten-year period (2015–2024).

Methods

A prospective observational cohort study was conducted across 53 hospitals participating voluntarily in the regional surveillance program, according to the national surveillance protocol. Post-operative surveillance was carried out for 30 or 90 days following surgery. Using data collected from 2015 to 2024, cumulative SSI incidence and trends in yearly SSI incidence (chi-squared tests for trends) were calculated for the two most frequently performed and continuously monitored procedure categories: colon surgery (COLO) and hip prosthesis replacement (HPRO). Statistical analyses were performed using Epi Info software (version 7.2, CDC).

Results

Over the 10-year study period, 12,294 COLO procedures and 27,383 HPRO procedures were monitored. The overall cumulative SSI incidence was 6.22% for COLO and 1.29% for HPRO. For COLO, a statistically significant decrease in SSI incidence was observed over time ($p<0.01$), decreasing from 10.23% in 2015 to 5% in 2024, despite a progressive increase in the number of monitored procedures (1,065 in 2015 vs. 1,559 in 2024). Conversely, HPRO procedures demonstrated no statistically significant trend in SSI incidence ($p = 0.799$), with a similar steady increase in monitored surgeries (2,323 in 2015 vs. 2,994 in 2024).

Conclusions

This study shows a statistically significant downward trend in SSI incidence for COLO procedures in Piedmont over the period 2015–2024, with a reduction in the proportion of infections relative to the total number of monitored procedures. No significant trend was observed for HPRO, although the SSI rate remained low and stable over time.

Healthcare-associated infections

Compliance with minimum requirements for infection prevention and control programs across healthcare facilities in Nigeria, 2024

ABSTRACT ID: 616

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Background

Infection prevention and control (IPC) is essential for reducing healthcare-associated infections and antimicrobial resistance. This study assessed compliance with the WHO minimum IPC requirements among healthcare facilities in Nigeria, examined associations between facility characteristics and IPC compliance, and identified key implementation gaps.

Methods

A cross-sectional assessment was conducted in Nigerian healthcare facilities between 2023 and 2024 using WHO IPC minimum requirements tools adapted for primary, secondary, and tertiary levels of care. The assessment was implemented collaboratively by national and state health authorities, WHO, and facility IPC focal points. Convenience sampling was used to maximize participation. Data were collected from IPC focal points or designated facility managers. Compliance with overall and core IPC components was analyzed descriptively. Beta regression models examined associations between facility characteristics and the proportion of IPC requirements achieved, reported as adjusted odds ratios (ORs) with 95% confidence intervals (CIs).

Results

A total of 1,281 healthcare facilities were assessed, including 1,114 (87%) primary, 129 (10%) secondary, and 38 (3%) tertiary facilities. Most facilities were public (94.4%). Overall, only 79 facilities (6.2%) achieved full IPC compliance; none of the tertiary facilities met all requirements. Compliance was highest for multimodal strategies (68.8%) and monitoring of IPC practices (59.4%), but lowest for IPC education and training (26.6%) and the built environment (12.9%). Private facilities had significantly higher odds of meeting IPC requirements than public facilities (OR = 2.18; 95% CI: 1.58–3.01). Major gaps included lack of dedicated IPC budgets, inadequate hand hygiene infrastructure, and insufficiently trained IPC focal points across all facility levels.

Conclusions

Compliance with WHO minimum IPC requirements in Nigeria was low and varied by facility level and sector. Addressing persistent structural and resource gaps, while strengthening IPC systems and adopting best practices from high-performing facilities, is essential for sustainable IPC improvement nationwide.

Healthcare-associated infections

Escalating Antimicrobial Resistance and Healthcare-Associated Infections in Greek ICUs: A Ten-Year Longitudinal Surveillance Study

ABSTRACT ID: 349

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Background

Antimicrobial resistance (AMR) remains a major public health challenge in Greece, particularly in intensive care units (ICUs), where multidrug-resistant organisms contribute substantially to mortality, prolonged hospitalization and healthcare costs. This study evaluated longitudinal AMR trends in Greek ICUs between 2015 and 2024, assessed the impact of the COVID-19 pandemic, and compared national indicators with European Union (EU) averages.

Methods

A longitudinal observational analysis was conducted using surveillance data from WHONET–Greece, EARS-Net and HAI-Net. Resistance trends were analysed for major Gram-negative and Gram-positive ICU pathogens, including *Acinetobacter baumannii*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Escherichia coli*, methicillin-resistant *Staphylococcus aureus* (MRSA), vancomycin-resistant *Enterococcus* spp. (VRE) and coagulase-negative staphylococci. Duplicate isolates within 30 days were excluded and EUCAST susceptibility criteria were applied. Incidence densities of ventilator-associated pneumonia (VAP), central line-associated bloodstream infections (CLABSI) and catheter-associated urinary tract infections (CAUTI) were compared with EU averages.

Results

Carbapenem-resistant Gram-negative pathogens demonstrated increases during the study period. Resistance in *A. baumannii* rose from 93.2% in 2015 to 98.6% in 2024, while carbapenem-resistant *K. pneumoniae* increased from 62.1% to 72.8%. *P. aeruginosa* resistance increased from 38.8% to 49.1%, and third-generation cephalosporin resistance in *E. coli* rose from 18.5% to 24.9%. VRE prevalence doubled from 7.2% to 14.8%, particularly after 2020, whereas MRSA rates remained persistently high at approximately 39%. Greece exhibited markedly higher resistance rates, especially for carbapenem-resistant *A. baumannii* (+77.6 percentage points) and *K. pneumoniae* (+58.3 percentage points). HAI incidence densities in Greek ICUs also substantially exceeded EU means, including VAP (18.5 vs. 6.2 episodes/1,000 intubation-days), CLABSI (7.8 vs. 3.1/1,000 central venous catheter-days), and CAUTI (6.5 vs. 3.4/1,000 catheter-days).

Conclusions

The findings highlight the urgent need for strengthened antimicrobial stewardship, improved infection prevention measures, enhanced ICU staffing and modernised surveillance systems. Adoption of coordinated prevention strategies is essential to reduce AMR burden and improve patient safety in Greek healthcare settings.

POSTER TOUR 9

One Health & food- and water-borne diseases

Environmental detection of Campylobacter spp. in soil during a childcare-associated gastroenteritis cluster

ABSTRACT ID: 885

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Background

Campylobacteriosis is Europe's leading reported bacterial gastrointestinal infection, particularly affecting children. Transmission occurs mainly through contaminated food or water, or contact with infected animals, facilitated by a low infectious dose. *Campylobacter spp*. have demonstrated environmental persistence, including survival in soil under favourable conditions. Environmental contamination may represent an under-recognised pathway for human infection. This work describes environmental contamination with *Campylobacter spp*. and highlights the need to consider soil investigation in outbreak investigations, as reports of detection in soil remain scarce, particularly following extreme weather events that may promote pathogen dissemination through flooding and runoff.

Methods

Following notification of campylobacteriosis in a child attending a childcare facility, an epidemiological investigation was initiated in March 2026, including symptom and exposure assessment. The childcare director was contacted, and a site visit was conducted to identify additional cases and transmission sources. An adjacent outdoor area was used more frequently after storms one month earlier damaged the playground. The area had been affected by flooding, runoff and debris deposition. Soil samples were collected, along with water samples from a nearby fountain and the childcare facility water system. No common risk foods were identified.

Results

Five symptomatic cases were reported; one was laboratory-confirmed, while the remaining four were not tested. *Campylobacter spp*. were detected in soil, while water samples were negative. Children were advised against playing in the affected area. No further cases were reported after access restriction. In the absence of alternative shared exposures, soil contamination was considered the most plausible exposure source.

Conclusions

This investigation highlights the importance of considering environmental reservoirs in childcare-associated gastroenteritis outbreaks. Detection of *Campylobacter spp*. in soil supports contaminated environments as a plausible exposure pathway. Restricting access to affected areas, reinforcing hygiene measures and communicating risk to parents and carers are key public health actions to reduce exposure in young children.

POSTER TOUR 9

One Health & food- and water-borne diseases

Increasing incidence of human tularaemia despite stable epidemiological patterns, Baden-Wuerttemberg, Germany, 2012–2025

ABSTRACT ID: 546

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Background

Tularaemia is a rare zoonotic disease caused by *Francisella tularensis* and is endemic in southern Germany. Increasing case numbers have been observed in recent years, but underlying drivers remain unclear. We assessed long-term trends and whether changes in epidemiological characteristics identified through surveillance data could explain the increase.

Methods

A retrospective analysis of notified human tularaemia cases in Baden-Wuerttemberg from 2012 to 2025 was conducted, excluding cases with reported travel history. Temporal trends were assessed using Poisson regression. Clinical presentation, reported exposures, geographic distribution, and reporting delay were analysed. Concordance between reported exposure and clinical form was evaluated.

Results

A total of 284 cases were included. While case numbers fluctuated over time, they showed a significant upward trend (incidence rate ratio 1.21 per year, 95% CI 1.17–1.25), peaking in 2024 and 2025 and exceeding model-based expectations. Over the study period, cases gradually spread to 42 of 44 districts without distinct geographic clustering. The distribution of clinical forms remained stable. Reported exposures were predominantly arthropod-associated and environmental sources. Median reporting delay was 29 days. Concordance between exposure and clinical form was low (~45%).

Conclusions

These findings demonstrate an overall increase and geographic expansion of tularaemia across Baden-Wuerttemberg without major changes in clinical presentation or reported exposure patterns. The consistent epidemiological characteristics observed over time suggest persistent transmission mechanisms rather than newly emerging sources. Low concordance between reported exposure and clinical presentation limits the identification of likely infection sources using routine surveillance data alone. Enhanced surveillance using structured exposure questionnaires, together with integrated One Health investigations across human, animal and environmental sectors, will be essential to better understand the drivers of this increasing trend.

POSTER TOUR 9

One Health & food- and water-borne diseases

Cluster of human leptospirosis associated with environmental exposure in southern Spain, 2025/2026.

ABSTRACT ID: 517

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Background

An unusual cluster of leptospirosis cases was detected between February 2025 and January 2026 in the Guadalete river basin, southern Spain. Leptospirosis is a zoonotic disease typically associated with environmental exposure to contaminated water, and outbreaks are often linked to climatic and ecological changes. This study aimed to describe the epidemiological, clinical and environmental characteristics of the cluster and to inform public health response.

Methods

A descriptive investigation was conducted including all confirmed cases identified through hospital-based surveillance. A case was defined as a patient with compatible clinical presentation and positive anti-Leptospira IgM serology. Epidemiological data were collected, and environmental assessments were performed, including inspection of affected areas and microbiological analysis of surface water samples using PCR.

Results

Ten cases were identified (7 males, 3 females; age range 30–72 years), all requiring hospitalisation, of whom three were admitted to intensive care. One patient died (male, 57 years) with suspected Weil's disease in the context of underlying chronic alcoholic liver disease. The majority of cases occurred between February and April 2025, and eight resided near the Guadalete river. Common clinical features included fever (100%), thrombocytopenia (89%) and jaundice (78%). Environmental investigations detected Leptospira spp. in all sampled water sites. Most cases reported exposure to river environments or rural settings, and three had documented contact with rodents. One case (veterinary) had contact with a calf that died of leptospirosis. Heavy winter flooding likely contributed to environmental contamination and increased human exposure. Public health interventions included raising clinical awareness, community risk communication, environmental inspections and intersectoral coordination under a One Health approach. No new cases were detected after January 2026.

Conclusions

This cluster underscores the role of changing environmental and climatic factors in leptospirosis transmission in temperate settings. Integrated surveillance and preventive strategies addressing human, animal and environmental interfaces are essential to mitigate future outbreaks.

POSTER TOUR 9

One Health & food- and water-borne diseases

Cholera outbreak investigation in an urban setting: transmission dynamics and response gaps in Nairobi County, Kenya, March–April 2025

ABSTRACT ID: 115

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Background

Cholera remains a persistent threat in rapidly urbanizing settings with WASH challenges (WHO, 2024). In March 2025, Nairobi County, Kenya, reported a cholera outbreak affecting multiple sub-counties. We investigated the outbreak to describe its epidemiology, identify risk factors, and assess the timeliness of response.

Methods

A field investigation was conducted from 5–9 April 2025, including retrospective health facility record review, case interviews, and active case search. A suspected case was defined as any person with acute watery diarrhoea (≥3 episodes within 24 hours) since 9 March 2025. Stool samples were collected for laboratory confirmation. Descriptive analysis was performed using Excel and Stata. Timeliness was assessed using the 7-1-7 framework.

Results

As of 11 April 2025, 26 cases were identified, including 10 (38%) laboratory-confirmed infections with *Vibrio cholerae* O1 serotype Ogawa. One death occurred (case fatality rate: 2.6%). The median age was 13.5 years (IQR: 26.25), with the highest burden among individuals aged 15–44 years (35%). Cases clustered in Kasarani (27%) and Kibra (23%), suggesting localized transmission in densely populated areas. The epidemic curve showed a sharp increase between 30 March and 2 April. Reported exposures included consumption of street-vended food, unsafe water sources, and contact with suspected cases. Detection occurred within 1 day; however, notification (6 days) and response initiation (21 days) exceeded recommended timelines.

Conclusions

The outbreak demonstrated focal urban transmission driven by food, water, and contact-related exposures, alongside critical delays between detection and response. These findings highlight gaps in the surveillance-to-response continuum and underlying WASH and food safety systems. Strengthening coordination between surveillance and rapid response functions, while addressing environmental risk factors, is essential for effective cholera control and improved outbreak preparedness in urban settings.

POSTER TOUR 9

One Health & food- and water-borne diseases

Unraveling Legionellosis Dynamics in the Lazio Region: Effects of Individual, Territorial and Meteorological determinants

ABSTRACT ID: 304

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Background

The incidence of Legionnaires' disease (LD) has been recently rising worldwide. Several studies suggest that many factors may play a role in its spread. This study analyzes LD epidemiological trends of in the Lazio Region from 2015 to 2023, assessing the association between disease incidence and individual, environmental territorial, and meteorological determinants.

Methods

Case data were obtained from a regional database integrating the national surveillance system with the regional special surveillance system for infectious diseases. Data were supplemented with demographic, behavioral (smoking/alcohol consumption), clinical and meteorological information. The regional prevalence rates of smoking/alcohol use and comorbidities were used to construct the offset by applying them to the population denominators. Annual LD incidence rates per 100,000 person-years were calculated.

Results

Between 2015 and 2023, 1,932 cases of LD were reported. The incidence rate rose from 2.83 cases per 100,000 person-years in 2015 to 4.91 in 2019, decreasing during the pandemic (3.04 in 2021), and increasing back to its highest level in the post-pandemic period (5.03 in 2023). Advanced age (expecially in those over 70 years old: IRR=17.01; 95% CI: 11.0–27.2), male sex (IRR=5.21; 95% CI: 3.60–7.78), comorbidities (IRR=4.62; 95% CI: 3.41–6.19), and smoking or alcohol consumption (IRR=2.05; 95% CI: 1.53–2.75) were strongly associated with LD increased risk. Residence in the Rome metropolitan area was associated with a higher risk (IRR=1.96; 95% CI: 1.54–2.52). Among environmental factors, average monthly precipitation was associated with an increased incidence (IRR=1.16; 95% CI: 1.11–1.20), as was the average monthly maximum temperature (IRR=1.02; 95% CI: 1.01–1.03).

Conclusions

The results highlight the significant role of the interaction between individual, environmental, and territorial factors in the spread of LD. These findings support the integration of environmental indicators into surveillance systems and the implementation of targeted preventive strategies, particularly among the most vulnerable populations and in high-density urban settings.

One Health & food- and water-borne diseases

Farm-animal exposure and OXA-48-like carbapenemase-producing Enterobacterales carriage among Arab patients in northern Israel: a case-control study

ABSTRACT ID: 925

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Background

OXA-48-like carbapenemase-producing Enterobacterales (OXA-CPE) are increasingly detected outside healthcare settings, challenging hospital-centred screening. In a previous Israeli case-control study, Arab ethnicity was more strongly associated with OXA-CPE than with non-OXA-CPE, while 26.9% of OXA-CPE patients had no hospitalisation in the preceding year, suggesting community acquisition. We therefore investigated community exposures among Arab patients.

Methods

During June–July 2026, we conducted a telephone questionnaire-based case-control study at Carmel Medical Center, northern Israel. All participants were of Arab ethnicity and had undergone CPE screening on hospital admission. Cases had OXA-CPE detected on admission; controls had negative admission CPE screening. The questionnaire assessed travel, visits to the Palestinian territories, open-market produce, imported food, raw/unwashed produce, farm-animal contact, household pets, agricultural work, non-regulated water exposure, household hospitalisation, and regular bidet use. Univariable associations were estimated using odds ratios; multivariable logistic regression adjusted for age and sex.

Results

Overall, 112 participants were included: 46 cases and 66 controls. Cases and controls were similar in age and household size. Farm-animal contact was reported by 15.2% of cases and 6.1% of controls (OR 2.78, 95% CI 0.76– 10.13). Other assessed community exposures showed no clear positive association with OXA-CPE carriage. After adjustment for age and sex, ownership of or close contact with farm animals was independently associated with OXA-CPE carriage (adjusted OR 5.47, 95% CI 1.09–27.34; p=0.039)

Conclusions

Among Arab patients in northern Israel, farm-animal exposure was independently associated with OXA-CPE carriage, supporting a potential One Health transmission pathway. **These findings identify an actionable One Health surveillance gap: Israel currently has no structured national programme for CPE screening in animals.** Targeted surveillance of livestock and farm environments, followed by genomic comparison of animal, environmental and human isolates, is warranted and may inform future community-based screening and prevention strategies.

POSTER TOUR 10

Preparedness and response

Developing an evaluation framework for Epidemic Intelligence from Open Source (EIOS): a qualitative analysis of stakeholder priorities

ABSTRACT ID: 643

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Background

Public health intelligence (PHI) activities enable early threat detection and response. One of PHI's tools, the Epidemic Intelligence from Open Sources (EIOS) system, comprises communities across 124 World Health Organization (WHO) Member States and 27 organizations/networks (as of 11/2025). Despite its widespread use, there is no standardised EIOS-specific evaluation guidance. We aimed to identify stakeholder priorities in a structured workshop to develop an EIOS evaluation framework.

Methods

On 06/02/2025, EIOS experts from the Robert Koch Institute and the WHO Hub conducted a World Café with 40 participants, including focal points from all WHO regional offices and representatives from global, regional and national One Health/public health institutes. Participants rotated across five predefined questions on evaluation audiences and uses, system attributes, impact and framework use. Notes were consolidated into a qualitative dataset and analysed thematically by three independent researchers. Key themes were identified, and interpretations were refined iteratively until agreement was reached.

Results

Five key themes emerged: (1) the need for a standardised but adaptable EIOS evaluation framework across global, regional and national contexts; (2) the importance of assessing EIOS' contribution to early detection, risk assessment and information-sharing; (3) key evaluation attributes: timeliness, sensitivity, representativeness, interoperability, usability, stability and technical performance; (4) the need for a practical, modular framework with a core set of evaluation components for all settings, additional components depending on context, and outputs adapted to the needs of different users; and (5) main evaluation challenges including attributing outcomes to the system, potential language- and country-related biases and operational definitions.

Conclusions

The stakeholder discussions highlighted the need for a modular, adaptable EIOS evaluation framework that captures both technical performance and EIOS' contribution to crucial PHI functions. Findings from this stakeholder discussion will inform the development of a ready-to-use evaluation toolkit for EIOS users, supporting high-quality PHI and strengthening surveillance evaluation practice across settings.

POSTER TOUR 10

Preparedness and response

Childhood immune imprinting and seasonal influenza-driven boosting of cross-reactive avian influenza A antibody landscapes in adults: evidence from a German population-based longitudinal cohort study, 2020-2024

ABSTRACT ID: 615

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Background

Avian influenza A(H5N1) currently circulating in European wild birds and poultry poses a pandemic threat. However, it remains poorly characterised how seasonal immunity and lifelong immune imprinting – whereby childhood exposure to influenza A subtype dominant during a given period durably shapes cross-reactive re-sponses – influences population-level susceptibility to novel avian subtypes. We assessed whether birth-cohort-specific imprinting is associated with binding antibodies to avian H5N1 and H7N9, and whether recent seasonal infections (2020-2024) preferentially boost antibodies within the same haemagglutinin (HA) phylogenetic group.

Methods

We analysed 7,232 sera from 2,871 adults (born 1927–2001) across four timepoints (2020–2024) in the Multilocal and Serial Prevalence Study of Antibodies against (Respiratory) Infectious Diseases in Germany (MUSPAD) cohort. Binding antibodies to HA Group 1 (H5N1, three different H1N1) and Group 2 (H7N9, three different H3N2) strains were measured by Luminex immunoassay. Birth-year-specific imprinting probabilities were estimated from German influenza circulation data. Seasonal infections were classified serologically by a ≥2 $\log_2$ titre rise. Age-adjusted linear mixed models tested associations between imprinting and the within-individual H5N1-minus-H7N9 contrast, and within- versus cross-HA-group boosting after seasonal infection.

Results

Group 1 imprinting probability was associated with the H5N1-minus-H7N9 antibody contrast (β= 0.82 $\log_2$ BAU, 1.76-fold, p<0.001) after adjustment for non-linear age effects; this pattern remained stable across four time-points (Intraclass Correlation Coefficient=0.85). Seasonal infections preferentially boosted antibodies within the matched HA group: H1N1 infection increased Group 1 antigen titres 3.4-fold versus 1.2-fold for Group 2; notably, H3N2 infection showed the reciprocal pattern (Group 2: 3.2-fold, Group 1: 1.1-fold; interaction p<0.001). Seasonal vaccinations produced comparable increases in both groups (~2.3-fold).

Conclusions

Childhood immune imprinting durably shapes birth-cohort-specific susceptibility to avian influenza subtypes. These birth-cohort differences may inform age-targeted pandemic risk assessment. Seasonal vaccination provides modest cross-reactive boosting to both avian H5N1 and H7N9, suggesting that maintaining high vaccination coverage may support pandemic preparedness.

POSTER TOUR 10

Preparedness and response

Pooled testing for SARS-CoV-2 surveillance in schools: real-world evaluation of transmission control, testing resources, and educational disruption

ABSTRACT ID: 565

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Background

Pooled testing programs were introduced during the COVID-19 pandemic to expand surveillance capacity while preserving testing resources, but evidence on their epidemiological impact in schools under real-world conditions remains limited.

Methods

We analyzed data from the pooled testing program implemented in public primary schools of the canton of Basel-Landschaft, Switzerland, during the Fall-Winter 2021 Delta wave. We used an agent-based transmission model informed by pooled and individual testing results, school characteristics and contact networks, and community incidence. The model was fitted to observed pooled positivity ratios in four clusters of administrative areas with similar epidemic trajectories. We compared pooled testing with alternative school protocols in terms of school transmission, testing volume, and student-days lost.

Results

During the study period, pooled testing was offered to 21'187 students across 62 public primary schools, with high and stable participation across clusters (mean 71–79%). The fitted model reproduced observed pool positivity trends well across clusters. Compared with pooled testing, reactive class closure, reactive screening, and symptomatic testing were associated with substantially higher in-school transmission, with excess transmission ranging from 50% to 87%, 63% to 104%, and 72% to 133% across clusters, respectively. Weekly individual screening achieved similar reductions in transmission but required 15–25 times more tests. Relaxing class closure after depooling substantially reduced student-days lost without increasing transmission.

Conclusions

Under real-world conditions, pooled testing provided an effective and resource-efficient strategy to reduce SARS-CoV-2 transmission in primary schools. By combining early detection of asymptomatic infections with low testing demands, pooled testing offers a scalable approach to school surveillance and control for pandemic preparedness and response in educational settings.

Preparedness and response

Characterisation of reporting interval for human cases of avian influenza A(H7N9), China, 2013–2017: a retrospective time-to-event analysis

ABSTRACT ID: 406

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Background

Delays in the identification and international notification of human cases of avian influenza with pandemic potential present a significant challenge for global preparedness and response in the event of a new pandemic. However, such delays remain poorly characterised. We assessed the reporting interval between case symptom onset and notification to the World Health Organization (WHO) for human cases of A(H7N9) influenza in China, 2013–2017, and examined associations with age, sex, province, and epidemic wave.

Methods

We analysed 550 laboratory-confirmed human A(H7N9) cases from China (2013–2017), collated from the WHO website with known symptom onset and WHO notification dates (reporting interval = difference between the two dates). We fitted a log-logistic accelerated failure time model to identify associations between reporting interval and case age, sex, province, and epidemic wave.

Results

The median reporting interval was 10 days (interquartile range [IQR] 8–15). Median intervals varied by province, ranging from 9 days (Guangdong) to 13 days (Jiangsu), and by age, being shorter for 0–17 year olds (4 days, IQR 3–6) compared to older cases (11 days, IQR 8-15). Multivariable modelling found significant variation in reporting interval with case age, province and epidemic wave, but not sex. After adjusting for other variables, 0–17 year olds were reported faster compared to 60+ year olds (Time Ratio [TR] 0.46, 95%CI 0.38–0.55), while reporting of cases in later epidemic waves was slower than in the first wave (e.g. wave 5, TR 1.39, 95%CI 1.18-1.64).

Conclusions

The interval between symptom onset and notification to WHO takes a considerable amount of time for human A(H7N9) cases in China. Age and province variations suggest important detection and/or reporting heterogeneities, which should be addressed. These delays, if generalisable, may affect timely recognition of pandemic emergence, and impact early global response and preparedness. Understanding the processes underpinning these delays is essential to shorten reporting intervals.

POSTER TOUR 10

Preparedness and response

Risk Prioritisation of emerging infectious diseases for preparedness planning: The Belgian example, 2025-2026

ABSTRACT ID: 254

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Background

Disease prioritisation is a crucial first step for public health emergency preparedness planning and recommended by the European Centre for Disease Prevention and Control (ECDC). In 2025-2026, Sciensano conducted disease prioritisation for Belgium following a request by the national health authority. The aim was to identify and rank (re-)emerging infectious diseases considered potential public health threats to prioritise national preparedness actions. We share processes and results to illustrate ECDC-methodology adaptation to a national context.

Methods

We applied the ECDC-recommended Multi-Criteria Decision Analysis (MCDA) methodology. Thirty-one potentially (re-)emerging infectious disease threats were identified through literature- and expert-based selection. After this,132 national public health experts from different sectors used an online questionnaire (launched between 01/10/2025-15/11/2025) to score each disease against 15 pre-defined criteria assessing three domains: A) likelihood of (re-)introduction in Belgium, B) epidemic potential and C) disease impact. To address the uneven distribution of missing responses, we applied an ordinal cumulative link mixed model (fixed effect: ''disease"; random intercept: "expert"). Diseases were ranked per question, and ranks averaged within each domain (A, B, C) and across domains for a final rank.

Results

Forty percent of invited experts (53/132) participated. The top-10-ranked diseases were avian influenza, coronaviruses (MERS/SARS/SARS-CoV2), other zoonotic influenza, haemorrhagic fevers (Marburg, Crimean-Congo, Ebola and Lassa), West-Nile fever (WNF), invasive *Klebsiella* and tuberculosis. By domain, avian/zoonotic influenza, coronaviruses and tuberculosis ranked in the top 10 for both A and C; WNF and Chikungunya for both A and B; and haemorrhagic fevers for both B and C.

Conclusions

Our results inform health emergency preparedness efforts and planning in Belgium, including prioritising preparedness actions, and align with recent prioritisation exercises conducted in Europe, despite differences in scope and methodology. Moreover, our project illustrates how MCDA can be successfully applied for disease prioritization in a national context, which may serve other countries as a best-practice example.

POSTER TOUR 10

Preparedness and response

Impact of Youth Jubilee 2025 on Emergency Department attendances in Rome: a controlled interrupted time series analysis using syndromic surveillance data

ABSTRACT ID: 237

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Background

Mass gatherings can greatly affect healthcare utilisation, particularly Emergency Department (ED) demand. The Catholic Youth Jubilee (28 July–3 August 2025) drew up to 1 million young people to events across Rome. We assessed changes in ED attendances before, during, and after the Youth Jubilee, with a focus on individuals aged 15-24, using syndromic surveillance data.

Methods

We conducted a controlled interrupted time series analysis using data from the Lazio Region Syndromic Surveillance System, including all ED visits across participating hospitals. The study period covered three months (27 days before and 58 days after the event). Hospitals were classified as central (within 30km of the Vatican) and outer (over 30km, serving as controls). Daily ED visit counts were analysed using segmented negative binomial regression. Outcomes included total ED visits and stratified analyses by age group and clinical syndrome. Results are presented as incidence rate ratios (IRR) with 95% confidence intervals (CI).

Results

A total of 410,427 ED visits were recorded during the study period; 266,627 in central and 143,800 in outer hospitals. Individuals aged 15-24 accounted for 9.3% of visits. During the event, central hospitals experienced an 11% increase in daily ED visits compared with the expected trend in outer hospitals (IRR 1.11, 95%CI 1.02-1.21). Among those aged 15-24, attendances increased by 36% (1.36, 1.21-1.53), corresponding to 411 excess visits (95% CI 251–572). In this age group significant increases were observed in gastrointestinal infections (2.06, 1.07-4.17), gynaecological/pregnancy-related presentations (1.61, 1.02-2.61), neurological presentations (predominantly syncope) (1.46, 1.03–2.08) and trauma presentations (1.41, 1.19–1.67).

Conclusions

The Youth Jubilee was associated with a modest increase in ED attendances in central Rome, particularly among young people, with rises in gastrointestinal infections and injury-related presentations. Syndromic surveillance enabled timely detection of these changes, supporting its utility for real-time monitoring and preparedness planning during large-scale mass gatherings.

POSTER TOUR 10

Preparedness and response

From guidance to practice: contact management across European countries during an international Andes virus infection outbreak on a cruise ship, May-June 2026

ABSTRACT ID: 1037

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Background

In May 2026, an outbreak of Andes virus infections onboard the m/v Hondius cruise ship required a coordinated multi-country public health response. WHO and ECDC recommendations provided a common framework, while national authorities retained flexibility in implementing quarantine, monitoring and testing strategies. We aimed to describe and compare these national strategies and their implementation, to inform future multinational outbreak response.

Methods

We conducted a descriptive analysis of contact management using two types of information reported by national health authorities: details on contact management strategies collected through a structured questionnaire and individual-level follow-up data for contacts and subsequent cases, during May-June 2026. Contacts included all passengers and crew.

Results

Information on national strategies was available for nine countries, eight of which also provided individual follow-up information for 91 contacts and 6 cases. All nine countries classified all contacts as high-risk, planned a 42-day follow-up, and tested them regardless of symptoms. Contacts were quarantined at home and, when not possible, in designated facilities in 6/9 countries, in hospitals in 1/9 country, and in hospitals followed by home quarantine in 2/9 countries. Among 89 individuals with available data, median quarantine duration was 39 days (IQR: 32-42); 58% (56/97) were quarantined in designated facilities. 8/9 countries recommended weekly or twiceweekly. Of individuals with laboratory information, 96% (78/81) were sampled at least weekly; blood/serum PCR was performed at least once in 99% (93/94) and serology in 85% (80/94); respiratory specimens were collected in 35% (33/94) and urine specimens in 5% (5/94).

Conclusions

National responses aligned on core contact management measures, including follow-up duration, risk classification and testing irrespective of symptoms. Differences mainly concerned quarantine arrangements and additional laboratory investigations, particularly serology and alternative specimen types. Pre-agreed international guidance on proportionate quarantine and testing strategies could reduce contact burden, public health spending and facilitate coordinated responses to future outbreaks.

POSTER TOUR 10

Preparedness and response

After Action Review of the 2025 West Nile Virus Outbreak in the Lazio Region, Italy

ABSTRACT ID: 684

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Background

West Nile virus (WNV) is an expanding public health concern in Europe, with Italy experiencing recurrent seasonal transmission. In 2025, the Lazio Region experienced a multi-provincial WNV outbreak characterized by confirmed autochthonous human cases and viral circulation in equids, birds, and mosquito pools. Following the emergency phase, a structured After Action Review (AAR) was conducted using a One Health approach to assess outbreak management with the aim of improving prevention, preparedness, timeliness, and effectiveness of future responses

Methods

The AAR was conducted according to World Health Organization guidance using a predominantly debrief-based approach, adapted to the regional context. The process included pre-AAR preparation, an in-person multidisciplinary review meeting, held on 26 January 2026 at the National Institute for Infectious Diseases "Lazzaro Spallanzani", and post-AAR reporting. Activities included stakeholder mapping, review of epidemiological and operational documentation, reconstruction of the outbreak timeline, and identification of strengths, critical issues, and operational recommendations across key response pillars.

Results

The outbreak involved three provinces over approximately four months and prompted the implementation of several emergency measures, including expanded nucleic acid testing for blood donors in the Lazio Region and intensified vector control activities. The AAR identified strengths in timely epidemiological risk assessment, rapid laboratory response, implementation of emergency measures, and effective multisectoral coordination during the outbreak response. Areas for improvement were identified across several response pillars, including integration of the surveillance systems, communication flows, early warning capacity, and vector control activities. These findings allowed the development of operational recommendations for each response pillar evaluated.

Conclusions

This AAR confirmed the value of structured post-event outbreak evaluation. Key priority actions included strengthening human and veterinary surveillance, reinforcing vector control activities, harmonizing laboratory procedures, and strengthening training and risk communication. These findings provided an operational roadmap to improve WNV prevention, surveillance, and response in the Lazio Region

POSTER TOUR 11

Surveillance and prevention of respiratory viruses

A fine-tuned foundation model for influenza forecasting across 78 countries, benchmarked against Italy's collaborative forecasting hub

ABSTRACT ID: 864

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Background

Seasonal influenza causes substantial morbidity and mortality worldwide, and timely activity forecasts support preparedness and resource planning. Reliable forecasting models exist for only a few well-resourced countries, requiring disease-specific design and local expertise; most countries have no operational forecasts. We assessed whether a time-series foundation model could be fine-tuned into a single influenza forecaster for many countries and compared it with purpose-built national models.

Methods

We fine-tuned Chronos-2, a pretrained time-series foundation model, on weekly influenza-like illness and acute respiratory infection records for 78 countries, selected from the WHO FluID global epidemiological surveillance database using predefined data-quality criteria. The model produced probabilistic four-week-ahead forecasts. We benchmarked it for the 2025/26 season against the models of Influcast, Italy's collaborative forecasting hub, using the pairwise relative weighted interval score (rWIS), where values below one beat the naive baseline. This season lay outside the fine-tuning data and post-dated Chronos-2's release, ensuring an out-of-sample test. We also evaluated Chronos-2 without fine-tuning (zero-shot).

Results

Across 16 weekly forecasting rounds, the fine-tuned model ranked second of all entries, with a pairwise rWIS of 0.71, ahead of the Influcast ensemble (0.74) and eight of nine participating models, behind only one (0.70). The zero-shot model achieved an rWIS of 1.01, no better than the naive baseline; fine-tuning reduced the rWIS by 30% and mean absolute percentage error from 23% to 17%. Prediction intervals were over-confident: 50% intervals covered 24% of observed values.

Conclusions

A fine-tuned foundation model produced influenza forecasts that matched the purpose-built models of the Italian forecasting hub, whereas the off-the-shelf model performed no better than a naive baseline. Because one model forecasts across 78 countries, the approach could extend influenza forecasting to countries lacking dedicated modelling capacity, supporting preparedness and resource allocation. Benchmarking against forecasting models in other countries is needed to confirm whether this generalises.

Surveillance and prevention of respiratory viruses

Vaccine effectiveness against influenza A(H3N2) infection and hospitalization in recommended target groups over four seasons: A Spanish test-negative study using surveillance data from 2022/23 to 2025/26

ABSTRACT ID: 772

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Background

In Spain, influenza A(H3N2) produced the first wave of the bimodal 2022/23 season, cocirculated with A(H1N1) in 2023/24 and also B in 2024/25, and dominated in 2025/26 (subclade K). We estimated influenza vaccine effectiveness (IVE) against A(H3N2) in seasons 2022/23 through 2025/26 among adults ≥65 years and children aged 6–59 months attending at primary care (PC) with acute respiratory infection (ARI) or hospitalised due to severe ARI (SARI).

Methods

We analysed data from the Spanish surveillance system (SiVIRA) using a test-negative design. ARI and SARI cases were systematically RT-PCR–tested for influenza and classified as cases if positive to A(H3N2) and controls if negative to any influenza and SARS-CoV-2 (only in ≥65-year-olds). Individuals were considered vaccinated if received it ≥7 days before symptom onset. Confounder-adjusted logistic regression (age, epidemiological week, sex, chronic conditions) with robust standard errors by region was used to estimate IVE as 1-Odds Ratio x100.

Results

Among ≥65-year-olds, we included 515/6759 cases/controls in PC and 1105/14,544 in hospitals. In seasons 2022/23 through 2025/26, IVE (95% Confidence Interval) in PC was, sequentially, 33% (-17;62), 4% (-44;36), 35% (-22;65) and 29% (6;47) and, in hospitals, 37% (-14;65), -4 (-40;23), 45% (29;57) and 45% (35;54). Among children we included 390/3383 cases/controls in PC and 72/753 in hospitals. In seasons 2023/24 (first with children vaccination) through 2025/26, IVE in PC was 35% (14;51), 63% (48;73) and 50% (21;68) and, in hospitals, 68% (-516;98), 26% (-96;72) and 57% (15;78).

Conclusions

Vaccination protected against influenza A(H3N2) ARI and SARI in both target groups. The lowest effectiveness in the 2023/24 season could be explained by dominant A(H3N2) clades showing reduced recognition by antibodies against the A/Darwin vaccine component. In contrast, effectiveness was maintained in the 2025/26 season, supporting evidence on the low impact of the drifted subclade K and the importance of monitoring IVE.

POSTER TOUR 11

Surveillance and prevention of respiratory viruses

Estimating the start of the influenza season using the Moving Epidemic Method (MEM) and GLM-based outbreak detection algorithms

ABSTRACT ID: 405

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Background

Influenza viruses cause winter seasonal epidemics in the Northern Hemisphere, with potential to cause severe disease and increased pressure on healthcare systems. In September 2025, a drifted H3N2 influenza A strain (subclade K, J.2.4.1) likely contributed to an early increase in influenza across Scotland. Timely notification of early influenza circulation guides vaccination planning, resource allocation, and enhanced epidemiologic monitoring.

Methods

At Public Health Scotland (PHS), the WHO-recommended moving epidemic method (MEM) is used to estimate the beginning of the influenza season based on 5 years of historical epidemics. Use of Generalized Linear Model (GLM) based outbreak detection algorithms (ODA), using data from a 7-week period over the previous 3 years (Farrington algorithm), to detect unusual increases in respiratory pathogen case counts has also been explored. Using data on lab-confirmed influenza positive cases in Scotland, the first week reported above baseline in MEM was compared to the first week an alarm was raised by ODA.

Results

In season 2025/26, lab-confirmed influenza incidence rates surpassed the MEM epidemic threshold in week 45, indicating the start of the season. ODA detected increasing influenza cases in week 40, five weeks earlier than MEM. In 2023/24 and 2024/25, incidence rates followed “normal” seasonal patterns and surpassed the epidemic threshold before ODA raised an alarm. These results underpinned development of our framework, with open-source R code, whereby MEM is used to estimate the start of “normal” influenza seasons, and “early” seasons are flagged by ODA.

Conclusions

These findings support the use of ODAs alongside MEM to determine the start of the influenza season, ensuring early influenza seasons are detected promptly to inform public health monitoring and response. Combining methods provides complementary epidemiological insight for detecting the start of the influenza season and supports preparedness during early influenza epidemics, such as those driven by drifted and reassorted strains.

POSTER TOUR 11

Surveillance and prevention of respiratory viruses

Serological evidence of substantial Respiratory Syncytial Virus infection burden among older adults residing in Swedish long-term care facilities

ABSTRACT ID: 330

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Background

Older adults (>65 years) residing in long-term care facilities (LTCFs) are at elevated risk of severe outcomes from respiratory infections. Infections often present atypically in this population leading to underdiagnosis and delayed response. We aimed to estimate the respiratory virus infection burden, independent of symptom presentation, among older adults in Swedish LTCFs.

Methods

We leveraged capillary blood samples and national registry data from 1622 LTCF residents (median age: 87 years) spanning 3.5 years post pandemic. A multiplex platform was used to quantify antigen-specific IgG and IgM responses to RSV (pre-/post-F, G-protein), influenza-A (H1N1/ H3N2 HA), influenza-B (HA) and SARS-CoV- 2 (spike). Linear mixed-effects models were used to demonstrate the dynamics of antibody levels over time, adjusted for age, sex and comorbidities.

Results

RSV-specific antibody responses peaked in spring-2022 ($p<0.001$), suggesting an impact of relaxed COVID-19-related restrictions on RSV exposure at LTCFs. RSV antibodies subsequently declined followed by an increase during autumn-2023 ($p<0.001$). Geographic variation in pre-F antibody levels suggested localised RSV outbreaks. Total estimated RSV burden at LTCFs was markedly higher than official reports of the Swedish Public Health Agency. As expected, influenza antibody dynamics reflected seasonal trends and were strongly influenced by annual vaccination. Random forest classifier including serological profiles, demographics, location and co-morbidities moderately predicted mortality (AUC-ROC=0.67). Higher levels of RSV pre-F-specific antibodies in autumn-2021 were associated with increased one-year mortality (OR=1.43, p=0.024), while age, sex, and comorbidities were not significant predictors. Survival analysis indicated a transiently increased risk of deaths related to RSV pre-F antibody levels during low population immunity (HR=4.50, p=0.087).

Conclusions

Substantial respiratory virus circulation was found in Swedish LTCFs. RSV exposure during periods of low population immunity was associated with increased mortality risk, underscoring the need for improved prevention strategies. Longitudinal serological surveillance provides a scalable approach to detect respiratory virus transmission in LTCFs independent of symptom presentation.

POSTER TOUR 11

Surveillance and prevention of respiratory viruses

Impact on RSV hospitalisations among infants in Sweden following the introduction of nirsevimab, season 2025-2026

ABSTRACT ID: 289

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Background

In Sweden, respiratory syncytial virus (RSV) prophylaxis with the monoclonal antibody nirsevimab was implemented autumn 2025. Children born between September 10, 2025 and May 17, 2026 are eligible for an injection of nirsevimab at birth. We investigated the impact of the intervention on RSV infant hospitalisations during the 2025-26 season in Sweden.

Methods

We assessed the incidence of RSV hospitalisations in infants aged 0-11 months, between September 10-April 15 for each season from 2017-2026, excluding the pandemic period (2019-2021). The target intervention group (infants aged 0-5 months) were enrolled on a rolling basis throughout the study period. We assumed protective effect for 5 months post-injection. To assess its impact, we compared pre-intervention seasonal hospitalisation incidence in infants aged 0-5 months with post-intervention incidence in the same age group. For comparative analysis, the same pre-and postintervention comparison was performed with infants aged 6-11 months (no assumed protection). Incidence rate ratios (IRRs) and 95% confidence intervals (CIs) were calculated using Poisson regression. The ratio of the IRRs (RIRR), obtained from a season-by-age-group interaction term, quantified the relative temporal differences in incidence by age-group.

Results

The incidence of hospitalisations was lower in all age groups in 2025-26 compared to 2024-25 (0-5m: IRR: 0.15, 95%CI: 0.12-0.19; 6-11m: IRR: 0.57, 95%CI: 0.46-0.70). The reduction in RSV hospitalisation incidence was greater in infants aged 0-5 months compared to those aged 6-11 months (RIRR: 0.27, 95%CI 0.20-0.36). The results were stable across all compared seasons.

Conclusions

Our results demonstrate the beneficial impact of the prophylactic approach on infant RSV hospitalisations in Sweden. We recommend continuing provision of nirsevimab to eligible infants in subsequent seasons.

Surveillance and prevention of respiratory viruses

Temporal trends and sociodemographic predictors of maternal influenza vaccination in Region Stockholm: A register-based cohort study

ABSTRACT ID: 222

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Background

Although influenza vaccination has been recommended during pregnancy in Sweden since 2013, research on uptake remains limited. Using the regional vaccination register of Stockholm (Vaccinera), we investigated temporal trends in maternal influenza vaccination, the impact of additional maternal vaccine recommendations, and sociodemographic differences in uptake. The aim was to improve understanding of maternal influenza vaccination uptake and inform policies and interventions to increase coverage.

Methods

The study included 264,929 women residing in Region Stockholm during pregnancies which reached gestational age ≥12 weeks during influenza seasons 2013/14–2024/25. The impact of other maternal vaccine recommendations was analyzed using seasonally adjusted interrupted time-series analysis. Sociodemographic differences were examined using Poisson regression to estimate relative risks (RRs) and 95% confidence intervals (CIs). For variables with multiple categories, RR ranges represent the lowest-to-highest RR across subcategories.

Results

Maternal influenza vaccination uptake increased in Region Stockholm from 13.8% in 2013/14 to 39.7% in 2024/25. Following the COVID-19 pandemic and introduction of maternal COVID-19 vaccination, uptake showed a non-significant decline relative to the expected trend (–0.5 percentage points, p=0.08), whereas it increased after the introduction of pertussis vaccination (+1.3 percentage points, p<0.001). Uptake was lower among younger women (RR 0.35, 95% CI 0.33–0.38), women born outside the Nordic countries (RR range 0.23–0.76), women with basic education (RR 0.54, 95% CI 0.50–0.59), women outside employment (RR range 0.41–0.68), multiparous women (RR 0.74, 95% CI 0.73–0.75), and women not cohabiting with the baby's father (RR range 0.74–0.81).

Conclusions

Since its introduction, maternal influenza vaccination uptake in Region Stockholm has increased but remains suboptimal. The increase may have been partly driven by the introduction of maternal pertussis vaccination. Significant sociodemographic differences in vaccine uptake highlight the need for targeted efforts to improve coverage.

POSTER TOUR 11

Surveillance and prevention of respiratory viruses

Uncovering Human Metapneumovirus Burden of Disease through the Belgian Severe Acute Respiratory Infections Surveillance Network

ABSTRACT ID: 139

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1. *Sciensano*

Background

Human metapneumovirus (hMPV) is an important yet under-recognized cause of severe acute respiratory infections (SARI). In the context of evolving respiratory virus epidemiology, driven by advances in respiratory syncytial virus (RSV) prevention and ongoing hMPV vaccine development, robust surveillance is essential to better quantify its burden and clinical impact. This study aimed to characterize the epidemiology and severity of hMPV using data from the Belgian Severe Acute Respiratory Infections (BELSARI) Network.

Methods

We conducted a retrospective analysis of SARI patients hospitalized between 21 June 2021 and 15 June 2025. Demographic and clinical characteristics, including hospital and intensive care unit (ICU) length of stay (LOS), were compared between hMPV-positive and hMPV-negative patients. Risk factor distributions were assessed overall and by age group.

Results

Among 13,560 SARI cases, hMPV circulation occurred predominantly from November to March, with occasional atypical peaks. The highest burden was observed in children aged 0–4 years, accounting for 54% of cases and showing the highest incidence and positivity rates. hMPV-positive patients had a longer median (IQR) hospital LOS than hMPV-negative patients (3 days (2-4) vs 2 days (2-4), $p<0.05$), particularly in young children. Respiratory symptoms, including cough, respiratory distress, and abnormal auscultation findings, were more frequent among hMPV-positive cases. Underlying risk factors were highly prevalent among SARI patients, especially in adults aged ≥65 years (>94%). However, a substantial proportion of hMPV-positive cases, particularly in younger age groups, occurred in individuals without reported risk factors.

Conclusions

hMPV contributes substantially to the burden of SARI, particularly among young children, and is associated with increased healthcare utilization. Seasonal variability highlights the importance of continuous, year-round surveillance. The BELSARI Network provides a robust system for integrated respiratory virus monitoring. Enhanced surveillance, including genomic characterization, will be critical to inform prevention strategies and support future hMPV vaccine implementation.

POSTER TOUR 12

Burden and prevention of vaccine-preventable diseases

Evaluation of Nirsevimab effectiveness in preventing RSV infection in infants under one year during the first two RSV seasons following its introduction in primary and secondary care

ABSTRACT ID: 770

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Background

Respiratory syncytial virus (RSV) is a major cause of acute lower respiratory tract infections and hospitalisation in infants. In June 2024, Germany introduced universal infant immunisation with Nirsevimab. Real-world evidence is needed to evaluate its impact. We assessed the effectiveness of Nirsevimab against symptomatic, laboratory-confirmed RSV infection among infants in primary (PC) and secondary care (SC) during the first two RSV seasons after introduction.

Methods

We conducted a nationwide test-negative case-control study during the 2024/25 and 2025/26 RSV seasons among infants under one year presenting with acute respiratory symptoms. Cases were RSV-positive, controls RSV-negative by qPCR. Adjusted odds ratios (aORs) were estimated using logistic regression adjusting for age, sex, month of symptom onset and underlying conditions. Effectiveness was calculated as (1 – aOR) × 100.

Results

In PC, 42 cases and 211 controls from 48 practices were included. Mean age was 5 months among cases and 6 months among controls. Most infants had no chronic conditions (100% of cases vs 85% of controls). Nirsevimab coverage was lower among cases than controls (31% vs 48%). Adjusted effectiveness of Nirsevimab in PC was 55% (95% CI: 4–79). In SC, 34 cases and 93 controls from six hospitals were included. Mean age was 4 months among cases and 3 months among controls. Most infants had no reported underlying conditions (91% of cases vs 87% of controls). Nirsevimab coverage was lower among cases than controls (15% vs 49%). Adjusted effectiveness of Nirsevimab in SC was 80% (95% CI: 39–93).

Conclusions

Nirsevimab showed moderate effectiveness against RSV infection in PC and higher effectiveness in SC among infants during the first two RSV seasons following introduction. These findings provide evidence supporting universal infant immunisation with Nirsevimab as an effective strategy to reduce RSV burden. Continued surveillance is essential to assess long-term impact and guide future RSV prevention strategies.

POSTER TOUR 12

Burden and prevention of vaccine-preventable diseases

Epidemiological profile and factors associated with death from meningococcal disease in the municipality of Belém, Pará State, northern Brazil, 2024–2025

ABSTRACT ID: 765

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Background

Between 2024 and 2025, an outbreak of meningococcal disease was recorded in the second most populous capital city in the Brazilian Amazon region, triggering a field epidemiological investigation and an analysis of factors associated with death.

Methods

A retrospective case series and cohort study was conducted between 1 August 2024 and 31 May 2025, including residents with confirmed meningococcal disease. Data included records from Notifiable Diseases Information and laboratory information systems, as well as medical and epidemiological investigation reports. Measures of central tendency and dispersion, absolute and relative frequencies, incidence and case fatality rates, and Fisher's exact test were analysed, adopting a 5% significance level.

Results

Seventy-five cases were identified, caused by serogroup B (92,0%; 69/75), among males (56,0%; 42/75), 20–59 years (53.3%; 40/75), and individuals of mixed race/ethnicity (81.3%; 61/75). All cases were confirmed by Polymerase Chain Reaction, and 28.1% were also confirmed by culture (18/75), with clonal complex ST-60 identified in 38,9% (7/18) of culture-confirmed cases. The median time between symptom onset and chemoprophylaxis of contacts was 3 days (IQR: 2–6). The incidence was 5.8 per 100,000 inhabitants and the case fatality was 11,0% (8 deaths). Edema and peripheral cyanosis were risk factors for death (RR=12.1; p<0.001; 95%CI: 4.8–39.5 and RR=12.2; p<0.001; 95%CI: 4.8–30.5, respectively), whereas meningeal irritation signs (RR=0.1; p<0.006; 95%CI: 0.0–0.6) and admission to a reference unit for meningitis (RR=0.1; p<0.001; 95%CI: 0.0–0.42) were protective factors. In the regression analysis, admission to a reference unit remained associated with a lower risk of death (RR=0.04; p<0.001; 95%CI: 0.00–0.35).

Conclusions

The identification of clinical signs associated with death and the protective effect of admission to reference units reinforce the need to raise awareness across the healthcare network regarding timely suspicion and access to specialised services. Strengthening communication between surveillance teams, primary healthcare, and hospitals is recommended to ensure more timely chemoprophylaxis.

POSTER TOUR 12

Burden and prevention of vaccine-preventable diseases

Coverage and timeliness for respiratory syncytial virus (RSV) immunisation and rotavirus vaccination in the National Immunisation Programme in the Netherlands

ABSTRACT ID: 669

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Background

In the Netherlands, RSV immunisation and rotavirus vaccination were recently (in 2025 and 2024, respectively) added to the National Immunisation Programme (NIP). RSV immunisation is offered to infants born April–September in September-October (catch-up group) and to those born October–March within 14 days after birth (primary group). Rotavirus vaccination is offered at 2 and 3 months. This study determined immunisation coverage and timeliness for these first birth cohorts.

Methods

Immunisation coverage was determined using the national vaccination registry Præventis. For RSV, data was extracted for infants born April 2025–March 2026 at the end of the RSV season, 28 April 2026. For rotavirus, data was extracted for children born in 2024 at 33 weeks of age on 9 March 2026. Timeliness was assessed by age of administration for rotavirus and the RSV primary group and date of administration for the RSV catch-up group.

Results

For the 2025/2026 RSV season, coverage was 77.1% in the catch-up group, 72.6% in the primary group, and 75.0% overall (including anonymous immunisations: 77,1%). By municipal health service (MHS) region, coverage ranged between 65.7%-82.5%. In the catch-up group, 81.2% received RSV immunisation within the preferred target period (between 15 September-15 October 2025) and 77.7% of the primary group received it within 14 days after birth. Rotavirus vaccination coverage was 72.8% (65.1% - 82.2% by MHS); 97.5% received the first dose within 12 weeks, and 92.7% received the second dose before 16 weeks of age.

Conclusions

Coverage for the first birth cohorts offered RSV immunisation and rotavirus vaccination was lower than for other infant vaccines (coverage around 87%). Timely administration was high for rotavirus vaccination. For RSV, slightly fewer children were immunised within the target period. These findings highlight the importance of research on factors and reasons associated with lower and less timely participation aiming to increase coverage and timely administration.

Burden and prevention of vaccine-preventable diseases

Measles outbreak in an occupational setting in Spain: informing elimination strategies

ABSTRACT ID: 459

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Background

On 26 January 2026, the European Regional Verification Commission confirmed the re-establishment of endemic measles transmission in Spain, despite sustained high vaccination coverage in cohorts targeted by systematic vaccination. However, recent seroprevalence data show immunity below 95% in cohorts born between 1978 and 2007. On 28 January, a measles outbreak was declared in an open-plan office building. We conducted an outbreak investigation to support public health response.

Methods

Cases were notified following the national measles surveillance protocol case definition, with broadened clinical criteria. We conducted a descriptive study assessing spatiotemporal patterns, demographics, symptoms, severity and immune status (based on vaccination registry data and serology). Probable transmission chains were reconstructed using interview data, exposure windows and serial intervals. Laboratory investigations included IgG/IgM serology, PCR and genomic characterization.

Results

As of 10 April, the outbreak comprised 34 cases with rash onset between 14 January and 28 February. Median age was 44 years (IQR: 43–47), and 66% were women. Rash (100%) and fever (88%) were the most frequent symptoms. Two cases required hospitalisation; no deaths occurred. Vaccination status was unknown in 66% of cases; 19% were unvaccinated, 9% had received one dose and 6% were fully vaccinated. Twenty-two cases had early positive Ig-G. Twenty-eight cases were classified as secondary, four as tertiary and one as fourth-generation. No transmission was observed from cases with early IgG. The same virus variant was identified in all 26 sequenced cases (D8-9171).

Conclusions

Outbreak investigations provide critical evidence to inform measles elimination strategies. Outbreaks occurring in occupational settings with a high concentration of adults from cohorts with lower seroprevalence represent a significant risk. In the frequent absence of reliable vaccination records, information on immunity profiles (including early IgG) can support the prioritisation of control measures. Strengthening surveillance and vaccination among the most susceptible cohorts remains essential to regain measles elimination.

Burden and prevention of vaccine-preventable diseases

Rotavirus epidemiology in the Netherlands before implementation of rotavirus vaccination, 2014-2023

ABSTRACT ID: 353

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Background
Rotavirus is the leading cause of acute gastroenteritis (AGE) in young children, resulting in a substantial disease burden. In January 2024, universal rotavirus vaccination was introduced in the Netherlands. Understanding pre-vaccination epidemiology is essential for evaluating vaccine impact.

Methods
We described the rotavirus epidemiology in the Netherlands in 2014–2023 using data on laboratory-confirmed detections, general practitioner (GP) consultations and hospitalizations for AGE in children <5 years, and circulating genotypes. To estimate the number of rotavirus-attributable hospitalizations, we applied negative binomial regression to estimate the number of AGE hospitalizations attributable to rotavirus using laboratory detections. We describe seasonal dynamics, disease burden, hospital length of stay, and genotype distribution.

Results
Annually, an average of 945 laboratory-confirmed rotavirus detections was reported, with typical seasonal peaks in March–April. In 2013/2014 and 2015/2016, detections were low (553 and 670, respectively) and peaks were delayed (May). During the COVID-19 pandemic, detections dropped to 467 in 2020/2021 but rebounded to 1,742 in 2021/2022, with a peak in December. Average weekly GP consultation rates ranged from 0.76 per 1,000 population in 2020 to 2.11 in 2015. On average, 3,090 rotavirus-attributable hospitalizations were estimated annually, peaking at 5,620 in 2014/2015. The median hospital length of stay for AGE was one night throughout the study period, with a statistically significant decreasing trend over time . There was a shift from G9P8 predominance (2014–2021) to G3P8 dominance from 2022 onwards.

Conclusions
By using multiple complementary data sources, this study provides a robust overview of rotavirus epidemiology and its significant disease burden among young children in the Netherlands prior to vaccination. The implementation of universal routine vaccination has the potential to significantly reduce this burden. Continued surveillance is crucial to assess the impact of public health interventions such as vaccination.

Burden and prevention of vaccine-preventable diseases

RSV-related hospitalisations in infants averted by nirsevimab during the first implementation seasons in Spain and Portugal

ABSTRACT ID: 221

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Background

Respiratory syncytial virus (RSV) is a leading cause of severe respiratory disease in young children. Infant immunisation with nirsevimab was introduced in Spain in the 2023–2024 RSV season and in Portugal in 2024–2025. We assessed the impact of immunisation on RSV-related hospitalisations in the eligible population during each country's first implementation season.

Methods

We conducted an ecological study using national birth statistics to identify infants eligible for nirsevimab in their first RSV season based on country-specific birth-date criteria (Spain: April/2023–March/2024; Portugal: August/2024–March/2025). Infants born before or during the immunisation campaign (≈1 October–31 March) were classified as catch-up or at-birth immunisation groups, respectively. RSV-related hospitalisations (October–March) were estimated in Spain by extrapolating rates from Spain's severe acute respiratory infections surveillance system to the study population and, in Portugal, from the national hospital discharge database using RSV-specific ICD-10 codes (J12.1, J20.5, J21.0 and B97.4). Site-specific nirsevimab coverage and effectiveness were applied by group, catch-up or at-birth, when available: in Spain (coverage 87.8%-92.3%; effectiveness 80.3%-83.1%) and in Portugal (coverage 84.7%-86.9%; overall effectiveness 79.1%). We estimated hospitalisation-averted rates per 100,000 infants (HARs/10^5), prevented fraction (PF), and number needed to immunise (NNI), using Monte Carlo simulations to calculate 95% confidence intervals (CI).

Results

In Spain, the catch-up and at-birth groups included 159,453 and 161,209 infants, respectively; HARs/10^5 were 1,623 (1,289–2,005) and 2,472 (1,937–3,083), PF was 70.4% (65.7–74.5) and 76.7% (72.2–80.3), and NNI was 54 (44– 68) and 37 (30–47). In Portugal, the catch-up and at-birth groups included 14,922 and 42,016 infants, respectively; HARs/10^5 were 1,722 (813–2,752) and 945 (441–1,531), PF was 67.1% (49.7–75.7) and 69.4% (51.0–77.7), and NNI was 49 (31–104) and 90 (57–197).

Conclusions

Nirsevimab substantially reduced RSV-related hospitalisations in both countries, preventing 67–70% of catch-up and 69–77% of at-birth cases. Similar impact despite different implementation contexts highlights programme robustness and the importance of sustaining high coverage.

POSTER TOUR 13

Data systems and surveillance

Nationwide epidemiology and machine learning-derived phenotypes of sepsis-associated delirium in Spain, 2017–2022

ABSTRACT ID: 775

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Background

Sepsis-associated delirium (SAD) is a frequent neurological complication among septic patients, particularly in older adults, and is linked to worse clinical outcomes and increased healthcare utilisation. However, large-scale epidemiological data and the clinical heterogeneity of SAD remain insufficiently characterised.

Methods

We conducted a retrospective nationwide cohort study using the Spanish Minimum Basic Data Set (MBDS), including adult patients hospitalised with sepsis between 2017 and 2022. Sepsis and delirium were identified using validated ICD-10-CM algorithms. Clinical variables, mortality, ICU stay, and hospital costs were analysed. Unsupervised k-modes clustering was applied to identify phenotypic subgroups of SAD.

Results

Among 1,187,393 patients with sepsis, 143,825 (12.1%) developed SAD. Patients with delirium were substantially older than non-delirium patients (median age 85 vs. 78 years; $p<0.001$). SAD was associated with longer ICU stay (9 vs. 5 days; $p<0.001$) and markedly higher healthcare expenditure, with an estimated 39% increase in hospital costs. Although crude in-hospital mortality was lower in SAD patients (15.8% vs. 22.0%), this finding was likely influenced by survivor bias and the predominance of lower-risk genitourinary infections. The incidence of SAD increased progressively during the study period, especially in patients aged >65 years. Cluster analysis identified four reproducible phenotypes: respiratory-dominant, genitourinary-dominant, severe renal dysfunction, and geriatric multi-morbidity. Mortality differed substantially between phenotypes, ranging from 9.5% in the genitourinary cluster to 24.3% in the respiratory phenotype.

Conclusions

SAD represents a growing clinical and economic challenge in Spain, particularly in elderly multimorbid patients. Machine learning analysis demonstrates that SAD is a heterogeneous syndrome with distinct prognostic phenotypes. These findings support the development of phenotype-oriented prevention and management strategies in septic patients.

POSTER TOUR 13

Data systems and surveillance

Data quality and reporting timeliness in Uzbekistan's infectious disease surveillance system: a baseline assessment for further strategical development

ABSTRACT ID: 678

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Background

Complete, valid, and timely reported infectious disease (ID) notification data are essential for effective surveillance and public health response. In 2024, Uzbekistan initiated the transition from a paper-based to an electronic ID surveillance system (IS EMID) to improve data quality and reporting efficiency. To support future evaluations of IS EMID, we assessed data completeness, data validity, and reporting timeliness as baseline indicators of functionality of the system in 2023.

Methods

All 208 local public health authorities (LPHA) in Uzbekistan were invited to participate in an anonymous voluntary online survey. Perceptions regarding data completeness, validity, and timeliness for 2023 were analysed descriptively. Survey findings were compared with routine surveillance data for 2023 collected on-site from paper-based notification and case management forms from five LPHA. Completeness was assessed across 15 mandatory fields on notification forms, while validity by comparing field-level consistency between notification and case management forms.

Results

Overall, 192 LPHA departments from all 14 regions participated in the survey (92%, range: 50-100%). Routine surveillance data were collected for 1343 cases. Perceived completeness (mean=75%; range: 35–90%) and validity (mean=76%; range: 56–89%) were lower than values extracted from notification forms (completeness: mean=87%, range: 20–99%; validity: mean=86%, range: 17–99%). Regarding timeliness, reporting delays exceeding 24 hours were perceived to occur either "rarely" or "never" by 74% of respondents. However, routine surveillance data revealed that only 49% of cases (432/882) were reported within the required 24-hour time-frame in 2023.

Conclusions

LPHA staff perceived data completeness and validity as lower, and timeliness as higher than observed in notification forms in 2023. Substantial delays in meeting the mandatory 24-hour reporting requirement in 2023 could hinder early warning and response activities. The results demonstrate the need for more automated and standardized approach to data collection and transmission and will build a baseline for comparison for future evaluations.

POSTER TOUR 13

Data systems and surveillance

From data to action: a regional epidemiological bulletin driving public health action in the Midlands region, England

ABSTRACT ID: 564

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Background

Timely use of surveillance data is critical for effective infectious disease control, yet the evidence on how routine epidemiological reporting drives action for outbreak detection and situational awareness at sub-national level is limited. The UK Health Security Agency (UKHSA) Field Service (FS) Midlands produces a weekly epidemiological bulletin. Providing an overview of the epidemiology of infectious diseases at city/district level and visualised in an interactive Power BI dashboard, to identify exceedances, detect emerging clusters, and inform risk assessment across stakeholders. Key messages are disseminated via a weekly email. We present the results of an evaluation and summarise the impact of the bulletin.

Methods

A mixed-methods evaluation assessed utility and impact, combining stakeholder survey responses, qualitative feedback, and usage analytics. Contribution to public health action was assessed by collating instances where the bulletin informed identification, investigation, or follow-up of outbreaks or clusters over 12 months.

Results

The bulletin demonstrates sustained and widespread use (100+ users; median of 38 weekly views; range29-68). Over the evaluation period, it supported the identification of 46 increases which were investigated by FS. Stakeholders reported improved situational awareness and stronger evidence for local risk assessment. Timeliness, clarity, and LA-level granularity were highlighted as key strengths. Weekly email summaries were identified as valuable, highlighting things of note to users. The bulletin is now embedded within routine health protection processes across the Midlands region.

Conclusions

This work demonstrates how routinely collected surveillance data can be operationalised to directly inform public health action. The Midlands epidemiological bulletin demonstrates an effective and adaptable approach that can be replicated by other public health and regional epidemiology teams. By structuring and communicating routine surveillance data effectively, the bulletin enables the detection of outbreaks, and supports coordinated, evidence-based public health action.

POSTER TOUR 13

Data systems and surveillance

Completeness of laboratory surveillance for four bacterial meningitis pathogens in the Netherlands, 2015-2024

ABSTRACT ID: 636

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Background

Laboratory surveillance for meningitis-causing bacterial pathogens is essential to monitor the impact of vaccine programmes and to detect clusters. The goal of this study was to investigate the completeness of invasive isolate submission data for *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Neisseria meningitidis* and *Haemophilus influenzae* to the Netherlands Reference Laboratory for Bacterial Meningitis (NRLBM) from 2015 to 2024.

Methods

We compared numbers of submitted isolates of each of the four pathogens with data from the automated national surveillance system for antibiotic resistance in the Netherlands (ISIS-AR). We assumed that all invasive isolates would be tested for antibiotic resistance and reported to ISIS-AR. Isolate counts stratified by medical microbiological laboratory (MML), year, age group and sample material were compared between NRLBM and ISIS-AR; the number of isolates recorded in ISIS-AR was used as the denominator. Additionally, three MMLs were invited for semi-structured interviews to gain more insight into isolate submission routines.

Results

The MMLs included in the analysis (n=47) submitted nearly all requested isolates to the NRLBM in 2022-2024 (99.5%), while over the whole study period, 2015-2024, 89.5% of requested isolates were submitted. For *S. pneumoniae*, completeness strongly increased between 2017 (62.4%) and 2021 (94.1%). For *S. pyogenes*, *N. meningitidis* and *H. influenzae* completeness was high (>90%) during almost the entire study period. Interviews with MMLs suggested that completeness of isolate submission improved with automated alerts in laboratory information management systems (LIMS) and through emphasizing importance of isolate submission during notable outbreaks.

Conclusions

Completeness of isolate submission to the NRLBM of the four included bacterial meningitis pathogens was very high. Completeness of S. pneumoniae isolate submission increased over thirty percentage points in just four years. Recommendations to maintain a high completeness include automated alerts in LIMS and continued feedback to MMLs from the reference laboratory, especially in the context of notable outbreaks.

POSTER TOUR 13

Data systems and surveillance

Epidemiological trends in non-polio enterovirus infections in England, 2012–2025

ABSTRACT ID: 553

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Background

Non-polio enteroviruses (NPEVs) typically cause mild infections but can rarely lead to severe disease including meningitis, sepsis and death. There are no antivirals licensed or in development, partly due to limited epidemiological data to inform therapeutic pipelines. Here, we describe long-term trends in enteroviral infections.

Methods

We analysed trends in NPEVs reported to the UK Health Security Agency national reference laboratory between 2012-2025, including samples submitted by English laboratories from patients with severe viral-like illness. We linked laboratory-confirmed infections to multiple national databases to evaluate intensive care admissions and fatal outcomes.

Results

23,136 genotyped NPEV samples with 21,282 infection episodes were identified. Children accounted for most detections: aged 0–3 months (7,712/23,136; 33%), 3–12 months (2,478/23,136; 11%), and 1–4 years (5,086/23,136; 22%). NPEV detections declined during the COVID-19 pandemic and then rebounded from 2022 , with the highest annual detections during 2023-2025. There were 255 deaths within 120 days, highest in infants aged 0–3 months (75/255; 30%). CV-A6 (3,214/23,136; 14%), E9 (1,903/23,136; 8.2%), EV-D68 (1,607/23,136; 6.9%), E6 (1,573/23,136; 6.8%), E30 (1,510/23,136; 6.5%) and CV-B5 (1,503/23,136; 6.5%) were the most prevalent genotypes. EV-D68 circulation increased during 2021–2024 with higher detections in 2021 (n=206), 2023 (n=266), and 2024 (n=723) than pre-pandemic years (range: 2–74 annually) and an annual rather than previously-observed biennial circulation. There were 535 paediatric intensive care admissions within ±30 days infection, with a median length of stay of 3 days (IQR:5); infants aged 0–3 months accounted for 48% of admissions (256/535).

Conclusions

Infants aged 0-3 months continue to have the highest incidence of severe NPEV infections, severe disease and fatal outcomes. NPEV surveillance is essential to detect outbreaks, monitor disease burden and identify emerging enterovirus serotypes. Further work is needed to correlate clinical syndromes with specific NPEV serotypes.

POSTER TOUR 13

Data systems and surveillance

Extraordinary excess mortality detected by EuroMOMO during the severe heatwave affecting Europe in June-July 2026

ABSTRACT ID: 1035

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Background

The European Mortality Monitoring Network (EuroMOMO) aims to detect early signals of excess mortality associated with major public health events in Europe, such as severe seasonal respiratory epidemics and extreme weather events.

Methods

We analysed pooled estimates of excess mortality from the 27 participating European countries for the weeks 26, 27, 28 and 29 of 2026, coinciding with the sudden extreme heatwave in Europe. Excess deaths were analysed for the total population and by age groups (0-14, 15-44, 45-64, 65-74, 75-84, and ≥85 years).

Results

Following normal mortality levels in the first part of June 2026, we detected a steep peak in week 26, with a total of 16,888 excess deaths, or 24% above the expected. This excess mortality was detected in both older and younger age groups, with the following excess deaths estimated (percentage above expected in brackets): 0-14 years: 51 (2,6%), 15-44 years: 363 (7,6%), 45-64 years: 1845 (15,1%), 65-74 years: 2684 (16,7%), 75-84 years: 4481 (17,0%), and ≥85 years: 7896 (17,4%). After week 26, mortality levels declined, with the following excess deaths estimated per week (all ages): Week 27: 8520 (10,3%), week 28: 4515 (5,5%) and week 29: 3506 (4,2%).

Conclusions

Excess heat-mortality in a single week at this high level has not been recorded previously in Europe, reaching levels almost similar to the mortality peaks seen during the coronavirus pandemic. Surprisingly, not only the older age groups but also younger adults were affected. Importantly, the excess heat-mortality were confined to a subset of countries, where excess deaths profoundly exceeded the numbers reported for Europe overall. Analysis of causes of death-data will be needed to fully understand the unusual heat-mortality observed. As extreme heat is expected to become more frequent due to climate change, heat-mortality monitoring systems to inform early warning and preventive actions will become increasingly important.

POSTER TOUR 14

Surveillance and outbreak investigations of AMR

Prevalence of MRSA nasal colonisation in patients undergoing elective total joint arthroplasty: implications for targeted preoperative screening

ABSTRACT ID: 251

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Background

Methicillin-resistant *Staphylococcus aureus* (MRSA) remains a major contributor to antimicrobial resistance and is associated with increased morbidity, mortality, and healthcare costs, particularly in surgical patients. Preoperative MRSA screening is widely implemented to reduce the risk of surgical site infections; however, up-to-date epidemiological data are essential to determine whether universal screening remains justified or whether targeted strategies may be more efficient. This study aimed to estimate the prevalence of MRSA nasal colonisation among patients undergoing elective total joint arthroplasty (TJA) and to assess demographic patterns relevant to screening strategies.

Methods

A retrospective review was performed for all adults scheduled for elective TJA between June 2024 and August 2025. Preoperative MRSA nasal screening using culture-based methods was conducted as part of routine preoperative assessment. Demographic data, including age and sex, were extracted from electronic medical records. Descriptive statistics were used to estimate MRSA prevalence and summarise patient characteristics.

Results

A total of 809 patients underwent screening. The mean age was 70.4 years (median 72; range 23–91), and 55.6% were female (n = 450). MRSA nasal colonisation was detected in 10 patients, corresponding to a prevalence of 1.2% (95% CI 0.60–2.28%). Of those colonised, 9 (90%) were aged ≥60 years and 8 (80%) were male. Overall, 98.8% (n = 799) of patients tested negative.

Conclusions

The prevalence of MRSA nasal colonisation in this elective arthroplasty population was low, suggesting that universal screening may have limited yield in similar settings. The higher proportion of colonisation observed among older patients indicates that risk-based or targeted screening strategies may warrant further evaluation. These findings support ongoing efforts to optimise preoperative screening protocols and antimicrobial stewardship. Further studies are needed to evaluate additional risk factors and assess the cost-effectiveness of targeted versus universal screening approaches.

POSTER TOUR 14

Surveillance and outbreak investigations of AMR

Investigating the effects of methodological de-duplication rules on routine bacterial antimicrobial resistance surveillance indicators in Germany 2023–2024

ABSTRACT ID: 67

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Background

Repeated sampling from patients can bias antimicrobial resistance (AMR) surveillance estimates. Although deduplication of repeated isolates is a core analytical step, its effect on national AMR surveillance estimates is insufficiently quantified. We assessed the impact of de-duplication rules on resistance estimates in Germany's Antimicrobial Resistance Surveillance (ARS) system.

Methods

We included *Staphylococcus aureus* and *Klebsiella pneumoniae* isolates reported to ARS, 01.01.2023–31.12.2024. We applied three scenarios of specimen selection: all isolates; isolates excluding screening samples, and invasive blood/cerebrospinal fluid isolates only, as in EARS-Net. Within each scenario, we compared no deduplication and six de-duplication rules. Firstly, four first-isolate rules: per person and species per year or quarter, with or without specimen-type stratification. Secondly, one first-isolate rule per 30-day episode and lastly, one most-resistant-isolate rule per person, species, and year. We calculated proportions of methicillin-resistant *S. aureus* (MRSA), carbapenem-resistant *K. pneumoniae* (CRKP), and the monthly proportion of isolates included by de-duplication rules.

Results

We included 1,789,121 isolates (1,222,836 *S. aureus*; 566,285 *K. pneumoniae*) from 1,017,679 patients. Without de-duplication, the MRSA proportion was 11.1% in all isolates, 6.8% after excluding screening isolates, and 4.8% in invasive isolates; across de-duplication rules, it ranged from 9.7%–10.5%, 5.9%–6.3%, and 4.3%–4.4%, respectively. The CRKP proportions were 1.7% (all isolates), 1.2% (excluding screening isolates), and 1.2% (invasive isolates) without de-duplication; across de-duplication rules, it ranged from 0.7%–1.1%, 0.6%–0.8%, and 1.2%–1.2%, respectively. The monthly proportion of included isolates declined over the year or quarter with calendar-year or calendar-quarter de-duplication rules but remained stable with the episode-based rule.

Conclusions

MRSA and CRKP proportions decreased with de-duplication and when excluding screening isolates. Estimates based on invasive isolates, as in EARS-Net, were less sensitive to de-duplication rule choice, supporting current approaches for aggregated annual surveillance. For sub-annual trends, episode-based rules may be preferable to calendar-based rules.

POSTER TOUR 14

Surveillance and outbreak investigations of AMR

Consumption of antimicrobials relevant for multidrug-resistant infections in Piedmont, Italy, 2023–2024: regional trends and implications for antimicrobial stewardship

ABSTRACT ID: 739

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Background

Antimicrobial resistance is a major public health threat, with multidrug-resistant (MDR) organisms driving increased mortality, prolonged hospitalization, and healthcare costs. Marked regional heterogeneity in resistance profiles and antibiotic consumption makes regional surveillance essential to inform locally adapted stewardship interventions. This study describes trends in hospital consumption of antimicrobials relevant for MDR infections in Piedmont (north-western Italy, 4.2 million inhabitants) during 2023–2024, benchmarked against national and European data.

Methods

Hospital antibiotic consumption data were extracted from Piedmont's regional administrative pharmaceutical database. Consumption was expressed as defined daily doses (DDD) per 100 bed-days, using the WHO ATC/DDD classification system. MDR-relevant antimicrobials were selected following the WHO AWaRe Reserve group classification and Italian medicines agency (AIFA) definitions. Twenty-seven molecules across six classes were analysed: penicillin/beta-lactamase inhibitor combinations, carbapenems, third- and fourth-generation cephalosporins and related agents, glycopeptides, aminoglycosides, other antibacterials.

Results

Total MDR-relevant consumption decreased between 2023-2024 from 30.86 to 28.59 DDD/100 bed-days (–7.4%), consistent with the Italian National Action Plan against Antimicrobial Resistance (PNCAR) target of reducing overall hospital antibiotic consumption by at least 5% by 2025. Reductions were observed across most classes: carbapenems (meropenem –6.0%, ertapenem –10.8%), glycopeptides (vancomycin –17.4%, teicoplanin –18.9%), and linezolid (–19.5%). Increases were recorded for imipenem/cilastatin/relebactam (+63.2%), dalbavancin (+32.1%), and fosfomycin (+11.3%). In 2024, broad-spectrum and/or last-resort antibiotics represented 48% of hospital consumption, below the national mean of 50.9% (AIFA, 2024) but exceeding the EU/EEA mean of 39.6% (ECDC ESAC-Net, 2024)

Conclusions

The observed reduction indicates a positive trend aligned with PNCAR targets, with consumption falling below the national average but above European benchmarks. Setting uniform national and European targets may inadequately reflect local epidemiological drivers, including endemic MDR burden and hospital case-mix. Regional surveillance, local analysis and interpretation of results enables context-specific target-setting and informs objectives of local stewardship programmes.

POSTER TOUR 14

Surveillance and outbreak investigations of AMR

Regional WGS surveillance identified a clinically relevant MDR Klebsiella pneumoniae ST15 cluster with possible intra-facility transmission

ABSTRACT ID: 653

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Background

A pilot regional whole-genome sequencing (WGS) surveillance network for multidrug-resistant (MDR) *Klebsiella pneumoniae* was implemented in the Netherlands. Sequence type 15 (ST15) was the second most frequently detected and most clonal type, with 23/26 isolates belonging to a single cluster, representing the largest regional cluster. ST15 is a globally disseminated high-risk clone associated with MDR, hospital outbreaks, and emerging hypervirulence. A key challenge in genomic surveillance is distinguishing endemic circulation from true transmission chains.

Methods

ST15 MDR *K. pneumoniae* isolates (one per patient per year; June 2023–October 2025) from hospitals, general practitioners, and long-term care facilities were included. Whole-genome sequencing (Illumina NextSeq500/550) was performed, with Kleborate and β-lactamase databases used for resistance and virulence profiling. Publicly available ST15 genome sequences (2014–present), obtained from Pathogenwatch, were included for comparison. Phylogeny was assessed using cgMLST (cluster cut-off ‹15 alleles). Epidemiological linkage was evaluated using electronic health records; probable, possible, and improbable links were defined by overlap in 4–5, 2–3, and 0–1 of institution, department, specialty (≤1 year pre-sampling), admission/visit dates, and 4-digit postcode.

Results

The regional ESBL-positive, carbapenemase-negative ST15 cluster (N=23), with trimethoprim/sulfamethoxazole and quinolone resistance genes, was genetically distinct from 1,907 Pathogenwatch genomes, including 47 from the Netherlands. Cluster isolates originated from three hospitals (N=10, 4, 1) and general practitioners (N=8). Possible epidemiological links were identified for 10 isolates, all from a single hospital, based on institutional, departmental, and specialty overlap.

Conclusions

Regional WGS surveillance identified a large *K. pneumoniae* ST15 cluster with possible intra-facility transmission using limited standardized metadata. Its resistance profile precluding oral treatment for complicated urinary tract infections underscores the clinical impact of undetected transmission chains or reservoirs. Integrating regional and national WGS surveillance offers opportunities to improve outbreak detection, but requires evaluation of minimum surveillance coverage and optimal metadata requirements under financial constraints and restricted data access.

Surveillance and outbreak investigations of AMR

30-day fatality of Klebsiella pneumoniae bloodstream infections in Emilia-Romagna, Italy, 2018-2025: a population-based study.

ABSTRACT ID: 622

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Background

Klebsiella pneumoniae bloodstream infections (KP-BSIs) represent a growing clinical and economic burden across Europe, driven by increasing incidence, the spread of multidrug-resistant strains, and the emergence of hypervirulent clones. Italy consistently reports among the highest carbapenem resistance rates in Europe. This study assesses the association between antimicrobial resistance and 30-day fatality in KP-BSIs occurring in Emilia-Romagna, Italy, from 2018 to 2025.

Methods

We conducted a population-based study on all KP-BSIs occurring in Emilia-Romagna residents aged ≥14, linking regional laboratory and administrative datasets, to obtain information on antimicrobial resistance phenotypes, demographics, baseline mortality risk score, polymicrobial BSI, clinical severity, and hospital-onset. KP-BSIs were classified as carbapenem-resistant (CR-KP), third-generation cephalosporin-resistant (3GCR-KP), or susceptible (S-KP) to the previous two classes. Cox proportional hazards regression was used to estimate crude and adjusted hazard ratios (HR) with 95% confidence intervals (CI) for 30-day fatality.

Results

We identified 13,418 KP-BSIs, of which 1,088 (8.1%) were caused by CR-KP, 1,603 (11.9%) by 3GCR-KP, and 10,727 (79.9%) by S-KP. Patients were predominantly male (62%), with a mean age of 73.4 years (SD 14.1); 49.5% of infections were hospital-onset. Overall, 30-day case fatality rate (CFR) was 25.3%, with group-specific rates of 34.7%, 28.5%, and 23.9% for CR-KP, 3GCR-KP, and S-KP, respectively. Crude 30-day fatality HRs were 1.53 (95% CI 1.38-1.70) for CR-KP and 1.22 (95% CI 1.10-1.34) for 3GCR-KP compared to S-KP. After multivariable adjustment, HRs were 1.31 (95% CI 1.17-1.46) and 1.10 (95% CI 0.995-1.22), respectively.

Conclusions

KP-BSI CFR in Emilia-Romagna region was substantial and consistent with the literature. CR-KP was independently associated with 30-day fatality, whereas the association for 3GCR-KP was attenuated after adjustment. Further analyses will address short-term fatality, length of stay, and readmission rates. The use of routinely collected data enables both local epidemiological monitoring and outcome-based surveillance, providing a replicable framework to inform targeted antimicrobial stewardship interventions.

POSTER TOUR 14

Surveillance and outbreak investigations of AMR

Prevalence of carbapenemase production in Enterobacterales with elevated imipenem MIC and low meropenem MIC in the Netherlands

ABSTRACT ID: 542

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Background

Carbapenemase producing Enterobacterales (CPE) are associated with a high disease burden, making early detection and control essential. The Dutch national laboratory guideline for the detection of CPE recommends additional genotypic or phenotypic carbapenemase confirmation if defined screening breakpoints for the minimal inhibitory concentration (MIC) are exceeded for either meropenem (>0.25 mg/L) or imipenem (>1 mg/L). However, it has been argued that confirmation tests are unnecessary if only the automated imipenem MIC is above the screening breakpoint (hereafter high imipenem). We analysed the prevalence of CPE among Enterobacterales isolates with solely a high imipenem.

Methods

From the Dutch national antimicrobial resistance surveillance system (ISIS-AR), we included *Escherichia coli*, *Klebsiella pneumoniae* and *Enterobacter cloacae* complex isolates, sampled in 2023 and 2024. Per patient, only an infection-related isolate with the highest MIC value for meropenem and/or imipenem and has a confirmation test results available was selected per year. We included only data from laboratories providing confirmation test results for 100% of patients with ≥1 high imipenem isolate. We calculated the percentage of isolates showing carbapenemase production, assessed the distribution of automated imipenem MIC values and described identified genotypes.

Results

We found 168 high imipenem isolates from 12 laboratories using the VITEK system for susceptibility testing. Out of these isolates, 5% were carbapenemase producing (6/49 for *E. coli*; 1/42 for *K. pneumoniae*; and 2/77 for *E. cloacae* complex) all with an MIC of 2 mg/L. In all genotypically confirmed isolates (n=5), OXA48 or OXA48-like genes were found.

Conclusions

Despite a meropenem MIC below the screening breakpoint, carbapenemase production in high imipenem Enterobacterales usually encoded by OXA48 or OXA48-like genes were found. This finding shows that additional testing for carbapenemase production remains recommended in case of solely elevated imipenem, especially for *E. coli* in which the confirmation of CPE was most notable.

POSTER TOUR 14

Surveillance and outbreak investigations of AMR

First reported outbreak of carbapenemase-producing Enterobacterales in a Belgian nursing home: investigation and management

ABSTRACT ID: 866

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Background

Carbapenemase-producing Enterobacterales (CPE) outbreaks in nursing home (NH) settings are rarely reported. Following identification of two index cases on a single ward of a 156-resident facility, extensive screening identified the first documented CPE outbreak in Belgium. This prompted an in-depth investigation into infection prevention measures and environmental reservoirs.

Methods

Rectal screening of 154 residents was performed in three waves. Fecal samples were cultured on selective chromogenic agar (CHROMID CARBA SMART, bioMérieux) and MacConkey agar supplemented with ertapenem and meropenem discs. Positive screenings were confirmed using OXA-48 K-SeT Rapid tests (Coris Biocept). Confirmed isolates underwent genotyping and clustering at the National Reference Centre. Visual inspections and microbiological sampling of the environment and staff hands were performed. Hand contamination was assessed via fingertip imprints and interdigital swabs. Colony counts were quantified on Tryptic Soy Agar, with significant contamination thresholds set at 50 CFU (fingertips), 500 CFU (hand swabs), and 100 CFU (surfaces).

Results

Twenty-one OXA-48 CPE carriers were identified. Genotyping of E. coli isolates (n=17) identified 3 clonal clusters of different MLST (ST69, n=6; ST38, n=2; ST10, n=2), suggesting potential cross-transmission. Three other species including 3 K. pneumoniae isolates (all of different MLST clones) harbored the same blaOXA-48-containing plasmid. Infection control analysis revealed critical gaps, including insufficient hand hygiene facilities. Staff sampling (n=17) revealed 5 unacceptable fingertip samples and 13 unacceptable interdigital swabs. Environmental assessment showed visible soiling of multiple surfaces, with 25 of 37 samples exceeding predefined CFU thresholds.

Conclusions

This outbreak demonstrated extensive environmental contamination and suboptimal hand hygiene facilitating OXA-48 CPE transmission. Targeted interventions, including mandatory infection control training, revised cleaning protocols, and enhanced auditing, were implemented. These findings emphasize the need for increased vigilance, structured outbreak management protocols, and strengthened infection control expertise in nursing homes, which could be effectively managed by a dedicated reference person.

POSTER TOUR 15

Artificial intelligence in public health

Scaling One Health Surveillance: AI-Driven Predictive Modeling of AMR Trends Using Municipal Wastewater in Pirkanmaa, Finland

ABSTRACT ID: 126

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Background

Antimicrobial resistance (AMR) demands proactive One Health surveillance. Traditional clinical monitoring in the EU often lags behind community transmission. In Finland, despite strict regulation of human and veterinary antibiotic use, the silent community spread of imported multi-drug resistant organisms such as Carbapenemase-producing *Enterobacteriaceae* (CPE) remains a critical threat. This study evaluates a machine learning framework applied to municipal wastewater to provide early warnings of AMR circulation prior to clinical manifestation.

Methods

We developed a hybrid spatial-temporal model utilizing Long Short-Term Memory (LSTM) networks. The model analyzed retrospective metagenomic sequencing data from the Tampere/Pirkanmaa municipal wastewater network alongside the Finnish Institute for Health and Welfare (THL) national repository. We cross-referenced targeted wastewater resistance gene markers with clinical isolate data from the ECDC's European Antimicrobial Resistance Surveillance Network (EARS-Net) to map cross-border and local transmission dynamics.

Results

LSTM model successfully identified anomalous spikes in CPE-associated resistance genes an average of 18 days (95% CI: 14–22 days) prior to their first detection in regional Pirkanmaa hospital diagnostics. The algorithm effectively filtered baseline agricultural run-off noise, achieving a 92% positive predictive value for identify-ing subsequent clinical clusters. Furthermore, spatial-temporal clustering accurately differentiated localized, domestic AMR amplification from resistance profiles mirroring broader Scandinavian and EU trends.

Conclusions

Applying deep learning to municipal wastewater transforms passive environmental monitoring into a highly actionable epidemic intelligence tool. By forecasting AMR emergence nearly three weeks ahead of clinical detection in Pirkanmaa, this One Health framework enables preemptive hospital infection control, targeted veterinary stewardship, and optimized public health resource allocation. Furthermore, it bridges the critical gap between environmental surveillance and clinical intervention, fostering real-time, data-driven collaboration between local health boards, THL and the agricultural sector. Ultimately, this scalable, cost-effective approach provides a concrete blueprint for harmonizing early-warning AMR systems across the European Union, bolstering resilient pandemic preparedness against future drug-resistant threats.

POSTER TOUR 15

Artificial intelligence in public health

Evaluating AI-assisted surveillance of healthcare-associated infections using a standard European point prevalence study in a regional hospital, the Czech Republic, 2025

ABSTRACT ID: 328

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Background

Healthcare-associated infections (HAI) remain a major burden in acute care hospitals. Traditional passive surveillance systems underestimate HAI incidence and lack reliability. Daily manual review of health records for HAI detection is not feasible. Artificial intelligence (AI) supported HAI surveillance system HAIDI for daily routine was implemented in the Regional Hospital Liberec in 2023. The aim of the study was to evaluate the methodology and the performance of an AI-assisted surveillance system (HAIDI) by comparing its results with a manual point prevalence survey (PPS). Specifically, we aimed to determine the system's capacity to ensure accurate and comprehensive detection of all HAI cases.

Methods

A three-step study was conducted at a large regional hospital on May 13th 2025. First, we performed a one-day PPS using ECDC methodology. Second, HAIDI was applied to the same patient cohort and its outputs were validated by epidemiologists. We then calculated Cohen's kappa and sensitivity.

Results

Among 749 patients, manual PPS identified 61 patients with 65 HAI (prevalence 8.1%), while HAIDI identified 62 patients with 65 HAI. Agreement between the two approaches was high (Cohen's kappa $\kappa = 0.8849$; observed agreement 0.9826). 55 patients were classified as HAI-positive by both methods, while 681 were classified as HAI-negative by both. Manual PPS and HAIDI both missed seven HAI but with different HAI ranges. Estimated sensitivity for both epidemiologists and HAIDI was 90.28%. Limitations of our study include its conduct in a single hospital and the one-day evaluation design.

Conclusions

Evaluation methodology proved useful and AI-assisted surveillance demonstrated high concordance with manual PPS while improving case detection and operational efficiency. The integration of AI into routine surveillance enables sustainable, hospital-wide, continuous daily incidence monitoring and provides a more accurate evidence base for infection prevention and control.

POSTER TOUR 15

Artificial intelligence in public health

Operationalizing LLM-based surveillance of healthcare-associated bloodstream infections: a data governance and de-identification framework

ABSTRACT ID: 223

Costanza Vicentini [1], ***Lorenzo Ramondetti*** [1], ***Daniele Citta*** [1], ***Daniele Consoli*** [1], ***Jacopo Ciani Sciolla Lagrange Pusterla*** [2], ***Jacopo Dirutigliano*** [2], ***Paolo Gardois*** [1], ***Gianfranco Michele Maria Politano*** [3], ***Alfredo Benso*** [3], ***Tommi Kärki*** [4], ***Angelo D'Ambrosio*** [4]

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Background

Healthcare-associated infection (HAI) surveillance remains heavily dependent on manual review of electronic medical records (EMRs), limiting scalability and reproducibility. Large language models (LLMs) may support automated extraction of clinically relevant information from unstructured text, but implementation in real-world surveillance is constrained by data protection, governance, and workflow integration challenges. We describe the data-processing framework developed within an ECDC-funded project on automated surveillance of healthcare-associated bloodstream infections (HA-BSIs) in Italian hospitals.

Methods

We developed a multicenter governance architecture and data processing framework combining: (i) a Data Protection Impact Assessment used as a design instrument; (ii) categorization of data into raw, derived, and aggregated tiers; (iii) an on-site, open-source, AI-assisted de-identification pipeline for EMRs; and (iv) a tiered LLM deployment model. LLMs are used exclusively for structured clinical information extraction from unstructured text; the final case classification is performed by processing the extracted data points through a transparent, deterministic, rule-based, algorithm based on the ECDC HAI case definitions.

Results

The project produced an operational workflow in which identifiable data remain under hospital control, pseudonymization is confined to hospital-level handling, and only anonymized records are transferred for downstream processing. An open-source assisted redaction tool was developed to support local anonymization of unstructured EMRs. Key implementation barriers included variable EMR maturity across hospitals, lengthy ethics and data protection approval cycles, and the continued need for supervised manual oversight despite AI-assisted redaction. Overall, the framework enabled development of LLM-based surveillance while preserving accountability, local control of raw data, and structured human oversight.

Conclusions

In a high-stringency EU regulatory setting, the main barriers to LLM-based surveillance are not only technical but organizational and governance-related. A locally deployable de-identification pipeline, combined with a constrained LLM-based clinical information extraction architecture and deterministic downstream case classification, may offer a practical and transferable pathway for implementing trustworthy AI-enabled infectious disease surveillance.

POSTER TOUR 15

Artificial intelligence in public health

Artificial Intelligence for Healthcare-Associated Infection prediction in Adult Intensive Care Units: a systematic review of prognostic models

ABSTRACT ID: 178

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Background

Identifying patients at high risk of Healthcare-Associated Infections (HAIs) is still a major challenge in Intensive Care Units (ICUs). Prognostic prediction models based on Machine Learning and Artificial Intelligence (ML/AI) methods can enhance individual-patient HAI risk estimation and enable preventive interventions. This systematic review (protocol: osf.io/bzqfp) aims to identify ML/AI-based prognostic models for estimating the HAI risk in adult ICU-patients and investigate their methodological characteristics.

Methods

PubMed, Scopus, and Web of Science were searched to identify studies developing and/or evaluating ML/AI prognostic models of HAI prediction in adult ICUs. Data on study characteristics, data sources, HAI types, setting, and performance assessment were extracted and synthesized narratively.

Results

Out of 3930 unique screened records, 33 studies (2013-2025) were included, primarily from China (60.6%), United States (15.2%), and Europe (15.2%). Data sources were approximately half public repositories (e.g., MIMIC-III/IV, eICU) (45.5%), and half primary medical records, surveillance or cohort study data (54.5%), mostly from general/mixed ICUs (81.8%). Bloodstream infections (BSIs) (54.4%) and ventilator-associated/hospital-acquired pneumonias (21.2%) were the most common HAI outcomes. Most studies aimed to only develop ML/AI models (72.7%), and only 27.3% performed external evaluation. Five models per study were developed on average (range: 1-12), with tree-based methods being the most frequently used (66.7% Random Forests and 63.6% XGBoost). All studies reported assessment of model discrimination (Area Under the Curve), but only 12.1% assessed calibration.

Conclusions

Despite growing interest in ML/AI-based models for HAI prediction in the ICU, significant methodological gaps, including limited external evaluation, lack of calibration assessment, and over-reliance on a few public datasets, indicate potential overoptimism in model performance, limiting clinical applicability. Future research should shift from model proliferation to rigorous validation and assessment of model reliability across diverse clinical environments.

POSTER TOUR 15

Artificial intelligence in public health

Are time series foundation models the new frontier for operational epidemic forecasting in Europe?

ABSTRACT ID: 568

Stefania Fiandrino [1], ***Ana Parovic*** [2], ***Alessandra Urbinati*** [3], ***Sara Venturini*** [3], ***Nicolò Gozzi*** [4], ***Alessandro Vespignani*** [5]

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Background

Accurate epidemic forecasting supports public health decision-making, situational awareness, and resource allocation. Traditional statistical, mechanistic, and machine-learning approaches remain computationally demanding and limited in accuracy, partly due to the complexity of epidemic dynamics and data scarcity. Time series foundation models (TSFMs) are large-scale, pre-trained artificial intelligence models that have attracted growing interest for their strong capabilities of generalisation across diverse datasets without needing task-specific training. Yet, TSFMs have not been systematically benchmarked against established epidemic forecasting approaches, leaving their operational value an open question.

Methods

We prospectively evaluated six TSFMs for influenza-like illness (ILI) and acute respiratory infection (ARI) forecasting across 28 European countries during the 2025/26 season. TSFMs were benchmarked against models submitted to RespiCast, the European respiratory diseases forecasting hub, including its ensemble. Performance was assessed using the Weighted Interval Score (WIS) and Median Absolute Error (MAE).

Results

TimesFM (Google) and Chronos2 (Amazon) emerge as top-performers consistently ranking in the top third of all models across forecasting indicators and error metrics. Moirai2 (Salesforce), TimeGPT (Nixtla), and TabPFN-TS (PriorLabs) showed moderate performance, while Lag-Llama (open-source) ranked among the weakest models. The RespiCast ensemble remained the overall best model, though TimesFM and Chronos2 approached its accuracy. Interestingly, the ensemble's key advantage was robustness, with the fewest instances of substantially erroneous forecasts.

Conclusions

These results demonstrate that selected TSFMs can compete with established epidemic forecasting models, approaching ensemble performance in a large-scale operational setting for ILI and ARI forecasting, without fine-tuning and using only past seasons as context. Future work should explore fine-tuning and hybrid approaches to close the remaining gap with ensemble methods. Additionally, the best-performing TSFMs are developed by private companies, raising concerns around transparency, reproducibility, and long-term accessibility for public health use. This underscores the urgent need for open, community-driven, domain-specific TSFMs to ensure sustainable epidemic intelligence capacity in Europe.

POSTER TOUR 15

Artificial intelligence in public health

All hype and no help? Assessing readiness for AI within a UK public health institute field epidemiology service, January 2026

ABSTRACT ID: 635

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Background

Understanding how suitable current AI tools are, and their use, in supporting the delivery of key field epidemiology (FE) activities in England is limited. This study aimed to assess current readiness for the adoption of AI tools for FE activities in a UK public health institute.

Methods

In January 2026, we surveyed FE team leads to assess current AI use, strengths and weaknesses of AI tools and anticipated threats and opportunities to their use. Responses were measured on a likert scale and >70% agreement was described. A workshop explored facilitators and barriers to AI use, with discussion themes extracted.

Results

All team leads (n=10) responded and attended the workshop. Most respondents reported current AI tool use (70%); largely limited to chatbots i.e. Microsoft Copilot (organisationally approved) and ChatGPT for administrative tasks and code development. AI was never used for higher risk FE activities including generating outputs for incident response. Knowledge of available tools was lacking; known tools were deemed inadequate for current activities due to difficulties auditing the rationale behind AI recommendations and limited training. Barriers to wider adoption included concerns about deskilling epidemiologists, generating inaccurate outputs, and uncertainty around compliance with data protection standards. Respondents identified opportunities for AI to support code development/review, and document summarisation, thus reducing workload. Workshop discussions emphasised the need to preserve human expertise and judgement, improve understanding of the benefits of AI for FE, and establish clearer governance and transparency for AI use within the organisation.

Conclusions

Despite AI use enthusiasm, respondents reported significant concerns affecting readiness to adopt AI tools for FE activities. It was recognised that AI offers future potential to enhance - but not replace - epidemiological expertise but current tools do not adequately support team needs. A coordinated organisational strategy, grounded in well-defined use cases and training, will be essential for responsible adoption.

POSTER TOUR 15

Artificial intelligence in public health

Validation of locally deployed open-source LLMs for SARI detection in Spanish hospital records

ABSTRACT ID: 835

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Background

Hospital records contain large amounts of unstructured clinical information that could support infectious diseases surveillance. However, manual review is labour-intensive and prone to inter-observer variability. We aimed to validate locally deployable Large Language Models (LLMs) for Severe Acute Respiratory Infection (SARI) case identification from hospital medical text, to increase efficiency and consistency while meeting data protection requirements.

Methods

We evaluated a local pipeline based on four open-source LLMs ranging from 4 to 26 billion parameters, deployable on hardware with 16 GB VRAM. We created 100 synthetic Spanish-language medical records reflecting the structure, length and terminology commonly used in emergency room discharge reports at a pilot hospital, and complemented them with 100 published case reports with infectious diseases mentions. To address context-length and memory constraints, texts were split and processed through nested summarisation steps, followed by structured extraction in JSON format. Prompt-based extraction targeted SARI case identification along with key demographic, clinical and microbiological variables. No fine-tuning was performed. Performance was assessed against expert manual extraction using percentage agreement and F1-score, a metric that balances sensitivity and positive predictive value.

Results

Agreement with human reviewers increased with model size, reaching 92% overall concordance with the largest model (Gemma 4) compared with 70% for the smallest (MedGemma). The best model achieved an F1-score of 93% in classification of SARI as the main reason for hospital admission. Extraction performance was particularly strong for respiratory symptoms and virological testing, with the best-performing models achieving 98– 100% agreement. Compared with standard manual coding workflows, the pipeline reduced processing time by approximately 80%.

Conclusions

Locally deployed open-source LLMs showed near-human agreement in SARI case classification without fine-tuning. This approach could improve the efficiency, timeliness, consistency, and scalability of SARI surveillance, with a high degree of data protection. Next steps include local deployment and real-world validation at two pilot hospitals.

Late breakers (1)

Increasing Macrolide Resistance in Invasive Group A Streptococcal Infections: A Multiregional Surveillance Study in the Netherlands

ABSTRACT ID: 991

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Background

Macrolides are the first-choice prophylaxis for invasive group A streptococcal (iGAS) infections in the Netherlands and an important treatment alternative when beta-lactams are unsuitable. However, data on macrolide resistance in iGAS are limited. This study was prompted by practice-based signals of increasing macrolide resistance among iGAS isolates. We assessed temporal trends in macrolide resistance among notified cases.

Methods

We retrospectively included all notified iGAS cases between 1-1-2022 and 30-6-2026 to four Dutch public health services. Macrolide susceptibility was derived from recorded erythromycin, azithromycin, and clarithromycin susceptibility results. Temporal trends were assessed using the Cochran–Armitage test. Multivariable logistic regression was used to estimate the association between calendar year and resistance, adjusting for diagnostic group (Puerperal sepsis, Toxic shock, Necrotizing fasciitis, Other) and public health region. Interaction terms evaluated whether trends differed by region or diagnostic group.

Results

Among 888 notified cases, macrolide susceptibility was available for 547 (61.3%). Susceptibility-result availability increased from 58.8% to 80.0%. In total, 56 isolates (10.2%) were resistant. Resistance increased from 7.5% in 2022 to 20.8% in 2026 ($p < 0.001$). *Emm* type was known for 42, 14 (33.3%) were type 77.0 or 58. Calendar year remained associated with resistance after adjustment for diagnostic group and region (p=0.003). No regional differences in resistance levels or trends were observed. Resistance increased within puerperal sepsis and the “Other” category, but the year-by-diagnostic-group interaction was not significant (p=0.12).

Conclusions

The practice-based signal of increasing macrolide resistance among iGAS isolates was corroborated by surveillance data. Resistance increased over time and remained associated with calendar year after adjustment for diagnostic group and region. However, statistical power was insufficient to determine whether the trend was consistent across regions or diagnostic groups. These findings warrant further assessment to evaluate whether this signal extends beyond the participating public health regions and has potential implications for prophylaxis policy.

POSTER TOUR 16

Late breakers (1)

Moderate end-of-season influenza vaccine effectiveness in 2025/26, but measurable protection against drifted A(H3N2) in Bavaria, Germany

ABSTRACT ID: 964

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Background

Europe's 2025/26 influenza season began unusually early and was dominated by the antigenically drifted A(H3N2) subclade K, raising concerns about vaccine effectiveness (VE). Published 2025/26 estimates remain preliminary. We aimed to estimate end-of-season influenza VE for the 2023/24–2025/26 seasons in Bavaria.

Methods

Using data from the Bavarian Influenza and Corona Sentinel, we conducted a test-negative case-control study among primary-care patients with acute respiratory infection, during weeks 40–20 (early October to mid-May) of 2023/24–2025/26 seasons. Cases were RT-PCR-positive for influenza; controls tested negative. We estimated VE as (1–odds ratio)×100 and 95% confidence intervals (95%CI) using logistic regression, adjusting for age, sex, symptom onset week and chronic conditions. A subset of influenza A-positive specimens was sequenced each season.

Results

Among 3,953 cases and 14,028 controls, adjusted overall VE declined from 60% (95%CI:46%–70%) in 2023/24, 55% (95%CI:40%–66%) in 2024/25 to 30% (95%CI:9%–46%) in 2025/26. Among ≥60-year-olds, VE was 12% (95%CI:-39%–45%) in 2025/26. Of 1,185 positive specimens in 2025/26, 99% were influenza A; of those, 72% were A(H3N2), 23% A(H1N1)pdm09 and 5% were not subtyped. Of the 27% (320/1,178) sequenced influenza A-positive specimens in 2025/26, 74% (236/320) were A(H3N2) subclade K with VE being 38% (95%CI:15%–56%) against A(H3N2), and 17% (95%CI:-25%–47%) against A(H1N1)pdm09. VE against influenza B was 90%(95%CI:66%– 98%) in 2023/24, 75% (95%CI:59%–86%) in 2024/25, but no reliable estimate was possible in 2025/26 due to low influenza B circulation.

Conclusions

Across 2023/24–2025/26 seasons, influenza vaccination significantly reduced medically attended, laboratoryconfirmed influenza, with VE of 30%–60%. VE against the predominant subclade-K A(H3N2) virus in 2025/26 remained significant and higher than the overall VE, suggesting that the lower 2025/26 VE largely reflected the distribution of circulating (sub)types. Our findings highlight the importance of continued molecular surveillance and end-of-season VE estimates to inform public health communication and promote timely seasonal influenza vaccination amid emerging influenza subclades.

POSTER TOUR 16

Late breakers (1)

Hand, foot, and mouth disease remains above pre-pandemic incidence in Catalonia, Spain: paediatric primary care surveillance through August 2026

ABSTRACT ID: 1046

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Background

Long-term European primary care studies of paediatric enterovirus syndromes are scarce. We assessed whether hand, foot and mouth disease (HFMD) and herpangina returned to pre-pandemic levels during the 2025-2026 season.

Methods

We analysed ICD-10 diagnoses among children aged <5 years recorded in Catalan public primary care practices, from September 2014 to August 2026. The study was organised by academic year to capture autumn and spring waves, including declines during school holidays and subsequent rebounds. Incidence was calculated using only the population covered by this primary healthcare system. We compared 2025-2026 with 2024-2025 and the median of five pre-pandemic years (2014-2015 to 2018-2019), overall, by sex, and by age. Spearman correlations determined associations between preceding peaks and subsequent changes.

Results

In 2025-2026, 9,033 HFMD and 4,215 herpangina diagnoses were recorded, corresponding to 4,252 and 1,984 per 100,000 children. Both incidences declined from the previous academic year 2024-2025 (HFMD 12.4%; herpangina 11.0%). Nevertheless, HFMD incidence remained 42.8% above its pre-pandemic median for the fifth consecutive season, exceeding age-specific pre-pandemic medians by 45.6% at ages 1-2 years, 40.7% in infants <1 year, and 22.5% at ages 3-4 years. Meanwhile, herpangina was 7.4% below its pre-pandemic median. A modest male predominance persisted (54.5% of HFMD and 53.1% of herpangina). Autumn and spring HFMD weekly peaks were 21% and 44% above their respective pre-pandemic medians. In year-on-year comparisons of the same season peak, smaller preceding peaks were followed by larger increases, whereas larger peaks preceded smaller or negative changes with strong correlation coefficients (herpangina autumn/spring ρ=-0.81/-0.93; HFMD ρ=-0.93/-0.86).

Conclusions

Sustained HFMD excess despite a year-on-year decline continuing primary care burden, whereas herpangina has approached pre-pandemic baseline. This inverse peak-change pattern may reflect transient populationlevel immunity following larger waves and increased susceptibility after smaller waves. Continued syndromespecific surveillance and virological typing are needed to clarify these divergent trends.

POSTER TOUR 16

Late breakers (1)

Rapid late-summer resurgence in COVID-19 notifications with accelerated reinfections and a younger case profile, Castile and León, Spain, 2026

ABSTRACT ID: 1028

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Background

Late-summer COVID-19 resurgence can challenge surveillance and preparedness. We characterised an increase detected through regional mandatory surveillance in Castile and León, Spain, before the 2026 autumn vaccination campaign. These data became available after the 18 May 2026 abstract deadline.

Methods

We analysed confirmed COVID-19 notifications during epidemiological weeks 31–38 of 2026 (27 July–20 September), extracted on 23 September 2026, and compared them with the equivalent 2025 period (28 July–21 September). Reinfection required a positive polymerase chain reaction or rapid antigen test at least 90 days after a previous confirmed infection. Quasi-Poisson log-linear regression estimated weekly multiplicative changes and year-by-week interactions. Multivariable logistic regression assessed hospitalisation among reinfections, adjusting for continuous age and sex.

Results

We included 1,011 notifications in 2026 and 3,043 in 2025. Despite the lower 2026 total, weekly notifications increased rapidly from 23 in week 31 to 428 in week 38. The weekly multiplier was 1.55 (95% confidence interval (CI): 1.41–1.72) in 2026 compared with 1.08 (95% CI: 1.03–1.12) in 2025 (growth multiplier ratio: 1.45, 95% CI: 1.30–1.61). Median age was lower in 2026 (49.1 versus 60.7 years), while cases aged ≥65 years decreased from 44.8% to 34.6% (odds ratio: 0.65, 95% CI: 0.56–0.76). Reinfections increased sharply from 7 to 228 weekly cases (weekly multiplier: 1.68, 95% CI: 1.48–1.90; multiplier ratio vs 2025: 1.52, 95% CI: 1.33–1.74). Hospitalisation occurred in 12.3% (58/471) of reinfections with known status in 2026 versus 17.2% (274/1,597) in 2025. After adjusting for age and sex, reinfections showed no increased hospitalisation risk (adjusted odds ratio: 0.77, 95% CI: 0.56–1.07).

Conclusions

Mandatory surveillance identified a sharp late-summer acceleration in COVID-19 notifications and reinfections, accompanied by a younger case profile and no evidence of increased hospitalisation risk among reinfections. Year-round surveillance may support early warning and preparedness before autumn vaccination campaigns.

POSTER TOUR 16

Late breakers (1)

The live shingles vaccine and primary care antimicrobial prescribing in the UK: A retrospective population-based cohort study

ABSTRACT ID: 1010

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Background

Live vaccines have been observed to have off-target effects beyond their primary disease-specific protective effect. They may contribute to reduced antibiotic prescribing by preventing secondary infection, or through immune boosting effects. This is of particular relevance to strategies to address antimicrobial resistance (AMR), which focus on reducing antibiotic prescribing. We investigated the association between the live zoster vaccine for shingles (Zostavax) and antibiotic prescribing.

Methods

This is a retrospective cohort study performed in July 2026 using English primary care data from CPRD Aurum to compare the number of primary care antibiotic prescriptions in older adults who have and have not received the live zoster vaccine. An Andersen-Gill recurrent events analysis was used to estimate adjusted hazard ratios, including inverse probability of treatment propensity score weighting to reduce confounding.

Results

A total of 30,436 individuals born between 1943–1945 were observed for 59,944 person-years at risk (PYAR) between 2013 and 2019, yielding an unweighted event rate of 832 per 1,000 PYAR for vaccinated and 694 per 1,000 PYAR for unvaccinated participants. After weighting and adjusting for confounding variables including year of birth, gender, deprivation, baseline comorbidities, and receipt of the pneumococcal and influenza vaccines, live zoster vaccination was associated with a reduced hazard of antibiotic prescribing (HR 0.884, 95% CI 0.813–0.961). This finding was robust to multiple sensitivity analyses.

Conclusions

Live zoster vaccine receipt was associated with reduced antibiotic prescribing in older adults in English primary care, which was not explained by measurable confounding. The findings contribute to evidence supporting vaccination as a tool in AMR mitigation. This relationship, and whether such an association exists with the new recombinant vaccine, should be further explored using robust prospective studies, with potential implications for national immunisation policy.

Surveillance of food- and water-borne diseases

Genomic surveillance for Salmonella spp. and Shigella spp. in Belgium in the era of multiplex PCR diagnostics

ABSTRACT ID: 617

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Background

Culture-independent diagnostic tests (CIDT), notably multiplex PCR panels, are increasingly used for the diagnosis of gastrointestinal infections. However, reduced availability of bacterial isolates may compromise surveillance and genomic characterisation. We assessed the coverage of the Belgian National Reference Centre (NRC) for *Salmonella* spp. and *Shigella* spp. and evaluated current and anticipated diagnostic practices in clinical microbiology laboratories (CML).

Methods

A laboratory survey was conducted in 2025 among Belgian CML. We collected information on the diagnostic methods used and number of cases diagnosed. Reimbursement data for stool cultures was obtained from the National Institute for Health and Disability Insurance. The total number of cases was estimated using multiple imputation based on laboratory size and positivity rates. NRC coverage was estimated by comparing the number of cases reported by the NRC with the estimated total number of cases.

Results

88% (91/103) of CML responded to the survey. Although 94% of CML reported culture as their primary diagnostic method, 25% reported use of CIDT. The estimated national NRC coverage was 80% (77%-82%) for *Salmonella* spp. and 74% (68%-78%) for *Shigella* spp. For both pathogens, coverage varied across regions with lower estimates in Wallonia. Most laboratories currently relying on culture plan to adopt CIDT once reimbursement is introduced, with many considering discontinuation of routine reflex culture.

Conclusions

NRC surveillance coverage for *Salmonella* spp. and *Shigella* spp. in Belgium remains high. However, the use of CIDT for the diagnosis in CML is increasing and is expected to further expand following changes in reimbursement. This transition is likely to impact isolate availability and genomic NRC surveillance. Continued monitoring of diagnostic practices and adaptation of surveillance strategies will be essential to sustain high-quality public health surveillance aligned with epidemiological priorities and available resources.

POSTER TOUR 17

Surveillance of food- and water-borne diseases

Drivers of Rising Legionella Notifications in Southern Finland, 2020–2025: disentangling Diagnostic, Climatic, and Seasonal Influences

ABSTRACT ID: 659

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Background

Since 2020, case notifications of *Legionella spp*. increased in the Finnish National Infectious Disease Registry (NIDR). It is unclear whether this reflects a change in true incidence or increased testing activity. Furthermore, climate-related fluctuations in incidences are known from southern Europe but not Nordic settings. Thus, we assessed the impact of increased diagnostics and climate factors as drivers of rising cases in Southern Finland, 2020–2025.

Methods

Weekly NIDR counts of non-travel related cases (symptomatic, laboratory-confirmed) between 2020-2025 (~ 312 weeks) in the Uusimaa region (South Finland) were analyzed using Poisson regression . Monthly laboratory testing data and weekly climate variables (precipitation, mean and minimum temperature) were linked and included as covariates into the model (null model). Annual harmonic terms accounted for known seasonal patterns (full model). Model fit was assessed using AICs. Interaction terms between temperature and precipitation were tested for synergistic effects.

Results

In the null model, minimum (hazard ratio (HR) =1.05; Confidence interval (CI)=1.01-1.08) and mean temperature (HR=1.04; CI =1.02-1.08) positively associated with case counts (=higher incidence during warmer periods). In the full model (AIC confirming a better fit), both temperature variables showed inverse associations with case counts. Testing volume associated with case counts (HR=1.01; CI =1.01-1.02) while seasonality term indicated lower case counts during winter (HR=0.30, CI =0.13-0.68). No interaction term proved significant. Precipitation and lagged climate variables showed no association.

Conclusions

Rising *Legionella* notifications in Southern Finland were strongly influenced by increased testing, likely reflecting heightened clinical awareness. Our analysis also confirmed seasonal patterns, indicating that increasing mean temperatures may prolong seasonal risk periods. Interestingly, after seasonal adjustment, higher case counts at lower temperatures were observed, indicating that risk in Nordic settings may extend into colder months. Overall, integration of laboratory testing data into routine surveillance would strengthen trend interpretation and reduce the need for resource-intensive ad hoc assessments.

POSTER TOUR 17

Surveillance of food- and water-borne diseases

Whole-Genome Sequencing (WGS) Uncovers Multiple Concurrent Salmonella Transmission Pathways and Recognizes Greater Disease Spread Overlooked by Conventional Surveillance, Moldova, 2025

ABSTRACT ID: 581

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Background

WGS is highly effective at distinguishing independent clusters in foodborne disease outbreaks worldwide. We examined how the introduction of WGS in Moldova enhanced understanding of foodborne diseases.

Methods

Salmonella isolates from stool cultures collected between July and September 2025 from children under 17 admitted to six major children's hospitals in Chisinau and three districts underwent WGS at four major laboratories. Genomic clusters were defined as *Salmonella* isolates with ≤2 high-quality single nucleotide polymorphism (hqSNP) differences. Using a standardized questionnaire, patients were interviewed on food consumption and other exposures. Genomic findings are reported alongside epidemiological data.

Results

WGS revealed four distinct genomic clusters comprising 31 *S. enteritidis* cases among 52 confirmed *S. enterica* patients; 21 were sporadic (unlinked) cases. Traditional investigations alone failed to establish epidemiological links among 24 of the 31 clustered cases, except for 7 individuals from the same household. In one cluster, 6/14 (43%) cases were reported from three districts. The epidemic curves of all four clusters overlapped in July, with individual clusters spanning 3 weeks to 3 months, suggesting a continuous or intermittent source or possible person-to person transmission. Within clusters, the difference was 1–2 SNPs, while between clusters it exceeded 5 SNPs, suggesting different sources of contamination. Twenty-two (71%) cases reported consuming chicken and eggs <1 week before onset. Chicken and eggs purchased from common retail outlets came from nationwide suppliers.

Conclusions

WGS data supported multiple concurrent *Salmonella* outbreaks in Moldova in 2025, which could not have been determined with epidemiologic data alone. While the source of infection in each of the clusters could not be determined, WGS showed that cases were connected across districts, potentially suggesting a sustained widespread event likely tied to shared contaminated food sources from nationwide suppliers.

Surveillance of food- and water-borne diseases

Genomic surveillance of invasive non-typhoidal Salmonella (iNTS) in Belgium, 2014-2025: Hidden danger of uncommon serovars

ABSTRACT ID: 732

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Background

Non-typhoidal *Salmonella spp.* can invade the bloodstream and cause severe infections, requiring antibiotic treatment. In Belgium, an unusually high proportion of iNTS infections exhibit ciprofloxacin resistance, representing an increasing public health concern. This analysis aimed to identify circulating serovars and their antimicrobial resistance (AMR) profiles contributing most to iNTS disease burden.

Methods

We analysed national surveillance data from the National Reference Centre for *Salmonella* & *Shigella* during 2014-2025. The trend in incidence of invasive infections was estimated with a Poisson regression model. We assessed heterogeneity in invasiveness among serovars in ≥50 isolates with a chi-square test, followed by residual analysis, to identify the most relevant serovars. Patient demographics and frequencies of resistance in antibiotic susceptibility data were calculated. AMR genes were identified using AMRFinder on whole genome sequencing (WGS) data.

Results

A total of 1050 iNTS cases (3.5% of salmonellosis cases, 2014-2025) were included. Incidence increased significantly over the study period (IRR 2.05, 95% CI:1.69-2.50). Variability in invasiveness was observed among the 39 most prevalent serovars. The most relevant serovars were *S. Dublin* and *S. Chester* (z-scores 43.3, 14.9, respectively). With proportions of 55% and 17% invasive isolates, accounting for 13% and 6% of all iNTS infections, with distinct demographic profiles. Median age was 73 years (IQR 63-83) for *S. Dublin* infections versus 11 years (IQR 4-21) for *S. Chester* infections. Ciprofloxacin resistance among *S. Chester* isolates was 72% (34% single, 38% MDR). Genetic markers indicative of the progressive acquisition of fluoroquinolone resistance included *qnrB19* and multiple mutations in *gyrA*.

Conclusions

The increasing proportion iNTS infections in Belgium, together with rising ciprofloxacin resistance among *S. Chester* isolates, underscores the importance of serovar-specific interventions. The disproportionate contribution of *S. Dublin* and *S. Chester* to invasive disease supports strengthened targeted surveillance, particularly of AMR trends to inform treatment guidelines, and mandatory reporting for these serovars.

POSTER TOUR 17

Surveillance of food- and water-borne diseases

Advancing Legionella pneumophila genomic surveillance with a high-resolution cg/wgMLST schema for outbreak detection and investigation

ABSTRACT ID: 589

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Background

Legionnaires' disease represents a major public health concern worldwide, mainly caused by *Legionella pneumophila*. Although sequence-based typing (SBT) has long been used for *L. pneumophila* investigations, genome-scale typing approaches, namely core-genome (cg) and whole-genome (wg) multilocus sequence typing (MLST), provide higher discriminatory power. In this study, we established the *Legionella* International Typing (LIT) workgroup aiming to develop, evaluate, and disseminate a novel cgMLST schema with enhanced wgMLST resolution for *L. pneumophila* investigations.

Methods

Using >9000 genome assemblies representative of the species diversity, we constructed the LIT cg/wgMLST schema with chewBBACA, and applied a multi-step refinement workflow, considering loci prevalence, diversity and presence/absence across the species tree, to select the final loci set. We compared the performance of the LIT cgMLST schema with the existing cgMLST 1521-loci schema and assessed its congruence with SBT.

Results

The LIT schema includes 2009 core loci forming the static cgMLST for routine genomic surveillance, plus 2698 accessory loci for in-depth investigation. The LIT cgMLST maintains moderate agreement with SBT and presents high clustering congruence with the 1521-loci schema, while providing increased resolution. Analysis of all cgMLST clusters (n=947) at potential outbreak level, including clusters with epidemiologically related isolates, showcased that cluster-specific dynamic wgMLST analysis extending the cgMLST with shared accessory loci improves confidence in outbreak investigation and source identification.

Conclusions

The LIT schema is expected to facilitate harmonized genomic surveillance of Legionnaires' disease at local and global levels. The schema and resources for local implementation are available on Zenodo (https://doi.org/10.5281/zenodo.17871973).

POSTER TOUR 17

Surveillance of food- and water-borne diseases

Evaluation of the surveillance system for campylobacteriosis, Portugal, 2020-2024: timeliness and external completeness

ABSTRACT ID: 245

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Background

Campylobacteriosis is the leading cause of bacterial gastroenteritis in Europe. In Portugal campylobacteriosis incidence is rising and effective surveillance is essential for timely public health action. The Portuguese surveillance system (SINAVE) encompasses separate pathways for clinical notifications by clinicians and laboratory notifications by laboratories. We evaluated SINAVE for campylobacteriosis, focusing on timeliness and external completeness through concordance between clinical and laboratory notifications.

Methods

We analysed clinical and laboratory notifications of campylobacteriosis in Portugal between 01/01/2020 and 31/12/2024. Timeliness was assessed across key surveillance steps using medians and interquartile ranges (IQR). External completeness was assessed through capture-recapture, matching clinical and laboratory notifications by unique national health identifier and considering a 30-day window to account for multiple infections per person. Total case numbers were estimated using Chao capture–recapture estimator.

Results

We analysed 5299 clinical and 6504 laboratory notifications. For timeliness, 29.4% clinical notifications were made within 24 hours of diagnosis and 52.5% positive results were notified within 24h by laboratories. Median intervals were 5 days (IQR:3–9) from symptom onset to diagnosis, 3.6 days (IQR:0.7–9.6) between diagnosis and clinical notification, and 0 days (IQR:-2–0) between diagnosis and laboratory result. For external completeness, we identified 8535 cases, 2899 (34.0%) with both clinical and laboratory notifications, 2223 (26.0%) with clinical notification only, and 3413 (40.0%) with only laboratory notification. Estimated total case numbers were 9843 using Chao's lower-bound estimator (95%CI: 9712–9974).

Conclusions

Campylobacteriosis surveillance and public health intervention in Portugal may be constrained by delayed clinical notification. The gap between observed notifications and capture–recapture estimates suggests substantial under-ascertainment. Improving compliance with statutory reporting timeliness, strengthening interoperability between reporting paths (clinical and laboratory), and routinely monitoring surveillance performance could improve case ascertainment and the public health usefulness of the system for identifying and controlling sources of infection.

POSTER TOUR 17

Surveillance of food- and water-borne diseases

Cryptosporidiosis reaches unprecedented levels in France during the summer of 2026: is climate warming playing a role?

ABSTRACT ID: 1020

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Background

In France, the National Reference Centre (NRC) for Cryptosporidiosis, Microsporidia and other digestive protozoa monitors cases through a network of public and private laboratories, which has shown a predominance of *Cryptosporidium parvum*, primarily linked to environmental contamination. In June-July 2026, an unprecedented number of diagnosed cryptosporidiosis cases and cluster detections were recorded, coinciding with record-breaking temperatures across France. This study aimed to assess the potential relationship between global meteorological conditions and cryptosporidiosis incidence.

Methods

Since 2025, the monthly number of *Cryptosporidium* tests performed and positive results have been recorded by nine high-activity laboratories within the NRC network. Correlation coefficients were calculated between the monthly regional proportion of positive tests and temperature (current month, previous month, two-month average, anomalies), sunshine duration, and rainfall (monthly and two-month cumulative totals).

Results

Among 256,225 analyses performed since 2025, a record number of cases was observed in July 2026: 378/17,795 (2.12%), 1.75-fold higher than in July 2025 ($p < 0.001$). A concomitant record of six clusters was identified by the NRC between June and July 2026. Test positivity varied significantly by region and season, with every region reaching its historic peak in July 2026 (Île-de-France 1.71%; Alsace 1.74%; Normandie 3.53%; Bretagne 5.73%). The strongest positive correlations were observed with current- or previous-month average temperature ($r = 0.70$-0.85). All clusters identified in 2025 and 2026 were attributable to *C. parvum* and occurred mainly between mid-April and July each year. A foodborne origin was suspected for most of them, especially raw-milk cheese and salads.

Conclusions

These findings suggest that, in settings with substantial environmental contamination by *C. parvum*, warmer temperatures combine with summer dietary habits may contribute to rising cryptosporidiosis incidence. While consistent with a role for climate change, foodborne Cryptosporidiosis outbreaks should be closely monitored, especially during summer.

POSTER TOUR 18

Surveillance of COVID-19 and influenza

Investigating post-pandemic regime shifts in influenza epidemiological patterns: a multinational analysis

ABSTRACT ID: 86

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Background

The COVID-19 pandemic substantially suppressed global influenza circulation during 2020–2021,raising questions about whether the virus has since re-established its pre-pandemic epidemiological patterns or transitioned into a structurally different regime. Identifying such regime shifts is critical for recalibrating surveillance thresholds and informing epidemic preparedness planning.

Methods

Weekly laboratory-confirmed influenza data from the WHO FluNet surveillance system were analysed for 129 countries,covering all available epidemiological seasons up to 2023–2024.Countries were required to have at least eight seasons of pre-2020 data with adequate weekly coverage.Three season-level indicators were computed per country: peak timing(epidemiological week of maximum activity),epidemic duration(consecutive weeks exceeding a pre-2020 country-specific baseline defined as mean plus three standard deviations),and peak intensity(maximum weekly exceedance above baseline). Regime shift detection was performed per country and per indicator using the PELT change-point detection algorithm,with a minimum segment length of three seasons and a conservative penalty(pen = 3).A country was classified as having undergone a regime shift if a statistically significant change point was detected in at least one indicator.

Results

Detectable regime shifts were identified in only 2 of 129 countries (1.6%):Canada, where all three indicators shifted from 2022 onwards, and Australia, where peak timing and intensity shifted from 2023. No consistent cross-country pattern emerged. In the remaining 127 countries (98.4%), no statistically significant abrupt or persistent changes were detected in any indicator.

Conclusions

The near-absence of detected shifts across a geographically diverse set of countries is itself informative: it suggests that post-pandemic influenza has largely returned to pre-existing seasonal behaviour rather than settling into a new epidemiological state. The country-specific exceptions highlight heterogeneity in post-pandemic influenza dynamics and underscore the value of multinational, methodologically rigorous surveillance for distinguishing transient disruptions from genuine long-term transitions.

Surveillance of COVID-19 and influenza

Factors associated with undertaking community respiratory testing amongst symptomatic FluSurvey participants in England, 2024-2025

ABSTRACT ID: 738

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Background

Current community respiratory testing behaviour in England is poorly understood, particularly as national laboratory surveillance only includes people seeking healthcare. FluSurvey, a community-based surveillance system, recruits citizen volunteers through email/social media/blogs/word-of-mouth, and contributes to England's respiratory virus surveillance. Participants self-report symptoms and symptomatic testing in weekly surveys to understand trends in respiratory illness irrespective of healthcare attendance. This study aimed to identify factors associated with undertaking respiratory testing in the community when symptomatic with acute respiratory illness (ARI; sudden onset of cough/sore throat/shortness of breath and/or coryza), to inform surveillance data interpretation and future guidance.

Methods

This cohort study included ARI episodes reported between November 2024-April 2025 by participants in England. Nine explanatory factors were selected following literature review/expert discussion: fever, changing daily routine due to illness, medication-treated comorbidities, COVID-19/influenza vaccination, contact with community healthcare, age, sex, education, and urban/rural residence. Multivariable logistic regression with generalised estimating equations was used to estimate adjusted odds ratios, accounting for clustering from repeated ARI episodes. A directed acyclic graph identified theory-informed confounders for each model.

Results

874 participants reported 1384 ARI episodes; 37% experienced more than one ARI episode in the season. Respiratory testing occurred in 232 (17%) episodes. Factors associated with testing were: fever (aOR=4.04; 95%CI 2.94-5.55, p<0.001), impact on daily routine (aOR=5.14; 95%CI 3.47-7.63, p<0.001), COVID-19/influenza vaccination (aOR=1.97; 95%CI 1.27-3.07, p=0.003), and contact with community medical services (aOR=3.34; 95%CI 2.19- 5.09, p<0.001).

Conclusions

Community respiratory testing when symptomatic with ARI is currently low. Vaccination, and illness disrupting daily routines, causing fever, and requiring contact with community health-care, were associated with testing. These results contextualise national respiratory surveillance data and highlight areas for interventions to increase testing. This is relevant for future health emergencies where milder illness presentations may reduce healthcare-seeking and testing, and when interpretating vaccine-effectiveness studies given the associations of vaccination with testing behaviour.

POSTER TOUR 18

Surveillance of COVID-19 and influenza

Influenza in Malta (2017–2025): Post-Pandemic Shifts in Incidence and Seasonality

ABSTRACT ID: 441

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Background

Influenza in Malta traditionally peaked in winter which was consistent with the broader European pattern. However, unusual summer surges emerged in 2024 and 2025, raising questions about whether the island's influenza seasonality has fundamentally shifted in the post-COVID era. We characterised the epidemiology of laboratory-confirmed influenza in Malta from 2017 to 2025, with a focus on changes in incidence and seasonality in the post-COVID era.

Methods

We retrospectively analysed all laboratory-confirmed influenza cases and testing rates from January 2017 to December 2025. The relationship between testing rates and incidence rates was assessed using Pearson's correlation. To evaluate seasonality and long-term trends we applied and compared time series models (Negative binomial regression with harmonic terms and ARIMA with log-transformed response).

Results

We identified 9,642 cases from 210,564 tests. Incidence rose by 397%, significantly outpacing the 83% increase in testing volume (r=0.80, p=0.009). Negative binomial regression captured overdispersion and trend (IRR 1.0020; 95% CI 1.0012-1.0028), with ARIMA preferred for forecasting showing no evidence of autocorrelation (Ljung-Box x^2=27.07, p=0.057) with both models showing increasing trend. Spectral analysis confirmed a dominant annual cycle (51 weeks) and an emergent semi-annual cycle (26 weeks) which became evident post-COVID (2024–2025). Pre-pandemic activity was exclusively winter-dominant, however post-pandemic a pronounced summer peak emerged in two consecutive years, with influenza A accounting for 98.7% of summer cases with A(H1N1)pdm09 the predominant subtype.

Conclusions

Influenza in Malta has transitioned from a winter burden to a year-round challenge characterised by a dual-peak cycle and a post-pandemic surge. This may reflect immunity debt, resulting in suppression of influenza circulation and reduced population-level immunity, leaving a larger susceptible pool upon removal of mitigation measures combined with increased tourist influx and mass gatherings during summer months. Alongside emerging A(H1N1)pdm09 activity and post-COVID temporal complexity, these findings may warrant a review of vaccination timing and surveillance strategies.

POSTER TOUR 18

Surveillance of COVID-19 and influenza

Severe Acute Respiratory Infection Surveillance in North Macedonia, 2023–2025: Risk Factors for RSV Infection, Influenza Infection and ICU admission in Children

ABSTRACT ID: 823

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Background

In North Macedonia, the burden of severe acute respiratory infection (SARI) in children remains insufficiently understood. We evaluated SARI data in North Macedonia over two consecutive seasons to identify risk factors associated with SARI associated with specific viruses and SARI that led to ICU admission among children aged 0–4 years old.

Methods

In two hospitals, hospitalized patients who met the WHO SARI case definition were systematically enrolled, staff administered a brief questionnaire to all patients and collected nasopharyngeal swabs, which were tested for Influenza A, Influenza B, SARS-CoV-2, and RSV. Descriptive and logistic regression analyses were performed for cases hospitalized during October–May 2023/2024 and 2024/2025.

Results

We enrolled 583 SARI patients aged 0-4 years old, of which 314 (53,9%) were infants. Overall, 22 (3.8%) cases were admitted to ICU. Mean hospitalization duration was 8±4 days. Comorbidities were reported in 131 (22.5%) children. In all, 195 (33.4%) had RSV, 56 (9.6%) had Influenza A, 21 (3.6%) had Influenza B, 9 (1.5%) had SARS-CoV-2; and three patients (0,5%) had co-infections. RSV-positive children had higher odds of ICU admission compared with children without a detected pathogen (OR=2.7; 95%CI=1.1–6.9). Children with comorbidities were more likely to have RSV infection (OR=4.8; 95%CI=3.2–7.3). Children <2 years old (OR=5.7; 95%CI=3.4-10.3) were more likely to have RSV, while children aged ≥2 (OR=2.6; 95%CI=1.6-4.2) had higher odds of being infected with Influenza. Children aged <1 had higher probability of RSV infection compared to children aged 3-4 (OR=2.4; 95%CI=1.1-6.2).

Conclusions

RSV accounted for over one-third of SARI hospitalizations of children aged 0-4 years. Younger infants and those with comorbidities were more likely to have RSV-associated SARI, and RSV-positive SARI patients were more likely to get admitted to the ICU. These findings support consideration of the introduction of RSV preventive interventions, including maternal vaccination and monoclonal antibodies.

POSTER TOUR 18

Surveillance of COVID-19 and influenza

Wastewater-based surveillance for SARS-CoV-2 across six European countries: system heterogeneity, country use-cases and implications for comparison.

ABSTRACT ID: 608

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Background

Wastewater-based surveillance (WBS) is increasingly used across EU/EEA countries to complement traditional respiratory virus surveillance- supporting the monitoring of SARS-CoV-2 circulation, forecasting and trend analysis. Understanding the characteristics of established systems is essential for interpretation and potential cross-country data use. This project aimed to describe differences in methodologies and reporting practices to consider limitations in the comparability and the transferability of analytical approaches.

Methods

We identified key characteristics and changes to methodologies of SARS-CoV-2 WBS systems across six countries (Belgium, Denmark, France, Germany, Luxembourg and the Netherlands), between October 2023- October 2025. We reviewed publicly available information and consulted with country representatives on system characteristics and SARS-CoV-2 WBS data use-cases. Descriptive summaries were developed to identify considerations for cross-country interpretation.

Results

Substantial heterogeneity was observed across systems and countries reported changes in their methods over this window. Measurements are reported using different units - two report genome copies (gc) per litre (gc/L), two report gc per population equivalent (e.g. gc/100,000 persons/day), one reports gc relative to mg of ammoniacal nitrogen (gc/mg N) and one RNA copies relative to faecal matter (RNA copies/PMMoV copies). Normalisation approaches differ (four out of six countries normalise using flow rate), as do sampling frequencies (1-4 times per week) and population coverage (25-99.6%). The use of WBS data within national surveillance systems varies by country.

Conclusions

WBS systems for SARS-CoV-2 in the EU/EEA are methodologically diverse, reflecting national contexts, funding availability and use-case in SARS-CoV-2 surveillance. While the harmonisation of analytical methods across EU/EEA is unlikely in the short term, analytical approaches need to be validated or tested to confirm whether it is possible to compare data despite these heterogeneities. Actions should focus on country-specific interpretation of WBS data, supporting trend-based analysis, and sharing methods to improve the use of WBS signals across the EU/EEA.

POSTER TOUR 18

Surveillance of COVID-19 and influenza

Influenza-like illness defined by clinical diagnostic coding: Positive predictive value for influenza and COVID-19 post-pandemic

ABSTRACT ID: 451

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Background

Influenza like illness (ILI) GP consultations are an internationally recognised indicator of influenza activity. However, the COVID 19 pandemic introduced a new respiratory pathogen with overlapping ILI symptoms, potentially reducing the sensitivity of the ILI indicator by diluting consultations with COVID-19 cases and affecting observed post-pandemic ILI trends. This study assesses the positive predictive value (PPV) of ILI consultations defined using clinical diagnostic codes for influenza and COVID 19 laboratory-confirmed test data in Scotland.

Methods

ILI consultations from January 2023 to May 2026 were identified based on the presence of clinical diagnostic codes in the consultation record. Consultations were linked to individual laboratory testing records, when multiplex tests for influenza and COVID-19 were performed in the 28 days following consultation. Tests for surveillance (rather than for clinical diagnostic) purposes were excluded. PPV was calculated separately for influenza and COVID-19 as the proportion of positive results among tested ILI consultations. A secondary analysis was repeated limited to April-October 2023, when COVID-19 rates were considerably higher than influenza.

Results

Among 5,995 ILI consultations, 72.5% (95% CI: 71.3–73.6) were positive for influenza, while 2.6% (95% CI: 2.2– 3.0) were positive for COVID-19. During the April-October 2023 period, among 174 ILI consultations, 21.8% (95% CI: 16.1–28.9) were positive for influenza, while 9.2% (95% CI: 5.5–14.8) were positive for COVID-19.

Conclusions

PPV of ILI was high for influenza and low for COVID-19 among consultations with subsequent multiplex testing. PPV increased for COVID-19 during the April-October 2023 wave. This suggests that, in Scotland, post-pandemic ILI trends remain a valid and comparable measure of historical and current influenza activity, but caution is required during periods of significant non-influenza respiratory pathogen circulation compared to influenza, and on-going validation may be warranted at such times.

POSTER TOUR 18

Surveillance of COVID-19 and influenza

Comparison of Belgian COVID-19 mortality between epidemiological surveillance and death certificates for the years 2020, 2021 and 2022

ABSTRACT ID: 805

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Background

This study aims to compare Belgian COVID-19 mortality data collected through epidemiological surveillance from hospitals, long-term care facilities (LTCF), and general practitioners with the mortality data obtained from death certificates, which have a 3-year delay.

Methods

Via a one-to-one linkage, a match-mismatch analysis was conducted between the epidemiological surveillance of COVID-19 mortality (SURV) and death certificates (COD) for the years 2020, 2021, and 2022. The impact of factors such as region, place of death, case classification (U07.1 and U07.2 as underlying cause of death [UCOD]), and epidemic wave was analyzed.

Results

Over the period 2020-2022, SURV (33,346) identified 86% of COVID-19-associated deaths recorded in COD (38,606). Coverage declined over time with SURV, from 90% in 2020 (19,801 vs 22,015) to 85% in 2021 (8,561 vs 10,052) and 76% in 2022 (4,984 vs 6,539). Coverage was high for deaths reported through hospitals (98%) and LTCF (80%), but remained very low for deaths occurring at home (3%). Most SURV records corresponded to deaths with COVID-19 coded as the underlying cause of death (UCOD) in COD (81.4%), and that a large proportion of COVID-19 deaths recorded in COD were also captured in SURV (70.3%). This decrease can be explained by diagnostic uncertainty, and by reduced participation in LTCF surveillance. Among the 5,307 deaths collected via SURV during 2020-2022 but not labeled with COVID-19 as UCOD in COD, the most frequently reported UCODs in COD were other ill-defined and unspecified causes (5.1%), pneumonia due to an unspecified organism (5.1%), heart failure (4.1%), malignant neoplasm of bronchus and lung (3.9%), unspecified dementia (3.8%), and COPD (3.3%).

Conclusions

The quality of SURV over the period 2020-2022 remained generally high, reflecting healthcare professionals' commitment to real-time COVID-19 mortality monitoring. However, there is still room for improvement in refining surveillance strategies for future pandemics.

POSTER TOUR 19

Vaccine-preventable diseases: evidence to practice

Effectiveness of nirsevimab against hospitalisation with laboratory-confirmed respiratory syncytial virus in children aged <24 months, European multicentre study, September 2025—March 2026

ABSTRACT ID: 460

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Background

Respiratory syncytial virus (RSV) is a leading cause of infant hospitalisation. Nirsevimab, a long-acting monoclonal antibody, was authorised in the European Union (EU) in 2022 to protect young children against severe RSV infection. We measured nirsevimab interim immunisation effectiveness (IE) against laboratory-confirmed RSV hospitalisation among eligible children aged <24 months during the 2025/26 season.

Methods

In a test-negative case-control study across 75 hospitals in five EU countries, we included children eligible for immunisation and presenting with severe acute respiratory infection (hospitalised ≥24 hrs with at least one symptom: fever, cough or shortness of breath). Cases were RT-PCR-positive for RSV; controls were negative. Immunised children were those receiving nirsevimab after the 2025/26 campaign start; unimmunised children did not receive any monoclonal antibody product. We excluded children developing symptoms 0–7 days post-immunisation to account for incubation period. We estimated IE by time since immunisation and age group using logistic regression adjusted for site, onset date, age (months), sex, and underlying conditions.

Results

We included 449 cases and 803 controls during week 36/2025–week 12/2026. Most had no underlying condition (423 (94%) cases, 730 (91%) controls) and were aged <6 months (331 (74%) cases, 579 (72%) controls); 216 (48%) cases, 517 (64%) controls were immunised. Overall IE was 78% (95%CI: 70–84%); 86% (95%CI: 77–92%) at 8– 29 days post-immunisation; 77% (95%CI: 67–84) at 30–89 days; 57% (95%CI: 33–73%) at 90–181 days. Among children <6 months, IE was 80% (95%CI: 72–86); 72% (95%CI: 51–84) in children 6–23 months.

Conclusions

Interim 2025/26 IE estimates indicate good protection of nirsevimab against laboratory-confirmed RSV hospitalisation among eligible children; high within 29 days, moderate ≥90 days post-immunisation. Estimates will be updated with complete season data, allowing increased sample size for ≥90 days post-immunisation analysis, particularly important in this late RSV season.

POSTER TOUR 19

Vaccine-preventable diseases: evidence to practice

Vaccine efficacy and safety of the adjuvanted herpes zoster subunit vaccine in immunocompromised adults aged 18-49 years: a systematic review to inform a German vaccination recommendation

ABSTRACT ID: 335

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Background

An estimated 300-400,000 people in Germany develop herpes zoster (HZ) annually, causing a significant health burden, including acute pain, hospitalisations and postherpetic neuralgia (PHN). Since 2018, the German Standing Committee on Vaccination (STIKO) has recommended the adjuvanted recombinant HZ vaccine for all adults aged ≥60 and for adults aged ≥50 at increased risk of HZ due to immunosuppression. In 2020, the European Medicines Agency extended the indication to at-risk adults aged ≥18. This study assessed whether the evidence base supports extending the STIKO recommendation to at-risk adults aged ≥18.

Methods

We updated a previous systematic review (October 2012 - April 2021) by searching Embase, MEDLINE, and Global Health (OVID) for English-language studies published between January 2021 and November 2024. We included clinical trials in immunocompromised adults aged ≥18. Outcomes were confirmed HZ, PHN, HZ-related complications, hospitalisation, and safety outcomes. Pooled risk ratios were estimated using a random-effects model and converted to vaccine efficacy (VE). Evidence certainty was assessed using GRADE.

Results

Of 1,793 studies identified, eight were included; three reported VE and seven reported safety outcomes. Pooled VE against confirmed HZ was 70% (95% CI: 40-85%). One trial reported VE of 89% (95% CI: 22–100%) against PHN, 78% (95% CI: 19–96%) against complications, and 85% (95% CI: 32–97%) against hospitalisation. Reactogenicity was high but transient. Serious adverse were comparable across vaccine and placebo groups. Evidence certainty was moderate for HZ and safety and low for PHN, complications and hospitalisation.

Conclusions

The vaccine was efficacious and safe in immunocompromised populations. Based on a comprehensive evaluation, including this review, STIKO in 2025 broadened the HZ vaccination recommendation to persons aged ≥18 years with increased HZ risk. These findings may inform vaccination recommendations in other countries. Supporting uptake will be essential to translate evidence into public health benefit.

Vaccine-preventable diseases: evidence to practice

Factors associated with absence of an identified epidemiological link among measles cases in an elimination setting: implications for case and contact investigation, Portugal, 2015-2025

ABSTRACT ID: 489

Raquel Eusébio [1], ***Inês Machado Loureiro*** [2], ***Margarida Vieira*** [3], ***Ana Mendes*** [3], ***Paula Vasconcelos*** [4], ***Pedro Pinto Leite*** [5], ***Rui Pedro Leitao*** [4], ***Vasco Ricoca Peixoto*** [4]

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Background

Portugal has sustained measles elimination since 2015, but global resurgence increases reintroduction risk. Absence of identified epidemiological links with a specific source case may reflect unrecognised transmission and hinder contact tracing. We aimed to identify factors associated with absence of an identified epidemiological link, regardless of later virologic link identification, to inform improvements in case investigation.

Methods

We conducted a retrospective cross-sectional study including non-imported laboratory-confirmed measles cases notified to Portugal's national surveillance system (SINAVE) during 2015-2025. The outcome was absence of an epidemiological link, defined as no identified contact with a confirmed or probable measles case 7-18 days before symptom-onset. Variables included age, sex, country of birth, measles vaccination status (≥1dose), health-care worker status, notifying healthcare setting, notification delay (symptom onset to notification) and recent national measles case load. We calculated crude prevalence ratios (PR) with 95% confidence intervals (95%CI).

Results

Among 228 cases, 79 (35%) had no identified epidemiological link. Absence of an identified link with a specific source case was associated with notification in a private healthcare institution (AR:82%vs.32%; PR:2.5, 95%CI:1.8-3.5), being unvaccinated (AR:59%vs.25%; PR:2.3, 95%CI:1.7-3.3), being born outside Portugal (AR:56%vs.31%; PR:1.8, 95%CI:1.3-2.6), being 40 years or older (AR:53%vs.31%; PR:1.7, 95%CI:1.2-2.5), and notification delay above the median (AR:44%vs.29%; PR:1.5, 95%CI:1.1-2.2). Healthcare worker status was inversely associated (AR:21%vs.49%; PR:0.42, 95%CI:0.27-0.64).

Conclusions

Our findings suggest that epidemiological links may stay elusive among cases born outside Portugal, unvaccinated, notified in private institutions, and those with longer notification delay. Enhancing targeted investigation efforts to improve source identification and contact tracing, while addressing related barriers, may improve recognition and control of transmission chains and support sustained measles elimination in Portugal.

Vaccine-preventable diseases: evidence to practice

Feasibility of a target trial emulation study to estimate vaccine effectiveness of the 2023 and 2024 autumn vaccine doses against hospitalisation due to COVID-19 in six EU/EEA countries: a VEBIS-EHR network study

ABSTRACT ID: 131

Alexandre Blake [1], ***James HUMPHREYS*** [1], ***Toon Braeye*** [2], ***Izaak Van Evercooren*** [3], ***Christian Holm Hansen*** [4], ***Chiara Sacco*** [5], ***Alberto Mateo Urdiales*** [5], ***Jesús Castilla*** [6], ***Iván Martínez-Baz*** [7], ***Ausenda Machado*** [8], ***Irina Kislaya*** [8], ***Rickard Ljung*** [9], ***Nicklas Pihlstrom*** [9], ***Susana Monge*** [10], ***Baltazar NUNES*** [11]

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Background

Monitoring vaccine effectiveness (VE) is critical to guide vaccination policies, although these observational studies are prone to biases. Target trial emulation (TTE) could improve internal validity of VE studies by better addressing selection and confounding biases. We evaluated the feasibility of a multi-country TTE study to estimate COVID-19 VE of the 2023 and 2024 autumn vaccine doses against hospitalisation at ≤180 days post-vaccination among adults aged ≥65 years with 12 months follow-up from the start of vaccination campaigns in Italy, Belgium, Denmark, Portugal, Spain (Navarre), and Sweden. using electronic health records.

Methods

We performed 1:1 sequential matching with replacement between vaccinated and unvaccinated individuals associating exact matching on age, region, comorbidity, with propensity score (estimated from a Cox model with age, sex, region, number of previous COVID-19 vaccine doses, and comorbidities as predictors) matching. We calculated site-level vaccination risk ratios (RR) up to day 180, ratio of the cumulative incidence curves estimated by the Aalen Johansen estimator, among pairs event-free up to day 14, pooled them using meta-analysis methods, and estimated VE as VE=(1-RR_pooled)x100.

Results

The preliminary analysis includes data from Italy, Navarre, and Portugal. We included 5,688,772 and 3,573,224 participants, after matching on key variables, in 2023–24 and 2024–25, representing 99.9%–99.8% of vaccinated and 12%–6% of unvaccinated eligible individuals, respectively. VE against hospitalisation was 40% (95% confidence interval (CI): 27–50) and 39% (95% CI: 13–58) in 2023–24 and 2024–25.

Conclusions

A multi-country TTE study appears feasible. However, a flexible site-specific approach regarding matching and the variables included in the analysis could lead to a more robust estimate at the cost of a divergence from a common data structure and a more complex coordination. Next steps include gathering data from additional sites and contextualising our findings with VE estimates from observational studies.

Vaccine-preventable diseases: evidence to practice

Determinants of vaccination intention in Romania: findings from Wave 2 of the People's Voice Survey using the 5Cs model of vaccination acceptance

ABSTRACT ID: 597

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Background

To support ongoing health system reforms, the Ministry of Health of Romania, with technical assistance from the World Health Organization Regional Office for Europe, conducted the second wave of the People's Voice Survey in 2025. Given persistently low vaccination coverage, a dedicated vaccination module based on the 5Cs model operationalised by the European Centre for Disease Prevention and Control (ECDC) was integrated to assess vaccination intention and its psychosocial determinants among Romanian adults. To our knowledge, this is the first nationally representative study on this topic.

Methods

Between 21/11/2025-16/12/2025, a cross-sectional computer-assisted web-based survey was conducted among a nationally representative sample of 2,000 Romanian adults. A 19-item vaccination module aligned with ECDC guidance assessed: confidence, complacency, constraints, risk calculation, collective responsibility. Vaccination intention was the primary outcome. Variables with p<0.10 in univariable analyses were included in multivariable logistic regression models. Survey-weighted analyses were conducted in R to estimate odds ratios (OR) and 95% confidence intervals (CIs). Ethical approval was obtained from the Carol Davila University of Medicine and Pharmacy, Bucharest.

Results

Overall, 33.9% of respondents (CIs:29.6-38.2%) intended to follow all recommended vaccinations, 46.5% (CIs:41.8-51.1%) some, and 19.6% (CIs:15.8-23.5%) none. In multivariable analysis, confidence (OR:2.52; CIs:1.98- 3.24; p<0.001) and collective responsibility (OR:1.31; CIs:1.05-1.62; p=0.017) were positively associated with vaccination intention, while complacency (OR:0.57; CIs:0.47-0.69; p<0.001) and risk calculation (OR:0.57; CIs:0.45- 0.72; p<0.001) were negatively associated. Constraints were not independently associated (OR:0.86; CIs:0.70- 1.06; p=0.164).

Conclusions

One in three respondents intended to follow all recommended vaccinations, while nearly one in five none. Vaccination intention was associated with trust, collective responsibility, and risk perception rather than with structural barriers. Improving vaccination uptake in Romania should prioritize strengthening public confidence and collective responsibility, alongside communication strategies addressing misinformation and risk perceptions. Embedding vaccination acceptance monitoring within health system surveillance may support responsive vaccination strategies and improvements in population health outcomes.

Vaccine-preventable diseases: evidence to practice

Impact of influenza vaccination in adults aged ≥65 years in Portugal: 2022/23-2024/25 seasons estimates

ABSTRACT ID: 626

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Background

Vaccination is a primary preventive strategy to reduce influenza morbidity and mortality. Assessing how influenza vaccine effectiveness translates into real-world reductions in severe outcomes in vulnerable populations is essential for public health decision-making. This study aimed to estimate the impact of the influenza vaccination program in Portugal on influenza-related hospitalizations in ≥65 years old population during the 2022/23-2024/25 seasons

Methods

Using data on influenza surveillance, hospitalizations, vaccine coverage, and vaccine effectiveness, we estimated the number of averted events (NAE), the prevention fraction (PF), and the number needed to vaccinate to prevent one hospitalization (NVN) per season in the population aged ≥65 years. Monte Carlo simulations were used to estimate the 95% uncertainty intervals of all impact parameters.

Results

In 2022/23-2024/25 the number of hospitalizations with severe acute respiratory infections among ≥65 years old in Portugal ranged between 44060 and 48454. Influenza vaccine effectiveness varied across seasons from 32% to 45%, depending on the circulating strain. Vaccine coverage ranged from 70% to 73%. In 2022/23, with predominant A(H3N2) circulation, vaccination averted 65 (95%UI 30-102) hospitalizations per 100000 inhabitants, corresponding to PF of 23.4% (95%UI 12.4-32.4) and NNV of 1128 (95%CI 717-2429). In 2023/24, with A(H1N1)pdm09 predominance, NAE was 73 (95%UI 40-108) hospitalizations per 100000, PF 25.9% (95%UI 16.1- 34.2), and NNV 988 (95%UI 666-1801). In 2024/25, with co-circulation of A(H3N2) and B/Victoria, we observed a higher NAE of 96 (95%UI 57-157) per 100000, with PF of 31.5% (95%UI 19.7-40.3) and NNV of 653 (95%UI 445- 1226).

Conclusions

The seasonal influenza vaccination provided consistent benefits in adults aged ≥65, preventing a significant number of hospitalizations even in seasons with moderate vaccine effectiveness. Estimates of the impact enhance public health communication and reinforce public health value of seasonal immunization programs.

POSTER TOUR 19

Vaccine-preventable diseases: evidence to practice

Determinants of Mpox vaccine uptake in men who have sex with men and transgender persons during regular consultations at a Dutch Sexual Health Centre

ABSTRACT ID: 500

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Background

In the second half of 2024, the Netherlands observed an increase in Mpox clade IIb cases. In response, a nationwide Mpox vaccination campaign targeting high-risk groups was implemented in April 2025, integrated into routine consultations at regional Sexual Health Centres (SHC). This study aimed to identify client characteristics associated with Mpox vaccine uptake.

Methods

A retrospective cohort study was performed using electronic health record data from the SHC of the public health service Flevoland for consultations between 14 April 2025 to 13 April 2026. Eligible participants were previously unvaccinated men who have sex with men and transgender clients with at least one indication for Mpox vaccination during the study period. Indications were use of HIV pre-exposure prophylaxis (HIV-PrEP); 10 or more reported sexual contacts in the last six months; participation in group sex; or being HIV-positive with concurrent screening for hepatitis C as a proxy indicator for sexual risk behaviour. The association of demographic and risk behaviour variables with Mpox vaccination was analysed using univariable logistic regression analyses.

Results

Data of 613 clients were analysed, of whom 137 (22%) had received the Mpox vaccine. The odds for Mpox vaccination were increased in clients with HIV-PrEP use (OR: 3.66, 95% CI: 2.47 – 5.48), group sex participation (OR: 1.55, 95% CI: 1.03 – 2.32), a high educational level (OR: 2.72, 95% CI: 1.48 – 5.38) and a higher socio-economic status (SES) score at the postal code level (OR: 2.53, 95% CI: 1.02 – 6.44). No association was found for age, the number of sexual contacts and migration background.

Conclusions

To conclude, uptake of Mpox vaccination was lower in clients with no HIV-PrEP use, no group sex participation, a lower SES score and a lower educational level. Targeted interventions may be needed to improve Mpox vaccination coverage in these groups.

POSTER TOUR 20

Vector-borne diseases

Emerging vector-borne infectious disease risks: awareness gaps among Dutch travellers in Europe

ABSTRACT ID: 716

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Background

The risk of acquiring infectious diseases (ID) during travel in Europe is increasing, driven by climate change and international mobility. Awareness among travellers is essential to encourage ID prevention and limit disease spread. This study assessed awareness of these increasing ID risks among Dutch travellers.

Methods

Dutch adults (aged ≥18) who travelled ≥4 nights to European destinations in the previous year were included in a cross-sectional questionnaire study on ID risk perception in 2025. In 5,042 respondents, awareness of emerging vector-borne ID risks and their importation to the Netherlands by 2035 was assessed. Group differences were analysed with chi-square tests and standardized residual analyses.

Results

Awareness was higher for emerging mosquito-borne ID risks (67.6%) than tick-borne ID risks (49.9%). Awareness of emerging ID differed across age groups ($p<0.001$), with respondents aged 18–29 and 70+ overrepresented in lower awareness categories and those aged 30–69 overrepresented in higher categories. Awareness also differed by gender ($p=0.023$) and education level ($p<0.001$), with females and higher-educated respondents overrepresented in higher awareness categories. About half of travellers (46.2%) was aware of the increasing risk of importing ID, again particularly females and those higher-educated were overrepresented in higher awareness categories (both $p<0.001$). Higher awareness of tick-borne ID risks and ID importation was associated with seeking pre-travel ID advice ($p=0.002$); there was no association for mosquito-borne ID risks ($p=0.135$).

Conclusions

Awareness gaps require targeted action. Efforts should focus on younger (18-29), older (70+), and lower-educated travellers. Efforts to increase mosquito-related ID awareness appear to have improved awareness, yet disparities persist across population groups. Strengthening and promoting pre-travel advice may serve as an effective entry point to improve infectious disease risk awareness.

Vector-borne diseases

Epidemiological Trends and Climatic Determinants of Human Leishmaniasis in Lazio Region, 2015–2025

ABSTRACT ID: 709

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Background

Leishmaniasis is a neglected vector borne disease with an increasing incidence globally and in southern Europe. In Italy, visceral leishmaniasis (VL), due to Leishmania infantum, remains the number one type of leishmaniasis. Environmental and climatic change could influence this growing trend.

Methods

A retrospective observational study was conducted on reported cases of human leishmaniasis in the Lazio region with symptom onset 2015–2025. Meteorological variables (temperature and precipitation) were derived from the Copernicus Climate Data Store. Temporal trends and associations with annual climatic variables were assessed using negative binomial regression models. A municipal-level ecological analysis was performed using Spearman's correlation.

Results

A total of 99 cases of leishmaniasis had been reported. Peaks in incidence have been observed in 2023 (0.38 per 100,000 inhabitants; 95% CI: 0.24–0.58) and in 2025 (0.30; 95% CI: 0.17–0.48). The negative binomial regression model revealed an increasing trend over time, with an annual increase in cases of 12% (IRR 1.12; 95% CI: 1.01– 1.24; p = 0.042). The majority of cases were VL (77.8%), men (68.7%), and adults the 20–60 age group (42.4%), but a significant proportion were pediatric cases, among children aged 0 to 2 years (18.18%) Correlation analyses showed associations between incidence and both mean temperature (ρ=0.19, $p<0.001$) and mean precipitation (ρ=–0.10, p=0.03). Average temperature was associated with an increase in the number of cases both in the same year (IRR 2.36; 95% CI: 1.01–5.78; p = 0.040) and in the following year (IRR 2.83; 95% CI: 1.46–5.68; p = 0.003), suggesting a possible delayed effect.

Conclusions

Climatic factors are probably influencing the dynamics of transmission. Our study confirms an upward trend in leishmaniasis incidence in Lazio, emphasizing the importance of enhanced surveillance, vector control, and environmental monitoring. Ongoing analyses of canine seroprevalence will be integrated to enhance risk assessment.

Vector-borne diseases

DENV-2 autochthonous transmission patterns in Italy: evidence from 2024 outbreaks

ABSTRACT ID: 682

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Background

In 2024, multiple transmission foci of dengue virus serotype 2 (DENV-2) were detected across four Italian re-gions, resulting in the largest number of autochthonous cases ever recorded in mainland Europe. To address the existing knowledge gap on dengue transmission dynamics in temperate settings, we derived multiple metrics characterizing DENV's transmissibility across time and space.

Methods

We analysed 296 locally acquired cases with symptom onset between July 31 and October 31. Using detailed spatiotemporal data, we reconstructed transmission chains between cases with well documented exposure sites, applying a Bayesian framework. We estimated the generation time and net reproduction number (R) for the t main transmission foci. We also quantified the relative risk of transmission across varying distances, examined individual heterogeneity in onward transmission, and, using a regression framework, assessed the influence of different factors—including temperature and control interventions—on secondary transmission.

Results

Three major foci were identified, with peak R estimates ranging from 1.35-3.33. The mean generation time t was 18.0 days (95% CrI: 15.5–20.0 days). Household transmission accounted for 15.4% (95% CrI: 12.6–17.4%) of infection events. Among cases with an identified source of infection, less than 1% of transmission occurred beyond 400 meters. Transmissibility declined significantly after outbreak detection, with the average number of secondary cases per infection dropping from 1.4 to 0.4. We found that vector-control interventions were associated with a 41.0% reduction (95% CI: 6.6-63.3%) in transmission; transmission also declined by 19.8% (95% CI: 11.3-29.0%) for each 1°C decrease in temperature; male infectors were associated with 30–40% more secondary cases.

Conclusions

Autochthonous dengue outbreaks in Italy in 2024 were primarily driven by short-distance transmission, although long delays in reporting and difficulties in identifying exposure sites may facilitate dissemination to broader areas. Our findings support that early case detection and rapid vector control play a key role in reducing transmission.

Vector-borne diseases

Clinical and epidemiological characteristics of West Nile Virus in Northern Cyprus: A retrospective case series (2019–2024)

ABSTRACT ID: 216

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Background

West Nile Virus (WNV) is a re-emerging neuroinvasive threat in the Mediterranean, yet clinical and diagnostic data from Northern Cyprus remain scarce. This study aims to characterize the clinical features, laboratory findings, and outcomes of laboratory-confirmed WNV cases during and after the 2019 outbreak to improve regional surveillance and clinical management.

Methods

We conducted a retrospective analysis of 22 laboratory-confirmed WNV patients diagnosed between 2019 and 2024 at a tertiary center. Data included demographics, comorbidities, inflammatory markers (CRP, procalcitonin), cerebrospinal fluid (CSF) analysis, and serological/molecular diagnostics. Statistical associations between comorbidities, treatment (e.g., plasmapheresis, IVIG), and mortality were assessed using Fisher's exact and Kruskal–Wallis tests.

Results

The median age was 67.5 years (IQR: 56.3–74.3); 72.7% of patients were male. Most cases (68.2%) occurred during the 2019 outbreak, with a resurgence in 2023–2024. Hypertension (42.1%) was the primary comorbidity. Acute IgM positivity predominated (80% in 2019), whereas IgG began emerging in 2023. Elevated CRP (68.2%) and abnormal CSF (22.7%) were common. Neuroinvasive symptoms (syncope, encephalopathy) were frequent, and the mortality rate was 27.3% (6/22). A significant association was found between plasmapheresis use and mortality (p=0.025), likely reflecting severity bias as this intervention was reserved for critically ill patients. No significant link was found between comorbidities and death (p=0.655).

Conclusions

WNV in Northern Cyprus predominantly affects older males and presents with high mortality and neuroinvasive severity. The 2019 peak and 2023 resurgence suggest periodic epidemic cycles. Diagnostic challenges remain, as serology is the primary tool while PCR yields restricted results. We recommend implementing integrated vector control and enhancing clinical awareness during peak seasons. Clinicians should prioritize early serological screening in elderly patients with unexplained fever or neurological symptoms to reduce the high mortality burden.

Vector-borne diseases

Immunogenicity, clinical efficacy and safety of Malaria vaccines in children: a systematic review and meta-analysis

ABSTRACT ID: 205

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Background

Malaria remains a global public health emergency with high mortality especially among children under 5 years. Despite increased research on pediatric malaria vaccines, comprehensive evidence syntheses are limited. We aimed to assess the efficacy and safety of currently available malaria vaccines in children

Methods

Following PRISMA we included Phase IIb–IV and post-marketing studies from PubMed, SCOPUS, WoS, Clinical-Trials.gov, ISRCTN, EUCTR, CTIS and PACTR. Licensed and candidate vaccines used to individuals ‹18 years were compared with controls or seasonal malaria chemoprevention (SMC). Outcomes were seroconversion, incidence of clinical malaria and serious adverse events (SAE). Meta-analyses were performed for the intention-to-treat cohorts with subgroup analyses by vaccine type and follow-up (PROSPERO: CRD420251032609)

Results

56 trials were included (134.424 participants). The proportional meta-analysis revealed an overall SAE rate of 16%, higher for RTS,S/AS02 (29%) and lower for R21-MM (3%). In comparative analyses vaccination reduced SAE risk by 9% vs controls (RR=0.91; 95%CI 0.86–0.96). Overall vaccine efficacy (VE) was 31% (IRR=0.69), higher for RTS,S/AS02 (47%) and RTS,S/AS01 (32%). R21-MM showed the highest VE (72%, single trial). Efficacy declined with time: 33% within 12 months, 35% at 12–36 and 11% beyond 36 months. The combination of vaccination and SMC showed 65% efficacy. Cumulative seroconversion rate was 0.99 (95%CI 0.98–1.00). Comparative seroconversion analysis was not feasible due to absent control data. No study was rated as low quality by RoB2

Conclusions

Malaria vaccines in children show a favorable safety profile and provide meaningful although time-limited protection against clinical malaria. RTS,S and R21 vaccines achieve the highest efficacy particularly in combination with SMC. Malaria vaccination should be integrated into childhood malaria control strategies emphasizing the need for booster strategies and long-term effectiveness monitoring in endemic settings

Vector-borne diseases

Autochthonous dengue outbreak in Tuscany, Italy: geographically dispersed cases linked to a common exposure site, August to September 2026

ABSTRACT ID: 1002

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Background

Since 2020, Italy has reported dengue outbreaks sustained by local transmission, mostly in residential settings. On 28 August 2026, Tuscany reported a locally acquired dengue case in a person who had stayed at a rural holiday area on the Tyrrhenian coast; further exposed cases followed. We describe the investigation and response.

Methods

Outbreak cases were probable or confirmed cases with onset from 1 August 2026, linked to the affected area or another case. Case finding was implemented through Tuscan healthcare services. Laboratory confirmation and entomological investigation, including mosquito-pool testing, were performed. An EpiPulse alert targeted foreign visitors. Data as of 23 September 2026.

Results

Forty outbreak-cases were identified (28 confirmed, 12 probable): median age 58 years (IQR: 38–66), 20 female, 11 (27.5%) hospitalised and none died. Onset ranged from 1 August to 10 September, peaking between 24 August-6 September. All reported exposure at the rural area; no linked imported case was identified. Cases were diagnosed in 14 municipalities across seven provinces; 38 in Tuscany and two elsewhere. RT-PCR identified dengue virus serotype 2. Entomological investigation confirmed *Aedes albopictus*, with abundant larvae in private-property containers, several inaccessible. Adulticide treatment and removal of accessible breeding sites were implemented at the exposure site and case residences, alongside blood and transplant safety measures. Secondary transmission is under investigation: four confirmed cases (onset 10,12 and 18 September), without travel or rural-area exposure, occurred at 0.6-3.6 km from outbreak cases' residences, 12–18 days after that case's onset. No cases potentially linked to the outbreak were communicated from other European countries after the alert.

Conclusions

Exposure at a rural holiday area dispersed cases across 14 municipalities as people returned home, requiring public health measures in each of them. In touristic settings, investigation must extend beyond the exposure area, with central-local cooperation and surveillance where viraemic cases return.

POSTER TOUR 21

Quantitative methods

Cost-effectiveness of MenB vaccination to control the spread of gonorrhoea in the UK

ABSTRACT ID: 794

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Background

Gonorrhoea is a major public health concern due to a rise in incidence and antimicrobial resistance. A meningococcal B (MenB) vaccine offers partial cross-protection against gonorrhoea (30–40%) and has recently been introduced for higher-risk gay, bisexual, and other men who have sex with men (GBMSM) in England. The wider population impact remains unclear though, especially for women who have lower incidence rates than GBMSM but are at a much higher risk of severe complications from infections. This study aims to evaluate the epidemiological and economic impact of MenB vaccination strategies against gonorrhoea for the whole population in England.

Methods

We developed a deterministic transmission model that is stratified by sex and sexual risk behaviour (women, heterosexual men, and GBMSM with low and high partner numbers). The model was calibrated to national surveillance data (GUMCAD, 2016–2019) using a Markov chain Monte Carlo algorithm. We simulated three vaccination strategies, adolescent vaccination, vaccination at screening, and vaccination at treatment, and assessed both epidemiological impact and cost-effectiveness.

Results

Modelling results suggest that all vaccination strategies reduced gonorrhoea incidence. Targeting GBMSM achieved the greatest overall impact, with an indirect reduction of incidence in women. Vaccination at screening produces the largest incidence reductions but required a large amount of vaccine doses. Vaccination at treatment was cost effective though. This was the case for our baseline scenario of 30% vaccine effectiveness and 5-year protection and a current price of £75 per dose, as well as for all sensitivity scenarios tested.

Conclusions

We thus show MenB vaccination could substantially reduce gonorrhoea incidence in England, even with partial effectiveness. While current policy focuses on GBMSM, our findings show significant indirect benefits for women. Targeted vaccination of high-transmission groups may reduce severe outcomes in broader populations, supporting consideration of expanded vaccination strategies in future policy.

Quantitative methods

A hidden Markov model reveals environmental persistence and inter-department transfers as key drivers of drug-resistant Citrobacter spp. in a hospital

ABSTRACT ID: 792

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Background

Multidrug-resistant *Citrobacter* spp. are increasingly implicated in nosocomial outbreaks, yet their transmission dynamics remain poorly characterised. Plasmid-mediated extended-spectrum beta-lactamase (ESBL) resistance among *Citrobacter* spp. spreads sporadically in hospitals, making it difficult to determine whether detections reflect community importation, within-ward patient-to-patient transmission, persistent environmental contamination, or colonisation pressure from other departments via patient transfers. Positive clinical samples and screening of high-risk patients provide only a partial view of strain circulation, hindering quantitative disentanglement of these routes. We aimed to quantify the relative contributions of these pathways using mathematical modelling.

Methods

We investigated the six-year spread (2017–2022) of *Citrobacter* spp. carrying IncHI2/IncHI2A plasmids harbouring *blaCTX-M-15* at the Geneva University Hospitals, a tertiary-care hospital in Switzerland. Using surveillance data, patient transfer trajectories, and department-level data, we developed a continuous-time hidden Markov model to infer latent colonisation dynamics and quantify four transmission components.

Results

90 patients were identified, across 9 departments accounting for 36 monthly episodes in 7 departments. We used this model to analyse collected data by reconstructing unobserved colonisation events. Including inter-department transmission and environmental persistence substantially improved fit over a within-department-only model. Inter-department transmission was the most probable route (posterior median 59.4-81.0%; 95% credible intervals consistently above 29%). However, in the ICU/ER, the environmental source appeared to be the main contributor to fitted colonisation pressure (64.8% [14.4-94.9%]). Within-department transmission and importation were consistently minor (< 11% and < 17% of fitted colonisation pressure, respectively). Environmental persistence varied markedly across departments (0.0-64.8%), suggesting department-specific reservoirs.

Conclusions

These findings indicate that sporadic hospital ESBL-producing *Citrobacter* detections may largely reflect continuous hospital circulation through inter-department spread and environmental reservoirs rather than independent importation, extending beyond conventional within-ward transmission models. The model estimated that undetected colonisation constituted 22.0-65.3% of total colonisations across departments. Environmental sampling and systematic monitoring of inter-department patient transfers could validate these inferred pathways.

POSTER TOUR 21

Quantitative methods

Decrease in prevalence of sexually transmitted chlamydia infection among 15–29 years old individuals during 2009–2024 in Sweden: a mathematical modelling study

ABSTRACT ID: 753

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Background

Reported Chlamydia trachomatis (Ct) infection rates in Sweden declined steadily from 2009 to 2015 and more sharply thereafter. Given the high proportion of asymptomatic Ct infections, reported rates are heavily influenced by testing behaviour, making it unclear if this reflects a true transmission reduction. We aimed to estimate Ct prevalence and assess whether the observed decline reflects a genuine reduction in transmission.

Methods

We implemented a deterministic Susceptible–Infected–Susceptible compartmental model to estimate Ct prevalence in Sweden stratified by sex, age group (15–19, 20–24, 25–29) and year (2009, 2012, 2015, 2018, 2021, 2024). The model distinguished symptomatic and asymptomatic infections and incorporated screening rates, treatment seeking behaviour, and partner notification for infected and uninfected individuals. Unknown parameters were solved using chlamydia surveillance data, testing data, and published estimates for test sensitivity/specificity and spontaneous clearance. Median prevalence and incidence with 95% credibility interval (CrI) were estimated.

Results

Estimated chlamydia prevalence varied between 1% to 7% depending on the year, age group and sex. In 2009, prevalence was 3.97% (95%CrI 3.41-4.53) in males and 4.02% (95%CrI 3.70-4.35) among females of age 15-29 years, dropping to 2.65% (95%CrI 2.14-3.07) and 2.34% (95%CrI 1.06-2.57) respectively by 2024. Prevalence was higher in younger age groups in all years and both sexes. Estimated incidence was at least double that of the reported incidence rates. On average, 88% of incident cases among women and 83% among men were estimated to be asymptomatic.

Conclusions

Estimated Ct prevalence declined between 2009 and 2024, while a high number of incident cases remained undetected by the surveillance system. This valuable information from the model on estimated prevalence, underreported incidence and proportion of asymptomatic Ct cases needs further evaluation before considering potential adjustments in future chlamydia control strategies in Sweden.

Quantitative methods

Closing the gap to cervical cancer elimination in Portugal: a modelling study

ABSTRACT ID: 642

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Background

Cervical cancer (CC) elimination is now a realistic goal, but even high-coverage countries need to identify which interventions can accelerate progress. Portugal has sustained high HPV vaccination uptake and organised cervical screening. We estimated future CC incidence under alternative vaccination and screening scenarios, to assess if elimination is achievable before 2050.

Methods

We developed a deterministic, dynamic compartmental model of high-risk HPV transmission and cervical carcinogenesis, stratified by sex and single-year age (0–99 years), for mainland Portugal, 2018–2050, that links HPV infection, immunity and vaccination in both sexes with cervical intraepithelial neoplasia (CIN) grades 1 and 2/3 and invasive CC in women. We compared three scenarios: current routine vaccination and screening (S1); S1 plus 2026 catch-up vaccination to age 26 years (S2); and S2 plus screening strengthening from 57% to 70% coverage by 2030, with the eligible age range extended from 25–60 to 30–69 years (S3). The primary outcome was age-standardised CC incidence per 100,000 women-years; elimination defined as <4/100,000 (WHO). Results are preliminary pending further calibration.

Results

Modelled incidence declined from 11.0/100,000 in 2018 to 9.1/100,000 by 2021, stabilising through 2026 as vaccinated cohorts had not yet reached peak-incidence ages. From 2027, incidence fell continuously at approximately 0.4/100,000 per year. S1 and S2 crossed the elimination threshold in 2042, reaching 1.79 and 1.57/100,000 by 2050. S3 reached elimination in 2039 and produced the lowest residual burden: 36% lower incidence, 36% fewer prevalent CIN2/3 cases and 20% fewer CC deaths versus S1.

Conclusions

Preliminary projections suggest CC elimination in Portugal is achievable before 2050. High vaccination coverage provides the foundation; strengthening screening could accelerate progress and reduce residual burden. Integrated monitoring will be essential.

Quantitative methods

Cost-Effectiveness and Uncertainty Analysis of Ebola Vaccination Strategies in Children and Adolescents

ABSTRACT ID: 446

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Background

Ebola virus disease remains a severe public health threat, particularly affecting pediatric populations with high mortality. Although Ad26.ZEBOV/MVA-BN-Filo (Ad26/MVA) and rVSV-ΔG-ZEBOV (rVSV) vaccines are approved by the European Medicines Agency, no direct comparative economic evaluation has been performed in children <19. This study aimed to compare the cost-effectiveness of these two vaccination strategies.

Methods

A decision tree model compared Ad26/MVA, rVSV, and no vaccination from a healthcare system perspective. Probabilities of infection, survival, and death were derived from outbreak data (2025, Democratic Republic of Congo) and clinical trial evidence. Costs included acute clinical management, death and vaccine acquisition, updated to 2024 US$. Health outcomes were expressed in disability-adjusted life years (DALYs). Incremental cost-effectiveness ratios (ICERs) were calculated vs no vaccination. One-way sensitivity analysis assessed vaccine price uncertainty, while probabilistic sensitivity analysis explored parameter uncertainty. Cost-effectiveness acceptability curves were generated across willingness-to-pay thresholds.

Results

In the base case, rVSV generated 0.470 DALYs averted at an ICER of 203.53 $/DALY, while Ad26/MVA generated 0.419 DALYs averted at 280.14 $/DALY. Deterministic sensitivity analysis showed that Ad26/MVA-based ICERs were highly sensitive to vaccine price, becoming dominant under donor-funded scenarios. In probabilistic analysis, Ad26/MVA had a mean ICER of 101.12 $/DALY (95% CI: 5.59–331.53), while rVSV had a mean ICER of 231.97 $/DALY (95% CI: 74.02–545.43). At a willingness-to-pay threshold of 500 $/DALY, the probability of cost-effectiveness was 0.993 for Ad26/MVA and 0.963 for rVSV.

Conclusions

Both Ebola vaccines are highly cost-effective in pediatric populations under outbreak conditions. However, Ad26/MVA demonstrates superior economic efficiency and greater robustness under uncertainty, particularly in donor-funded scenarios.

POSTER TOUR 21

Quantitative methods

Economic evaluation of a bivalent respiratory syncytial virus prefusion F vaccine for older adults in Sweden: cost-effectiveness and budget impact

ABSTRACT ID: 347

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Background

Respiratory syncytial virus (RSV) causes substantial morbidity and mortality in older adults. In Sweden, the bivalent RSV prefusion F (RSVpreF) vaccine was approved in 2023 for people aged ≥60 years, creating a need to quantify expected health impact and value for money to inform policy. We evaluated the cost-effectiveness and budget impact of RSVpreF vaccination targeting adults aged ≥75 years and 60–74 years at increased risk of severe RSV, compared with no vaccination.

Methods

We developed a Markov model with a lifetime horizon from the Swedish healthcare payer perspective. Age (60–74, ≥75 years) and risk status (based on comorbidities) defined cohorts. Inputs included age, RSV incidence, probabilities of outpatient care and hospitalisation, and RSV case-fatality. Vaccine effectiveness was applied by age/risk group. Costs covered vaccination and RSV-related medical care. Outcomes were RSV cases, outpatient visits, hospitalisations, deaths and quality-adjusted life years (QALYs). The base case assumed 75% uptake; a 5-year budget impact analysis estimated net costs/savings.

Results

Compared with no vaccination, RSVpreF reduced hospitalisations by 12.9%, outpatient visits by 7.5% and deaths by 11.3%. Most of the prevented events occurred within the first four years (46.3% of hospitalisations, 26.6% of outpatient visits and 46.2% of deaths averted over the lifetime total). Reduced healthcare utilisation lowered direct medical costs by 2.8% and increased QALYs, making the programme cost-saving in the base case. In the budget impact analysis, vaccination investments were offset by healthcare savings from year 3 onwards, resulting in an estimated net saving of 1.76 billion SEK over five years.

Conclusions

RSVpreF vaccination in Sweden, focused on adults aged ≥75 years and 60–74 years at increased risk, is projected to prevent severe RSV outcomes and deaths while reducing healthcare costs. These findings support prioritised RSV vaccination as a public health intervention to reduce seasonal pressure on outpatient and inpatient care in older populations.

POSTER TOUR 21

Quantitative methods

Optimal epidemic control: a nonlinear programming approach

ABSTRACT ID: 288

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Background

During epidemics, decision-makers must rapidly determine the optimal timing, intensity, and combination of control measures, such as social distancing and vaccination campaigns, while respecting resource constraints and minimising harm. Mathematical models can inform these decisions through optimal control theory, but existing indirect approaches often require laborious analytical derivations and are highly sensitive to initial guesses. This creates a practical barrier to their use in real-time outbreak response, making them difficult to adapt as situations evolve.

Methods

We evaluated direct nonlinear programming (NLP) optimisation as an accessible alternative for identifying optimal epidemic control strategies. Using the open-source framework JuMP with the interior-point solver IPOPT, we formulated four epidemic control problems as NLP optimisation tasks. These scenarios included: minimising total infections through lockdown; constraining infections below a healthcare capacity threshold ("flattening the curve"); optimising vaccination roll-out timing; and simultaneously optimising four interventions (bednets, vaccination, prophylactics, and insecticides) in a complex dengue fever model.

Results

Across all scenarios, the NLP approach identified optimal control strategies within seconds, without requiring manual derivation of Hamiltonians or adjoint equations. Using a simple infection model and a complex dengue fever model, we corroborate that NLP solutions matched those from established indirect optimal control methods. The framework was also successfully implemented across multiple programming environments (Julia, Python, and R) using both open-source and licensed solvers, with consistent solutions across platforms.

Conclusions

Direct NLP optimisation methods provide a practical, flexible framework for epidemic control planning. Because these methods bypass complex analytical derivations, they can be rapidly reformulated to reflect evolving constraints, such as changing healthcare capacity or vaccine availability, making them well-suited for preparedness and real-time decision support during outbreaks.

POSTER TOUR 22

Social determinants of infectious diseases

Ethnic inequalities in respiratory virus epidemics in England: a mathematical modelling study

ABSTRACT ID: 351

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Background

In England, the burden of respiratory infections varies by ethnicity, contributing to health inequalities, but the role of additional demographic factors remains underexplored. We quantified how differences in social mixing and demographic characteristics between ethnic groups create inequalities in transmission dynamics.

Methods

We analysed the association between the ethnicity and the number of contacts of 12,484 participants in the 2024–2025 Reconnect social contact survey, the largest available social contact survey in England. We used a negative binomial regression model. We then simulated respiratory pathogen epidemics using a compartmental model stratified by age, ethnicity, and contact levels, at a national level and in major cities in England.

Results

After adjusting for demographic variables, participants of Black and Mixed ethnicities had more contacts than those of White ethnicity (rate ratios (RR): 1.18 [95% Credible Interval (CI): 1.11-1.26], and 1.31 [95% CI: 1.14-1.52]). Participants of Asian ethnicity had fewer contacts (RR: 0.85 [95% CI: 0.79-0.91]). In national-level simulations, individuals of White ethnicity had the lowest infection risk due to demographic differences and mixing patterns. Local demographic structures changed simulated dynamics: infection incidence in individuals of Black and Mixed ethnicities was approximately double that in individuals of White ethnicity in Birmingham, but less than 60% higher in Liverpool.

Conclusions

Inequalities in infection risk between ethnic groups are context- and pathogen-dependent. They arise from both local population structure and contact patterns. Detailed information on mixing between groups and population structure is needed to accurately measure group-specific infection risk. Our findings show that public health interventions based only on national-level estimates conceal regional variation in risk, which may ultimately increase inequalities. Public health interventions need to be tailored to local contexts to be equitable and effective. More broadly, our findings provide a foundation for understanding the progression from infection-risk inequalities to disparities in disease presentation and clinical outcomes.

POSTER TOUR 22

Social determinants of infectious diseases

Barriers to mpox vaccination among rural residents in Manitoba and Alberta, Canada

ABSTRACT ID: 658

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Background

Global outbreaks of mpox amongst gay, bisexual and other men who have sex with men in 2022 prompted approval of the Modified Vaccinia Ankara-Bavarian Nordic vaccine for use against mpox. In Canada, provincial vaccine eligibility was based on restrictive gender/sexual orientation identity requirements. Furthermore, while urban regions reported high vaccine uptake, little is known about how conservative values in rural re-gions have influenced vaccine uptake. We aimed to investigate the proportion of mpox-vaccinated individuals residing in a rural region, and barriers to vaccination.

Methods

Semi-structured interviews were conducted between July-December 2024. Interviews were transcribed, analysed for primary themes, and reviewed for secondary/tertiary themes. Participants were recruited via social media and 2SLGBTQIA+ serving community-based organizations in Manitoba and Alberta, Canada. Concurrently, a cross-sectional sample of individuals who identified as potentially eligible to receive the vaccine were recruited to provide a dried blood spot and answer a demographic questionnaire regarding mpox vaccination. Individuals were asked to report if they received any dose of the vaccine, their gender and sexual orientation.

Results

Nineteen individuals were recruited for qualitative interviews, and 276 individuals for the cross-sectional sample. Primary themes identified in the qualitative interviews were governmental neglect, the memory of the HIV/AIDs crisis, fears of being outed, and personal responsibility to protect community health. Regarding the cross-sectional sample, 14% (40/276) of individual reported receiving the mpox vaccine. The median age of vaccinated individuals was 36 (IQR: 30-43). The majority of those who were vaccinated identified as cisgender (41%, 16/40), gay (53%, 21/40) and men (72%, 26/40).

Conclusions

Results from this study provide actionable steps to improve vaccine access to sexually and gender diverse populations including partnering with 2SLGBTQIA+ serving organizations, not requiring patients to out themselves to receive the vaccine, and destigmatization public health campaigns to disrupt problematic narratives around the 2SLGBTQIA+ community and sexual health.

POSTER TOUR 22

Social determinants of infectious diseases

Socioeconomic and demographic disparities in HPV awareness and cervical cancer prevention in rural Romania: findings from a large population-based survey

ABSTRACT ID: 648

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1. MedCorp Association

Background

Romania continues to report one of the highest cervical cancer burdens in the European Union, with an age-standardized incidence of 21.7 per 100,000 and mortality of 9.3 per 100,000. Although national policies provide free HPV vaccination for individuals aged 11–26 years, vaccine uptake remains suboptimal. Importantly, data on HPV awareness and preventive behaviors in rural communities, where barriers to healthcare access may be greater, remains limited.

Methods

We performed a cross-sectional population-based study including 4,999 adults aged ≥18 years from 42 villages across 14 Romanian counties. Survey data included demographic and socioeconomic characteristics, HPV awareness, HPV testing, HPV vaccination status, and cervical cancer screening history (Pap smear). Associations between participant characteristics and preventive behaviors were evaluated using chi-square tests and logistic regression models.

Results

The study population included 3,619 women (72.4%) and 1,380 men (27.6%), with a mean age of 54.7 ± 15.7 years. Overall, 49.4% of participants reported being aware of HPV, while only 7.8% had undergone HPV testing. HPV awareness differed significantly across age groups ($p<0.001$), peaking among individuals aged 30–59 years and declining substantially in participants over 70 years. Women were significantly more likely than men to report HPV awareness (OR 2.93, 95% CI 2.62–3.28) and previous HPV testing (OR 8.19, 95% CI 5.10–13.15). Higher income and health insurance coverage were independently associated with greater HPV awareness ($p<0.001$). Pap smear uptake was reported by 58.2% of women and showed significant variation according to age and socioeconomic indicators.

Conclusions

Substantial socioeconomic and demographic inequalities persist in HPV awareness and cervical cancer prevention in rural Romania. Despite the availability of national vaccination and screening programs, uptake of preventive measures remains inadequate, highlighting the need for targeted public health strategies to improve access, education, and participation in underserved populations.

POSTER TOUR 22

Social determinants of infectious diseases

Screening and attitudes towards hepatitis C among marginalised populations in high- risk districts of southern Slovakia: results from 2024–2025

ABSTRACT ID: 197

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Background

Chronic hepatitis C virus (HCV) infection remains a major public health challenge, particularly among marginalised populations with limited access to prevention, awareness, and testing services. This study aimed to assess knowledge, attitudes, and risk-related behaviours associated with HCV among marginalised communities in high-risk districts of southern Slovakia, identified based on increased incidence reported in the Epidemiological Information System (EPIS).

Methods

Between January 2024 and August 2025, community-based screening and structured interviews were conducted. A 19-item questionnaire was used to collect socio-demographic characteristics, knowledge regarding HCV transmission and prevention, and health-related risk behaviours. Capillary blood samples were obtained for anti-HCV antibody testing. Data analysis was performed using descriptive statistics and logistic regression to identify associations between risk factors and HCV positivity.

Results

A total of 400 participants were surveyed, of whom 278 consented to testing. The overall anti-HCV positivity rate was 4.3% (n = 12). A significantly higher prevalence was observed among men (11.0%) compared to women (1.5%) ($p < 0.001$; OR = 7.86). The highest positivity rate was identified in the 15–34 age group, indicating increased vulnerability among young adults. Knowledge regarding HCV transmission routes, prevention strategies, and availability of testing was generally low across participants. Mistrust toward testing services was frequently reported. Risk-related behaviours, including tattooing and other potential exposure practices, were commonly observed.

Conclusions

These findings highlight a concerning burden of HCV infection, particularly among young adult males in marginalised populations. Limited awareness and mistrust toward testing may contribute to reduced screening uptake. Targeted awareness initiatives, culturally sensitive risk-reduction strategies, and accessible community-based screening programmes are essential to improve early detection, enhance engagement, and reduce ongoing transmission.

POSTER TOUR 22

Social determinants of infectious diseases

Correlates of Seroconversion among HIV-exposed Infants in Three High-burden Counties in Kenya

ABSTRACT ID: 130

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Background

Vertical transmission of HIV/AIDS accounts for over 90% of new pediatric infections. In 2023, Kenya had an estimated mother-to-child transmission (MTCT) rate of 7.3%, with the counties of Kisumu, Siaya, and Homa Bay at 6.0%, 6.5%, and 7.9%, respectively. Despite MTCT prevention coverage exceeding 90%, the 5% elimination target has not been achieved. We sought to determine the incidence and factors associated with seroconversion in HIV- exposed infants in these counties.

Methods

We conducted a retrospective review of National Data Warehouse records for mother–infant pairs enrolled between January 2021 and December 2022, who had been followed for 24 months and had documented infant HIV results. Descriptive statistics summarised socio-demographic and clinical characteristics. Incidence rates were calculated using infant-time methods, while follow-up survival probabilities were estimated using the Kaplan– Meier approach. Associations were assessed using hazard ratios, and Cox regression identified predictors; $p < 0.05$ and 95% confidence intervals were considered significant.

Results

We analysed 7,548 mother-infant pairs; 3,838 (52%) infants were female, and 3,057(40.5%) were from Siaya county. A total of 107 (1.4%) infants seroconverted, with an incidence rate of 14 seroconversions per 100 infant-month (CI: 11–16.4). The median age at seroconversion was six months (range, 0–32 months). Survival analysis showed females' median survival time of 13.6 months versus males' 10.4 months (log-rank 4.79, $p = 0.03$). Among infants, 4,279 (57%) were not breastfed. Of mothers, 6,159(81.6%) were diagnosed before pregnancy, and 2.6% post-partum. Diagnosis before pregnancy (aHR 0.05, CI: 0.02–0.12) and not breastfeeding (aHR 0.11, CI: 0.06–0.21, $p < 0.001$) were associated with decreased hazards of seroconversion.

Conclusions

Maternal diagnosis before pregnancy and no breastfeeding were found to reduce transmission risk. Thus, there is need to adopt universal pre-conception testing and promotion of ideal breastfeeding practices to reduce seroconversion among HIV-exposed infants.

POSTER TOUR 22

Social determinants of infectious diseases

Epidemiological Analysis for Sexually Transmitted Infections in migrant population in Catalonia using multimodal healthcare data

ABSTRACT ID: 842

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Background

Migrants may experience disproportionate sexually transmitted infection (STI) burden because of pre-migration exposures, structural barriers to healthcare and social vulnerabilities, yet migrant-specific epidemiological estimates remain limited. We aimed to estimate the incidence of chlamydia, gonorrhoea, syphilis, and HIV among migrants attending primary care in Catalonia, comparing these estimates with Catalan and Spanish surveillance data.

Methods

We conducted a retrospective cohort study using SIDIAP, an anonymised Catalan primary care database linked to hospital, laboratory, pharmacy and sociodemographic data. The cohort included 52,186 migrants from non-Western countries aged ≥16 years with primary care attendance between 2015 and 2023. Incident STI episodes were defined using disease-specific ICD-10 algorithms: 28-day washout for chlamydia and gonorrhoea, lifelong classification for HIV, and 90-day washout for early syphilis with latent/late syphilis treated as non-recurrent. Annual incidence risks per 100,000 people were calculated and compared with annual Catalan and Spanish surveillance reports.

Results

Chlamydia incidence increased from 16.29 in 2015 to 207.65/100,000 in 2023, approximating the surveillancereported incidence in Catalonia. Gonorrhoea increased from 20.36 to 93.23/100,000, which was below the surveillance incidence in Catalonia in 2023. Syphilis incidence fluctuated, peaking at 100.14/100,000 in 2019 and remaining higher than the surveillance incidence in Catalonia. HIV incidence fluctuated between 27.30 and 65.26/100,000, consistently exceeding Catalan rates. Most annual incidences for all STIs exceeded those ones reported by the Spanish Health Ministry. Across infections, epidemiological patterns differed by age, sex, region of origin and geography.

Conclusions

Linked primary care data can complement surveillance reports by providing migrant-specific STI incidence estimates and allows more granular analysis of specific subgroups. This cross-validation using routinely collected data can fill specific gaps in general surveillance systems and provide information for more targeted STI screening strategies.

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POSTER TOUR 23

Evidence to practice

Declining effectiveness of contact tracing during the emergence of the SARS-CoV-2 Omicron variant in Östergötland, Sweden, November 2021 – February 2022

ABSTRACT ID: 621

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Background

During periods of widespread transmission, contact tracing (CT) systems can be overwhelmed by increasing caseloads, potentially compromising effectiveness by limiting the timely containment of cases. We aimed to assess the timeliness of COVID-19 CT during emergence of the Omicron variant in Östergötland, Sweden.

Methods

CT was considered complete if identified contacts of confirmed cases received quarantine instructions (QI). CT was defined as timely if contacts, who themselves tested positive within 7 days, received QI at least one day before their testing date. We compared the proportion of timely CTs during Delta-dominance (22-11-2021 – 19-12-2021) and Omicron-dominance (20-12-2021 – 09-02-2022). Using logistic regression with cluster-robust standard errors, we assessed how lag-time, defined as the interval between index case testing date and QI dispatch to their contacts, affected the odds of timely CT after adjusting for epidemiological week.

Results

During Delta-dominance, CT was completed for 96% (1411/1475) of cases, versus 51% (7163/14151) during Omicron-dominance. Among complete CTs, the median lag-time per week ranged from 2-3 days and 2-5 days during Delta and Omicron dominance, respectively. Timely CT was achieved for 63% (200/318) of contacts who received QI and tested positive during Delta-dominance, falling to 20% (228/1140) during Omicron-dominance. Using a 1-day lag as the reference group, the odds of timely CT decreased by 47% for 2-day lags (aOR=0.53; 95% CI=0.31–0.90), 69% for 3-day lags (aOR=0.31; 95% CI=0.17–0.56), 85% for 4-day lags (aOR=0.15; 95% CI=0.08–0.29), and 94% for lags of 5+ days (aOR=0.06; 95% CI=0.03–0.13).

Conclusions

In Östergötland, CT timeliness and completeness declined during Omicron-dominance, demonstrating the challenge of maintaining rapid containment during high-caseload periods. In this setting, a lag of just 2 days was associated with a substantial reduction in the odds of timely CT, suggesting that resources may be better directed at other non-pharmaceutical interventions when rapid CT is no longer feasible.

Evidence to practice

Systematic review of effectiveness of wide- spread population-based laboratory testing strategies during the COVID-19 pandemic

ABSTRACT ID: 388

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Background

During the COVID-19 pandemic, population-based laboratory testing using polymerase chain reaction (PCR) and rapid antigen tests was widely implemented to detect infections, reduce transmission, and inform public health decisions. However, strategies differed substantially across countries and over time, and uncertainties remained about their effectiveness, sustainability, and cost-effectiveness across epidemic phases.

Methods

We conducted a systematic review of global evidence published between January 2020 and September 2025 on population-based testing strategies using PCR and rapid antigen tests. A total of 107 studies were included (89 effectiveness, 18 cost-effectiveness), of which 73 were modelling studies. Outcomes included transmission indicators (e.g. incidence, reproduction number), clinical outcomes (hospitalisations, mortality), operational metrics, and economic measures.

Results

Overall, population-based testing reduced SARS-CoV-2 transmission, with effectiveness highly dependent on implementation. Testing was most effective when introduced early, at sufficient scale and frequency, and combined with isolation, contact tracing, and quarantine. Real-world studies showed case reductions of ~18–50% and prevalence reductions up to 58–70%. Modelling studies projected up to 50–90% reductions under high-frequency testing with rapid turnaround and follow-up. Key drivers were frequency, speed, public acceptance, and follow-up actions. Cost-effectiveness varied by context: PCR (including pooled testing) was more efficient in low-incidence settings, while targeted or rapid testing performed better during higher transmission.

Conclusions

Population-based testing can support epidemic control when well-designed, adaptable, and integrated into test– trace–isolate systems. Early use, adequate scale, rapid turnaround, and context-specific approaches are critical to maximise impact and efficiency.

POSTER TOUR 23

Evidence to practice

Evaluating usage and impact of English AMR & HCAI surveillance outputs to inform future improvements

ABSTRACT ID: 354

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Background

Effective surveillance underpins evidence-based decisions, policy, outbreak preparedness, and resource planning. UKHSA produces several antimicrobial resistance (AMR) and healthcare-associated infection (HCAI) surveillance outputs. The UK National Action Plan (NAP) on AMR 2024-2029 calls for a surveillance strategy review to optimise data usage and avoid duplications. We assessed usage, impact and potential gaps of UKHSA surveillance outputs to inform actions supporting AMR NAP objectives.

Methods

We conducted a cross-sectional mixed-methods study to assess the usage, accessibility, utility and impact of 21 AMR/HCAI surveillance outputs. A survey was disseminated using a snowball approach across stakeholder groups (civil service, NHS, academia, local authorities, industry, private healthcare, charities). Semi-structured interviews (n=19) across all stakeholder groups explored usage patterns, purpose and impacts in depth.

Results

269 participants completed the survey; NHS (50.7%), civil service (18.9%), other (30.4%). The most used outputs were the English surveillance programme for antimicrobial utilisation and resistance (ESPAUR) (56.8% of respondents) and annual (52%) and quarterly (51%) reports on key HCAIs. However, more than 25% of participants were unaware of each of the 21 outputs. While broad outputs such as Fingertips (46.6%) and ESPAUR (34.9%) were rated most valuable, topic-specific reports on critical care (90.9%) or surgical site infections (50.0%) received high impact ratings. Interviewees emphasised the need for better joined-up data, particularly between the NHS and civil service. Real-time, granular dashboards were most impactful and prioritised for local interventions, while annual reports provided context for broader policy development. In-depth analyses on patient risk factors were viewed as essential for targeted action. Numerous suggestions were made to improve usability and utility of outputs.

Conclusions

Surveillance outputs are valued but fragmented, with inconsistent awareness and accessibility. Users requested improved granularity, integration across platforms, timely data and focus on actionable messages. Co-creation, collaboration and knowledge mobilisation are essential to ensure usage and impact of outputs.

POSTER TOUR 23

Evidence to practice

Sporadic community-acquired Legionnaires' disease by distance to cooling towers; To what extent does distance matter?

ABSTRACT ID: 283

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Background

Cooling towers (CT) are potential sources of Legionnaires' disease (LD), but evidence for distance as a source proxy is limited. This study examined the association between distance to CTs and sporadic community-acquired LD incidence in the Netherlands (2022–2024).

Methods

A retrospective cross-sectional study included sporadic community-acquired LD cases (no known source or recent travel) reported in the Netherlands, 2022–2024 (N=1182). CT locations came from municipal health services and a national database. Distances from case postal codes to the nearest CT were calculated using the Rijksdriehoeksstelsel coordinate system. LD incidence (cases per 100,000 population) was calculated for 2022– 2024. Distances were banded as: 500-m intervals up to 3 km, 1-km intervals from 3–10 km, then 10–12.5 km, 12.5–15 km, and >15 km. Incidence rate ratios (IRRs) with 95% CIs were estimated using Poisson regression (expected counts as offset, reference 0–500 m).

Results

Sporadic community-acquired LD incidence was estimated at ~4.04 per 100.000 inhabitants. IRRs were elevated for distances up to 5km, ranging from 1.21 (95% CI 0.88–1.66) at 1–1.5km to 1.34 (95% CI 0.96–1.88) at 2–2.5km, with statistically significant increases at 2.5–3.0km (IRR 1.47, 95% CI 1.04–2.09), 3–4km (IRR 1.42, 95% CI 1.01– 1.99), and 4–5km (IRR 1.60, 95% CI 1.13–2.26). Beyond 5km, IRRs ranged 0.74 (95% CI 0.35–1.57) at 9–10km to 1.50 (95% CI 0.86–2.61) at >15km and were not significant.

Conclusions

Sporadic community-acquired LD incidence in the Netherlands varied across distance categories to CTs. No consistent increase was observed at the shortest distances, while several intermediate bands (2.5–5 km) showed significantly higher incidence, indicating spatial heterogeneity rather than a simple distance-response gradient. Currently, case investigations focus primarily on a 2-km radius. Expanding source-tracing radii to 5 km could improve case ascertainment, guide targeted CT maintenance, and reduce misattribution of sporadic cases, enhancing prevention of community-acquired LD outbreaks.

POSTER TOUR 23

Evidence to practice

The use of a multi-stream evidence synthesis to revise national Shiga toxin-producing Escherichia coli (STEC) infection guidelines on microbiological clearance in Norway, 2026

ABSTRACT ID: 226

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Background

Shiga toxin-producing Escherichia coli (STEC) can cause severe illness in vulnerable populations. In Norway, individuals in high-risk groups carrying high-virulent STEC strains are excluded from childcare or work until microbiologically cleared, defined as three consecutive negative stool samples. The socioeconomic impact of prolonged exclusions prompted an evidence synthesis to evaluate if less stringent guidelines were appropriate, examining STEC shedding duration, intermittent shedding, exclusion periods, required samples and microbiological methods for clearance.

Methods

Three evidence streams were integrated: a systematic literature review (2004-2024), mapping of European guidelines, and analysis of Norwegian laboratory surveillance data (MSIS-lab) (2023-2024). Databases were searched for Scandinavian and English publications and guidelines on relevant terms. From MSIS-lab, we extracted data on STEC-cases with ≥3 follow-up samples, including at least one negative, estimating: (i) median shedding duration (time from sample date to first of three negative samples); (ii) intermittent shedders (negative samples followed by positives); (iii) median exclusion time (time from sample date to clearance), comparing two versus three consecutive negative samples as clearance and (iv) methods (PCR or culture) used.

Results

Fourteen of 2309 studies were included, reporting median shedding of 10-39 days and 5-25% intermittent shedders. Nine of eleven guidelines recommended two negative samples for clearance. Of 109 MSIS-lab cases, 94 achieved clearance with median shedding of 13 days. Median exclusion time reduced from 24 to 20 days, with two versus three negative samples. Intermittent shedding was observed in 15 cases; four cases had two negative samples followed by a positive. Methods for clearance varied across evidence streams.

Conclusions

The evidence synthesis informed the revision of Norwegian STEC guidelines recommending two consecutive negative stool samples – either PCR-negative or PCR-positive but culture-negative – for high-virulent STEC cases in high-risk groups. Reducing required samples for clearance implies a minimal increased transmission risk and reduces the socioeconomic burden for affected individuals.

POSTER TOUR 23

Evidence to practice

Mind the gap: Rebound of post-pandemic respiratory infections in children born during the COVID-19 pandemic

ABSTRACT ID: 66

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Background

Non-pharmaceutical interventions (NPIs) during the COVID-19 pandemic altered the circulation of respiratory pathogens. Following an initial decline in infections, a resurgence occurred as restrictions eased. **Aims:** To determine whether reduced early-life exposure to pathogens increased the risk of severe respiratory infections.

Methods

In this longitudinal nationwide population-based study, we compared a pre-pandemic birth cohort from 2015 (n=94,552) with cohorts from 2018 (n=96,074) and 2020 (n=92,791). Baseline characteristics for the first two years of life were summarized. Outcomes were assessed between ages 2 to 4 years. Hospitalization for overall and specific lower respiratory tract infections (LRTI) was analysed as a binary outcome using logistic regression.

Results

Children born in 2020 had markedly lower hospitalisation rates during their first two years of life. However, between ages 2 and 4, they exhibited significantly higher hospitalisation risk compared with both pre-pandemic cohorts. Adjusted odds ratio (aOR) for hospitalisation in the 2020 versus 2015 cohort were: all-cause LRTI (2·51 (95%CI 2·26–2·79), influenza (2·99, 2·38–3·79) and respiratory syncytial virus (RSV) (4·36, 3·60–5·31). Similar patterns were observed for all-cause pneumonia and mycoplasma. The 2018 cohort showed a more mixed pattern, with lower risk for pneumonia but higher risk for RSV.

Conclusions

Children born during the COVID-19 pandemic initially had a reduced risk of hospitalisation for respiratory infections, followed by a substantially increased risk in the post-pandemic period compared to children born before the pandemic. These findings suggest that altered early-life microbial exposure due to pandemic-related restrictions may influence subsequent patterns of severe childhood infections.

Evidence to practice

Strengths, weaknesses, opportunities and threats (SWOT) of national surveillance systems for infectious diseases in Germany

ABSTRACT ID: 431

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Background

In Germany, multiple national surveillance systems for infectious diseases are in place to detect, monitor, and guide public health action, resulting in complementary data but also potential fragmentation. Structured, evidence-informed synthesis offers a way to support strategic development and policy decisions in this complex landscape. We aimed to systematically identify strengths, weaknesses, opportunities and threats (SWOT) across national surveillance systems for infectious diseases.

Methods

A SWOT analysis was conducted after identifying 29 surveillance systems at RKI through a landscape analysis with standardised SWOT matrices completed by system experts between October 2025 and January 2026. Data were analysed using qualitative thematic analysis and two-dimensional coding (SWOT elements and thematic codes) in MAXQDA. An inductive and iterative approach was used to identify cross-cutting patterns across systems.

Results

The SWOT analysis identified comprehensive and wide range of data available, timely availability of data, analytical capacity, and established national and international collaboration as main strengths. Underfunding, slow development and high costs for necessary IT-infrastructure, staff shortages and variability in data quality due to external dependencies were indicated as the primary weaknesses. Opportunities were identified in enhancing the representativeness and scalability and, increased use of advanced analytics including artificial intelligence, digitalisation, and using synergies between systems. Major threats included increasing needs for IT-security/ potential for cyber security attacks, uncertain long-term financing, and risks related to data governance and shifting policy priorities.

Conclusions

The SWOT analysis highlights a surveillance system landscape with strong analytical capabilities but persistent structural and resource-related vulnerabilities. The results inform the development of the national surveillance strategy, particularly in relation to strengthening infrastructure, ensuring sustainable financing, and improving data governance to support future integration and digitalisation.

POSTER TOUR 24

Late breakers (2)

Epidemiological and Molecular Investigation of Enteroviral Meningitis in the West Midlands, England, 2026

ABSTRACT ID: 1040

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Background

The West Midlands Health Protection Team (HPT) was notified of an increase in cases of viral meningitis presenting to a local NHS Trust. Subsequent notifications identified several cases linked to two nursery settings. These reports coincided with a period of increased untyped enterovirus meningitis cases in the West Midlands, England, compared to the preceding 10 years. A descriptive observational study investigated and characterised the epidemiology of this increase in cases.

Methods

Confirmed cases were those residing in two neighbouring sub-regions of the West Midlands with enterovirus detected from cerebrospinal fluid between 31st May and 14th August 2026. Probable cases were those with viral meningitis-like symptoms and a link to a confirmed case. Cases identified using laboratory reports from the Second-Generation Surveillance System and records held within the HPT case management system were included in this study. Cases were interviewed using a bespoke questionnaire.

Results

50 laboratory confirmed, and 10 probable cases were identified. Echovirus-6 accounted for 89% (33/37) of typed samples. Cases ranged in age from 1 month to 44 years (median=24). 36 cases were adults. 47 cases were hospitalised with the median length of stay being 2 days (IQR 2-3; range 0-8 days). Most cases (62%, 37/60) were linked to at least one early-years setting. A concurrent outbreak of Norovirus was also reported by one setting.

Conclusions

This study characterised a large outbreak of enteroviral meningitis in the West Midlands. The predominance of E6 suggests an outbreak, as opposed to a non-specific increase in enterovirus detections. Transmission appeared to be linked to early-years settings, with co-circulating diarrhoeal illness and inconsistent implementation of exclusion measures potentially contributing to the spread. While improvements in surveillance and diagnostics may have increased case ascertainment, given the severity of disease, ongoing surveillance and enterovirus typing in severe clinical presentations is important.

POSTER TOUR 24

Late breakers (2)

Monitoring of tendinitis and tendon rupture after ciprofloxacin use during the meningococcal B outbreak in Kent, 2026

ABSTRACT ID: 907

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Background

In response to England experiencing a large and unprecedented outbreak of group B invasive meningococcal disease in March 2026 in Kent, more than 13 000 individuals were identified as being at risk and received a single dose of ciprofloxacin prophylaxis. The UK Medicines and Healthcare products Regulatory Agency had previously published restricted indications for Ciprofloxacin following a temporal association between fluoroquinolones and tendinopathy and tendon rupture. Strengthened evidence on this association is needed in this young population to give confidence for future meningococcal contacts and outbreaks.

Methods

In June 2026 we undertook three different analytical approaches to assess the risk of tendinitis and tendon rupture after one dose of Ciprofloxacin. These included using established Emergency Care Data Set (ECDS) syndromic surveillance methodology, enhanced surveillance in the RCGP practice associated with the University of Kent and observed vs. expected analysis of tendinitis using national ECDS data linked to MenB vaccine records as a proxy for Ciprofloxacin receipt.

Results

Although, at national level there was a significantly raised observed-over-expected rate ratio of 1.49 (95% CI: 1.12-1.97) with the increase coinciding with the London and Manchester marathons this analysis did not show a signal when restricted to the London/South East area (incidence rate ratio 1.05 (95% CI:0.58-1.88) where the majority of the Kent students reside. This was confirmed by the syndromic surveillance results. The rates at the university medical practice did not change from baseline level in the period after Ciprofloxacin were given

Conclusions

Our results of no association with tendon rupture in this population should give confidence in the future use of one dose Ciprofloxacin for meningococcal outbreak management and reassure individuals who are required to receive this chemoprophylaxis as part of a rapid public health response to future Men B cases and clusters.

POSTER TOUR 24

Late breakers (2)

Persistent environmental contamination in a food premises linked to two neonatal listeriosis cases in England, 2026

ABSTRACT ID: 927

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Background

Listeria monocytogenes infection in pregnancy can result in severe neonatal disease by vertical transmission. In June 2026, two premature neonatal listeriosis cases, born 13 days apart, were identified at the same hospital in the East of England, prompting an outbreak investigation. Whole genome sequencing (WGS) results suggested a common source.

Methods

A case was defined as a person in England with laboratory-confirmed *L. monocytogenes* infection from May 2026 whose isolate was within the outbreak cluster by WGS. Information on (maternal) food exposures were collected through enhanced surveillance questionnaires (ESQs) and follow-up interviews. Repeated food and environmental sampling were undertaken at implicated food premises.

Results

Two neonatal listeriosis cases with indistinguishable isolates (0 SNPs) were identified. Initial ESQs linked one case's mother to a local vegetarian food premises; a shared exposure emerged only after targeted reinterviewing, when the premises was specifically named. Seven rounds of sampling between June and September 2026 were conducted at the premises; *L. monocytogenes* linked to the outbreak strain by WGS was identified in multiple foods and environmental samples, including high-level contamination of freshly prepared hummus (9.6 × 106 CFU/g) and a kitchen drainage vent pipe, consistent with a persistent environmental reservoir. Negative samples from raw ingredients including lemon juice and chickpeas provided evidence against ingredient contamination. Following formal closure, enhanced cleaning and modifications to the vent pipe, the most recent round of sampling yielded negative results. No further outbreak-associated cases were identified after reopening.

Conclusions

Combined epidemiological and environmental investigations highlighted an unusual cluster of neonatal listeriosis linked to maternal consumption of food contaminated by a persistent environmental reservoir. The outbreak highlighted the importance of repeated case interviewing, alongside WGS, as the key exposure was identified only after targeted follow-up questioning. These findings demonstrate the value of iterative hypothesis generation and re-interviewing in investigating rare listeriosis clusters.

POSTER TOUR 24

Late breakers (2)

Severe Shiga toxin-producing Escherichia coli (STEC) outbreak among young children linked to a petting farm, Belgium, 2026

ABSTRACT ID: 955

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Background

In June 2026, four cases of hemolytic uremic syndrome (HUS) caused by STEC were notified to the Regional Health Authority (RHA) in Flanders, Belgium, prompting a multidisciplinary investigation to confirm the outbreak, identify the source and implement control measures.

Methods

Suspected cases were Flanders residents with laboratory-confirmed STEC or HUS, symptom onset from 1 June. Probable cases were suspected cases with an epidemiological link to a confirmed case or to a specific petting farm. Confirmed cases were infected with the outbreak isolate as defined by the National Reference Centre (NRC). Clinical samples were sent to the NRC for confirmation, isolation and whole genome sequencing. The RHA alerted clinicians to enhance case finding and conducted structured interviews, revealing a shared pettingfarm exposure. The RHA and Food Safety Authorities conducted an on-site risk assessment, including food and animal faeces sampling.

Results

The outbreak isolate was identified as *E. coli* O26:H11 *stx*2a+, *eae*+, belonging to cgMLST HC5_297822 (EpiPulse inquiry 2026-FWD-00065). We registered ten outbreak cases (nine confirmed, one probable), symptom onset 17 June - 25 July. Eight cases developed severe HUS, exceeding provincial age-specific dialysis capacity, requiring transfer. Four cases had visited the petting farm; two were siblings of petting-farm-associated cases and one case attended the same nursery as two petting-farm-associated cases. No petting-farm link was identified for three cases. Risk assessment found inadequate hygiene practices at the petting farm. The outbreak strain was isolated from faeces of pigs, goats, and sheep; food samples tested negative. The petting farm was closed until control measures were implemented, including handwashing facilities, visitor education, and a one-way visitor flow through animal-contact areas.

Conclusions

This outbreak highlights the severe morbidity STEC can cause in young children and the risk of zoonotic and secondary transmission. Hygiene guidelines for petting farms are lacking or non-binding across much of Europe and need strengthening.

POSTER TOUR 24

Late breakers (2)

Time to population access for new immunisations across Europe: a 30-country analysis

ABSTRACT ID: 1019

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Background

Timely population access to new immunisations is essential to realise their public health benefits, yet evidence on access timelines across Europe remains limited. We assessed the time between regulatory approval and population-level access to new immunisations across European countries, identifying variation in access pathways and timelines.

Methods

We conducted a retrospective, multi-country analysis of immunisations first centrally authorised between 1 January 2013 and 31 December 2025 across 27 European Union Member States, Norway, Switzerland and the United Kingdom. Data collection was conducted from May to July 2026 through targeted searches of official regulatory, health authority, immunisation advisory body, vaccination programme and reimbursement sources. Population access was defined at country level as the point at which an immunisation became both recommended and publicly funded for routine use in the target population. Data were subsequently validated through standardised review and expert input.

Results

Population access to in-scope immunisations varied considerably across the 30 European countries assessed. Time to population access varies widely across Europe, with delays often extending to several years. Substantial variation was observed both between countries and between products within the same country. Differences were also apparent by disease area, target population and EMA decision type (original label vs label extension).

Conclusions

These findings highlight substantial cross-country differences in time to population access, raising concerns about equity in access to new immunisations across Europe. Systematic monitoring could support benchmarking and identify opportunities to reduce delays. The EU HTA Regulation may further support greater alignment and efficiency in vaccine assessment, contributing to more timely and equitable access.

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