



Final Programme

IMMEM XIV

**14th International Meeting on
Microbial Epidemiological Markers**

A photograph of a modern building facade with a complex, angular, and faceted concrete structure, set against a clear blue sky. The building's surface is composed of large, irregular concrete panels that create a dynamic, geometric pattern. The sky is a solid, vibrant blue.

**Porto, Portugal
17–20 September 2025**

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Hilton Porto Gaia Hotel

IMMEM/ESCMID 2025 - Pedro Santos
Rua Carvalhosa 114
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Welcome

Distinguished Colleagues,

On behalf of the European Society of Clinical Microbiology and Infectious Diseases (ESCMID) and the ESCMID Study Group for Epidemiological Markers (ESGEM), it is our privilege to extend a cordial welcome to the 14th edition of the International Meeting on Microbial Epidemiological Markers (IMMEM XIV).

In this edition, this esteemed gathering convenes in Porto, Portugal, from 17 to 20 September 2025, and will feature sessions dedicated to the theme of **“Microbial Typing: from Fundamental to Daily Microbiology.”** The meeting provides a crucial forum for scientists worldwide working on microbial epidemiology, to share methods and tools, to deepen their understanding of microbial evolution and to promote equity and equality in their research. Our comprehensive and meticulously curated scientific programme—developed by ten experts—showcases the latest advancements in the fields of Genomic Epidemiology and Microbial Typing. Over these four days, participants will have the opportunity to engage in stimulating conversations on a diverse array of topics, including strain or plasmid epidemiology, bioinformatics tools, genotypic resistance, novel typing methods, genomics for public health, and the evolution of vaccine-preventable pathogens. These crucial conversations will transpire during the oral and poster sessions, as well as during the scheduled social events.

The ESGEM-PHA4GE supported hackathon, which will precede the meeting, will bring together bioinformaticians and scientists from various international backgrounds to address pivotal challenges in microbial epidemiology and typing. The outcomes of this collaborative endeavor will be formally presented during IMMEM XIV.

IMMEM is ideal for promoting new connections and sharing experiences, especially between early-career researchers and senior colleagues, due to its friendly and relaxed atmosphere. This unique character of IMMEM extends from previous editions and is fostered by the lovely and pleasant city of Porto. Porto, Portugal’s second-largest city, provides a magnificent setting for our meeting, distinguished by its picturesque Douro River, Atlantic coastline, and historically significant architecture. We encourage you to allocate time to experience the city’s culinary specialities—such as Francesinha or Tripas à Moda do Porto—and perhaps partake in a tasting of the globally renowned Port wine from the contiguous Douro Valley.

We wish you an inspiring and professionally enriching conference experience and trust that you will enjoy the time spent in Porto.



Sincerely,

Natacha Couto
Chair of the Programme Committee

Programme Committee



Natacha Couto
United Kingdom
Chair of the Programme
Committee



Ângela Novais
Portugal



Sandra Reuter
Germany



Sylvain Brisse
France



Benjamin P. Howden
Australia



Luísa Peixe
Portugal
Local Committee member



Ana Raquel Freitas
Portugal
Local Committee member



Senjuti Saha
Bangladesh



Duncan MacCannell
United States



Kat Holt
United Kingdom

Faculty

Allison Lopatkin, Rochester, US
Amber Hartman Scholz, Leibniz, Germany
Ana Freitas, Porto, Portugal
Ângela Novais, Porto, Portugal
Angeline Ferdinand, Melbourne, Australia
Beatriz Guerra, Parma, Italy
Benjamin Howden, Parkville, Australia
Deborah Williamson, London, UK
Ed Feil, Bath, UK
Emma Griffiths, Vancouver, Canada
Erik Alm, Stockholm, Sweden
Francesc Coll, Valencia, Spain
Guido Werner, Wernigerode, Germany
Hillary Craddock, Dublin, Ireland
Jacob Moran-Gilad, Be'er Sheva, Israel
Jane Hawkey, Melbourne, Australia
João A Gama, Madrid, Spain
John Rossen, Groningen, Netherlands
Josefina Campos, Berlin, Germany
Kat Holt, London, UK
Laurent Poirel, Fribourg, Switzerland
Leonid Chindelevitch, London, UK
Lorena López Cerero, Seville, Spain
Luísa Peixe, Porto, Portugal
Mael Bessaud, Paris, France
Maria Chuvochina, Brisbane, Australia
Martin Antonio, Banjul, Gambia
Nabil Fareed-Alikhan, Oxford, UK
Natacha Couto, Oxford, UK
Nicki Tiffin, Cape Town, South Africa
Norelle Sherry, Melbourne, Australia
Sandra Reuter, Freiburg, Germany
Senjuti Saha, Dhaka, Bangladesh
Sylvain Brisse, Paris, France
Teresa Coque, Madrid, Spain
Theo Sanderson, London, UK
Torsten Seemann, Melbourne, Australia
William Matlock, Oxford, UK
Zam Iqbal, Bath, UK

Scientific Programme

Registration opens each day at 8 am local time.

Time	Wednesday 17 September	Thursday 18 September	Friday 19 September	Saturday 20 September
08:30 – 09:00		Session 3 Novel typing and nomenclature approaches	Session 7 Role of environmental surveillance in controlling infectious diseases and AMR	Session 9 Genomics informed resistance profiling
09:00 – 09:30				
09:30 – 10:00		Break	Break	
10:00 – 10:30				
10:30 – 11:00		Session 4 Genomics implementation at the public health interface	Session 8 Pathogen data sharing and equity	
11:00 – 11:30				
11:30 – 12:00	Integrated Symposium Organized by Standard Biotools			Prize announcements
12:00 – 12:30	Light lunch	Lunch	ESGEM Awards	
12:30 – 13:00				
13:00 – 13:30	Session 1 Plasmid Typing for Surveillance	Session 5 Genomics to inform vaccine strategies	Lunch	Closing session
13:30 – 14:00				
14:00 – 14:30		Break	Poster session (even numbers)	Farewell Cocktail
14:30 – 15:00				
15:00 – 15:30	Session 2 Bacterial strain typing - when, how and where?	Session 6 What's new in Bioinformatics	Poster session (odd numbers)	
15:30 – 16:00				
16:00 – 16:30				
16:30 – 17:00				
17:00 – 17:30		Break		
17:30 – 18:00		Opening Ceremony		
18:00 – 18:30				
18:30 – 19:00				
19:00 – 19:30				
19:30 – 20:00	Cocktail	Faculty Dinner	Conference Party	Break
20:00 – 20:30				Scientific Programme
20:30 – 21:00				Networking Reception
21:00 – 21:30				

Scientific Programme

Wednesday, 17 September 2025

11:30-12:00 Integrated Symposium

Organized by Standard Biotoools

11:30-12:00 **Identifying multiple pathogens and ARGs simultaneously**

*Roberto Spada
(Strasbourg, France)*

12:00-13:00 **Light lunch**

13:00-15:00 **Plenary Session**

Plasmid typing for surveillance

*Chairs: Teresa Coque (Madrid, Spain)
Ed Feil (Bath, United Kingdom)*

13:00-13:30 **Evolution and distribution of plasmids and resistance genes**

João A Gama (Madrid, Spain)

13:30-14:00 **Plasmid dynamics in One Health**

William Matlock (Oxford, United Kingdom)

14:00-14:30 **Determinants of plasmid acquisition and selection**

Allison Lopatkin (Berkeley, United States)

14:30-14:45 **A 12-year survey of vancomycin-resistant *Enterococcus faecium* in a tertiary hospital reveals the rise in bac43 prevalence and emergence of linear Vana plasmids**

*Ana Almeida Santos
(Porto, Portugal)*

14:45-15:00 **Plasmid dynamics and local clonal spread of carbapenem-resistant *Klebsiella pneumoniae* over nine years**

Stefano Gaiarsa (Pavia, Italy)

15:00-15:30 **Break**

15:30-17:00 **Debate Session**

Bacterial strain typing: when, how and where?

*Chairs: Jacob Moran-Gilad (Be'er Sheva)
Ângela Novais (Porto, Portugal)*

15:30-15:45 **Introduction to current typing methods**

Guido Werner (Wernigerode, Germany)

15:45-16:15 **Tailoring strain typing workflows in high-income countries: balancing innovation and cost-effectiveness**

Lorena López Cerero (Seville, Spain)

16:15-16:45 **Challenges and opportunities for bacterial strain typing in resource-limited settings**

*Senjuti Saha
(Dhaka, Bangladesh)*

16:45-17:00 **Discussion**

17:00-17:30 **Break**

Scientific Programme

Wednesday, 17 September 2025

- 17:30–21:30 **Opening Ceremony**
Chairs: *Luisa Peixe (Porto, Portugal)*
 Benjamin Howden
 (Parkville, Australia)
- 17:30 – 17:40 **Welcome from ESCMID EC**
 Robert Skov
 (Copenhagen, Denmark)
- 17:40 – 17:50 **Welcome from ESGEM**
 Natacha Couto
 (Oxford, United Kingdom)
- 17:50 – 18:00 **Welcome from local committee**
 Ana Freitas (Porto, Portugal)
- 18:00–18:45 **How to translate genomics
epidemiology into policy
making?**
 Deborah Williamson
 (London, United Kingdom)
- 18:45–19:30 **Carbapenemases: where and
how? The rise in livestock and
food products**
 Laurent Poiriel
 (Fribourg, Switzerland)
- 19:30–21:30 **Welcome cocktail**

Scientific Programme

Thursday, 18 September 2025

08:30–10:00	Plenary sessions	11:00–11:30	Principles for evaluating the utility of pathogen genomics for surveillance and outbreak response <i>Angeline Ferdinand (Melbourne, Australia)</i>
	Novel typing and nomenclature approaches		
<i>Chairs:</i>	<i>Senjuti Saha (Dhaka, Bangladesh)</i> <i>Sandra Reuter (Freiburg, Germany)</i>	11:30–12:00	Global initiatives to supportive effective implementation and utilisation of pathogen genomics <i>Josefina Campos (Berlin, Germany)</i>
08:30–09:00	GTDB species classification and nomenclature <i>Maria Chuvochina (Brisbane, Australia)</i>	12:00–12:15	An overview of metagenomic environmental sampling from a melioidosis-endemic area <i>Chalita Chomkatekaew (Cambridge, United Kingdom)</i>
09:00–09:30	LIN codes – Novel bacterial strain taxonomy <i>Sylvain Brisse (Paris, France)</i>	12:15–12:30	Genomic surveillance and antimicrobial resistance of <i>Vibrio cholerae</i> in Africa: insights from the PulseNet Africa Network <i>Ebenezer Foster-Nyarko (London, United Kingdom)</i>
09:30–09:45	LIN codes for the genomic taxonomy of <i>Corynebacterium diphtheriae</i> strains <i>Jose Francisco Delgado-Blas (Paris, France)</i>		
09:45–10:00	Fourier transform infrared (FT-IR) spectroscopy for discrimination between global <i>Escherichia coli</i> sublineages <i>Astrid Rasmussen (Copenhagen, Denmark)</i>	12:30–13:30	Lunch Break
10:00–10:30	Break		
10:30–12:30	Plenary session		
	Genomics implementation at the public health interface		
<i>Chairs:</i>	<i>Guido Werner (Wernigerode, Germany)</i> <i>Deborah Williamson (London, United Kingdom)</i>		
10:30–11:00	Application of pathogen genomics in public health decision-making <i>Benjamin Howden (Parkville, Australia)</i>		

Scientific Programme

Thursday, 18 September 2025

13:30–15:00	Plenary session	16:15–16:30	Enhancing AMR research and surveillance: introducing the AMRgen R package for gene and phenotypic resistance interpretation <i>Matthijs S. Berends (Groningen, Netherlands)</i>
Genomics to inform vaccine strategies			
<i>Chairs:</i>	<i>Sylvain Brisse (Paris, France) Beatriz Guerra (Parma, Italy)</i>		
13:30–14:00	Vaccine surveillance for invasive bacterial infections in children <i>Martin Antonio (Banjul, Gambia)</i>	16:30–16:45	Enhancing genomics-based surveillance with ReporTree and the added value of dynamic cg/wgMLST approaches in outbreak detection and investigation <i>Verónica Mixão (Lisbon, Portugal)</i>
14:00–14:30	Global polio diversity and vaccination strategies <i>Mael Bessaud (Paris, France)</i>	16:45–17:00	Bacterial taxonomic identifier (BACTAX-ID): a novel method for bacterial classification <i>Val Fernandez Lanza (Madrid, Spain)</i>
14:30–14:45	Dynamics of antigenic turnover in the global <i>Klebsiella pneumoniae</i> population <i>Erkison Ewomazino Odih (Edmonton, Canada)</i>		
14:45–15:00	Emergence of macrolide-resistant <i>Bordetella pertussis</i> in France, 2024: out of China <i>Carla Rodrigues (Paris, France)</i>		
Break		17:00–19:00	Poster session (odd numbers)
15:00–15:30	Break		
15:30–17:00	Bioinformatics session		
What's new in Bioinformatics?			
<i>Chairs:</i>	<i>Nabil Fareed-Alikhan (Oxford, United Kingdom) Jane Hawkey (Melbourne, Australia)</i>		
15:30–16:00	Hackathon results <i>Nominated Hackathon representative</i>		
16:00–16:15	Fast and accurate <i>in silico</i> antigen typing with Kaptive 3 <i>Tom Stanton (Melbourne, Australia)</i>		

Scientific Programme

Friday, 19 September 2025

08:30–10:30 Plenary session

Role of environmental surveillance in controlling infectious diseases and AMR

Chairs: Ana Freitas (Porto, Portugal)
Natacha Couto
(Oxford, United Kingdom)

08:30–09:00 **Wastewater and AMR: control and monitoring within the One Health framework**
Hillary Craddock (Dublin, Ireland)

09:00–09:30 **Wildlife monitoring for pathogen surveillance**
Jacob Moran-Gilad
(Be'er Sheva, Israel)

09:30–10:00 **The value of wastewater surveillance at the hospital level**
John Rossen
(Groningen, Netherlands)

10:00–10:15 **Genomic insights into linezolid-resistant *Enterococcus* spp. from clinical, community and environmental samples from Victoria, Australia**
Jia Qi Beh (Melbourne, Australia)

10:15–10:30 **Tracking MRSA in the sewer: early insights from urban wastewater genomic surveillance**
Jennifer Guthrie
(London, Canada)

co-organised with the ESCMID Study Group for Food and Water-borne Infections (EFWISG)

10:30–11:00 Break

11:00–13:00 Panel discussion

Pathogen data sharing and equity

Chairs: Josefina Campos
(Berlin, Germany)
Torsten Seemann
(Melbourne, Australia)

11:00 – 11:20 **Data standards to support sharing**
Emma Griffiths (Vancouver, Canada)

11:20 – 11:40 **Models for data sharing and governance**
Nicki Tiffin
(Cape Town, South Africa)

11:40 – 12:00 **Pathoplexus – a new platform for data sharing**
Theo Sanderson
(London, United Kingdom)

12:00 – 13:00 **Panel Discussion**
Emma Griffiths (Vancouver, Canada)
Theo Sanderson
(London, United Kingdom),
Nicki Tiffin
(Cape Town, South Africa)
Erik Alm (Stockholm, Sweden)
Amber Hartman Scholz
(Leibniz, Germany)

13:00–14:00 Lunch Break

14:00–16:00 **Poster session**
(even numbers)

19:30–21:30 Conference party

Scientific Programme

Saturday, 20 September 2025

09:00–11:00	Plenary session	12:10 – 13:30	Lectures
	Genomics informed resistance profiling		ESGEM Awards
<i>Chairs:</i>	<i>Kat Holt (London, United Kingdom) Zam Iqbal (Bath, United Kingdom)</i>	<i>Chairs:</i>	<i>Natacha Couto (Oxford, United Kingdom) Fidelma Fitzpatrick (Dublin, Ireland)</i>
09:00–09:30	Application of genomics for AMR testing at clinical and public health interface <i>Norelle Sherry (Melbourne, Australia)</i>	12:10 – 12:35	ESGEM Lifetime Achievement Awardee presentation <i>Marc Struelens (Bruxelles, Belgium)</i>
09:30–10:00	Predicting AMR phenotypes from genomic data: the need for big data, improved curation, and new prediction methods <i>Francesc Coll (Valencia, Spain)</i>	12:35 –13 :00	ESGEM Young Investigator Awardee presentation <i>Carla Rodrigues (Paris, France)</i>
10:00–10:30	Building a WHO-endorsed catalogue of mutations for <i>Mycobacterium tuberculosis</i> <i>Leonid Chindelevitch (London, United Kingdom)</i>	13:00–13:30	Closing session
10:30–10:45	AMRrules: expert-curated interpretive standards for AMR genotypes <i>Jane Hawkey (Melbourne, Australia)</i>	13:00–13:30	Farewell cocktail
10:45–11:00	Creating rules for interpreting genetic determinants of antimicrobial resistance in <i>Neisseria gonorrhoeae</i>: insights and challenges <i>Leonor Sánchez-Busó (Valencia, Spain)</i>		
11:00–11:30	Break		
11:30–12:00	Prize announcement		

Poster presentations

At IMMEM XIV selected paper posters will be shown during two dedicated poster sessions.

Thursday, 18 September 2025: Poster session (odd numbers): 17:00–19:00 WEST

Friday, 19 September 2025: Poster session (even numbers): 14:00–16:00 WEST

During these sessions the presenting author will be standing next to their poster and lively discussions are encouraged. Refreshments and snacks will be offered, while the sessions are taking place, for the presenters and attendees.

1. New or updated bioinformatics tools

Poster	Abstract title	Presenter
P139	Bringing custom visual reporting to Bactopia workflows	Read, Timothy
P140	Sub-lineage clusterings and classifications of global pneumococcal bacteria using PopPUNK lineage model	Lu, Xi
P141	Towards a new sequencing era - Oxford Nanopore Technologies sequencing as a method for bacterial characterisation and outbreak investigation?!	Deneke, Carlus
P142	Barbet: a deep learning approach to bacterial taxonomic classification	Wirth, Wytamma
P143	Diana: a WebAssembly-powered tool for transposon-directed insertion-site sequencing (TraDIS) data exploration and analysis	Wirth, Wytamma
P144	Snippy-NG: the next generation of microbial variant calling	Wirth, Wytamma
P145	Scalable sequence alignment with kbo	Mäklin, Tommi
P146	Bioinformatics toolbox for comparative clustering evaluation of whole-genome sequencing (WGS) pipelines for bacteria routine surveillance and outbreak investigation	Pereira, Joana
P147	Efficient and interactive wg/cgMLST analysis of bacterial pathogens with chewBBACA 3	Ramirez, Mario
P148	Bait design for target-enrichment of bacterial pathogens with proBait	Ramirez, Mario
P149	BakRep – a searchable large-scale web repository for bacterial genomes, characterisations and metadata	Schwengers, Oliver
P150	Generalisable machine learning framework for viral classification based on dinucleotide frequency signatures	Gajdov, Vladimir
P151	A species-specific framework for bacterial genome assembly quality control	Alikhan, Nabil-Fareed
P153	Computational workflow for identifying borderline-oxacillin resistant <i>Staphylococcus aureus</i> variants	Adegoke, Joseph
P154	Comparison of two commercial whole genome-based analysis for carbapenemase-producing <i>Pseudomonas aeruginosa</i> ST175 typing	Lopez Cerero, Lorena

Poster presentations

2. Resistance profiling using genomics data

Poster	Abstract title	Presenter
P160	Ciprofloxacin resistance in <i>Klebsiella pneumoniae</i> : phenotype prediction from genotype and global distribution of resistance determinants	Tsang, Kara
P161	Dru repeats and the origin of the Staphylococcal Cassette Chromosome mec (SCCmec)	Worning, Peder
P162	Exploring the effect of genetic variations in oxidative stress pathways and iron transporters on cefiderocol susceptibility in <i>Klebsiella pneumoniae</i>	Daoud, Lana
P163	<i>Mycobacterium tuberculosis</i> lineage typing and drug resistance prediction direct from culture free sputum nanopore sequencing	Coin, Lachlan
P165	Converging resistance and virulence in <i>K. pneumoniae</i> species complex isolates from a large UK tertiary referral centre	Ferreira, Ana
P166	Novel genomic determinants of trimethoprim-sulfamethoxazole resistance in <i>Staphylococcus epidermidis</i>	Sieber, Raphael
P167	Connecting the dots: phenotypic and genotypic antimicrobial resistance in <i>Gardnerella</i>	Ribeiro Gonçalves, Teresa
P168	Mobile genetic elements carrying macrolide resistance genes among pharyngeal <i>Streptococcus pyogenes</i> isolates	Ramirez, Mario
P169	Uncommon genomic rearrangements drive vancomycin resistance in vanB-positive <i>Enterococcus faecium</i>	Xanthopoulou, Kyriaki
P170	Epidemiology of <i>Achromobacter xylosoxidans</i> in Belgium and evaluation of phenotypic and genotypic antimicrobial resistance based on genomic data	Michel, Charlotte
P172	Leveraging artificial intelligence to uncover genetic determinants of susceptibility to novel diazabicyclooctanes in <i>Escherichia coli</i>	Al Marzooq, Farah
P173	Congruence between phenotypic determination and genomic prediction of macrolide, lincosamide, and tetracycline resistance in <i>Streptococcus pyogenes</i> : great but not perfect	Ramirez, Mario
P174	Bioinformatic improvements in genotypic AMR prediction in <i>Enterococcus faecium</i>	García-González, Neris
P175	Surveillance of antimicrobial resistance genes in wastewater from hospital and community sources using high-throughput qPCR: insights from the United Arab Emirates	Shouqair, Douha
P176	Interlaboratory comparison of WGS-based detection of genetic AMR markers in <i>Salmonella</i> and <i>Campylobacter</i>	Ligowska-Marzeta, Malgorzata
P177	Molecular characterisation of <i>Escherichia coli</i> isolates, and other Enterobacterales, recovered from hospital patients in Quetta, Pakistan	Habib, Samia

Poster presentations

2. Resistance profiling using genomics data

Poster	Abstract title	Presenter
P179	Antimicrobial resistance of <i>Salmonella</i> Newport isolated in poultry flocks in 2011-2020 in Poland	Kwit, Renata
P180	Prevalence and molecular epidemiology of <i>Klebsiella pneumoniae</i> producing dual carbapenemases	Daoud, Lana
P182	Genomic characterisation of a KPC-producing <i>Klebsiella pneumoniae</i> clinical isolate resistant to meropenem-vaborbactam, imipenem-relebactam, and ceftazidime-avibactam	Wan, Yu
P184	Genome wide next-generation sequencing for determining <i>Helicobacter pylori</i> antimicrobial resistance	van Der Reijden, Wil
P186	Concordance between the presence of the mupA gene and phenotypic resistance in MRSA	Bartels, Mette Damkjær
P187	Antimicrobial resistance: a fresh look at SCCmec diversity in multidrug-resistant MRSA	Rønning, Torunn
P190	Integrated wastewater-based surveillance for antimicrobial resistance monitoring in Dubai, United Arab Emirates: a focus on <i>Staphylococcal</i> species	Shouqair, Douha
P191	Red foxes (<i>Vulpes vulpes</i>) as a reservoir of resistant <i>Escherichia coli</i>	Skarzynska, Magdalena

Poster presentations

3. Strain or Plasmid epidemiology

Poster	Abstract title	Presenter
P001	Genomic epidemiology of ESBL-E carriage among infants in Haydom, Tanzania: assessing the role of probiotics, birth setting, and age	Hetland, Marit
P002	<i>Phytobacter</i>, an environmental reservoir of plasmids carrying acquired class A, B and C beta-lactamases and metal resistance genes in the hospital-built environment	Guerra Pinto, Natalia
P003	Same swab, same clone? Split k-mer analysis reveals single nucleotide variants in core-genome concordant ESBL-producing <i>Klebsiella pneumoniae</i> isolates from the same patient swabs	Maechler, Friederike
P004	<i>Serratia sarumanii</i> in hospital outbreaks in Andalusia	Lopez Cerero, Lorena
P006	Applying rearrangement distances to enable plasmid epidemiology with pling	Frolova, Daria
P007	Simultaneous presence of different carbapenemase-producing <i>Enterobacteriaceae</i> species harboring the same carbapenemase gene in individual patients: a potential driver of plasmid-mediated outbreaks	Celar Šturm, Andraž
P008	Diversity and taxonomic classification of <i>Campylobacterota</i> plasmids and development of a <i>Campylobacter</i> plasmid typing scheme	Duim, Birgitta
P009	Swiss outbreak of VIM-1 carrying <i>Enterobacter</i> displays plasmid transmission between sequence types	Seth-Smith, Helena
P010	IncHI2 plasmids drove dissemination of carbapenemase gene <i>bla</i>_{IMP} among healthcare-associated Enterobacterales in the UK, 2014-2022	Jauneikaite, Elita
P011	Cross-domain plasmid mediated AMR transmission	Koeck, Rebekka
P012	Core genome MLST scheme for <i>Klebsiella pneumoniae</i> with high-discriminatory-power	Ovsepijan, Armen
P013	Population genetics of antibiotic-resistant <i>Campylobacter jejuni</i> in broilers in Finland – vertical transmission, fact or fiction?	Jaakkonen, Anniina
P014	The ICU environment contributes to the persistence and evolution of <i>Klebsiella</i> species in hospitals	Guerra Pinto, Natalia
P015	The benefits of routine genome-oriented surveillance for <i>Pseudomonas aeruginosa</i>	Rath, Anca
P016	Norwegian linezolid resistant enterococci show great diversity and novel mobile genetic elements	Hegstad, Kristin

Poster presentations

3. Strain or Plasmid epidemiology

Poster	Abstract title	Presenter
P017	The plasmidome and resistome of mercury-resistant Enterobacterales from healthy children living in urban polluted areas	López López, Carolina
P018	Characteristics and epidemiology of the novel OXA-48-like carbapenemase OXA-1207 from <i>E. coli</i>	Sommer, Julian
P019	Plasmid networks of ESBL-producing <i>E. coli</i> from humans and different environmental sources in Slovenia	Maric, Leon
P020	Genomic surveillance of diarrheagenic <i>Escherichia coli</i> unravels the diversity of Enteropathogenic <i>E. coli</i> (EPEC) lineages circulating in Europe	Silva Nodari, Carolina
P022	Plasmid-mediated convergence of carbapenem-resistance and hypervirulence in <i>Klebsiella pneumoniae</i> from an Indian tertiary care hospital	Kulkarni, Sanika
P023	Isolation of hospital-associated vancomycin resistant <i>Enterococcus faecium</i> clones from German rivers	Higgins, Paul G.
P024	Prevalence and serotype distribution of <i>Streptococcus pneumoniae</i> among preschool children attending immunisation clinics in Sri Lanka	Ip, Margaret
P025	Phage-plasmids as an overlooked mobile element in gastrointestinal pathogens	Barker, Clare
P026	Comparative longitudinal epidemiology of vancomycin-resistant <i>Enterococcus faecium</i> from bloodstream infections at four tertiary care hospitals in Bavaria, Germany	Rath, Anca
P028	Genomic epidemiology of 12 bp duplications in <i>ftsI</i> in clinical isolates of <i>Escherichia coli</i> in a tertiary hospital in Denmark	Schønning, Kristian
P029	Exploring the epidemiology and genetic complexity of <i>Escherichia coli</i> in vertically integrated pig farming in Spain using whole genome sequencing. A retrospective study, 2018–2022	Migura-Garcia, Lourdes
P030	Categorising the diversity of plasmids harboured by <i>Klebsiella pneumoniae</i> , <i>Escherichia coli</i> and related <i>Enterobacteriaceae</i> from diverse One Health settings	Feil, Edward
P031	A fly in the ointment: IncX3 plasmids harbouring blaSHV-12 isolated from patients and flies in a hospital in Italy	Gibbon, Marjorie
P032	Comparative genomic analysis of methicillin-resistant <i>Staphylococcus aureus</i> strains isolated from humans and companion animals	Yin, Nicolas
P033	Understanding within-patient plasmid dynamics to better understand AMR genes spread	Alice, Ledda

Poster presentations

3. Strain or Plasmid epidemiology

Poster	Abstract title	Presenter
P035	Epidemiological investigations involving plasmids– finding uniqueness in chaos	Hasman, Henrik
P036	One Health approach reveals an IncI1 plasmid-<i>Escherichia coli</i> clone association responsible for bla_{CTX-M-32} ESBL gene inter-ecological transmission	Favieres, Javier F.
P038	Spread and copy number change in a common small tetracycline resistant plasmid of <i>Staphylococcus aureus</i> over the past 70 years inferred from public sequence data	Read, Timothy
P040	Carbapenem-resistant <i>Acinetobacter baumannii</i> in patients and environment of a tertiary hospital in Hong Kong, 2014 - 2022	Li, Carmen
P041	ST398 methicillin-susceptible <i>Staphylococcus aureus</i> in Portugal were associated to severe atopic dermatitis	Araújo , Mariana
P042	Plasmid diversity of carbapenamase-producing <i>Escherichia coli</i> isolated from southern Brazil	Martins, Andreza
P043	Mobile genetic elements of hypervirulent KPC-producing <i>Klebsiella pneumoniae</i> ST11 disseminating in Oman	Al Bulushi, Mohamed
P044	Widespread of CTX-M variants among <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> lineages of humans, livestock and wildlife origin from Western Uganda	Migura-Garcia, Lourdes
P045	A ten-year genomic landscape of <i>Streptococcus pyogenes</i> causing bloodstream infections in an Italian hospital	Gaiarsa, Stefano
P047	Thirteen months of routine <i>Staphylococcus aureus</i> surveillance and typing using whole genome sequencing at a Danish University hospital	Simonsen, Jo
P048	Complete genome reconstruction of <i>Salmonella Enteritidis</i> using hybrid approach	Kamińska, Ewelina

Poster presentations

4. Novel typing methods

Poster	Abstract title	Presenter
P050	Comparative analysis of short-read and long-read sequencing technologies for characterising <i>Staphylococcus aureus</i> clinical isolates	Haugan, Ingvild
P051	Advancing <i>Legionella pneumophila</i> genomic surveillance with a high-resolution cg/wgMLST schema for outbreak detection and investigation	Mixão, Verónica
P052	Comparison of McRAPD and FTIR for high-throughput pre-sequencing screening of <i>Klebsiella</i> isolates: validation by WGS and results of one-year continuous monitoring of clonality in three ICUs	Raclavsky, Vladislav
P053	Comparison of two methods for whole genome sequencing of hepatitis C virus	Paulsen, Sarah
P054	Conserved spectral signatures across culture conditions enable FT-IR- based identification of major bloodstream infection pathogens	Martins, Rita
P055	<i>Streptococcus pneumoniae</i> carriage and serotype distribution in children after the end of COVID-19 restrictions in Portugal: a saliva-based study	Sá-Leão, Raquel
P056	Next-generation sequencing (NGS)-based pathogen characterisation: from culture-based genomic typing to advanced syndromic-panel metagenomic sequencing	Oh, Sujin
P057	Timely detection and subtyping of upper respiratory pathogens using a microfluidics-based workflow	Spada, Roberto
P058	FT-IR spectroscopy for the rapid and accurate prediction of capsular types in <i>Acinetobacter baumannii</i>	Roca, Ignasi
P059	A novel amplicon-based nanopore sequencing method for rapid <i>Klebsiella pneumoniae</i> typing	Capitani, Valerio
P060	From Sanger sequencing to MAMA-PCR: differentiation of <i>Klebsiella pneumoniae</i> species complex (KpSC) via <i>rpoB</i> gene	Sharmin, Mehbooba
P061	Discriminating closely related <i>Enterococcus</i> species via FT-IR-based biochemical profiling and machine-learning	Novais, Angela

Poster presentations

5. Genomics for public health

Poster	Abstract title	Presenter
P063	Phyletic patterns-based model to inform the emergence rate of transmissible traits in bacterial population	Batisti Biffignandi, Gherard
P065	The evolutionary trajectory of <i>Klebsiella pneumoniae</i> ST147 in India is defined by multiple introductions and capsular shifts	Shamanna, Varun
P066	Enhancing European Union genomic surveillance through the ECDC and EFSA One Health WGS System	Rossi, Mirko
P067	VaccinesWatch: monitoring of vaccine targets and interventions using global genome data	Alikhan , Nabil-Fareed
P068	Game of clones: sequential emergence and expansion of multi- and extensively-drug-resistant <i>Shigella</i> in Australia	Sherry, Norelle
P069	The microbiome and resistome in the "ICU patient-care environment", a longitudinal multi-omic study using pooled faecal sampling	Aracil-Gisbert, Sonia
P070	FOGS: a novel time-aware index of bacterial genome plasticity to predict emerging high-risk clones	Gaiarsa, Stefano
P071	Accurate genotyping of three major respiratory bacterial pathogens with ONT R10.4.1 long-read sequencing	Crestani, Chiara
P072	Evidences of adaptation of <i>Staphylococcus aureus</i> to atopic dermatitis skin lesion	Araújo, Mariana
P073	Comparing genomic-based machine learning approaches for source attribution of <i>Salmonella Typhimurium</i>	Paganini, Julian
P074	Implementing a pathogen genomics program at the BC Centre for Disease Control Public Health Laboratory, British Columbia, Canada	Zlosnik, James
P075	amr.watch – monitoring antimicrobial resistance trends from global genomics data	Couto, Natacha
P076	Setting up a regional AMR surveillance network in the Netherlands: challenges and opportunities	Koopman, Pieter
P077	<i>Candida</i> spp. sweep-metagenomics to study species and strain diversity within and between patients in a large hospital cohort	Sassera, Davide
P078	Genomic insights into a neonatal outbreak of <i>Klebsiella pneumoniae</i> in a rural Gambian hospital	Foster-Nyarko, Ebenezer
P079	Multi-country and intersectoral assessment of cluster congruence between different bioinformatics pipelines for genomics surveillance of bacterial pathogens	Mixão, Verónica
P080	Evolutionary dynamics and virulence factor variability in invasive <i>Streptococcus pyogenes</i> in Norway, 2017-2023	Brynildsrud, Ola

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5. Genomics for public health

Poster	Abstract title	Presenter
P081	Six years (2018–2023) of WGS-based national sentinel surveillance of <i>Clostridioides difficile</i> linked to hospital/ community-associated infection data, all-cause mortality, and patient home addresses	Persson, Soren
P082	Genomic surveillance of antimicrobial resistance reservoirs in the critical care environment	Verkerk, Anne
P084	Thirty years of adaptation: genomic insights into the Danish epidemic strain of <i>Achromobacter ruhlandii</i>	Gabrielaite, Migle
P086	Genomic diversity of <i>Enterobacteriaceae</i> on food-processing surfaces: an overlooked non-clinical setting with public health implications	Antunes, Patricia
P087	SOFI – a platform for sequence-based, cross-sectoral, one-health-based surveillance of foodborne infections in Denmark	Rømer Villumsen, Kasper
P088	Evaluation of routine One Health WGS-based surveillance of <i>Salmonella enterica</i> in the Netherlands	Stege, Paul
P089	Metagenomic surveillance of antimicrobial resistance genes in rivers used for drinking water production	Novais, Carla
P090	<i>Bordetella pertussis</i> resurgence and outbreak in Israel during 2023–2024 – a genomic and epidemiological study	Rokney, Assaf
P091	From sex to septicemia, <i>E. coli</i> bloodstream infections with a urinary focus in young women	Gladstone, Rebecca
P092	Source attribution of Shiga-toxin-producing <i>Escherichia coli</i> (STEC): a multinational study in Europe using virulence profiles and core-genome multi locus-sequence typing	Schadron, Tristan
P093	STEC virulence barcoding for capturing pathogenic potential of Shiga toxin producing <i>Escherichia coli</i>	Sim, Eby
P094	Detection of XDR Shigella spp. clusters through national genomic surveillance in the Netherlands, 2022-2024	van Der Putten, Boas
P096	Human infections by the novel zoonotic species <i>Corynebacterium silvaticum</i>	Dangel, Alexandra
P097	Genomics uncover resistant and virulent <i>Klebsiella</i> on foods: a potential risk to human health	Yap, Min
P098	Resistance to extended-spectrum cephalosporins and carbapenems in wildlife in France	Haenni, Marisa
P099	Genomic diversity of <i>Klebsiella pneumoniae</i> species complex in the human gut: evidence of infection-related strains with food-chain origins	Nova, Lúcia

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5. Genomics for public health

Poster	Abstract title	Presenter
P100	Genetic characterisation of carbapenem-resistant <i>Klebsiella pneumoniae</i> isolates from a Ukrainian hospital	Sobkowiak, Annika
P101	Comparative genomics and pangenome analyses of global <i>Staphylococcus lugdunensis</i> isolates	Jauneikaite, Elita
P102	The caveats and (im)possibilities of tracking outbreaks directly from swabs in neonates	Ayala Montaña, Stefany
P103	Factors impacting hospital-associated microbial communities composition and stability	Linares Ambohades, Iván
P104	Insight into the distribution of antimicrobial resistance through wastewater-based surveillance	Stoffers, Karelina
P105	Molecular epidemiology and transmission dynamics of Carbapenem-resistant <i>Acinetobacter baumannii</i> in a tertiary hospital	Keidar-Friedman, Danielle
P106	Increasing burden of ST398 methicillin-susceptible <i>Staphylococcus aureus</i> bloodstream infections in Portugal: a nationwide survey	Conceicao, Teresa
P108	Tracing <i>campylobacter</i> in Danish broilers: persistence, clonal spread, and human infection links	Persson, Søren
P109	Prospective WGS for surveillance and outbreak investigation at a Danish University Hospital	Vognbjerg Sydenham, Thomas
P110	Genomic surveillance of <i>Yersinia enterocolitica</i> in Norway reveals an absence of dominant cluster types	Pires, João
P111	Identification and characterisation of bactericidal tailocins against high-risk clones of <i>Pseudomonas aeruginosa</i>	Sarkar, Himadree
P112	Epidemiology of <i>Klebsiella pneumoniae</i> resistant to extended-spectrum cephalosporins and carbapenems in French companion animals	Haenni, Marisa
P113	The role of OXA-48/-181/-244-producing <i>Enterobacter</i> spp. in OXA-48 epidemiology in Poland by 2023	Izdebski, Radosław
P114	Genomic surveillance strategy for tuberculosis in Catalonia: TB-SEQ	Escalas Bordoy, Antoni
P115	Sequence Type 485 <i>Escherichia</i> Clade I represent a potentially diarrheagenic clone	Dada, Rotimi
P116	Bacterial composition of sewage in relation to COVID-19 containment measures in Rotterdam, the Netherlands	Kerkvliet, Jesse
P117	Identification of clinical non- <i>Enterobacteriaceae</i> isolates using 16S rRNA sequencing	Akter, Sumona

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5. Genomics for public health

Poster	Abstract title	Presenter
P118	Discrimination or typing of streptococci? Identification of endocarditis causative agents in the genomic era	Norskov-Lauritsen, Niels
P119	Emergence of the high-risk <i>Enterobacter hormaechei</i> ST121 clone harboring the bla _{NDM-1} gene in a tertiary hospital in Brazil	Martins, Andreza
P120	Rapid genotyping of <i>Salmonella</i> using nanopore-only sequencing for outbreak investigation	Souque, Celia
P121	<i>Salmonella</i> serovar determination: comparison between whole genome sequencing results from a regional microbiology department and the National Reference Laboratory	Skov, Marianne Nielsine
P122	The molecular epidemiology of <i>Klebsiella pneumoniae</i> in Iraq: multidrug resistance, polyclonal dissemination and virulence.	Al-Hassan, Leena
P123	Detection of SARS-CoV-2 variants of concern in Swiss wastewater without prior lineage classification	Kociurzynski, Raisa
P124	Acquired azole resistance in the <i>Aspergillus niger</i> complex in the Netherlands	Punt, Maarten
P125	Metagenomic insights into the impact of quaternary ammonium compounds on microbial communities in rivers used for drinking water production	Novais, Carla
P126	Nanopore sequencing for rapid VRE outbreak detection: evaluating data quality thresholds	Koeck, Rebekka
P127	High occurrence of <i>Staphylococcus aureus</i> in wild ungulates used for human consumption in Brandenburg, Germany	Lienen, Tobias
P128	First experience from changing strategy for surveillance of vancomycin-resistant enterococci in a Danish region	Kemp, Michael
P129	Closing the gap: Oxford Nanopore R10 sequencing enables accurate cgMLST- and SNP-based bacterial outbreak investigation, with results comparable to Illumina sequencing when accounting for methylation-related errors	Bogaerts, Bert
P130	Can two cases of invasive group B <i>Streptococcus</i> ST283 infections in Portugal suggest the potential emergence of this uncommon lineage in Europe?	Ramirez, Mario
P131	Evaluation of nanopore metagenomic sequencing of cell-free DNA from plasma, for the detection of <i>Borrelia burgdorferi</i> sensu lato	Ellegaard, Kirsten
P133	An overwhelming diversity – Gram-positive rods in positive blood cultures	Hansen, Dennis Schröder

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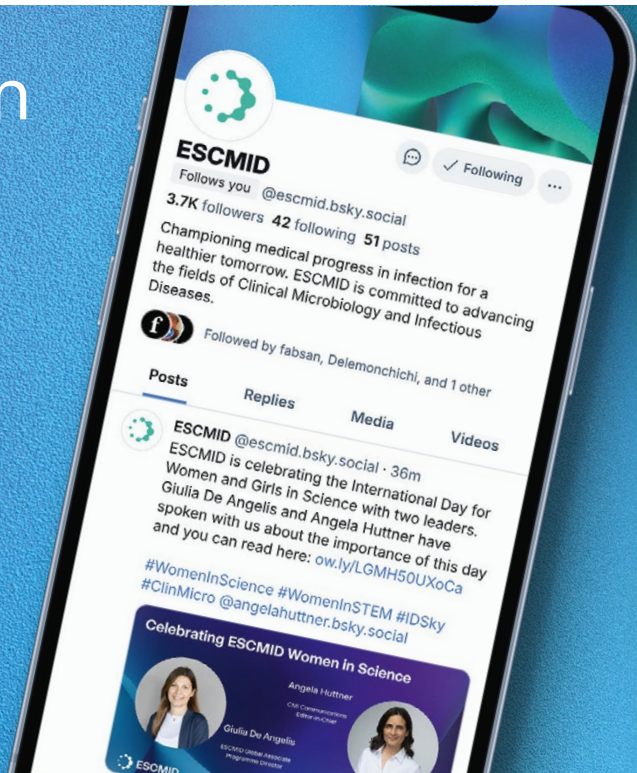
6. Evolution of vaccine-preventable pathogens

Poster	Abstract title	Presenter
P134	Prevalent chromosome fusion in <i>Vibrio cholerae</i> O1	Cuénod, Aline
P135	Distribution of GBS serotype and protein vaccine targets in disease-causing GBS in the UK (2009-2024): implications for GBS vaccine rollout	Jauneikaite, Elita
P136	Increased incidence and serotype dynamics of invasive pneumococcal disease in Israel, 2024-2025	Rokney, Assaf

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Upcoming ESCMID Courses and Workshops in 2025–January 2026	Location	Date
Implementation of new rapid diagnostic and antimicrobial susceptibility testing methods for bloodstream infections	Istanbul, Turkey	15 Oct – 17 Oct
Communication with patients in decision making on antibiotic prescribing in primary and outpatient care	Online	30 Oct – 31 Oct
Update on endocarditis and endovascular infections	Milan, Italy	6 Nov – 8 Nov
Unlocking women’s sexual health: the intersection of forensics and microbiomes	Online	11 Nov – 12 Nov
Implementation in infection prevention and control	Zurich, Switzerland	13 Nov – 14 Nov
Antimicrobial stewardship and infection prevention and control	Athens, Greece	21 Nov – 23 Nov
Enhancing hospital surveillance and rapid diagnostics of critical pathogens through metagenomics sequencing	Groningen, Netherlands	25 Nov – 27 Nov
The structure & position of AMS and antimicrobial stewardship aspect of management of infections	Ljubljana, Slovenia	27 Nov – 28 Nov
Multidrug-resistant (MDR) Gram-negative infections in Mediterranean hospitals: know them, prevent them, and beat them!	Barcelona, Spain	11 Dec – 12 Dec
Antifungal stewardship from primary to tertiary care	Leuven, Belgium	29 Jan – 30 Jan 2026



ESCMID Events 2025

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- Reviewing the current microbial typing methods and providing recommendations for their appropriate use.
- Encouraging and supporting collaborative research between scientists that fosters the development, implementation, and evaluation of microbial typing and epidemiology systems.
- Promoting the education of young scientists on the most recent developments on microbial typing and epidemiology.

ESGEM cordially invites colleagues actively interested in these areas to join and contribute to the 'critical mass' in this exciting international field.

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