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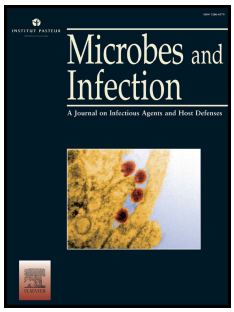


Conference report: The second Bacterial Genome Sequencing Pan-European Network conference

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# Conference report:

# The second Bacterial Genome Sequencing Pan-European Network conference

Kuangyi Charles Wei*[1], Srinithi Purushothaman*[2], Francesca Azzato[3, 3b], Kate S. Baker[1], Kira Waagner Birkeland[4], Sofia Brunet[5], Josefina Campos[6], Thomas R. Connor[7,7b], Christian G. Giske[8], Gilbert Greub[9], Erika Tång Hallbäck[5], Dag Harmsen[10], Emma B. Hodcroft[11,11a,18], Matthew T.G. Holden[3], Jobin Jacob[12], Andre Kahles[13], Amaya Campillay Lagos[14], Samuel Lipworth[15], Elin Loo[8], Paolo Miotto[16], Richard A. Neher[17,18], Aitana Neves[18], Derren Ready[19], Tim Roloff[2], Ashley Rooney[2], Emilie Rousseau[20], Jacques Schrenzel[21], Martin Sundqvist[14], Sofia Viegas[22], Fanny Wegner[2], Hege Vangstein Aamot[+,23, 24], Stefan Niemann[+,20], Deborah A. Williamson[+,3], Paula Mölling[+,14], Adrian Egli[+,2]

* Equally contributed to the work, + equally contributed to the work

[1] Pathogen Dynamics Unit, Department of Genetics, University of Cambridge, Cambridge, United Kingdom
[2] Institute of Medical Microbiology, University of Zurich, Zurich, Switzerland
[3] School of Medicine, University of St. Andrews, St. Andrews, United Kingdom
[3b] Victorian Infectious Diseases Reference Laboratory, University of Melbourne, Melbourne, Australia
[4] Department of Microbiology, Innlandet Hospital Trust, Brumunddal, Norway
[5] Department of Clinical Microbiology, Sahlgrenska University Hospital, Gothenburg, Sweden
[6] Unit Head Genomics and Analytics, World Health Organization, Geneva, Switzerland
[7] School of Biosciences, Cardiff University, Cardiff United Kingdom
[7b] Public Health Wales NHS Trust, Cardiff, United Kingdom
[8] Karolinska Institute, Stockholm, Sweden
[9] Institute of Medical Microbiology, University Hospital Lausanne, Lausanne, Switzerland
[10] Department of Periodontology, University of Münster, Münster, Germany
[11] Swiss Tropical and Public Health Institute, Allschwil, Switzerland
[11a] University of Basel, Basel, Switzerland
[12] Department of Microbiology, Christian Medical College Vellore, Vellore, India
[13] Eidgenössische Technische Hochschule Zürich, Zürich, Switzerland
[14] Department of Laboratory Medicine, Clinical Microbiology, Faculty of Medicine and Health, Örebro University, Örebro, Sweden
[15] Nuffield Department of Medicine, University of Oxford, Oxford, United Kingdom
[16] IRCCS Ospedale San Raffaele, Milano, Italy
[17] Biozentrum, University of Basel, Basel, Switzerland
[18] SIB Swiss Institute of Bioinformatics, Geneva, Switzerland
[19] UK Health Security Agency, London, United Kingdom
[20] Molecular and Experimental Mycobacteriology, Research Center Borstel, Germany.
[21] Division of Clinical Bacteriology, University Hospital Geneva, Geneva, Switzerland
[22] Instituto Nacional de Saúde, Marracuene, Mozambique
[23] Department of Microbiology and Infection Control, Akershus University Hospital, Lørenskog, Norway
[24] Department of Nursing, Health and Laboratory Science, Østfold University College, Fredrikstad, Norway

Correspondence:
Prof. Adrian Egli, MD PhD
Institute of Medical Microbiology
University of Zurich
Gloriastrasse 28/30
8006 Zurich
Email: aegli@imm.uzh.ch

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## Introduction

Advancements in sequencing technologies have transformed the diagnostic and public health landscape of microbiology, particularly in the areas of antimicrobial resistance (AMR) surveillance, outbreak monitoring, and pandemic preparedness. Each technological leap introduces both new opportunities and challenges, emphasizing the need for collaborative scientific efforts to establish standardized frameworks that ensure accuracy, reproducibility, cost-effectiveness, and clinical utility.

Standardization and data sharing have emerged as critical enablers for the successful integration of whole genome sequencing (WGS) into healthcare systems. Harmonized methodologies ensure reproducibility across laboratories and geographies, laying the groundwork for global research, regulatory compliance, clinical accreditation, and policy development. Sequenced data is increasingly shared in multi-country outbreaks e.g., as recently shown in a large European *Corynebacterium diphtheriae* outbreak [1] and acts as the vital fuel for machine learning (ML) algorithms, which increasingly underpin predictive tools in microbial genomics [2]. To achieve their full potential, access to FAIR (Findable, Accessible, Interoperable, Reusable) data is required [3]. The availability of large, diverse, and well-annotated datasets enhances genotype-to-phenotype prediction, supports real-time outbreak tracking, local infection prevention and control measurements, and strengthens antimicrobial stewardship (AMS). In this context, fostering a culture of data sharing is essential for progressing resilient public health infrastructure, e.g., the Swiss Pathogen Surveillance Platform [4] or the National Genomics Platform developed by Genomic Medicine Sweden [5]. The initiatives of national data sharing are in the next step paving the way for international data sharing.

International collaboration is essential to align scientific expectations, identify operational needs, and navigate the regulatory frameworks governing sequencing-based diagnostics and surveillance. The “Bacterial Genome Sequencing Pan-European Network” was launched to foster such collaboration and to catalyse the integration of genomics into routine clinical and public health settings. Following the success of its inaugural edition [6], the second edition of the conference was convened in Engelberg, Switzerland, from March 13$^{th}$ to 16$^{th}$, 2025.

Co-organized by Adrian Egli (Switzerland), Paula Mölling (Sweden), Deborah Williamson (UK), Hege Vangstein Aamot (Norway), and Stefan Nieman (Germany), the event brought together a diverse, international and interdisciplinary group of researchers, clinicians, and public health experts. The conference hosted a total of 35 speakers (**Table 1**) and featured scientific presentations from diverse, early-career scientists to senior researchers, panel discussions, an interactive workshop and brainstorming session, and networking opportunities (**Figure 1**). Our aim was to advance the use of WGS in clinical microbiology and to drive consensus around key challenges such as the implementation of sequencing for clinical diagnostics and surveillance, ethical data-sharing policies, learning about ML models, and the role of sequencing in shaping public health policy. This report provides a structured summary of the sessions and collaborative outcomes from the four-day meeting.

## Surveillance and AMR

Day 1 of the conference highlighted advancements in genomic surveillance methods and AMR, exploring the innovative sequencing technologies, pipeline developments, and strategic frameworks aimed at enhancing bacterial pathogen tracking, outbreak management, and AMR monitoring at national and international scales.

### 1.1 *Reliable and reproducible whole-genome genotyping for bacterial genomic surveillance with Nanopore sequencing data*

Dag Harmsen evaluated the Oxford Nanopore sequencing (ONT) method for genotyping 80 ESKAPE bacterial isolates [7]. Results demonstrated substantial improvements in accuracy and reproducibility when combining Dorado 5.0 model base calling, Medaka v2.0 with a bacterial methylation-aware model, and a novel ONT core genome multi-locus sequence typing (cgMLST)-polisher algorithm. This approach showed superior identification and localization of AMR genes compared to Illumina sequencing. A multicentre ring-trial further validated these methods, potentially showing that ONT sequencing may become sufficiently reliable for genomic surveillance purposes.

### 1.2 *Evidence review and recommendations for implementation of genomic AMR surveillance*

Kate S. Baker highlighted AMR as a complex, multi-pathogen challenge for surveillance, emphasizing the critical role genomics can play compared to traditional methods. Baker summarized findings from the Surveillance and Epidemiology of Drug-Resistant Infections Consortium (SEDRIC) genomics working group, outlining key recommendations including standardized surveillance frameworks, capacity building, data governance, improving stakeholder interactions, funding for cost-effectiveness studies, and investing in genomic innovations [8]. Baker also discussed ongoing United Kingdom initiatives, like TargetAMR (https://www.targetamr.org.uk/), designed to foster transdisciplinary collaborations and strategic alignment to enhance real-world genomic AMR surveillance and address implementation barriers.

### 1.3 *National and international WGS surveillance and outbreak alerts*

Martin Sundqvist emphasized the transformative potential of WGS for real-time surveillance of infectious diseases and AMR, highlighting successful platforms such as EpiPulse, European Gonococcal Antimicrobial Surveillance Programme (Euro-GASP), and GISAID. Sundqvist underscored the necessity of robust infrastructure, timely data sharing, and cross-sector collaboration exemplified by Sweden's Genomic Medicine platform (https://genomicmedicine.se) and Swiss Pathogen Surveillance Platform (https://spsp.ch/). Sundqvist concluded by illustrating how prospective WGS combined with machine learning offers an avenue to enhance outbreak detection, promoting faster, more precise public health interventions internationally.

### 1.4 *Evolution of Mycobacterium tuberculosis multidrug-resistant lineage strains toward global epidemic success*

Emilie Rousseau demonstrated the rapid global emergence of multidrug-resistant tuberculosis (MDR-TB), focusing on lineage-specific evolutionary traits that underpin its success. Using genomic and *in vitro* approaches, Rousseau revealed that lineage-2 strains acquire resistance mutations, particularly to rifampicin, at rates significantly faster than lineage-4 strains (unpublished). Rousseau highlighted that recent lineage-2 outbreaks have increasingly displaced endemic strains in Central Asia during humanitarian crises, suggesting these genetic traits confer substantial advantages in drug resistance acquisition and global dissemination.

### 1.5 *Targeted capture-based sequencing: bridging the gap in Neisseria gonorrhoeae genomic surveillance*

Francesca Azzato evaluated the effectiveness of targeted metagenomic next-generation sequencing (capture-based mNGS) for directly detecting and characterizing AMR in clinical samples of *N. gonorrhoeae*. Utilizing a modified RNA bait-based enrichment used in the detection of other sexually transmitted infections [9] to selectively capture *N. gonorrhoeae* directly from clinical samples. Azzato demonstrated high concordance between direct sequencing and traditional culture methods in identifying AMR determinants and genomic diversity. Given its practical challenges like cost and bioinformatics complexity, targeted mNGS was shown to be highly suitable for reflexed testing, focusing on characterizing pathogens that are relevant to public health, rather than using it as a single approach for identification and surveillance.

### 1.6 *Genomic characterization of Pseudomonas aeruginosa from Swedish cystic fibrosis patients*

Elin Loo investigated genomic and phenotypic characteristics of *P. aeruginosa* isolates (n=26) from cystic fibrosis patients at Karolinska University Hospital. Using WGS and cgMLST-based phylogenetics, she identified significant genomic diversity with the presence of an epidemic strain ST-242 (AUST-03). Phenotypically, the isolates showed high AMR rates, driven by the accumulation of chromosomal mutations under high selective pressure (unpublished). These findings show potential genetic diversity and evolutionary pressures shaping AMR in *P. aeruginosa* within a cystic fibrosis population in Sweden. However, these are samples from a single centre and need to be confirmed.

### 1.7 *Predicting drug-resistant bacteria from WGS data*

Christian G. Giske evaluated the capability of WGS to accurately predict AMR across various bacterial pathogens. He emphasized the complexity of the genotype-phenotype relationship, detailing successes with species like *Mycobacterium tuberculosis* and *Staphylococcus aureus*, while noting significant predictive challenges in species like *Acinetobacter baumannii*, *P. aeruginosa*, and *N. gonorrhoeae*. Giske highlighted advancements in databases, machine learning methods, and standardized regulatory frameworks essential for integrating genomic predictions into clinical practice, advocating further international coordination to refine genomic antimicrobial susceptibility for routine clinical implementation.

### 1.8 *Designing, validating, and implementing an AMR pipeline into a local and national framework*

Tim Roloff described the development of IMMense (https://gitlab.uzh.ch/appliedmicrobiologyresearch/immense, [10]), a modular nextflow-based sequencing pipeline designed to enhance reproducibility, scalability, and flexibility in AMR monitoring. Initially tailored for local clinical microbiology needs, the pipeline expanded nationally via the Swiss Pathogen Surveillance Platform (https://spsp.ch/, [4]), incorporating comprehensive benchmarking against phenotypic resistant profiles. Roloff emphasized key implementation challenges, including standardisation, stakeholder alignment, and resource management, underscoring the importance of rigorous quality control and stakeholder-driven iterative development for effective national integration and sustainability.

***Panel discussion: What is needed for efficient molecular surveillance?***

Gilbert Greub and Hege Vangstein Aamot co-moderated a panel themed “Key requirements for efficient molecular surveillance”, during which panelists outlined the essential elements for an effective surveillance framework. They noted that "rapid detection" timelines are context-dependent, ranging from one to two days for hospital outbreaks to slightly longer for community scenarios. Real-time sequencing was highlighted as critical for outbreak management, along with promptly identifying virulent and epidemiologically distinct pathogens.

The panel advocated streamlined, interoperable, and automated reporting systems tailored specifically for clinicians, bioinformaticians, and public health authorities. Emphasis was placed on maintaining trust through rigorous quality control and skilled personnel verifying data accuracy, while cautioning against oversimplification in electronic medical records.

Data sharing should follow a proactive, default-public approach with clear governance frameworks for privacy, anonymization, and ethics. This concept signifies a fundamental philosophical shift towards making molecular surveillance data, particularly genomic and associated epidemiological information, publicly available by default. This is critical in supporting public health measurements.

A practical "traffic light" system (green, yellow, red) was recommended to manage data sensitivity, especially regarding genomic data and associated metadata.

Training emerged as essential, with panelists proposing mandatory genomic microbiology certification and comprehensive education for laboratory staff, clinicians, public health officials, and regulators. Continuous training and skill updates were emphasized as crucial for maintaining surveillance standards despite stakeholder resistance.

## Emerging concepts

Day 2 focused on the integration of genomic sequencing technologies, specifically long-read sequencing and ML models. The speakers highlighted how the combination of cutting-edge genomic technologies and advanced computational methods can significantly improve real-time outbreak investigations, rapid AMR detection, and predictive analytics in clinical settings.

### 2.1 *Long-read shotgun metagenomic sequencing in CNS infections*

Kira Waagner Birkeland presented on the use of long-read shotgun metagenomic sequencing (mNGS) to investigate central nervous system infections [11]. The study aims to develop a protocol for pathogen identification in cerebrospinal fluid (CSF) samples using ONT and validate it against commercially available ZymoBIOMICS Microbial Community Standard with MS2 phage and Cytomegalovirus, and AMPLIRUN® TOTAL SARS-COV-2/FLUA/FLUB/RSV CONTROL (SWAB) with ZymoBIOMICS Spike-in Control II (Low-microbial load). Initial testing of a new protocol demonstrated the ability to detect viruses (Enterovirus B and Varicella-zoster virus) in CSF samples to reduce diagnostic turnaround time, offering a promising alternative to traditional methods. The integration of ONT sequencing into diagnostic workflows could serve as a model for hospitals, enhancing infection management capabilities.

### 2.2 *Long-read whole-genome sequencing to highlight MRSA´s adaptive potential within host*

Amaya Campillay Lagos discussed the genomic plasticity of methicillin resistant *S. aureus* (MRSA) in long-term carriers [12]. By using long-read sequencing, the study observed the evolution of MRSA within hosts, revealing a mutation rate of 10 SNPs per year and significant genomic diversity. This project was part of a broader genomic medicine initiative, focusing on integrating genomics into a broad national clinical diagnostic [13]. This research highlights MRSA's adaptive potential, emphasizing the need for personalized surveillance for long-term carriers. The importance of genomic medicine initiatives lies in improving patient-specific data integration, which could reshape treatment approaches for chronic infections.

### 2.3 *Long-read shotgun metagenomics to rapidly detect colonization with AMR directly from rectal swabs*

Srinithi Purushothaman explored the use of long-read shotgun metagenomics to detect Antimicrobial Resistance Genes (ARGs) directly from rectal swabs [14]. The study achieved significant reductions in turnaround time (TAT) to 24 hours, focusing on high-risk patients. However, there is still the need to further improve the sensitivity of certain resistance mechanisms in the current applied protocol. The research highlighted ONT sequencing as a potential tool for AMR surveillance in clinical settings. By reducing the TAT for detecting ARGs and pathogens, the study emphasizes the role of culture-independent genomic sequencing in improving the TAT for clinical diagnosis and surveillance [15].

### 2.4 *Integration of long-read sequencing for rapid whole-genome analysis in outbreak investigations*

Hege Vangstein Aamot discussed integrating long-read sequencing for outbreak investigations of multidrug-resistant pathogens (ESBL-producing *K. pneumoniae* and Methicillin-resistant *S. aureus*) and surveillance of *Pseudomonas spp., C. difficile,* and *Stenotrophomonas spp*. The use of ONT sequencing enabled real-time identification of pathogen transmission in healthcare-associated infections, providing a rapid and accurate method for outbreak control. The implementation of ONT sequencing as part of genomic diagnostics networks is crucial for rapid outbreak response. Different genomic sequencing

pipelines can streamline public health efforts by quickly identifying clusters and transmission routes, which is essential for controlling outbreaks.

### 2.5 *Holistic approach to unravel AMR in East Africa (HATUA)*

Matt Holden presented the HATUA project, an interdisciplinary initiative aimed at investigating AMR drivers in East Africa. The project combines genomic data with socioeconomic factors, analysing patterns in urinary tract infection pathogens from Kenya, Uganda, and Tanzania [16]. By integrating genomic surveillance with social science research, HATUA provides a holistic approach to understanding AMR. The HATUA project exemplifies the importance of interdisciplinary approaches to combat AMR, blending genomics with social and environmental factors. It shows the need for global collaborations that address AMR through a multifaceted lens, connecting microbiological, clinical, and societal data.

### *2.6 Machine learning for bacterial genomics*

Andre Kahles discussed the role of ML in bacterial genomics, focusing on how ML models are applied to genomic data for predicting AMR, virulence, and pathogen characterization. The talk highlighted the various ML approaches for analysing genomic sequences and emphasized the importance of large, well-curated datasets for training effective models. ML is becoming increasingly important in bacterial genomics, particularly in AMR prediction. The ability to predict resistance patterns using genomic data is enhanced by ML algorithms, which could ultimately support more personalized treatment strategies for infections.

### *2.7 What is the role of machine learning in AMR prediction?*

Samuel Lipworth explored ML's role in predicting AMR in *Escherichia coli* and *Klebsiella spp.* in bloodstream infections. The study utilized ONT sequencing and ML models to predict antibiotic resistance and optimize therapy. Lipworth emphasized the importance of large, diverse datasets and external validation for the effectiveness of ML models. Lipworth's research illustrates the promise of ML in improving AMS through better prediction of resistance patterns [17]. However, challenges in data quality and label accuracy underscore the need for more comprehensive, validated datasets to improve the reliability of ML predictions. While genotypic data is crucial for predicting AMR, challenges remain in accurately linking it to phenotypic resistance, requiring refined models and better catalogues of mutations.

### *Panel discussion: How can we implement long-read sequencing and machine learning in clinical practice?*

Moderated by Ashley Rooney and Jacques Schrenzel, the panel including Hege Vangstein Aamot, Matt Holden, Andre Kahles, and Samuel Lipworth discussed integrating long-read sequencing and ML clinically.

The panel identified key implementation hurdles, particularly selecting high-yield cases and clinician hesitation due to a lack of validated tools and standardized workflows. Examples from oncology precision medicine and HIV antiviral treatment underscored the value of successful integration models. Long-read sequencing was highlighted for its potential in community

surveillance through wastewater and saliva, emphasizing the need for rapid, actionable, point-of-care data delivery and robust local bioinformatics infrastructure.

Immediate clinical applications include infection control, outbreak prediction, and resistance tracking, with bacterial population genetics poised as an emerging clinical tool. Despite enthusiasm, challenges persist, especially the gap between technological capacity and clinical uptake. Harmonizing genotype-to-phenotype datasets remains a critical task. The panel urged focusing on identifying and harmonizing relevant data locally.

Regulatory hurdles remain significant, suggesting infection control as a feasible starting point. Panelists recommended initiating a focused pilot project on a specific pathogen or disease to generate localized evidence, demonstrate cost-effectiveness, and effectively engage stakeholders and regulatory bodies.

## Routine diagnostics

Day 3 focused on the critical aspects of implementing WGS in routine diagnostics, highlighting the challenges and importance of standardization, quality control, and efficient data sharing. Speakers presented innovative methods and real-world experiences from diverse international settings, emphasizing the need for streamlined robust systems.

### *3.1 National implementation of 16S Nanopore sequencing*

Sofia Brunet reported findings from a nationwide Swedish multicentre study, including 20 different laboratories, evaluating 16S ONT sequencing for bacterial identification, highlighting protocol harmonization and bioinformatics pipeline comparisons. Results showed varying success in species identification linked to primer specificity and database selection. Optimization with enzymatic pretreatment enhanced detection sensitivity. Nanopore sequencing via GMS-16S demonstrated user-friendliness and accuracy suitable for clinical diagnostics [18].

### *3.2 Exploring algorithms for outbreak detection for AMR bacteria*

Charles Wei examined current genotyping methods for pathogen surveillance, identifying limitations such as suboptimal resolution. Using a dataset of *Shigella sonnei* isolates, Wei highlighted the clustering inaccuracies arising from static thresholds and single-linkage methods. Wei proposed adaptive threshold clustering to improve outbreak detection, emphasizing that integrating genotyping with AMR data enhances actionable surveillance. Wei concluded that refined, adaptive algorithms could significantly advance public health response capabilities, balancing resolution, speed, and accuracy.

### *3.3 Leveraging microbial genomics for diagnosis and public health: the Indian perspective*

Jobin Jacob detailed high infectious disease and AMR burden in India, highlighting challenges including fragmented surveillance and diagnostic limitations. Jacob showcased institutional efforts to integrate genomics into clinical diagnostics, notably using rapid Nanopore sequencing for real-time diagnosis and outbreak management. Jacob stressed genomics' role

in identifying resistance mechanisms, optimizing antimicrobial therapy, and supporting vaccination strategies, underscoring its transformative potential for public health in resource-limited settings facing extensive disease burdens.

### *3.4 Genomic applications in public health bacteriology*

Derren Ready discussed genomic sequencing's crucial role within the UK's public health services, particularly emphasizing outbreak detection and AMR profiling. Through case studies of *Klebsiella pneumoniae* and STEC O145:H28 outbreaks [19], Ready illustrated genomics' powerful capabilities in identifying transmission pathways, informing clinical interventions, and shaping public health policies. Genomic methods offer superior resolution over traditional typing techniques, significantly refining epidemiological investigations and response actions, thereby enhancing patient care and outbreak management at both local and national levels.

### *3.5 Necessary quality steps for implementing whole genome sequencing in routine diagnostics*

Erika Tång Hallbäck outlined essential quality control stages for integrating genomic sequencing into clinical microbiology, including meticulous validation of DNA extraction, library construction, sequencing quality, bioinformatics analysis, and external quality assessments. Hallbäck emphasized challenges such as bioinformatics expertise, IT infrastructure, data security, and standardized data sharing. Hallbäck highlighted the importance of harmonized national strategies for genomic implementation, advocating rigorous quality management and comprehensive staff training to ensure reliable diagnostic and surveillance outcomes across Sweden [13].

### *3.6 Ten simple rules for the sharing of bacterial genotype-phenotype data on AMR*

Aitana Neves emphasized the importance of structured, standardized, and machine-readable formats for sharing AMR genotype-phenotype data. Highlighting platforms such as SPSP, COMPARE (https://www.compare-europe.eu/), ANRESIS (https://www.anresis.ch/#), and CARD (https://card.mcmaster.ca/), she outlined guidelines for metadata standardization, ontology utilization, and transparent reporting of resistance determinants. Neves advocated for open, accurate, and interoperable data sharing to enhance AMR surveillance, recommending clear licensing, consistent versioning, and efficient data accessibility mechanisms (**Table 2**).

### *3.7 Realising national, end-to-end accredited, pathogen genomics services for diagnostics and surveillance*

Tom Connor described Wales's successful development and accreditation of comprehensive pathogen genomic services, from sequencing to clinical action. Through detailed examples such as SARS-CoV-2 and *Clostridioides difficile*, Connor demonstrated the impact of

integrated genomics on public health surveillance, outbreak management, and patient care [20]. Connor emphasized modularization, robust bioinformatics infrastructure, and close integration with public health authorities as critical success factors, highlighting the significant public health benefits derived from streamlined genomic data use and interdisciplinary collaboration.

### *Workshop: Key steps to translate sequencing into routine diagnostics*

The 2-hour workshop addressed critical aspects for integrating genomic sequencing into routine diagnostics, emphasizing five main areas: bioinformatics, validation and accreditation, automation, artificial intelligence (AI), and reporting strategies.

Bioinformatics emphasized reproducibility, secure backups, metadata integration, and sustainable IT platforms with user-friendly interfaces. Community engagement among academia, industry, and clinics was vital for broad genomic adoption. Validation discussions prioritized clear SOPs, modular workflows for flexibility, adherence to ISO standards, regular external quality assessments (EQAs), audits, and workforce training. Automation was acknowledged for error reduction and efficiency, though cost and maintenance challenges persist. Integrated sequencing systems were recommended for smaller labs. AI was particularly valued for outbreak prediction, AMR forecasting, and identifying novel resistance mechanisms, despite challenges with prospective validation. Developing unbiased AI models was crucial for generalizable results. Effective reporting tailored to various stakeholders, with clear confidence indicators, was key for clinical integration. Multidisciplinary teams were proposed to enhance genomic report interpretation and clinical decision-making.

## Sequencing meets politics

Day 4 focused on the integration and long-term sustainability of sequencing in public health, emphasizing its crucial role in monitoring and controlling infectious diseases. The discussions centered on how WGS can be implemented into routine surveillance systems, with a particular focus on financial sustainability, workforce development, data management, and policy integration. Sustainability, scalability, and global collaboration emerged as key drivers for ensuring the success and longevity of genomic surveillance programs.

### *4.1 Translation of pathogen genomics to public health policy*

Deborah Williamson underscored that effective translation of genomic research into evidence-based policies is essential for influencing decision-making at governmental, institutional, and societal levels. Such translation ensures real-world applications that impact public health and healthcare practices. Williamson presented the application of genomic sequencing to track SARS-CoV-2 variants that played a pivotal role in the development of vaccines and the implementation of public health interventions such as border controls, lockdowns, and vaccination strategies, along with the integration of real-time genomic epidemiology in sexually transmitted infection control which faces challenges in balancing data sharing, privacy concerns, and clinical integration, but offers a unique opportunity to enhance public health interventions.

### *4.2 Integrating sequencing into local TB control guidelines in high incidence settings*

Sofia Viegas presented on the integration of WGS into National TB testing algorithms in Mozambique. She highlighted the country's high TB burden and the role sequencing can play in providing more accurate drug resistance profiles and faster diagnostics. Viegas also discussed the establishment of local capacity for sequencing and the strategic partnerships necessary to support sustainable sequencing programs. Viegas' talk emphasizes the importance of building local sequencing capacity to enhance TB management in high-burden settings. The integration of WGS in Mozambique is a crucial step towards improving drug-resistant TB diagnosis and treatment, requiring both infrastructure investment and global partnerships for long-term success.

### *4.3 Pathoplexus - building a new kind of pathogen database*

Emma Hodcroft discussed the limitations of existing pathogen sequence-sharing platforms, in particular difficulty of data upload and access, sometimes untransparent governance, and limitations in ensuring sequence generators are protected from 'scooping.' These issues hinder reproducibility, broader data integration, and the development of open analysis ecosystems. Hodcroft introduced Pathoplexus (https://pathoplexus.org/) as a new open-source, community-driven database designed to address these issues [21]. Pathoplexus focuses on ease of submission, improving data accessibility, clear data use terms, transparent governance, and the ability for researchers to submit pathogen sequences while reserving the right to publish first. Hodcroft's presentation highlighted the need for more transparent and accessible pathogen databases to encourage quick data sharing for public health response and foster a collaborative sharing environment. Pathoplexus is positioned as a solution to enhance data sharing, aid global collaboration and promote ethical use of genomic data, which is crucial for accelerating research and improving public health responses.

### *4.4 Sustainability of sequencing programs*

Paolo Miotto explored the key components necessary for the sustainability of sequencing programs, which requires a multifaceted approach that balances financial stability, robust infrastructure, skilled workforce retention, and the ability to adapt to evolving technological and public health needs. Central to this is the adoption of standardized frameworks. Miotto outlined the role of the WHO TB mutation catalogue in standardizing drug-resistant TB sequencing and discussed the importance of international collaborations and capacity-building efforts to ensure the long-term viability of sequencing programs. When integrated with public health systems, these efforts ensure genomic data informs real-time diagnosis, surveillance, and treatment. Miotto's talk emphasized that sustainability in sequencing programs depends on interdisciplinary collaboration, cost-efficiency, and workforce training. By integrating sequencing into routine diagnostic algorithms, especially for TB, sequencing programs can become a cornerstone for improving public health surveillance and disease management. Yet challenges remain, particularly in procurement, data sharing, and aligning stakeholders around clear, measurable goals. Embracing a One Health approach and fostering cross-sector collaboration can help overcome these gaps and ensure sequencing becomes a sustainable tool for global health.

## Conclusion

The second edition of the four-day “Bacterial Genome Sequencing Pan-European Network” conference successfully gathered international experts to discuss recent advances and address critical challenges in bacterial genome sequencing. Central themes included standardization, quality assurance, and efficient implementation of genomic methods, especially long-read sequencing technology into routine diagnostics and public health surveillance. Discussions underlined the necessity of rigorous validation, standardized reporting, and effective data sharing frameworks to facilitate accurate genomic interpretation and meaningful clinical translation. Importantly, the conference highlighted the transformative potential of emerging technologies such as long-read sequencing and AI, alongside considerations for sustainable practices and ethical guidelines.

**Declarations.** ChatGPT4 with the GPT-4-turbo model (April 2024) version is used to support writing and editing the first draft of the manuscript. The manuscript has substantially changed during the human writing course. Every author checked and edited the manuscript.

**Declaration of generative AI and AI-assisted technologies in the writing process**

During the preparation of this work the authors used ChatGPT4 with the GPT-4-turbo model (April 2024) version in order to to support writing and editing the first draft of the manuscript. After using this tool/service, the authors reviewed and edited the content as needed and takes full responsibility for the content of the publication. The manuscript has substantially changed during the human writing course. Every author checked and edited the manuscript.

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## Figure and table legends

**Figure 1:** The international participants of the second Bacterial Genome Sequencing Pan-European Network conference from eight different countries.

**Table 1**. List of participants and their corresponding affiliations.

**Table 2**: Ten recommendations for good data sharing practice for bacterial genotype-phenotype data. EUCAST, European Committee on Antimicrobial Susceptibility Testing (https://www.eucast.org/); CLSI, Clinical and Laboratory Standards Institute (https://clsi.org/); API, application programming interface; SPARQL, standard query language and protocol for Linked Open Data on the web or for RDF triplestores; IRI, Internationalized Resource Identifier (https://lincsproject.ca/docs/terms/internationalized-resource-identifier).

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**Table 1**. List of participants and their corresponding affiliations.

| Name | Country | Affiliation | Website link |
|---|---|---|---|
| Hege Vangstein Aamot | Norway | Akershus University Hospital & Østfold University College | www.ahus.no<br>www.hiof.no |
| Francesca Azzato | Australia | University of Melbourne | https://biomedicalsciences.unimelb.edu.au/departments/microbiology-Immunology/research/centre-for-pathogen-genomics |
| Kate S Baker | United Kingdom | University of Cambridge | https://www.pdu.gen.cam.ac.uk/kate-s-baker |
| Kira Waagner Birkeland | Norway | Innlandet Hospital Trust & University of Oslo | www.sykehuset-innlandet.no<br>www.uio.no |
| Sofia Brunet | Sweden | Sahlgrenska University Hospital | https://www.sahlgrenska.se/en/ |
| Josefina Campos | Argentina | *Unit Head Genomics and Analytics-World Health Organization* | https://www.who.int/news/item/20-05-2023-who-launches-global-network-to--detect-and-prevent-infectious-disease-threats |
| Tom Connor | United Kingdom | Cardiff University | https://profiles.cardiff.ac.uk/ |
| Adrian Egli | Switzerland | University of Zurich | https://www.imm.uzh.ch/<br>https://appliedmicrobiologyresearch.net/ |
| Christian Giske | Sweden | Karolinska Institutet and Karolinska University Hospital | https://ki.se/en |
| Gilbert Greub | Switzerland | Lausanne University Hospital & University of Lausanne | https://www.chuv.ch/fr/microbiologie/imu-home<br>https://www.gu.se/en |
| Erika Tång Hallbäck | Sweden | Sahlgrenska University Hospital | https://www.sahlgrenska.se/en/ |
| Dag Harmsen | Germany | University Hospital Münster, Münster, Germany | https://www.ukm.de/university-hospital-muenster |
| Emma Hodcroft | Switzerland | Swiss Tropical and Public Health Institute & Swiss Institute of Bioinformatics | https://www.swisstph.ch/en/<br>https://www.sib.swiss/ |
| Matt Holden | United Kingdom | University of St Andrews | https://research-portal.st-andrews.ac.uk/en/ |

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|---|---|---|---|
| Jobin Jacob | India | Christian Medical College, Vellore, India | https://www.cmch-vellore.edu/ |
| Andre Kahles | Switzerland | ETH Zurich | https://ethz.ch/en.html |
| Amaya Campillay Lagos | Sweden | Örebro University Hospital & Örebro University | https://www.regionorebrolan.se/en/care-and-health/universitetssjukhuset-orebro/<br>https://www.oru.se/english/ |
| Samuel Lipworth | United Kingdom | University of Oxford | https://www.expmedndm.ox.ac.uk/ |
| Elin Loo | Sweden | Karolinska Institutet & Karolinska University Hospital | https://ki.se/en |
| Paolo Miotto | Italy | IRCCS San Raffaele Hospital | https://research.hsr.it/en/ |
| Paula Mölling | Sweden | Örebro University Hospital & Örebro University | https://www.regionorebrolan.se/en/care-and-health/universitetssjukhuset-orebro/<br>https://www.oru.se/english/ |
| Richard Neher | Switzerland | University of Basel & Swiss Institute of Bioinformatics | https://www.biozentrum.unibas.ch/<br>https://www.sib.swiss/ |
| Aitana Neves | Switzerland | Swiss Institute of Bioinformatics | https://www.sib.swiss/ |
| Stefan Nieman | Germany | Forschungszentrum Borstel, Leibniz Lungenzentrum | https://www.dzif.de/en/ |
| Srinithi Purushothaman | Switzerland | University of Zurich | https://www.imm.uzh.ch/<br>https://appliedmicrobiologyresearch.net/ |
| Derren Ready | United Kingdom | UK Health Security Agency | https://www.gov.uk/government/organisations/uk-health-security-agency |
| Tim Roloff | Switzerland | University of Zurich | https://www.imm.uzh.ch/de.html |
| Ashley Rooney | Switzerland | University of Zurich | https://www.imm.uzh.ch/<br>https://appliedmicrobiologyresearch.net/ |
| Emilie Rousseau | Germany | Forschungszentrum Borstel, Leibniz Lungenzentrum | https://www.dzif.de/en/ |
| Jacques Schrenzel | Switzerland | University Hospital Geneva | https://www.hug.ch/en |
| Martin Sundqvist | Sweden | Örebro University Hospital & Örebro | https://www.regionorebrolan.se/en/care-and-health/universitetssjukhuset-orebro/ |

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|---|---|---|---|
| | | University | https://www.oru.se/english/ |
| Sofia Viegas | Mozambique | Instituto Nacional de Saúde | https://ins.gov.mz/ |
| Fanny Wegner | Switzerland | University of Zurich | https://www.imm.uzh.ch/<br>https://appliedmicrobiologyresearch.net/ |
| Kuangyi Charles Wei | United Kingdom | University of Cambridge | https://www.infectiousdisease.cam.ac.uk/ |
| Deborah Williamson | United Kingdom | University of St Andrews | https://research-portal.st-andrews.ac.uk/en/ |

| Rule | Rule Content |
|---|---|
| 1 | For phenotypic AMR, use ontologies/CVs, if possible, defined within European/global consortia |
| 2 | Use standardised resistance definitions (global standards (EUCAST, CLSI) and specify versions (e.g., year) for susceptible/intermediate/resistant (S/I/R) interpretation. |
| 3 | For bioinformatics results, follow PHA4GE specifications |
| 4 | For genotypic to phenotypic predictions, document the source of information (e.g., knowledge base and date of accession, or tool + version) |
| 5 | Provide minimal contextual metadata (e.g. strain name, collection date, location (country), host, compartment (human, animal, food, environment) |
| 6 | Publish phenotypic data openly on the INSDC (under BioSample) |
| 7 | Ensure data is accurate (correct/update where needed) |
| 8 | Make data findable, also for machines (API or SPARQL endpoints + use IRIs) |
| 9 | Make data accessible and reusable (i.e., define clear access models, explicit license) |
| 10 | Version data and metadata |

**Table 2**: Ten recommendations for good data sharing practice for bacterial genotype-phenotype data. EUCAST, European Committee on Antimicrobial Susceptibility Testing (https://www.eucast.org/); CLSI, Clinical and Laboratory Standards Institute (https://clsi.org/); API, application programming interface; SPARQL, standard query language and protocol for Linked Open Data on the web or for RDF triplestores; IRI, Internationalized Resource Identifier (https://lincsproject.ca/docs/terms/internationalized-resource-identifier).