

A selection of presentations featuring Oxford Nanopore sequencing

Friday, 20 June, 2025

CIV-IDS-206. Emerging and re-emerging arboviruses: pathogenesis, diagnostics and vaccines

01:45 pm–03:45 pm PT | 511ABC, LACC

Development of a field-applicable pan-serotype whole genome sequencing protocol for Dengue virus

M. Ulinici, *International Centre for Genetic Engineering and Biotechnology, Trieste, Italy*

Developing a novel amplicon-based next generation sequencing approach to determine West Nile virus transmission dynamics during an outbreak

S. Freed, Jr, *University of Nebraska Medical Center, Omaha, NE, United States*

Saturday, 21 June, 2025

AAR-IDS-303. Phage based therapeutics: progress/success?

08:15 am–10:15 am PT| 502A, LACC

A neonatal antibiotic resistant polymicrobial skin infection: a case report and laboratory investigation

F. Vaskoudis, *University of West London, London, United Kingdom*

Sunday, 22 June, 2025

CPHM-IDS-401. Tools and applications for utilizing whole genome sequencing data for outbreak investigations

08:15 am–10:15 am PT| 515B, LACC

Identifying and interrupting intra-hospital norovirus GII transmission using whole-genome sequencing

R. Potter, *Children's Hospital of Philadelphia, Philadelphia, PA, United States*

CPHM-IDS-410. Assessing the clinical impact of next-generation sequencing: where are we now?

01:45 pm–03:45 pm PT | 515B, LACC

When all methods fail. Rapid whole genome sequencing directly from positive blood culture

D. Navas, *AdventHealth Orlando, Orlando, FL, United States*

A selection of posters with rapid fire talks featuring Oxford Nanopore sequencing

Friday, 20 June, 2025

11:45 am–12:30 pm PT | AAR Track Hub, Exhibit Hall

AAR-RF-206. AAR Friday rapid fire

Genomic insights into carbapenem resistant *Acinetobacter baumannii* from different clusters

A. Uskudar Guclu, *Baskent University Faculty of Medicine, Ankara, Turkey*

11:45 am–12:30 pm PT | AES Track Hub, Exhibit Hall

AES-RF-205. AES Friday rapid fire: tiny microbes for tremendous tasks: using microbes as tools

Integrating DNA watermarks into genetically engineered microorganisms to support agricultural-runoff threat assessments

T. Cason, *University of Colorado Boulder, Boulder, CO, United States*

11:45 am–12:30 pm PT | EEB Track Hub, Exhibit Hall

EEB-RF-204. EEB Friday rapid fire

Exploring the drivers of bacteriophage diversity to gain insights into climate change in the North

A. Lehr, *University of Alaska Fairbanks, Fairbanks, AK, United States*

11:45 am–12:30 pm PT | HMB Track Hub, Exhibit Hall

HMB-RF-204. HMB Friday rapid fire

Nanopore adaptive sequencing recovers full bacterial genomes from the mosquito microbiome

J. Yuan, *Connecticut Agricultural Experiment Station, New Haven, CT, United States*

Saturday, 21 June, 2025

11:45 am–12:30 pm PT | CPHM Track Hub, Exhibit Hall

CPHM-RF-304. CPHM Saturday rapid fire

Investigating the genetic origins of West Nile Virus (WNV) in Southern Nevada

A. J. Tang, *University of Nevada, Las Vegas, NV, United States*

Sunday, 22 June, 2025

11:45 am–12:30 pm PT | AES Track Hub, Exhibit Hall

AES-RF-404. AES Sunday rapid fire: microbial pioneers: colonizing earth's unique habitats

Evaluation of psychrotrophic bacteria for biotechnological potential

Q. Faber, *Cold Regions Research and Engineering Laboratory, Hanover, NH, United States*

A selection of posters featuring Oxford Nanopore sequencing

Friday, 20 June, 2025

10:00 am–05:00 pm PT | Exhibit Hall

AAR-P-201. AAR01 Friday surveillance of antimicrobial resistance in clinical isolates: molecular typing and molecular epidemiology

Whole genome sequencing and characterization of the first macrolide-resistant *Bordetella pertussis* strain in Mexico: implications for public health and surveillance in Latin America

A. Da Costa, *American Society for Microbiology, Washington, DC, United States*

Detection of transferable antiphage defense mechanisms linked to antibiotic resistance genes with a one health approach

M. F. Ferreira, *Instituto de Higiene, Facultad de Medicina, Udelar, Montevideo, Uruguay*

From serotyping to genotyping. A rapid, accurate, and simplified protocol for *Streptococcus pneumoniae* typing by whole genome sequencing

J. Alexander, *Advent Health, Orlando, FL, United States*

Outbreak investigation of extensively drug resistant *Acinetobacter baumannii* of ST2 in the intensive care unit of a Lebanese hospital

I. Bitar, *Charles University, Plzen, Czech Republic*

AES-P-201. AES01 Friday agricultural systems microbiology

Advancing livestock production through long-read metagenomic sequencing and integrated omics approaches

B. A. Strickland, *Cmbio, Germantown, MD, United States*

Isolation and characterization of novel xylooligosaccharide-utilizing probiotics for enhanced poultry health and sustainability

X. Hu, *University of Tennessee, Knoxville, TN, United States*

AES-P-209. AES09 Friday marine and freshwater microbiology

Microbiome variability in the Hudson River over short and long timescales

I. Cohen, *Brooklyn College, Brooklyn, NY, United States*

CIV-P-201. CIV01 Friday clinical studies of adult infectious diseases

Analysis of genetic variability and prediction of T epitopes of the HPV16 E2 gene in a sample of asymptomatic women from Cajamarca, Peru

J. del Valle Mendoza, *Universidad Peruana de Ciencias Aplicada, Lima, Peru*

CPHM-P-202. CPHM03 Friday diagnostic bacteriology

Improving flow in the blood culture laboratory: direct full length 16S rRNA gene sequencing from positive blood culture flasks

D. S. Hansen, *Herlev Gentofte Hospital, Herlev, Denmark*

CPHM-P-207. CPHM12 Friday molecular and genome sequencing for diagnostics and AMR detection

Utilization of the ElysION automated sequencer to detect genetic markers predictive of hypervirulent *Klebsiella pneumoniae*

S. Stevenson, *University of Nebraska Medical Center, Omaha, NE, United States*

EEB-P-202. EEB02 Friday microbial evolution

Nitrophenol degradation is not a defining feature of *Arthrobacter nitrophenolicus*

R. Y. T. Shen, *The ISF Academy, Pokfulam, Hong Kong*

EEB-P-205. EEB05 Friday comparative genomics: host-associated microbes

Pathogenomes and resistance phenotypes of multi-drug resistant shiga toxin-producing *Escherichia coli*

S. Eppinger, *University of Texas at San Antonio, San Antonio, TX, United States*

Comparative genomic analysis of *Corynebacterium xerosis* yields clues about their role in the bovine respiratory tract

S. Howe, *University of Arkansas Division of Agriculture, Fayetteville, AR, United States*

Comparative genomics and virulence assessment of *Pectobacterium brasiliense* strains isolated from multiple hosts in Hawaii

V. Stewart, *University of Hawaii at Manoa, Honolulu, HI, United States*

Comparative genomics across diverse hosts: understanding the genomic variability of *Aeromonas veronii* in humans, fish, and medicinal leeches

N. Vargas, *University of Connecticut, Storrs, CT, United States*

HMB-P-202. HMB03 Friday basic science of pathogen during human infections

From biomarkers to whole-genome insights: comprehensive analysis of virulence mechanisms and plasmids of carbapenem-resistant hypervirulent *Klebsiella pneumoniae*

C.-Y. Kao, *National Yang Ming Chiao Tung University, Taipei, Taiwan*

MBP-P-202. MBP02 Friday stress responses and defenses

Identification of genetic and epigenetic changes linked to salt tolerance in *Escherichia coli*: implication on antimicrobial resistance (AMR)

P. Nagpal, *Indian Institute of Technology Delhi, New Delhi, India*

MBP-P-204. MBP04 Friday molecular and genome biology of microbes

Genetic and functional characterization of tumor-associated *Lactobacilli*

L. D. Boatright, *UT Health MD Anderson Graduate School of Biomedical Sciences, Houston, TX, United States*

MBP-P-205. MBP05 Friday metabolism, enzyme mechanics and physiology

Thermodynamic- and sequencing-guided on-site media design and culturing from diverse ecosystems

E. Miller, *Two Frontiers Project, San Diego, CA, United States*

MBP-P-208. MBP08 Friday fundamental phage biology, phage defense, and mobile genetic elements

Co-infection of bacteriophages (KHP30 and KHP40) with *Helicobacter pylori*

M. Shiraishi, *International University of Health and Welfare Graduate School, Narita, Japan*

Saturday, 21 June, 2025

10:00 am–05:00 pm PT | Exhibit Hall

AAR-P-301. AAR01 Saturday surveillance of antimicrobial resistance in clinical isolates: molecular typing and molecular epidemiology

First report of KPC-31 in Florida: redefining detection of KPC producing isolates with ESBL-like resistance pattern

J. Alexander, *Microbiology, Advent Health, Orlando, FL, United States*

AAR-P-304. AAR06 Saturday novel approaches: diagnostics/discovery and non-traditional therapies to combat drug-resistant infections

Methylation scores reveal antibiotic resistance in *Pseudomonas aeruginosa* using a machine learning model

S. Gan, *University of Texas Southwestern Medical Center, Dallas, TX, United States*

AAR-P-307. AAR10 Saturday phage therapy: clinical applications and consideration

Characterization of a novel *Drullisvirus* phage species against *Klebsiella pneumoniae* and *in vivo* assessment using the *Galleria mellonella* model

G. Quispe-Villegas, *Cayetano Heredia University, Lima, Peru*

AES-P-301. AES01 Saturday agricultural systems microbiology

Isolation and characterisation of four novel *Curtobacterium* spp. with plant growth-promoting potential

L. K. Y. Chow, *The ISF Academy, Pokfulam, Hong Kong*

Isolation and characterisation of two seed endophytic bacteria displaying antifungal activity

N. Cheung, *The ISF Academy, Pokfulam, Hong Kong*

AES-P-302. AES02 Saturday food systems & food fermentations microbiology

Evaluating real-time software-based host depletion for improved antimicrobial resistance surveillance

D. C. Wrenn, *University of Alaska Fairbanks, Fairbanks, AK, United States*

AES-P-303. AES03 Saturday engineered, built and urban environments microbiology

Duckweed surfaces are selectively colonized by a subset of environmental bacteria

I. Cohen, *Brooklyn College, Brooklyn, NY, United States*

AES-P-305. AES05 Saturday industrial microbiology: bioproductions, bioconversions and fermentations

Investigation of a unique pair of triacylglycerol lipases (EC 3.1.1.3) from *Staphylococcus pseudintermedius*

J. J. S. Luan, *The ISF Academy, Pokfulam, Hong Kong*

AES-P-307. AES07 Saturday source tracking: non-clinical microbial & AMR detection and monitoring

Long-read sequencing reveals antimicrobial resistance and pathogenicity markers in *Escherichia coli* and *Salmonella* isolates from retail meats

A. Ghorbani Tajani, *University of Wyoming, Laramie, WY, United States*

Isolation and characterisation of 9 strains of *Enterobacter mori* from Hong Kong reveals 4 new ACT beta-lactamase variants

A. Y. X. Huang, *The ISF Academy, Pokfulam, Hong Kong*

AES-P-309. AES09 Saturday marine and freshwater microbiology

Metagenomic insights of antibiotic resistance genes (ARGs) in Laguna Lake using nanopore sequencing

P. Vital, *University of the Philippines Diliman, Quezon City, Philippines*

CPHM-P-302. CPHM03 Saturday diagnostic bacteriology

Have you seen *Kerstersia gyiorium* on the bench? Reliable identification method and susceptibility profile

H. Miralles, *AdventHealth Orlando-Microbiology, Altamonte Springs, FL, United States*

CPHM-P-309. CPHM12 Saturday molecular and genome sequencing for diagnostics and AMR detection

Molecular characterization of the three genome segments of Crimean-Congo Hemorrhagic Fever Viruses (CCHFV) detected in 2020 in the Mopti Region, Mali

I. Guindo, *National Public Health Institute, NPHI-Mali, Bamako, Mali*

Development and validation of a 16S rRNA bioinformatic pipeline and curated reference database optimized for detection of bacterial pathogens from clinical specimens

N. P. G. Gauthier, *BugSeq Bioinformatics Inc., Vancouver, BC, Canada*

EEB-P-301. EEB01 Saturday microbial ecology

A characterisation of the TupABC-MobAB complex in *Vibrio* spp. isolates from Hong Kong coastal waters

A. N. H. Cheung, *The ISF Academy, Pokfulam, Hong Kong*

EEB-P-302. EEB02 Saturday microbial evolution

Variations in isaB and the Agr locus point to lineage-specific adaptations in *Staphylococcus saprophyticus*

P. S. K. Leung, *The ISF Academy, Pokfulam, Hong Kong*

EEB-P-303. EEB03 Saturday climate change: ecological interactions

Non-linear response in microbiome structure and soil respiration along a gradient of soil water filled pore space

J. Yuan, *The Connecticut Agricultural Experiment Station, New Haven, CT, United States*

EEB-P-307. EEB07 Saturday microbiome ecology and evolution

Oxford Nanopore sequencing enables strain-level metagenomics and reveals the structure and function of a mature compost microbiome

C. He, *Oxford Nanopore Technologies, Alameda, CA, United States*

HMB-P-304. HMB07 Saturday microbiome profiling

Exploring the connection between obesity and the human gut virome through long-read sequencing

G. Gulyás, *University of Szeged Albert Szent-Györgyi Medical School, Szeged, Hungary*

MBP-P-301. MBP01 Saturday gene expression, regulation and signaling

Decoding harmame biosynthesis in *Delftia tsuruhatensis*: RNAseq insights for novel malaria control strategies

P. Sai, *North Carolina State University, Raleigh, NC, United States*

MBP-P-304. MBP04 Saturday molecular and genome biology of microbes

Epitranscriptomic dynamics in T5 phage-infected *Escherichia coli*: a dual perspective on RNA modifications

L. Rivera Montero, *Ludwig-Maximilians Universität, Munich, Germany*

Sunday, 22 June, 2025

10:00 am–04:00 pm PT | Exhibit Hall

AAR-P-408. AAR08 Sunday new antimicrobial agents

(*in vitro* and *in vivo* studies)

Phenotypic and genotypic characterization of antimicrobial resistance (AMR) strains from the ATCC® collection: a key resource for diagnostics and therapeutic development

B. Benton, *ATCC, Manassas, VA, United States*

AES-P-402. AES02 Sunday food systems & food fermentations microbiology

Factors to consider for probiotic safety: discovery of a safe, high-GABA producing *Lactiplantibacillus plantarum*

A. Aditya, *Verb Biotics, Durham, NC, United States*

AES-P-404. AES04 Sunday wastewater and drinking water microbiology

Monitoring influenza A virus in wastewater: combining RT-ddPCR and nanopore sequencing for enhanced surveillance

A. A. Kalalah, *Michigan State University, East Lansing, MI, United States*

AES-P-407. AES07 Sunday source tracking: non-clinical microbial & AMR detection and monitoring

Evaluation of low biomass shotgun nanopore metagenomic sequencing for environmental microbial community profiling

Q. Dai, *Duke University, Durham, NC, United States*

A comparison of antimicrobial resistance in alpaca (*Lama pacos*) faecal isolates from six sites in China

E. J. S. Dong, *The ISF Academy, Pokfulam, Hong Kong*

AES-P-408. AES08 Sunday biotransformations: bioremediation, biodegradation, biofouling and biocorrosion

Isolation and characterization of acid-tolerant mo-reducing bacteria from a disused tungsten mine in Hong Kong

M. He, *The ISF Academy, Pokfulam, Hong Kong*

CPHM-P-404. CPHM08 Sunday diagnostic public health microbiology

Unmasking zoonotic tuberculosis: amplicon-based targeted metagenomics for *Mycobacterium orygis* diagnosis

B. T. Hugh, *University of Sydney, NSW, Sydney, Australia*

CPHM-P-406. CPHM12 Sunday molecular and genome sequencing for diagnostics and AMR detection

Characterizing the defective and intact HIV-1 proviral milieu in the spleen and brain using near full-length NGS sequencing

M. Collins, *Drexel University, Philadelphia, PA, United States*

Host-pathogen dynamics in tracheal aspirates during chronic critical illness

A. Gupta, *University of Pittsburgh, Pittsburgh, PA, United States*

Genetic characterization of *Francisella tularensis* detected in Georgia

G. Chanturia, *National Center for Disease Control and Public Health (NCDC), Tbilisi, Georgia*

EEB-P-407. EEB07 Sunday microbiome ecology and evolution: diversity of host-microbe interactions

Hidden palette: exploring the role of microbes on avian plumage coloration

K. Sharma, *The University at Buffalo (SUNY), Buffalo, NY, United States*

HMB-P-405. HMB07 Sunday microbiome profiling

Unravelling gut microbiota disparities in term and preterm infants: insights into bacterial strain contributions and modulation

E. Seo, *Seoul National University, Seoul, Republic of Korea*

MBP-P-401. MBP01 Sunday gene expression, regulation and signaling

Insights into the transcriptomic landscape of *Caviid gammaherpesvirus* 1 through long-read sequencing

Á. Dörmo, *University of Szeged Albert Szent-Györgyi Medical School, Szeged, Hungary*

MBP-P-404. MBP04 Sunday molecular and genome biology of microbes

Understanding unannotated regions of the *Leptospira* transcriptome

L. C. M. Salvador, *University of Arizona, Tucson, AZ, United States*