

## Norwegian Consortium for Microbial Genomics annual meeting

Norwegian Institute of Public Health, Lovisenberggata 8, Oslo, Norway

December 5<sup>th</sup>, 2024

### PROGRAM – [PRELIMINARY]

10:00 – 10:10	<b>Opening address:</b> N.N, NIPH
10:10 – 11:10	<b>Antimicrobial resistance (30 min) – Chair N.N.</b> <b>Sebastien Gagneux</b> , Swiss Tropical and Public Health Institute: Ecology and evolution of multidrug-resistant <i>Mycobacterium tuberculosis</i> <b>Helen Wang</b> , Uppsala: Plasmid copy number variation as a modulator of antibiotic resistance
11:10 – 11:30	<b>Coffee Break</b>
11:30 – 12:45	<b>Antimicrobial resistance (15 min) – Chair N.N.</b> <b>Dagfinn Skaare</b> , Sykehuset Vestfold: Cefotaxime-resistant <i>Haemophilus influenzae</i> in Norway <b>Veronika Pettersen</b> , UiT: Dynamics of gut resistome and mobilome in early life <b>Amulya Baral</b> , NMBU: The resistome of aquatic plastispheres <b>Andre Ingebretsen</b> , OUS: Outbreak of vancomycin-resistant <i>Enterococci</i> <b>Torunn Gresdal Rønning</b> , St. Olavs hospital: Trends and characteristics of multidrug resistant MRSA in Norway 2008-2021
12:45 – 13:45	<b>Lunch</b>
13:45 – 14:15	<b>Microbial evolution (30 min) – Chair N.N.</b> <b>Anna Dewar</b> , U. of Oxford: Cooperation and horizontal gene transfer in bacteria
14:15 – 15:00	<b>Microbial evolution (15 min) – Chair N.N.</b> <b>Jon Bråte</b> , NIPH: Hepatitis C in Norway [Tentative title] <b>Harry Thorpe</b> , UiO: Pan-pathogen deep sequencing of nosocomial bacterial pathogens in Italy in spring 2020: a prospective cohort study <b>Ole Herman Ambur</b> , OsloMet: DNA uptake sequence specificity of the <i>Neisseriales</i>
15:00 – 15:20	<b>Coffee Break</b>
15:20 – 16:35	<b>Bioinformatics and AI (15 min) – Chair N.N.</b> <b>Iain George Johnston</b> , UiB: Hypercubic inference: a machine learning approach to help understand AMR evolution <b>Erlend Gløer Teigset</b> , NTNU: Bioinformatics and AI [No title yet]

	<p><b>Arturo Vera Ponce De Leon</b>, NMBU: Genomic and functional characterization of the Atlantic salmon gut microbiome in relation to nutrition and health</p> <p><b>Marina Aspholm</b>, NMBU: Cracking a 50-year mystery: Unveiling the genes and composition of <i>Bacillus cereus</i> endospore appendages</p> <p><b>Erik Hjerde</b>, UiT: National pathogen data platform</p>
16:35 – 16:40	<p><b>Concluding remarks:</b> <b>N.N.</b>, NIPH</p>