

**Norwegian Consortium for Microbial Genomics Meeting**  
Norwegian Institute of Public Health, Lovisenberggata 8, Oslo, Norway  
December 8, 2022

**PROGRAM**

10:00 – 10:10	<b>Opening address:</b> Trygve Ottesen, NIPH
10:10 – 11:10	<b>Antimicrobial resistance (30 min) – Chair Tone Tønjum</b> Marko Virta, Univ. Helsinki: Antimicrobial resistance, the environment and human activities Pål Jarle Johnsen, UiT: Evolution, selection and spread of antibiotic resistance in <i>E. coli</i>
11:10 – 11:25	<b>Coffee Break</b>
11:25 – 12:55	<b>Antimicrobial resistance (15 min) – Chair Tone Tønjum &amp; Lene C. Olsen</b> Aasmund Fostervold, SUS: The Norwegian <i>Klebsiella pneumoniae</i> bacteremia study Håkon Kaspersen, VI: Highly conserved composite transposon harbouring aerobactin iuc3 in <i>Klebsiella pneumoniae</i> from pigs Helene Johannessen, SIV: Tn7100 - A novel integrative and conjugative element conferring multidrug resistance in <i>Haemophilus influenzae</i> Oddvar Oppegård, UiB: <i>Streptococcus dysgalactiae</i> in a One-health perspective Marte Dragset, NTNU: Disarm virulence and reduce resistance - in one go! Novel targets against tuberculosis Ahmed Bargheet, UiT: Probiotic treatment reshapes gut microbiota, resistome, and mobilome in extremely preterm infants
12:55 - 13:45	<b>Lunch</b>
13:45 - 14:15	<b>Population genomics/evolution (30 min) – Chair Lene C. Olsen</b> Nicholas Croucher, Imperial College London: Understanding epidemiology through evolutionary conflicts
14:15 – 15:15	<b>Population genomics/evolution (15 min) – Chair Iren Høyland Löhr</b> Marit Hetland, SUS: Within-host evolution and global dynamics of <i>Klebsiella pneumoniae</i> ST17 Xiangning Bai, UiO: Shiga toxin-producing <i>Escherichia coli</i> : A One Health perspective Ignacio Garcia Llorente, NIPH: Evolution of SARS-CoV-2 in Norway in response to vaccination Birgitte Freiesleben de Blasio, NIPH: Use of genomics data in modeling

15:15 - 15:30	<b>Coffee Break</b>
15:30-16:30	<b>Microbiome/metagenomics (30min) – Chair Yngvild Wasteson</b> <b>Josie Bryant</b> , Sanger Institute: Within-host evolution of lung pathogens <b>Knut Rudi</b> , NMBU: Linking 16S rRNA gene information to Metagenome Assembled Genomes (MAGs)
16:30 – 17:00	<b>Microbiome/metagenomics (15 min) – Chair Michael Koomey</b> <b>Eiric de Muink</b> , UiO: Developing single cell genomics to study human gut microbiota <b>Trine Ballestad Rounge</b> , UiO: Predicting colorectal cancer using gut microbiomes
17:00 - 17:05	<b>Concluding remarks:</b> <b>Dominique A. Caugant</b> , NIPH