International One Health Symposium 2025

One Health Symposium
Challenges in a rapidly changing environment
2025
13. – 15.10. | Berlin

ID der Kurzfassung : **307**

Nanopore-Based Methylome Profiling of Microbial Communities

Inhalt

The methylome, defined as the complete set of genome-wide methylation marks, provides an additional layer of information beyond the genetic sequence, yet remains largely underexplored in bacterial genomics. Recent advances in Nanopore sequencing now allow investigation of DNA methylation not only in isolates but also at the community level, opening new opportunities to study epigenetic variation in complex microbiomes and better understand microbial ecology and adaptation.

We are analyzing the metagenome and the metamethylome of seal microbiomes using Nanopore sequencing, as part of a project investigating antimicrobial resistance (AMR) acquisition on those sentinel species. By applying state-of-the-art ONT basecalling tools combined with in-house pipelines, we examine how DNA methylation varies across species and strains. A complementary study investigates Klebsiella pneumoniae isolates from wastewater, providing insights into how methylation patterns differ between environmental populations and those from host-associated communities.

Beyond biological insights, we aim to integrate methylation data into metagenomic workflows. We assess how methylation can improve early-stage classification by filtering out eukaryotic sequences and enhancing binning accuracy, especially in linking mobile genetic elements like plasmids to host genomes. These efforts contribute to a deeper understanding of epigenetic mechanisms in AMR and support a broader One Health approach connecting environmental, animal, and human health.

Keywords

metagenomics, methylation, Nanopore

Registration ID

OHS25-134

Professional Status of the Speaker

PhD Student

Junior Scientist Status

Yes, I am a Junior Scientist.

Track Klassifizierung: Genomics & Proteomics

Typ des Beitrags: Both options possible