



ID der Kurzfassung : 277

Legionella Genotype Map –Statewide Genomic Surveillance of Environmental Isolates

Inhalt

Background:

Despite their significant public health relevance, the epidemiological links between environmental *Legionella* sources and human infections remain poorly defined. This is due to limited strain-level resolution in standard detection methods and a lack of harmonized genomic surveillance data across environmental compartments. With climate change promoting conditions conducive to *Legionella* growth and transmission, the need for a robust molecular surveillance system is growing.

Objective:

To establish a genomic framework for routine environmental monitoring and genotyping of *Legionella* spp. in Lower Saxony using whole genome sequencing (WGS), in order to develop a state-level “*Legionella* Genotype Map” as a tool for outbreak preparedness and source attribution.

Methods:

Up to date around 100 environmental *Legionella pneumophila* (n = 93) most common and clinically relevant pathogenic *Legionella* species isolates from diverse geographic regions and water types across Lower Saxony. The isolates have already been collected and cultivated with high quality standard taxonomically verified using short-read sequencing (Illumina) and long-read sequencing (Oxford Nanopore), enabling high-resolution hybrid genome assemblies. Subsequent analyses include resistome/pathogenicity profiling using a custom-built bioinformatics pipeline in collaboration with the University of Duisburg-Essen and Universitätsmedizin Essen.

Results:

The survey sequencing results using short-read sequencing and WGS for core genome sequence multilocus typing (cgMLST, Ridom Seqsphere) analysis of *Legionella pneumophila* isolates (n = 93) showed different complex types (>50, CT) (Fig.). However, there were clustering samples resulting in clusters (>10), which gives a first look on surveillance data across environmental compartments as a tool for outbreak preparedness and source attribution.

Keywords

Legionella, Genomic Surveillance, sequencing, environment, preparedness

Registration ID

132

Professional Status of the Speaker

Senior Scientist

Junior Scientist Status

No, I am not a Junior Scientist.

Track Klassifizierung: One Health in Public Health

Typ des Beitrags: Both options possible