## **International One Health Symposium 2025**

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# Legionella Genotype Map –Statewide Genomic Surveillance of Environmental Isolates

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#### 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 custombuilt 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.

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