



## **Comparative Genomics of *Legionella pneumophila* Isolates from the West Bank/Palestinian territories and Germany Support Molecular Epidemiology of Legionnaires' Disease**

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*Legionella pneumophila* is an environmental bacterium and clinical pathogen that causes many life-threatening outbreaks of an atypical pneumonia called Legionnaires' disease (LD). Studies of this pathogen have focused mainly on Europe and the United States. A shortage in *L. pneumophila* data is clearly observed for developing countries.

To reduce this knowledge gap, *L. pneumophila* isolates were studied in two widely different geographical areas, i.e., the West Bank and Germany. For this study, we sequenced and compared the whole genome of 38 clinical and environmental isolates of *L. pneumophila* covering different MLVA-8(12) genotypes in the two areas. Genome sequences from 55 *L. pneumophila* strains, including 17 reference strains, were aligned with the genome sequence of the closest strain (*L. pneumophila* strain Alcoy). An analysis of the genomic population structure by SNP comparison divided the fifty-five *L. pneumophila* strains into six branches. Individual isolates in sub-lineages in these branches differed by less than 120 SNPs if they had the same MLVA genotype and were isolated from the same location. Overall, the selection of strains by MLVA and subsequent genomic characterization showed nearly the whole phylogenomic breadth of *L. pneumophila* as it was recovered within our study. SNP typing revealed a highly accurate typing superior to MLVA analysis.

When: Thursday, June 22<sup>nd</sup> 2023 at **3 pm**

Where: DSMZ lecture room, 4<sup>th</sup> floor, D.16

For participants who cannot attend in presence, a [Zoom link](#) is provided (Meeting-ID: 896 5418 0484; Kenncode: 918105)

Host: Dr. Boyke Bunk, DSMZ

Guests are welcome!

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