

The microbiome of sputum samples from legionellosis associated patients versus other pneumonia patients



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Introduction

A microbiome is the bacterial community that inhabits a specific host. Up until now, only a few studies investigated the lungs, the respiratory tract and the sputum microbiome. None of them have studied the sputum microbiome with regard to Legionellosis. Bacteria of the genus *Legionella* cause waterborne infections, resulting in severe pneumonia. *L. pneumophila* was reported as the cause of 84% of the cases world-wide. Humans become infected with *L. pneumophila* by inhaling aerosols from aquatic environments.

Aim

To analyze the bacterial community and the proportion of *Legionella* in sputum samples of pneumonia patients that cuse due to *Legionella* spp. and to compare it to the bacterial community in sputum samples of pneumonia patients that cue due to other pathogens.

Methods

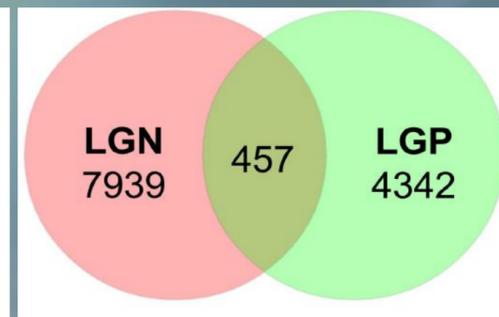
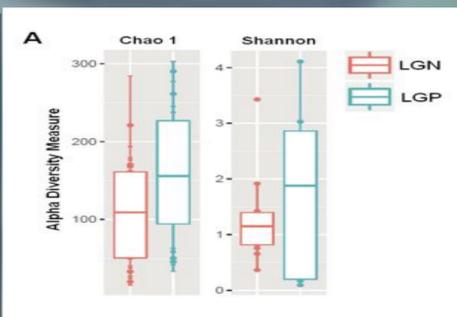
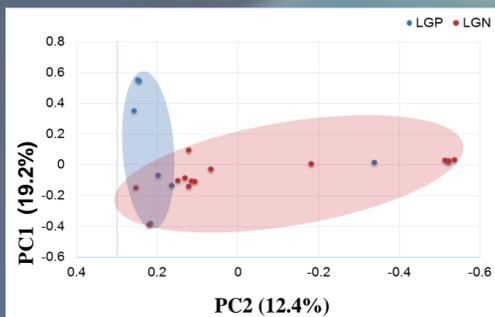
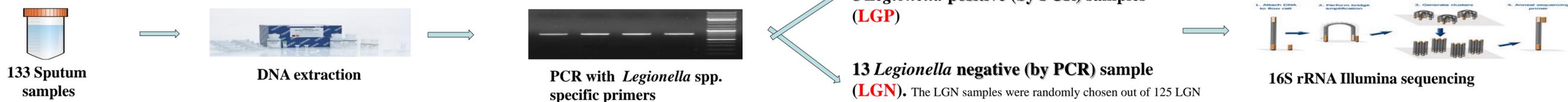
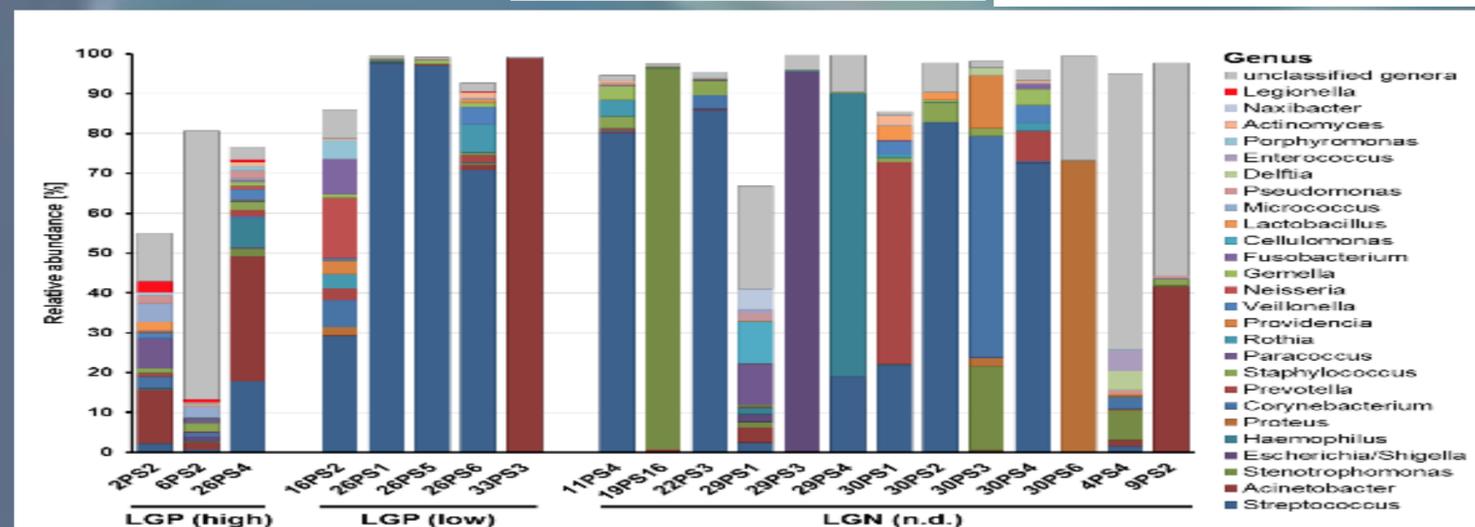


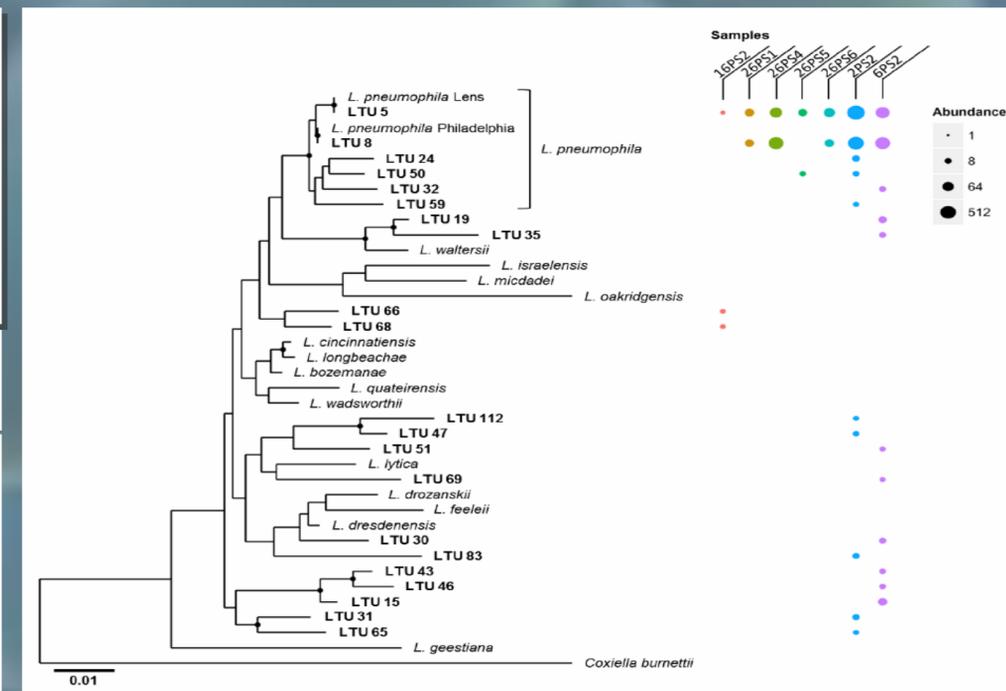
Figure 1. Principal Coordinates Analysis (PCoA) demonstrating the relations between LGP and LGN.

Diversity of sputum samples - α 2Figure based on data on the genus level.

. Venn Diagrams at distance 0.033Figure Number of unique and shared subsampled OTUs



: Phylogenetic diversity and abundance of Legionella operational taxonomic units (LTUs) in Legionella-positive (LGP) sputum 5Figure samples based on 16S rRNA sequence comparison. only clusters with ≥ 5 reads are shown. Nodes with bootstrap support of $\geq 50\%$ are indicated and the scale bar shows the number of substitutions per site.



: Phylogenetic 5Figure diversity and abundance of Legionella operational taxonomic units (LTUs) in Legionella-positive (LGP) sputum samples based on 16S rRNA sequence comparison. only clusters with ≥ 5 reads are shown. Nodes with bootstrap support of $\geq 50\%$ are indicated and the scale bar shows the number of substitutions per site.

Conclusions

- At the genera level, most of the sputum samples were dominated by OTUs belonging to one or two genera; *Streptococcus* and *Acinetobacter*
- The results demonstrate that at least for legionellosis, co-infection with other bacterial species occurs
- Our results show the importance of the next generation sequencing technique for receiving accurate bacterial composition identification of the sputum microbiome. This technique should be considered as a new molecular method for pathogens' diagnosis in pneumonia patients