

**P1002**  
**Paper Poster Session**  
**Microbiota**

**Sputum microbiome of legionellosis-associated patients vs. other pneumonia patients**

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**Background:** Bacteria of the genus *Legionella* cause water-based infections, resulting in Pontiac fever, a self-limited flu-like illness, or severe pneumonia called *Legionellosis* of which approximately 10% of the infections are fatal. Because of the difficulty in distinguishing *Legionellosis* from other forms of pneumonia, many cases are unreported. Our aim was to monitor the prevalence of *Legionellosis* in pneumonia patients by using both culture dependent and independent methods.

**Material/methods:** Primarily, the bacterial microbiome of clinical sputum samples was explored and particularly the prevalence of *Legionella* in those samples. Nine sputum samples out of the 133 analyzed were PCR positive by using *Legionella* genus specific primers. The limit of detection of the PCR was about 40 *Legionella* cells per 1 ml of sputum.

**Results:** *Legionella* was isolated by culture only from one of these samples. Illumina MiSeq 16S rRNA gene sequencing analyses of 21 sputum samples (8 PCR-*Legionella* positive and 13 *Legionella* negative), confirmed that indeed, *Legionella* was present in the PCR positive sputum samples. Interestingly, at the genus-level, most of the sputum samples were dominated by OTUs belonging to one or two genera; *Streptococcus* and *Acinetobacter*.

**Conclusions:** The results demonstrate that at least for legionellosis, co-infection with other bacterial species occurs. The next generation sequencing technique allowed the identification of the sputum bacterial composition. Further studies in larger scales are essential to evaluate the correlation between *Legionella* abundances in parallel to other pathogens in sputum samples. These may enable to create new tools for diagnostics of legionellosis.