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Paper Poster Session

Microbial pathogenesis and virulence

Comparative genomics on the re-emerged deadly bacterium *Fusobacterium necrophorum*

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Background: *Fusobacterium necrophorum* is a gram-negative, anaerobic bacterium that in the preantibiotic era was a relatively common cause of septicaemia in adolescents and young adults, most often with disseminated abscess formation and with a primary focus in the head (mostly the oropharynx). The disease is today known as necrobacillosis or Lemierre's syndrome and had an almost 100% mortality in the preantibiotic era. Between 1950-1990 very few cases of *F. necrophorum* septicaemia were described, but from the nineties *F. necrophorum* infections including invasive infections like Lemierre's syndrome have increased almost exponentially. Newer studies have also shown that *F. necrophorum* is involved in abscess formation, otitis media and may be as common as *S. pyogenes* (group A *Streptococcus*) in the aetiology of tonsillitis, especially recurrent/chronic tonsillitis. In addition, complications (peritonsillar abscesses and Lemierre's syndrome) due to *F. necrophorum* tonsillitis appear to be more common than complications arising from *S. pyogenes* tonsillitis including peritonsillar abscess, acute glomerulonephritis, and acute rheumatic fever. In spite of the reoccurrence of this deadly bacterium, virtually nothing is known about the genomics, phylogeny, pathogenesis and virulence of *F. necrophorum*. The keystone to answer many of the questions may be hidden in the genomes of *F. necrophorum*.

Material/methods: More than 200 well characterized isolates of *F. necrophorum* isolated from the Lemierre's syndrome patients (>50 isolates), patients with tonsillitis, peritonsillar abscesses and other localized infections (> 100 isolates), and healthy carriers (>50). The genomes are sequenced by Illumina technology, and five representative isolates have been sequenced with PacBio technology for closure of the genomes.

Results: The phylogenetic and comparative genomic analysis will be presented at ECCMID2016. Initial data shows that invasive isolates are phylogenetically different from non-invasive isolates and isolates from healthy carriers. Possible differences in virulence factors between the groups have to be determined. In addition, we are developing a typing scheme to identify invasive/virulent strains from non-invasive strains. Preliminary results of the typing scheme will be presented at ECCMID2016.

Conclusions: The resulting data and analysis of the genomes will greatly improve our general understanding of this emerging human pathogen in relation to phylogeny, virulence and genomics and the data will be the basis for further studies on this deadly bacterium. Our ultimately goal from the analysis is to development of quick tests to detect *F. necrophorum* directly from throat swabs similar to the Strep A test. This test will have the potential to greatly reduce complications such as peritonsillar abscesses and Lemierre's syndrome from an otherwise benign infection like tonsillitis. By reducing the number of complications, the medical cost will also greatly be reduced.