

Identification of *Streptococcus anginosus* virulence factors

Streptococcus anginosus (SAG, *Streptococcus milleri*) belongs to broad group of streptococci that until the 1980s was considered to be a non-pathogenic microorganism, rarely causing severe infections. Over the past 30-35 years, a growing number of complicated, life threatening infections caused by this group has been observed. The biology of these microorganisms is not fully understood, and the **mechanisms of virulence of these bacteria are mostly unknown**. Thanks to the development in genomic sequencing techniques, last 3-4 years brought a lot of information about this group of organisms and it opened new avenues to develop strategies to study SAG biology and pathogenesis. Unfortunately, genomic analyses shown that products that are encoded by about **50% of the genes can not be assigned a function** based on their homology to known genes. Moreover, usually genes are annotated as hypothetical, and even when the function is assigned based on the homology, it is not experimentally confirmed. There are only single reports describing experimentally confirmed identification of virulence factors in SAG. In addition, the pathogenicity traits of streptococci are often determined by the **interaction between the pathogen and the host** and depends on both "partners" involved in the infection process.

The major scientific problem we want to answer in this project is the **identification of virulence factors in SAG**. Genes involved in these processes can be identified by construction of "knock out" mutants without specific reading frames and analysis of their phenotype. Therefore, we plan to construct SAG mutants and screen them in search of phenotype that may be involved in virulence, such as interaction with human epithelial cells in vitro, or production of enzymes.