
Identification and characterization of genes contributing to the virulence of the major swine pathogen *Streptococcus suis*

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Streptococcus suis bacteria cause serious infectious diseases in piglets, associated with substantial piglet mortality and major economic losses to the pig industry. *S. suis* is also a zoonotic pathogen and human infections worldwide have increased significantly in the past years. Different isolates of *S. suis* are highly diverse in terms of genotype and serotype and asymptomatic carriage is common in pigs, hampering the development of effective control strategies. Our group is part of a European project aimed at increasing our understanding of *S. suis* disease mechanisms from the genomic sequences of more than 1800 *S. suis* strains isolated from healthy and diseased piglets from different countries including Denmark, Germany, Spain and the Netherlands. A genome-wide-association study was used to identify a set of genes that were highly enriched in the pathogenic isolates. To investigate the function of these genes in virulence, we generated KO mutants of selected genes in *S. suis* using a novel genome editing approach. These genetic mutants are being characterized in a variety of in vitro infection models mimicking relevant stages of infection, including organoid systems. This approach will increase our understanding of the mechanisms underlying *S. suis* infection and contribute towards the development of effective control strategies.