Poster Abstract

Genomic characterization of the FCT-like region in S. dysgalactiae subsp. equisimilis

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Streptococcus dysgalactiae subsp. equisimilis (SDE) is an emerging pathogen that is increasingly associated with invasive infections. It is a closest relative of *Streptococcus pyogenes* (Spy), the pathogen responsible for the 'flesh-eating' disease. Both species can co-exist and frequently exchange genes. No vaccine exists that confers immunity to SDE or Spy. However, a region in Spy encoding the Fibronectin-binding, Collagen-binding, and T-antigen proteins (FCT-region), involved in pilus formation is a prime target for vaccine development. Here the genomic architecture and diversity within SDE FCT-like region (SDE-FR) was investigated.

Methods: 20 genomes from diverse SDE isolates were utilized in this study. Six Spy genomes representing the most common FCT types (1-6) were independently annotated and imported for comparison. A multiple sequence alignment from protein sequences was used generate a phylogenetic tree

Results: 20 SDE genomes revealed 9 different FCT architectures. Each SDE-FR harbored between 2-4 sortase genes. Strikingly, *rofCG,* a homolog of Spy positive transcriptional regulator *rofA* was 98-99% similar. The fimbrial-associated (FaP) proteins in SDE showed the greatest difference in comparison to the backbone proteins (FctA, Tee6) in Spy. The sortases and collagen-binding proteins also showed high degree of variability. Moreover, some SDE strains harbored two fibronectin-binding genes which also function as ferrous iron transporters.

Conclusion: In general**,** SDE-FRs showed greater architectural conservation than the Spy FCT region. There are several proteins between SDE-FR and Spy FCT region that are highly conserved, and could form putative vaccine targets. Hypervariable loci within the SDE-FR region reflect genes whose products mediate host-cell adhesion and invasion.