

Hypervirulence and Group B Streptococcal infection

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The bacterium *Streptococcus agalactiae* also known as Group B Streptococci (GBS), is a leading cause of mortality in newborn babies in high- and low-income countries worldwide. Multi locus sequence typing (MLST) is commonly employed to identify and track GBS strains circulating globally with MLST sequence types (STs) further grouped into clonal complexes on the basis of these sharing a defined number of MLST alleles with a central ST. On that basis, 6 human associated GBS clonal complexes have been described each of which exhibiting varying degrees of virulence. For example, clonal complexes (CCs) 1, CC19 and CC23 are well adapted for colonisation of the mucosa with CC17 a known hypervirulent clonal complex due to its frequent association with neonatal sepsis and meningitis. Reasons for the increased propensity for CC17 isolates to cause invasive disease can be attributed to the presence of particular gene sets whose functions may facilitate persistence in the more hostile environments encountered in the host such as the blood stream.

In this presentation, I will be discussing some of these attributes and showing how genome sequence data can be used to improve our understanding of GBS populations. Using the core genome MLST scheme (h_ *S.agalactiae*_cgMLST v1.0) implemented in the genomics platform, PubMLST (<https://pubmlst.org/organisms/streptococcus-agalactiae>), genomes from large GBS datasets can be compared and their associations with clonal complexes, capsular loci and pilus islands explored. At the time of writing, (October 2021), over 2,000 genes had been defined in the database allowing the gene-by-gene annotation of GBS genomes. This allows us to explore the diversity of vaccine candidate genes while also for example, providing a resource for tracking the potential emergence of antimicrobial resistance in this species. Undertaking such studies allows us to understand the population biology of *S. agalactiae* and facilitates the global surveillance of this bacterium.