

Introduction: Group B Streptococcus (GBS) is a leading cause of mortality and morbidity in neonates worldwide. It is a pathobiont of the gastrointestinal and genitourinary tracts of healthy pregnant women and transmitted to the neonate during birth. The population structure of GBS is geographically distinct. To investigate the molecular epidemiology of GBS strains in Egypt Multilocus-sequence-typing (MLST) and serotyping was performed as a prerequisite for vaccine development.

Methods: GBS strains were collected in an earlier investigation. As part of the worldwide GBS surveillance study JUNO, whole-genome sequencing was performed at the Wellcome Sanger institute and MLST and serotypes were obtained from the genome data.

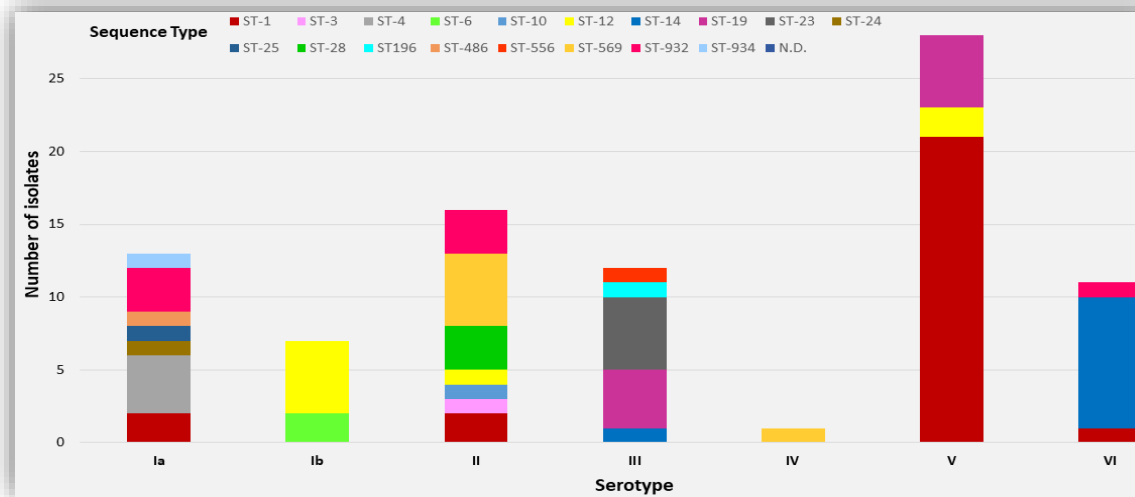


Fig. 1 Serotype and MLST distribution of colonizing GBS isolates from Egypt. Bars indicate the numbers of isolates per serotype in the collection of 90 isolates. The colored blocks indicate the sequence type (ST).

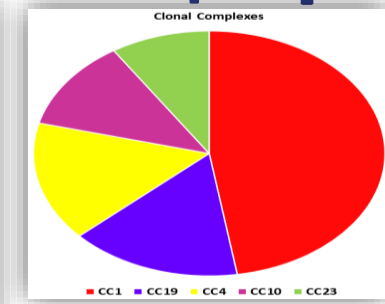


Fig. 2 Distribution of clonal complex among colonizing GBS in Egypt

Conclusion: Although the population structure of Egyptian strains resembles that of sequence types and serotypes found in the US and Europe, we identified local specificities in the distribution including a rather large proportion of ST 14, serotype VI strains. These findings may have potential implications for vaccine developments.

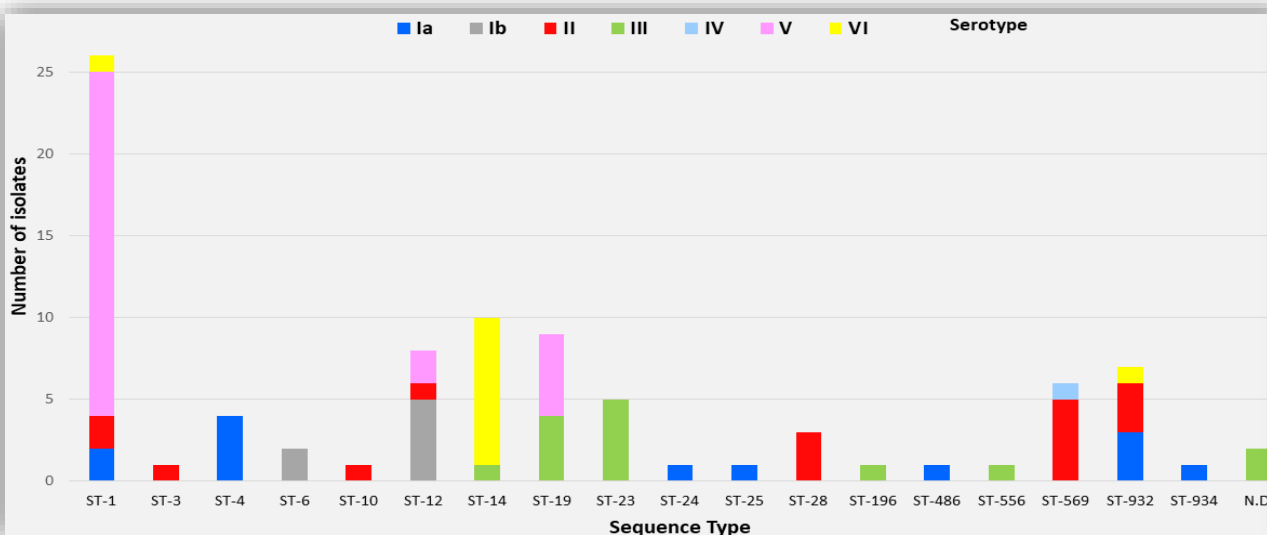


Fig. 3 Sequence type (ST) and serotype distribution of colonizing GBS isolates from Egypt. Bars indicate the numbers of isolates per ST in the collection of 90 isolates. The colored blocks indicate the serotype.

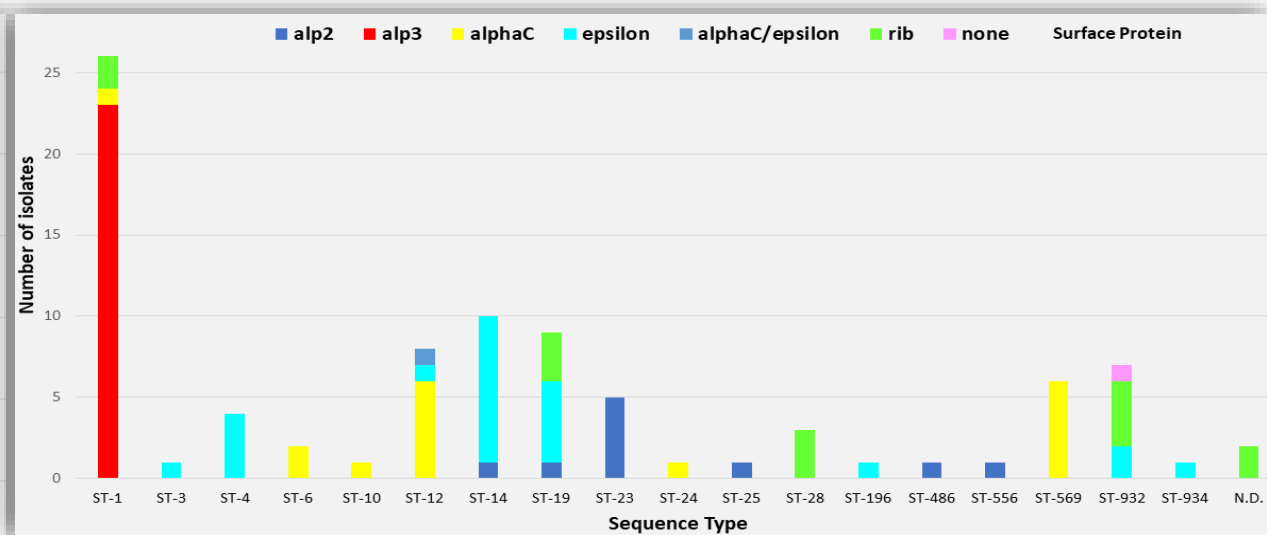


Fig. 4 Sequence type (ST) and surface protein distribution of colonizing GBS isolates from Egypt. Bars indicate the numbers of isolates per ST in the collection of 90 isolates. The colored blocks indicate the surface protein.