Genomic analysis of *Streptococcus agalactiae* ST103 recovered from different sources over 30 years in Brazil

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BACKGROUND

Group B *Streptococcus* (GBS) ST103 is emerging among bovine and human hosts. Genomic analysis of ST103 strains from various sources can lead to a better understanding of evolution and potential of this clone.

OBJECTIVES

Apply WGS for predicting the presence of major surface proteins, antimicrobial resistance genes, CRISPR elements and phylogenetic relationship among 15 serotype Ia/ST103 isolates recovered from human anovaginal specimens (AV; 11 strains from 2008-2019), human oropharynx (OP; 2 from 1990) and bovine milk (BM; 2 from 2006-2010) in Rio de Janeiro, Brazil.

MATERIAL & METHODS

Search for virulence factor and antimicrobial resistance genes; CRISPR elements and Phylogenetic relationship

RESULTS

Serotype Ia/ST103 strains clustered together, distant from outgroups (ST17, ST23, ST61) in the phylogenetic tree (Fig. 1), but were divided in two major subclusters (sc): scA comprised OP strains and the oldest BM while scB comprised AV strains and the most recent BM.

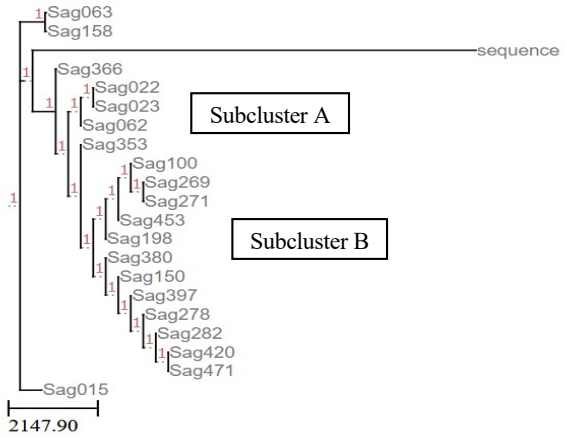

Fig. 1: Phylogenomic tree constructed with WGS data of GBS strains included in the study. The genome of GBS strains belonging to the lineages ST17 (Sag 158), ST23 (Sag 063) and ST61 (Sag 015), as well as the genome of another related beta-hemolytic streptococcal species *S. dysgalactiae* (sequence), were included as outgroups.

All strains had PI-2b and lacked *scp*B and *lmb* (bovine-related characteristics). Genes encoding Alp and AgI/II family proteins were found only in scB. Strains were mostly antimicrobial-susceptible and lacked *tet*M; *mef* was detected in both OP and *tet*O was found in both BM strains, being one of them also *erm*B-positive. All strains had CRISPR elements with 3 (BM) to 16 spacers (OP); consensus direct repeats were conserved within subclusters but different between scA and scB; identical spacers were shared among strains from all sources.

CONCLUSION

Serotype Ia/ST103 strains in this study present genomic characteristics that are common among bovine-adapted strains but are distantly related to other bovine and human lineages, suggesting this is a distinct but potentially zoonotic clone. Detection of ST103 subclusters presenting different resistance and virulence profiles and temporal distribution highlights the versatility of this clone and the possibility of a dynamic ongoing evolution.

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