

TITLE: GENOMIC ANALYSIS OF SEROTYPE Ia/ST103 *Streptococcus agalactiae* STRAINS RECOVERED FROM HUMAN AND BOVINE SOURCES OVER 30 YEARS (1990-2019) IN RIO DE JANEIRO, BRAZIL

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ABSTRACT:

Group B *Streptococcus* (GBS) is a leading agent of human invasive infections and contagious bovine mastitis. Strains belonging to ST103 clone are emerging among bovine and human hosts in different countries during the last years. Genomic analysis of ST103 strains from various sources can lead to a better understanding of evolution and potential of this clone. In this study, whole genome sequencing was applied 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. ST103 strains clustered together, distant from outgroup clones (ST17, ST23 and ST61) in the phylogenetic tree, 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, showing that division into sc did not correlate with clinical origin. All strains harbored genes for Srr1 and PI-2b proteins but lacked ScpB and Lmb genes, characteristics of bovine-adapted GBS strains. Genes encoding alpha-like proteins and Agl/II family proteins were found only in scB strains. ST103 strains were mostly antimicrobial-susceptible and lacked *tetM*; *mef* was detected in both OP strains and *tetO* was found in both BM strains, being one of them also positive for *ermB*. All strains had CRISPR-CasII elements containing 3 (BM) to 16 spacers (OP); consensus direct repeats were conserved within subclusters but different between scA and scB. However, identical spacers were shared among strains from all sources, suggesting a common evolutionary path. Overall, ST103 strains recovered from various sources in Rio de Janeiro presented genomic characteristics that are common among bovine-adapted strains and were distantly related to other bovine and human clones, suggesting this is a distinct but potentially zoonotic clone. Detection of subclusters containing strains from different origins and presenting different resistance and virulence profiles and temporal distribution within ST103 strains in this study highlights the versatility of this lineage and suggests the possibility of a dynamic ongoing evolution.

Keywords: *Streptococcus agalactiae*, Group B *Streptococcus*, zoonotic transmission, whole genome sequencing

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