

USA

United Kingdom





Characterization of the prophage content of Argentinean and global GBS strains by genomic analysis

Verónica Kovacec¹, Sabrina Di Gregorio¹, Mario Pajón¹, Tomás Poklepovich², Josefina Campos², Marta Mollerach^{1,3}, Laura Bonofiglio^{1,3,*}

in silico PCR (van der Mee-Marquet, 2018)

1 Universidad de Buenos Aires, Facultad de Farmacia y Bioquímica, Instituto de Bacteriología y Virología Molecular, Buenos Aires, Argentina, 2 Plataforma de Genómica y Bioinformática, INEI-ANLIS, Malbrán, Buenos Aires, Argentina, 3 CONICET, Argentina, 8 Ibonofi@ffyb.uba.ar

Introduction

The role of prophages in GBS epidemiology is still under study. Within the framework of an Argentinean Multicenter Study, we selected 10 human GBS strains (S1-S10) with different serotype, clinical origin and AMR profile to perform WGS analysis. We aimed to characterize the prophage content of the sequenced GBS strains and others publicly available, in the context of GBS genomic and epidemiological data.

Methods Assembly Quality Check Whole Genome Sequencing Reads Quality Check Assemblies Annotation De Novo Assembly 148 GBS assemblies from public databases Core gene alignment Single nucleotide polymorphisms extraction Illumina MiSeq v2 SPAdes 18 countries (5 continents), human and animal hosts Prokka FastQC / Kraken Quast / Manual Curation SNP-sites Maximum likelihood phylogenetic tree construction Serotype determination Antimicrobial resistance genes search Virulence factors search Plasmid replicon genes search RAxML (GTR+G model, 100 Bootstrap replicates) Blastn search of reference capsular genes (Sheppard, 2016) ABRicate on Galaxy Europe (ResFinder database) ABRicate on Galaxy Europe (VFDB database) ABRicate on Galaxy Europe (PlasmidFinder database) MLST prediction Prophage screening and classification according to GBS-prophage group (A-F)

Prophage screening and classification according to GBS-prophage-integrase (GBSint) type BLASTx against a GBSint database (Crestani, 2020)

Information integration and visualization

Results



Pathogewatch

ND / GBSint6.1

ND / GBSint8

Not detected

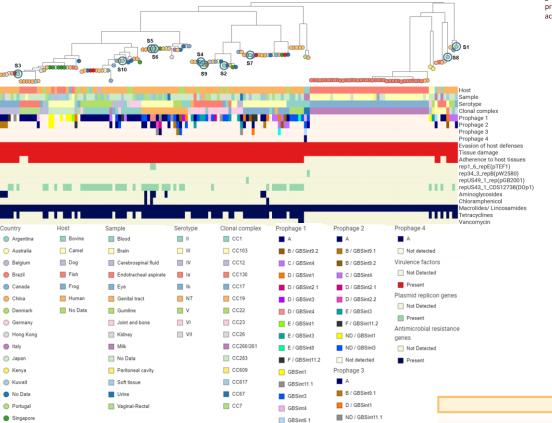


Figure 2: Distribution in the phylogeny of GBS strains (n=158) by clonal complex. Core-SNPs maximum likelihood phylogenetic tree, midpoint rooted, with nodes coloured by clonal complex. Argentinean strains (n=10) are circled and labeled. We detected the presence of up to 4 prophages per genome. Coloured blocks around the tree show serotype distribution in the phylogeny (inner layer) and prophage content of the genomes (prophage 1 to 4 from inside to outside). Each prophage is classified according to their prophage group (A-F) / prophage integrase type (GBSint).

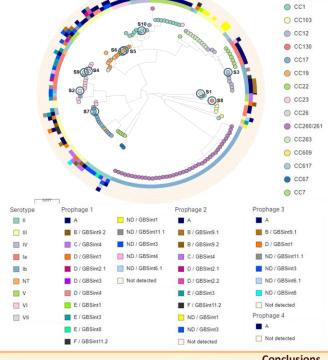
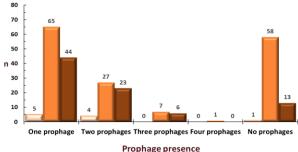
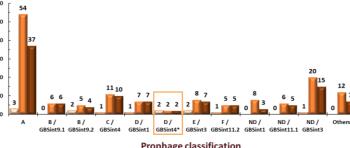


Figure 3: Prophage presence in Argentinean and global GBS strains.



☑ Argentinean strains (n=10) ■ Global strains (n=158) ■ Global human strains (n=86)

Figure 4: Classification of the prophages found in Argentinean and global GBS strains according to their prophage group (A-F) / prophage integrase type (GBSint).





Conclusions

Argentinean GBS are related to strains circulating globally

The implications in local GBS epidemiology of an exclusive prophage-type need to be studied

The relation between GBS distribution in the core-genome phylogeny and prophage content implies an important role of prophages in the spread of GBS strains.