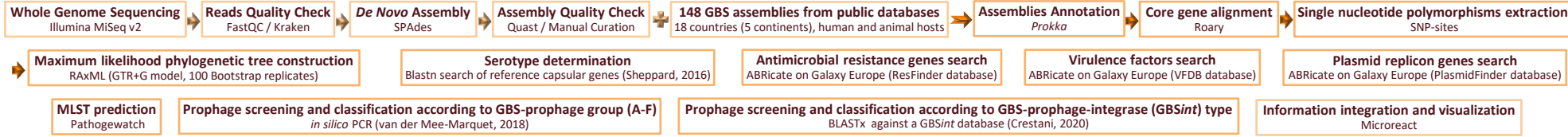


Introduction

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



Results

Figure 1: Epidemiological and genomic characteristics of the 158 GBS strains analyzed. Core-SNPs maximum likelihood phylogenetic tree, midpoint rooted, with nodes coloured by country of isolation. Argentinean strains (n=10) are circled and labeled. We detected the presence of up to 4 prophages per genome. Strain metadata, classification of the detected prophages, virulence genes, rep genes and AMR genes are coloured as described in the legend.

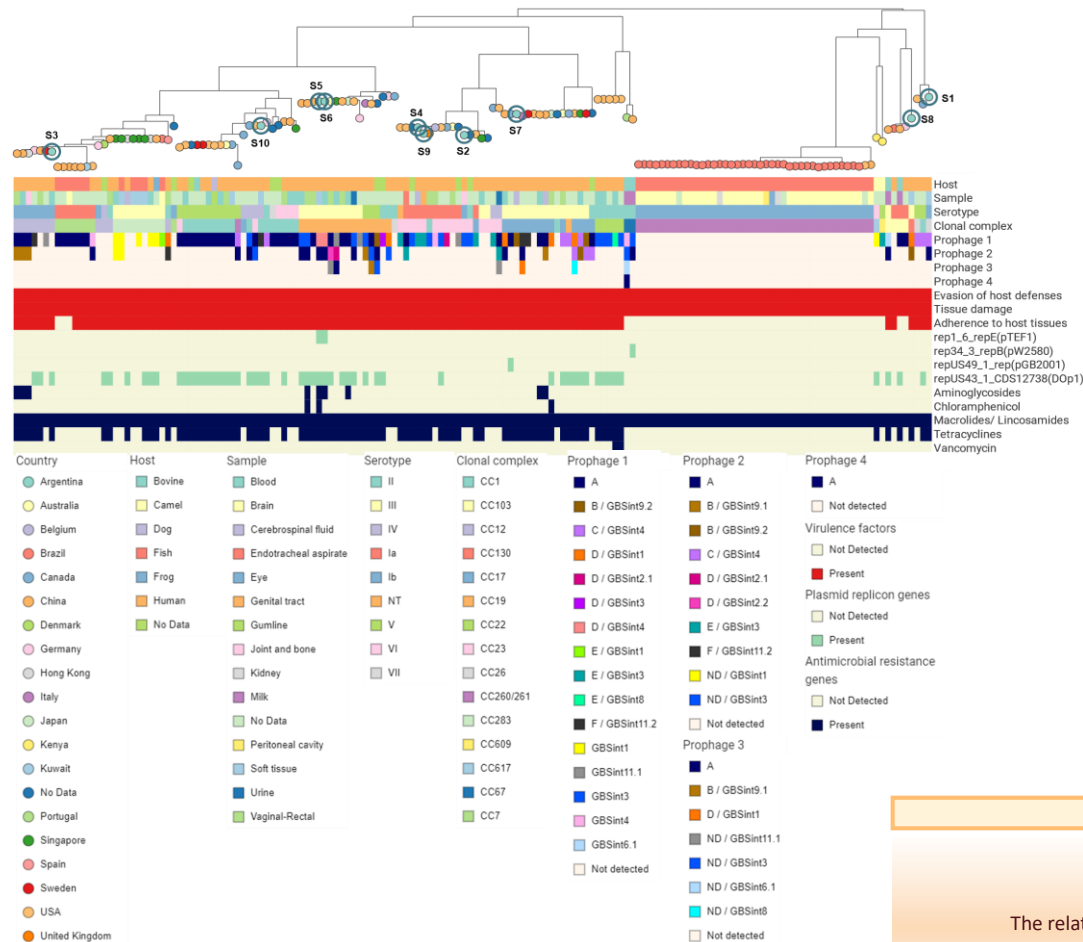


Figure 2: Distribution in the phylogeny of GBS strains (n=158) by clonal complex. Core-SNPs maximum likelihood phylogenetic tree, midpoint rooted, with nodes coloured by clonal complex. Argentinean strains (n=10) are circled and labeled. We detected the presence of up to 4 prophages per genome. Coloured 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).

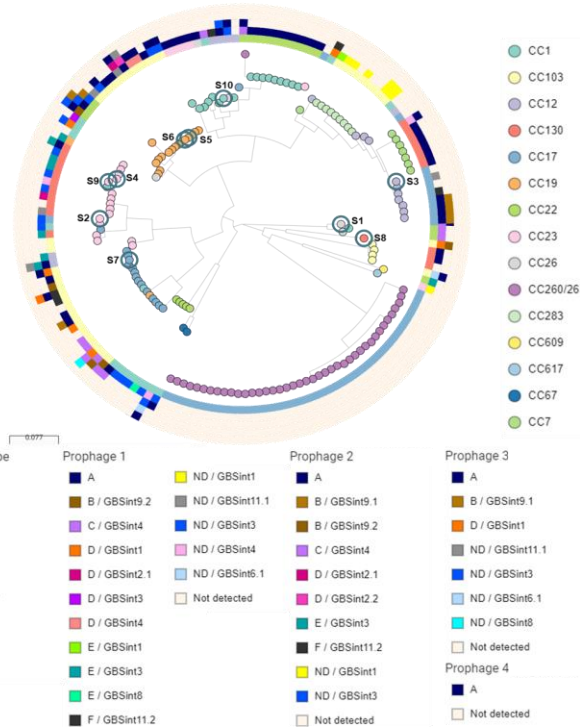


Figure 3: Prophage presence in Argentinean and global GBS strains.

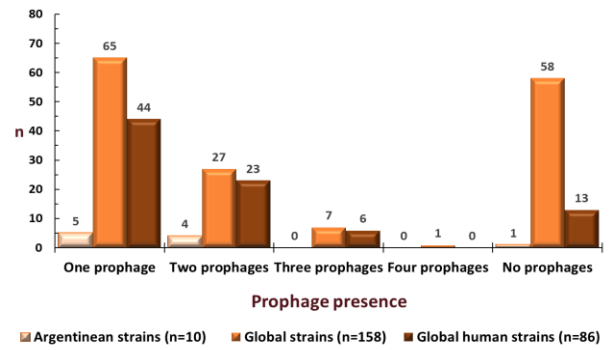
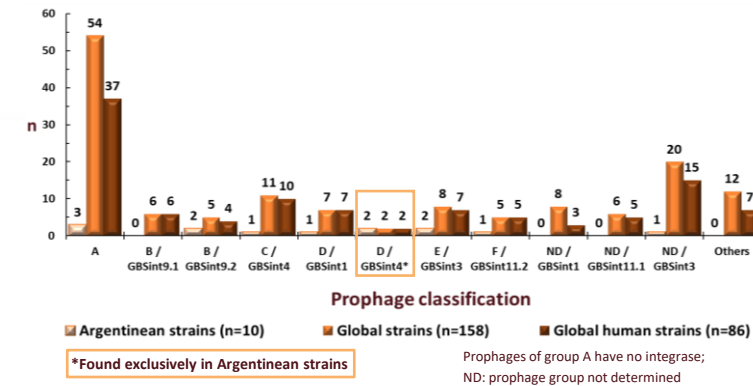


Figure 4: Classification of the prophages found in Argentinean and global GBS strains according to their prophage group (A-F) / prophage integrase type (GBSint).



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.