Comparing GPSCs and clonal complex clusters for *Streptococcus pneumoniae*

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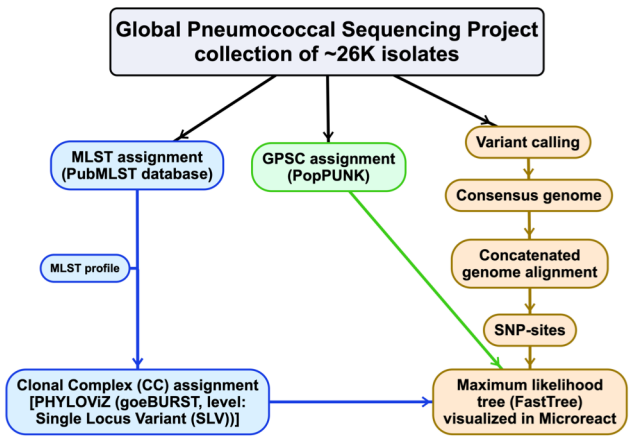
Introduction

Lineages in *Streptococcus pneumoniae* are defined based on clustering of MLSTs into clonal complexes (CCs) dependent on 7 housekeeping genes. This method lacks resolution with some of the genes subject to recombination and the results not easily comparable between studies. Also, the methodology is not very user-friendly and clustering is study specific. Recently, PopPUNK, a new method has been described that sketches the entire genome into k-mers and identifies Global Pneumococcal Sequence Clusters (GPSCs). Here, using a large global collection of pneumococcal isolates, we compare the clustering obtained by the two methods.

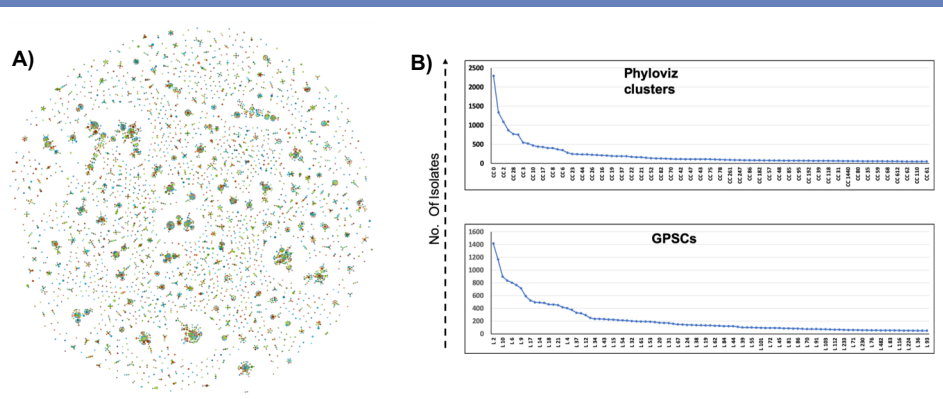
Aim

Comparing the genome based GPSCs against the MLST based CC assignment

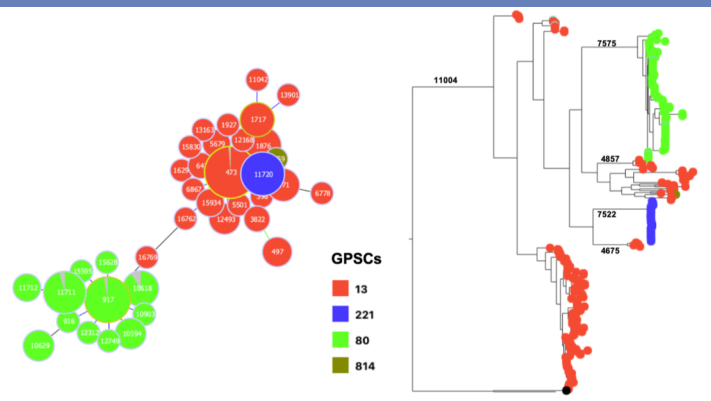
Methods



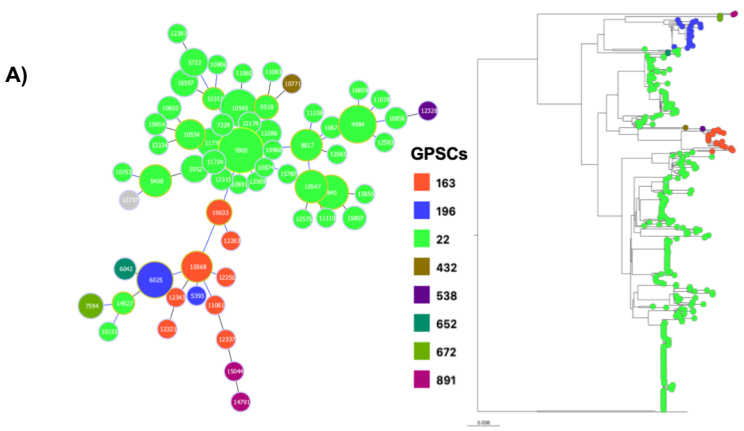
Results

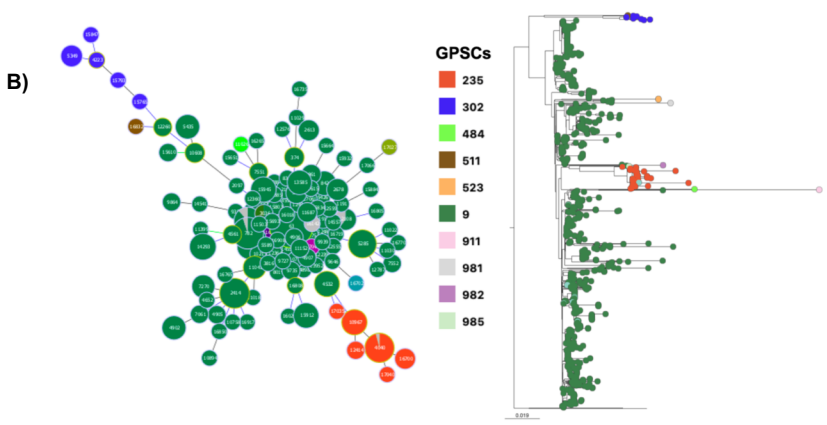


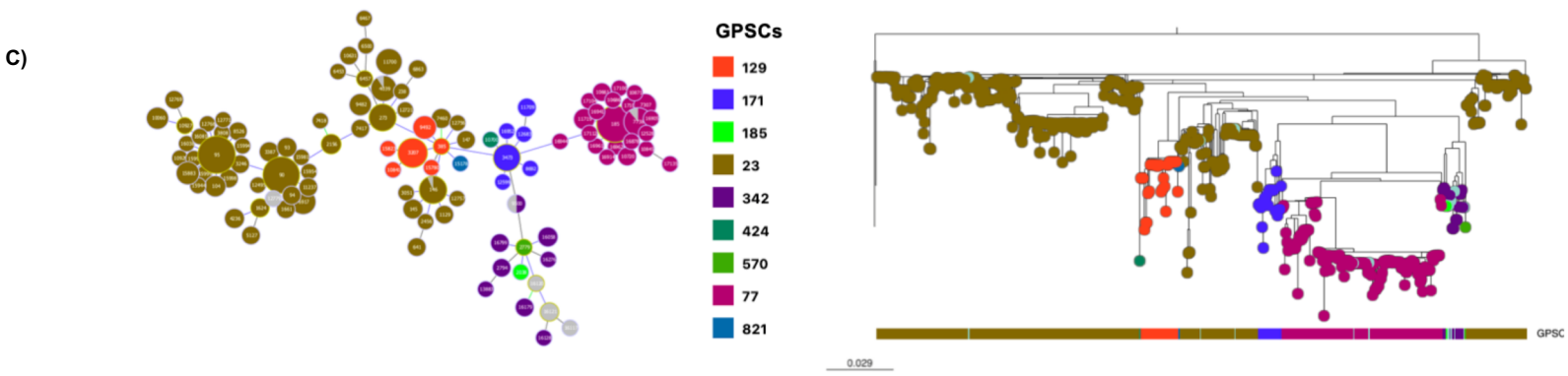
1. High diversity in GPS collection: The 26K isolates were clustered into 1657 clusters of which 810 (49%) were represented a single isolate. Using PopPUNK we identified 830 GPSCs of which 272 (32%) had a single isolate. Of the 1657 clusters there were 1608 (97%) with isolated belonging to a single GPSCs, showing a high concordance between the methods. 49 clusters had more than 1 GPSCs identified and were investigated further.



2. Cluster 14 (CC473) with 4 GPSCs: The figure above show that different GPSCs (coloured circles) are placed in distinct clusters within the phylogenetic tree. This is further supported by the single long branches reflects high genetic distance (number of SNPs) between the GPSCs.







3. A) Cluster 5 with 8 GPSCs; B) cluster 1 with 10 GPSCs; C) cluster 3 with 9 GPSCs: In the above three figures it can be again observed that the GPSCs form separate clusters separated by single long branches supportive of the higher genetic distances from other isolates. Therefore, GPSCs assignments provide a higher resolution when compared to CCs.

Conclusion

The sequence-based method for defining GPSC lineages presents a robust platform to study population structure of *S. pneumoniae* and enables comparisons of populations across regions to track the global spread of this pathogen.

Acknowledgements

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