

# GENOMIC STRUCTURE OF INVASIVE STREPTOCOCCUS PNEUMONIAE POPULATION FROM CHILDREN UNDER FIVE YEARS BEFORE AND AFTER VACCINE INTRODUCTION IN CASABLANCA, MOROCCO (ID 275)

## Presenter

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## Abstract

### Background

Pneumococcal infections remain a major cause of infections among children. In this study, a part of the Global Pneumococcal Sequencing (GPS) Project, we described the genomic structure of the pneumococcal population in Casablanca, Morocco, before and after vaccination introduction.

### Methods

DNA of 47 invasive isolates from children < 5 years old (32 isolates from pre-vaccine period, 15 isolates from post-vaccine period) were whole genome sequenced. Sequences were assembled, annotated and pangenome characterized. Core genome based phylogenetic trees were constructed. Finally, PopPUNK was used to group our isolates in different GPS Clusters (GPSC).

### Results

Pangenomic analysis revealed 1,396, 1,465 and 1,357 core genes for pre-vaccination period, post-vaccination period and the two periods combined, respectively; and 2,915, 2,405, 3,432 accessory genes for the same periods. Phylogenomic analysis showed two major clusters GPSC6 (serotype 14) and GPSC10 (Serotype 19A and non-vaccine serogroup 24). Both clusters are non-susceptible to penicillin. The two serogroup 24 isolates in GPSC10 were found in pre-vaccine (n=1) and post-vaccine periods (n=1), and both were resistant to erythromycin and tetracycline.

### Conclusions

The pneumococcal population in Casablanca was highly diverse regardless of serotype and period isolation. Several minor homogeneous and/or heterogeneous clusters were found with two major clusters.