Genetic diversity, serotype prediction and resistotyping of nasopharyngeal isolates of *S. pneumoniae* from Indian Hajj pilgrims by whole genome sequencing

Feroze Ganaie1, Geetha Nagaraj1, Vandana Govindan1, Avid Hussain1, RaviKumar KL1, Stephen Bentley2, Rebecca Gladstone2, Stephanie W. Lo2, Robert F. Breiman3, Lesley McGee4 and the Global Pneumococcal Sequencing Consortium

1 Central Research laboratory, Kempegowda Institute of Medical Sciences Hospital & Research Center, Bangalore, INDIA
2 Infection Genomics, The Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Cambridge, CB10 1SA, UK
3 Hubert Department of Global Health, Rollins School of Public Health, Emory University, Atlanta, GA 30322, USA
4 Respiratory Diseases Branch, Centers for Disease Control and Prevention, Atlanta, GA 30333, USA

Email- ferozeganaie@gmail.com

**Background and aim**

- The Islamic Hajj pilgrimage is the largest annual mass gathering in the world.
- The overcrowding and intermingling of people promotes the acquisition, spread and transmission of respiratory pathogens, including *Streptococcus pneumoniae*.
- We used whole genome sequencing approach to evaluate the genetic diversity, determine serotypes and resistotypes of *S. pneumoniae* isolated from pre and post Indian Hajj pilgrims.

**Methods**

- DNA was extracted from 83 NP pneumococcal isolates obtained from pre (n=36) and post (n=47) Indian Hajj pilgrim cohorts.
- Whole genome sequencing was performed at Sanger Institute using the Illumina Hiseq 2500 system, as part of Global Pneumococcal sequencing project. ([www.pneumogen.net](http://www.pneumogen.net))
- The Sanger Institute’s in-house bioinformatics pipeline was used to analyze genomic features.

**Results**

- Pre and post-Hajj isolates diverged into 12 and 9 clonal lineages, respectively.
- Among pre-Hajj isolates 15 known and 16 novel STs were identified. Similarly, among post-Hajj isolates 11 known and 30 novel STs were identified.
- The common serotypes in Pre-Hajj were 19F, 22F and 3 and post-Hajj were 28A, 31 and 6A.
- Genes coding for erythromycin (*ermB1, mef1*), tetracycline (*tetM1*) and co-trimoxazole (*dfrAS1*) resistance were present in 10, 20, 19 pre-Hajj and 14, 31, 27 post-Hajj isolates.

**Conclusion**

The study reveals high genetic diversity, changes in clonal types and increased carriage of resistance genes in post-Hajj *S. pneumoniae* isolates. Longitudinal genomic studies are needed to comprehend the relationship between carriage and disease in pilgrims.