

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

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## 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.

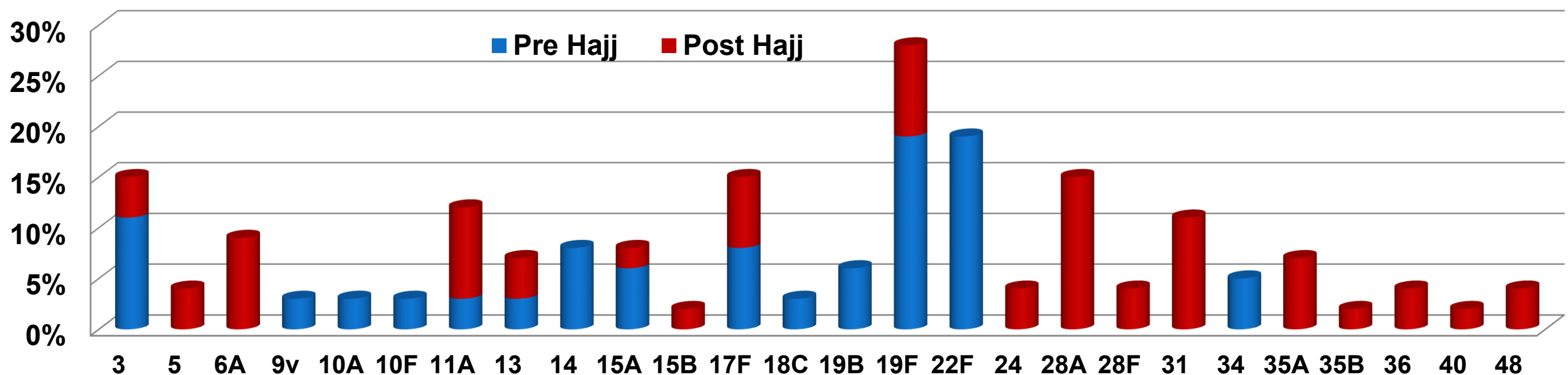
## Methods

- 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.

Pre Hajj			Post Hajj		
Sequence Type	No. of Isolates	Serotype	Sequence Type	No. of Isolates	Serotype
63	1	14	373	1	35B
236	2	19F	458	1	3
271	3	19F	505	1	3
334	1	9V	3214	3	35A
574	1	17F	4219	2	5
1915	1	14	6029	2	31
3135	1	10A	6441	2	48
3735	1	10F	7522	1	15B
4532	1	14	8958	1	40
5068	1	18C	11012	2	24
8152	2	19B	13262	1	15A
8509	1	19F			
11429	2	19F			
13262	1	15A			



## 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.



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The Global Pneumococcal  
Sequencing Project

A worldwide genomic survey of the impact of vaccination on the pathogen population



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