



## Evolutionary analysis of Influenza B Lineages in Pakistan during 2011-19: surveillance for vaccine effectiveness

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### Abstract:

Evolutionary dynamics of Influenza B viruses in humans are in a unique progression and HA gene has diverged into two antigenically and genetically distinct lineages known as B/Yamagata/16/88(B/Yam) and B/Victoria/2/87(B/Vic)-like viruses. Therefore assessment of the prevalent lineage and the group of viruses in circulation are important in order to decide whether the vaccine strain will match closely enough to protect the recipient population. In this study we analyzed genetic diversity in many Influenza B viruses circulating in Pakistan and determine their extent of closeness with vaccine strain. Throat and nasal swabs collected from ILI and SARI patients were processed for detection of influenza viruses according to CDC protocol. HA and NA genes of representative influenza B isolates were sequenced and Phylogenetic analysis were carried out using MEGA 6.0 by neighbor joining method. SPSS version 17 was used for statistical analyses. Out of 18036, 19% (n=1240) samples were positive for Influenza A or B. influenza A was detected in 72% while Influenza B accounted for 28%. Among the influenza B viruses, 40% were typed as B/Victoria while 60% were identified as B/Yamagata. Both B/Yam and B/Vic were seen at a higher proportion among children  $\leq 5$  yrs (31-32%) followed by adults between 21-30 yrs age (16-21%). Mean age was higher for B/Yam;  $24 \pm 22$  years as compared to B/Vic at  $19 \pm 16$  years. Phylogenetic analysis revealed that HA and NA genes of influenza B viruses circulating in Pakistan formed distinct clusters with globally circulating strains. The B/Victoria-isolate was grouped



in Clade (Group 1). Whereas Yamagata-like strains have common amino acid substitutions in HA gene of Influenza B and clustered with Clade 2 and 3. Clade 2 specific signature markers N181 and P187 for Clade 3 were found in our study strains. Some 2013 Yamagata Clade 3 isolates had the substitution from A to G at position 589 (characterized also by T541) characteristic of the B/Victoria-like lineages. This is the first report on molecular epidemiology of Influenza B viruses from Pakistan. Many of the presented in this report matched with the influenza B strain included in the vaccine recommended for northern hemisphere.

### Biography:

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### Publication of speakers:

1. R.K. Virk, Nazish Badar, V. Gunalan, P.A. Tambyah. Influenza infection in human host: challenges in making a better influenza vaccine. *Expert Rev Anti Infect Ther*, 14 (2016),