

Co-circulation of two Yamagata-lineage clades of influenza B viruses during the 2013 and 2014 influenza seasons in Thailand and implication for vaccine effectiveness

Content

Background: The low vaccine effectiveness (VE) against influenza B-Yamagata lineage viruses in Thailand during the 2013 (25%, 95% confidence interval [CI], -120% to 75%) and 2014 (23%, 95% CI, -236% to 82%) seasons was estimated in a VE study. The WHO recommended influenza B strains in the 2013 and 2014 Southern Hemisphere trivalent vaccine belong to Yamagata clade 3 (2013) and Yamagata clade 2 (2014), respectively.

Methods: We randomly selected 15 influenza B samples collected from vaccinated and unvaccinated children in the referred VE study. Genetic analysis was conducted to assess how closely related the 15 viruses were to the given vaccine strains.

Results: Phylogenetic analysis of the influenza B viruses sequenced showed that in 2013 and 2014, 12 tested, 9/12 (75%, 95% CI 47-91%) and 3 tested, 1 (33% CI 6-79%) did not match vaccine clade, respectively. For both years, we observed that all of the influenza B virus infections in vaccinated persons were from viruses belonging to different phylogenetic clades than the vaccine strain. Compared to vaccine strains, 4 amino acid mutations were observed at antigenic sites on the hemagglutinin 1 (HA1) protein of the viruses circulated in both seasons.

Conclusions: Two genetically different clades of influenza B-Yamagata lineage viruses were detected from a sub-set of infected children. Vaccinated individuals were infected with viruses belonging to different clades from those included in the vaccine. This implies that vaccine containing only one clade may not protect against the other clade and co-circulating of the two genetically different clades may contribute to low VE.

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