

Predominant of influenza A (H3N2) clade 3C.2a may have contributed to the low vaccine effectiveness against influenza A (H3N2) in the 2014 influenza season in Thailand

Content

Abstract

Background: The vaccine effectiveness (VE) against influenza A (H3N2) viruses [A(H3N2)] estimated from a VE study in Thailand was 73% (95% confidence interval [CI], -14% to 94%) and 6% (95% CI, -103% to 56%) in 2013 and 2014 seasons, respectively, when the given A (H3N2) vaccine strain belong to clade 3C.1.

Methods: A total of 15 A (H3N2) viruses from the referred VE study was used for complete genome sequencing. The viruses were from vaccinated children (n=5) and unvaccinated children (n=10).

Results: Phylogenetic analysis determined that the 2013-2014 viruses belonged to clade 3C.2 (5 strains from 2013) and clade 3C.2a (10 strains from 2014), while the vaccine strains from both seasons belonged to clade 3C.1. We found that vaccinated children from 2013 and 2014 seasons were infected with clade 3C.2 and 3C.2a, respectively. Two unique mutations were observed in the clade 3C.2a viruses from 2014, which caused a potential loss of a glycosylation site on epitope A but resulted in a potential gain of a glycosylation site on epitope B on the hemagglutinin (HA) protein. This mutation was absent in the 2013 3C.2 viruses.

Conclusions: We identified infection with A(H3N2) that were a different clade compared with the vaccine strain, from vaccinated children participating in a VE study during 2013 to 2014 seasons. This suggests that infection with viruses that were a mismatch to the vaccine strain may have resulted in breakthrough infections in vaccinated children. The predominance of clade 3C.2a in 2014 may have contributed to the low VE in the 2014 season.

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