

Phylogenetic analysis of influenza viruses in Bhutan during 2008-2017

Content

Background: Bhutan does not currently have an influenza vaccination program. Human influenza surveillance has conducted in Bhutan since 2008. Collected samples were tested by real-time RT-PCR (rRT-PCR) to detect and identify influenza viruses. This study aimed to examine the similarity between circulating influenza viruses in Bhutan and the annual vaccine strains through phylogenetic analyses.

Methods: A total of 277 influenza rRT-PCR positive specimens collected during 2008 to 2017 included 22 influenza A(H1N1), 86 A(H3N2), 79 A(H1N1)pdm09, and 90 B viruses. Sanger sequencing was performed to obtain hemagglutinin gene (HA) sequences from selected specimens and/or virus isolates. A phylogenetic tree was constructed using HA sequences and sequences from GenBank and Global Initiative on Sharing All Influenza Data (GISAID) databases

Result: Phylogenetic analysis revealed the influenza A(H1N1) viruses belonged to clades 2B (2008-2009); A(H1N1)pdm09 viruses belonged to clades 1 (2009), 3 (2010), 4 (2009-2010), 5 (2011), 7 (2012), 6C (2012), 6B (2013-2016), and 6B.1 (2016-2017); A(H3N2) viruses belonged to clades 1 (2009), 3C.2 (2012-2014), 3C.3 (2013), 3C.2a (2014-2016), 3C.2a1 (2016-2017) and 7 (2009); B Victoria-lineage viruses belonged to clades 1A (2009-2010, 2012, 2016-2017) and 1B (2009-2011); B Yamagata-lineage viruses belonged to clades 3 (2010-2011, 2013-2014, 2016) and 2 (2012).

Conclusion: This study summarizes the epidemiology of circulating influenza viruses over a 10 year period (2008-2017) in Bhutan. Bhutan experiences the same circulating influenza strains as its neighboring countries. The data indicates influenza viruses detected in Bhutan fall in the same clades as the vaccine strains and introduction of an influenza vaccine program would benefit the country.

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