Human Infection with Avian Influenza A(H9N2) Virus, Cambodia, February 2021

Appendix 1

Additional References


Figure. Maximum likelihood phylogenetic tree of hemagglutinin (A) and neuraminidase (B) genes of avian influenza A(H9N2) viruses detected in human and chicken specimens, Cambodia, 2021. Sequences were aligned using MAFFT v7.450 in Geneious Prime 2021.0.1 against 47 and 38 A/H9N2 HA and NA sequences, respectively, downloaded from the GISAID and Genbank database (Appendix 2, https://wwwnc.cdc.gov/EID/article/27/10/21-1039-App2.xlsx). Maximum Likelihood (ML) phylogenetic trees were inferred with IQ-Tree (v2.0.3) using the best-fit nucleotide substitution model (FLU+I+G4) and visualized using FigTree (v1.4.4) and gtree (v2.4.1). Phylogenetic support was estimated using 1,000 ultrafast bootstrap replicates. Candidate vaccine viruses are indicated in bold green, human A(H9N2)
viruses in bold blue, and 2021 Cambodian H9N2 viruses in bold red. Clade defining strains are indicated with an asterisk. Scale bars indicate the number of nucleotide substitutions per site. Genbank accession and GISAID isolate ID numbers are provided in Appendix 2.