

Canine Influenza Virus A(H3N2) Clade with Antigenic Variation, China, 2016–2017

Appendix

Appendix Figure (following pages). Dated phylogenies of the genome segments of H3N2 canine influenza viruses, China. The inferred most recent common ancestors of H3N2 canine influenza viruses isolated during 2016–2017 are indicated by blue dots. Timeline is in years. A) Polymerase basic 2; B) polymerase basic 1; C) polymerase acidic; D) hemagglutinin; E) nucleoprotein; F) neuraminidase; G) matrix; H) nonstructural protein.





