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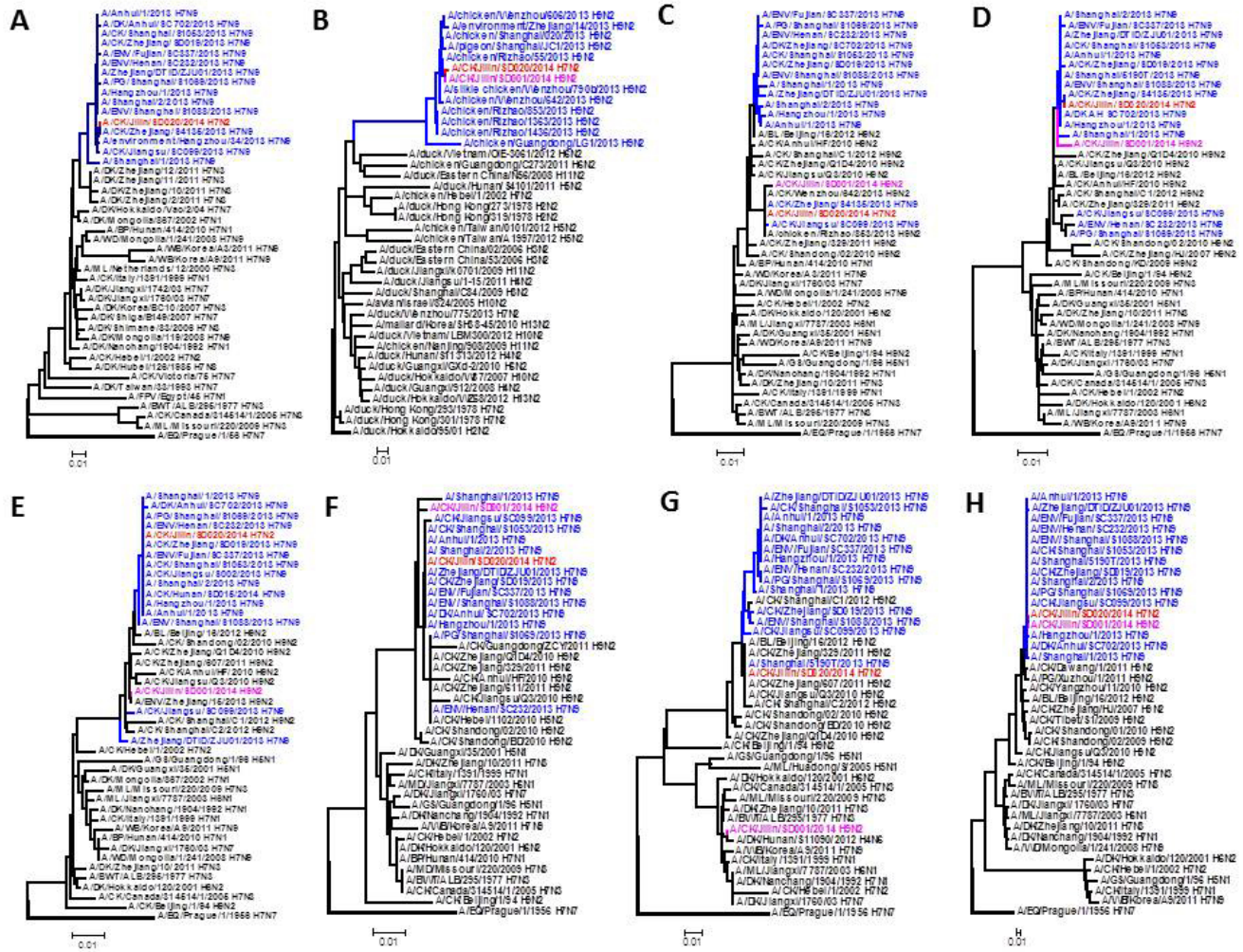
Novel Influenza A(H7N2) Virus in Chickens, Jilin Province, China, 2014

Technical Appendix



Technical Appendix Figure. Phylogenetic trees of avian influenza A(H7N2) virus. The tree topology was evaluated by 1,000-bootstrap analyses. The trees of H7 hemagglutinin (A), polymerase basic 2 (C), polymerase basic 1 (D), polymerase acidic (E), nucleocapsid (F), matrix (G), and nonstructural (H) were rooted to A/EQ/Prague/1/56 (H7N7), and the N2 neuraminidase tree (B) was rooted to A/duck/Hokkaido/95/01(H2N2). Viruses characterized in the present study are shown in red (H7N2) and pink (H9N2); the recent H7N9 viruses are shown in blue. BP, Baer's pochard duck; BWT, blue-winged teal; CK, chicken; DK, duck; ENV, environment; EQ, equine; ML, mallard; PG, pigeon; WB, wild bird; WD, wild duck. Scale bars indicate nucleotide substitutions per site.