

Supplementary Appendix

This appendix has been provided by the authors to give readers additional information about their work.

Supplement to: Zhu Q-Y, Qin E-D, Wang W, et al. Fatal infection with influenza A (H5N1) virus in China. *N Engl J Med* 2006;354:2731-2.

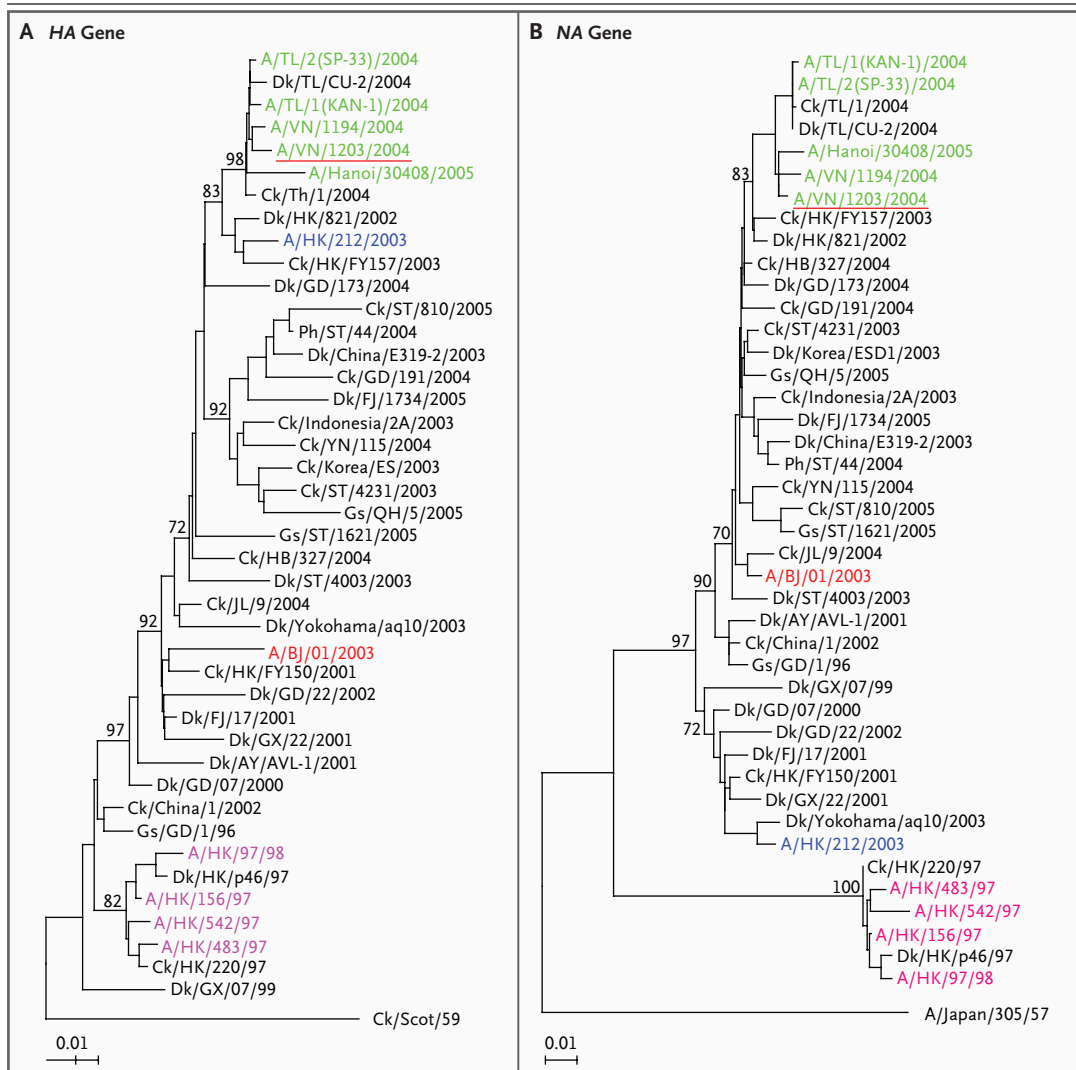


Figure 1. Phylogenetic Analyses of Representative Influenza A (H5N1) Viruses.

Panel A shows the phylogenetic tree of the hemagglutinin gene (HA) segment, which is rooted to the influenza A/Chick/Scotland/59 virus. Panel B shows the phylogenetic tree of the NA gene segment, which is rooted to the influenza A/Japan/305/57 virus. The trees were generated by the neighbor-joining method. Numbers to the left of the branches indicate neighbor-joining bootstrap values and bayesian posterior probabilities. Not all supports are shown owing to space constraints. The scale bar indicates 0.01 substitutions per site. Red represents the virus obtained from patients in Vietnam and Thailand in 2004 and 2005, green the viruses obtained from patients in China, pink the viruses obtained from patients in Hong Kong in 1997 and 1998, and blue the virus from a patient in Hong Kong in 2003. The proposed vaccine strain (A/Vietnam/1203/2004) is underlined. Ck denotes chicken, Dk duck, Gs goose, Ph pheasant, AY Anyang in Henan Province, FJ Fujian Province, GD Guangdong Province, GX Guangxi Province, HB Hubei Province, HK Hong Kong, JL Jilin Province, QH Qinghai Province, ST Shantou of Guangdong Province, TL Thailand, and VN Vietnam.