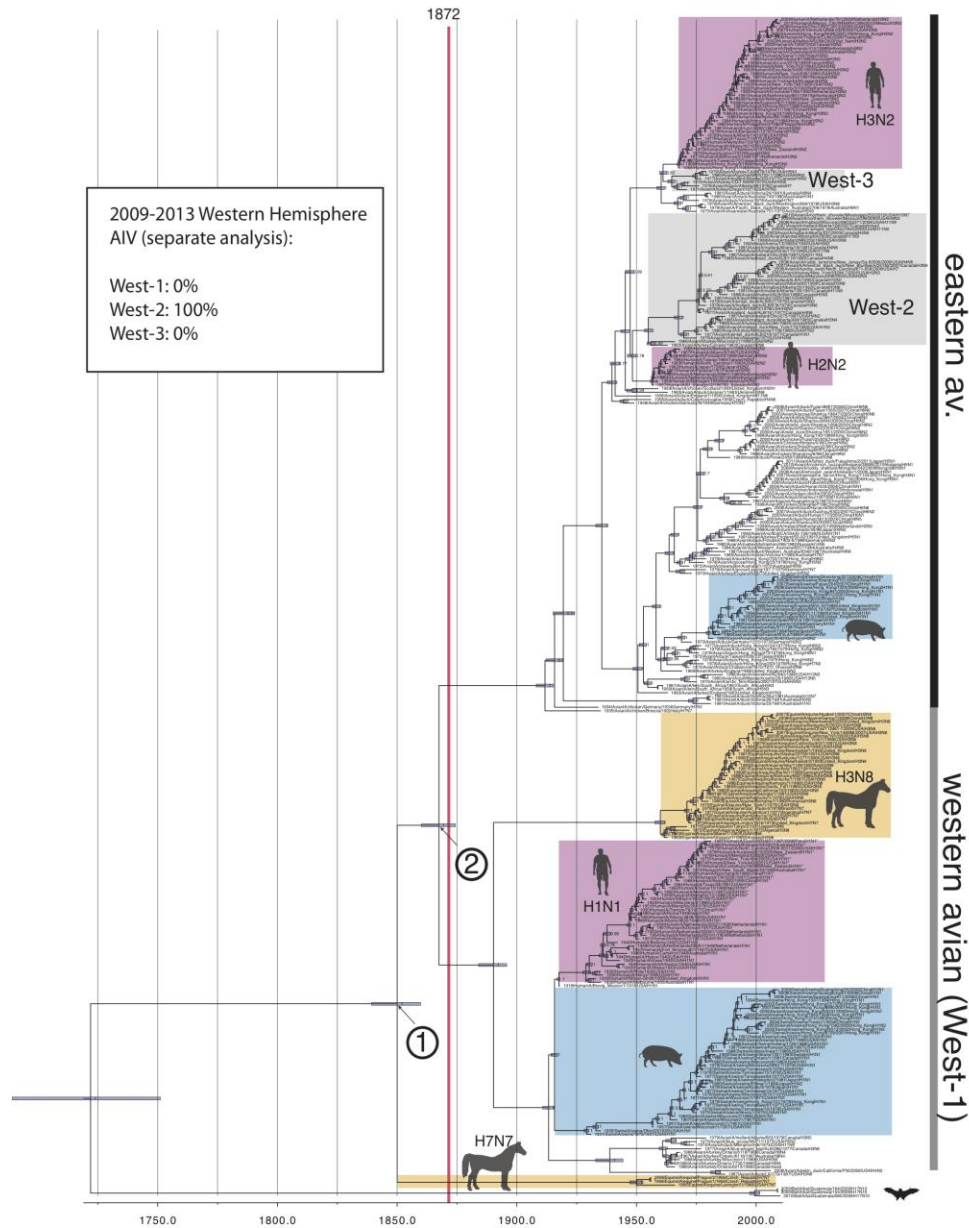
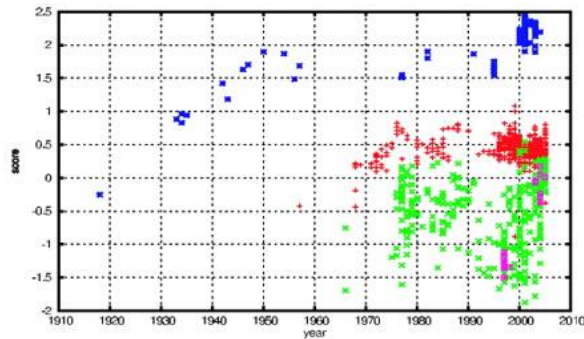


**Web Figure 1. MCC tree inferred for PB1 segment using a host-specific clock.** Figure is adapted from Worobey et al., (1). Branch lengths are in years. Node 1 depicts the most recent common ancestor (MRCA) of avian strains and equine H7N7 strains. Node 2 represents of the MRCA of Eastern and Western Hemisphere avian clades. The PB1 segments of both the human H2N2 and human H3N2 viruses are nested within the Eastern Hemisphere clade, as are avian clades ('West 2' and 'West 3') that moved between the 1950s and 1960s from the Eastern to Western Hemispheres.



**Web Figure 2. Data underlying Fig 1c from Rabadan et al. (2).** Log-odds scores of human and avian IAV nucleotide composition of the coding regions of the PB1 segment. Blue = human H1N1, purple = H5N1 found in humans, red = human H2N2 and H3N2, green = avian.



## References

1. Worobey M, Han G-Z, Rambaut A. A synchronized global sweep of the internal genes of modern avian influenza virus. *Nature* 508(7495):254-257.
2. Rabadan R, Levine AJ, Robins H. Comparison of avian and human influenza A viruses reveals a mutational bias on the viral genomes. *J. Virol.* 2006;80(23):11887–11891.