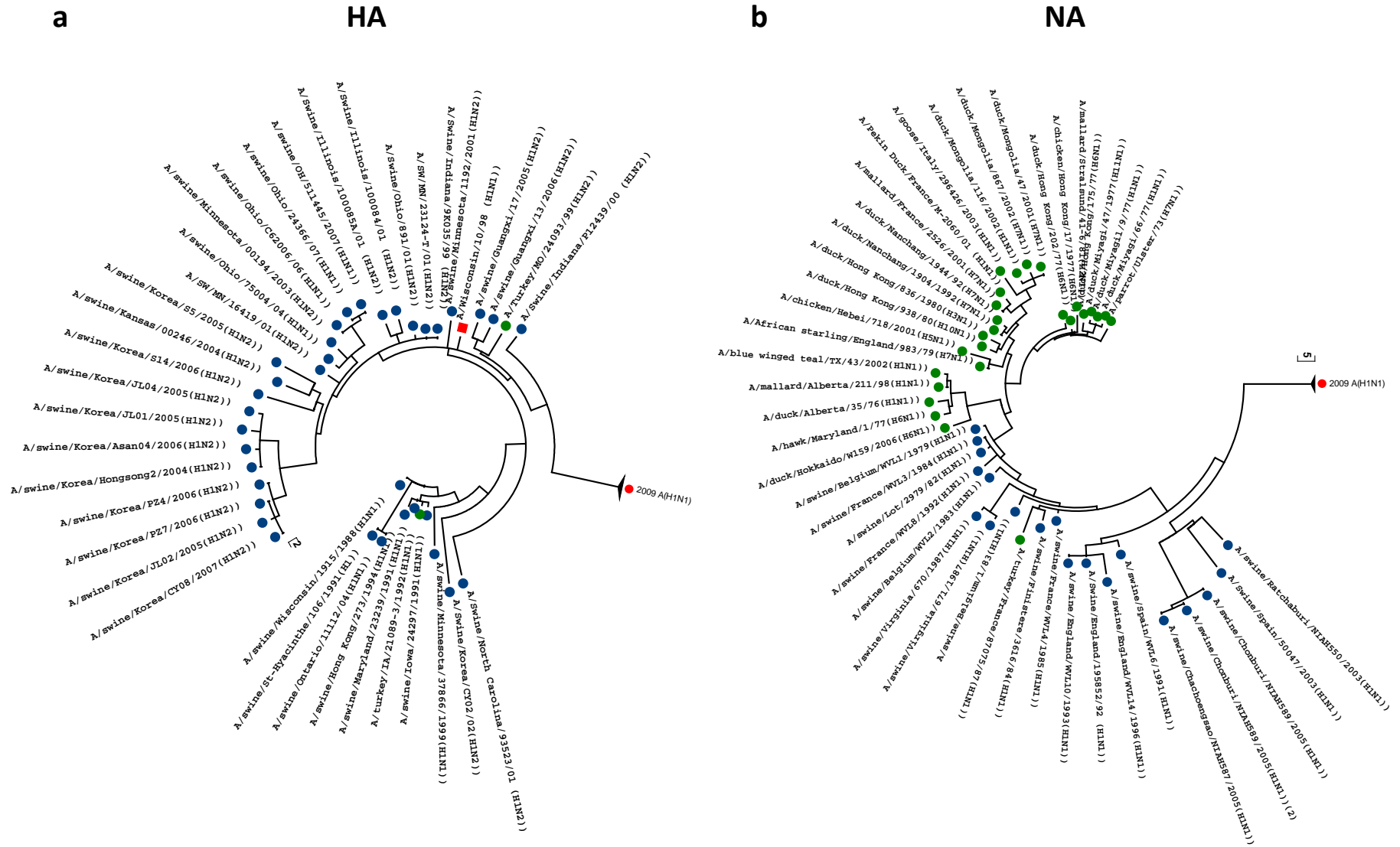


**Figure 1. Possible origins of the influenza 2009 A(H1N1) virus: a) hemagglutinin and b) neuraminidase proteins**



Protein sequences from the 2009 A(H1N1) virus were retrieved and used for BLAST searches versus the all-species NCBI nr protein database. Top-fifty best hits were retrieved from GenBank and used for phylogenetic tree reconstruction using the maximum parsimony method. Phylogenetic trees were rooted using the earliest influenza virus found with the analysis. Proteins from the 2009 A(H1N1) virus (red circles) showed close homology to proteins from swine influenza viruses circulating in Asia, Europe and US (blue circles) and swine influenza viruses that have infected humans in recent past (red squares). Protein relationships with avian influenza virus (green circles) were more distant. Scale bar indicates the number of changes over the whole sequence. Phylogenetic trees for PB2, PB1, PA, NP, MP1, and NS1 proteins, and details of statistical significance of branch order are provided in Supplementary Materials - Figure 1.