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Appendix A. Antigenic relatedness of representative circulating A/H1N1 viruses based on hemagglutinin (HA) phylogenetic analysis, 1918-2010

Methods

Amino acid sequences of H1 hemagglutinin (HA) were downloaded from the NCBI Influenza Virus Resource [1] and antigenic regions were extracted according to the scheme described by Soundararajan et al [2]. The dataset was then pruned to remove redundancy and sequences containing ambiguous residues, resulting in a final dataset containing 238 representative 1918-2010 H1 hemagglutinin antigenic regions. The Geneious tree builder [3] was used to construct a phylogeny using the UPGMA algorithm and a Jukes-Cantor genetic distance model. The resulting tree was visualized in FigTree [4] and is shown here as **Figure A1**.

References

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2. Soundararajan V, Tharakaraman K, Raman R, et al. Extrapolating from sequence--the 2009 H1N1 'swine' influenza virus. Nat Biotechnol. 2009;27:510-3.
3. Drummond AJ, Ashton B, Cheung M, et al. Geneious v4.8. 2009; http://www.geneious.com/
4. Rambaut A. FigTree. 2009. http://tree.bio.ed.ac.uk/software/figtree/

Figure A1. Antigenic relatedness of representative circulating A/H1N1 viruses based on hemagglutinin phylogenetic analysis, 1918-2010