Phylogenetics and Pathogenesis of Early Avian Influenza Viruses (H5N1), Nigeria

Technical Appendix

Neighbor-joining phylogenetic trees shown on the following pages were generated based on the A) hemagglutinin, B) neuraminidase, C) nucleocapsid protein, and D) nonstructural sequences of influenza viruses (H5N1). Influenza (H5N1) clades (2.2.1, 2.2.2 or 2.2.3) are indicated on trees. Viruses sequenced in this study are shown in **boldface**. Numbers indicate bootstrap values. Complete nucleotide sequences were aligned by using the Clustal program (*1*), and phylogenetic analyses were performed by using the PAUP program, version 4.0 beta 10 (*2*), with the neighbor-joining method using the HKY85 distance formula. Bootstrap analyses were conducted with 1,000 to place confidence values on groupings within trees (*3*).

References

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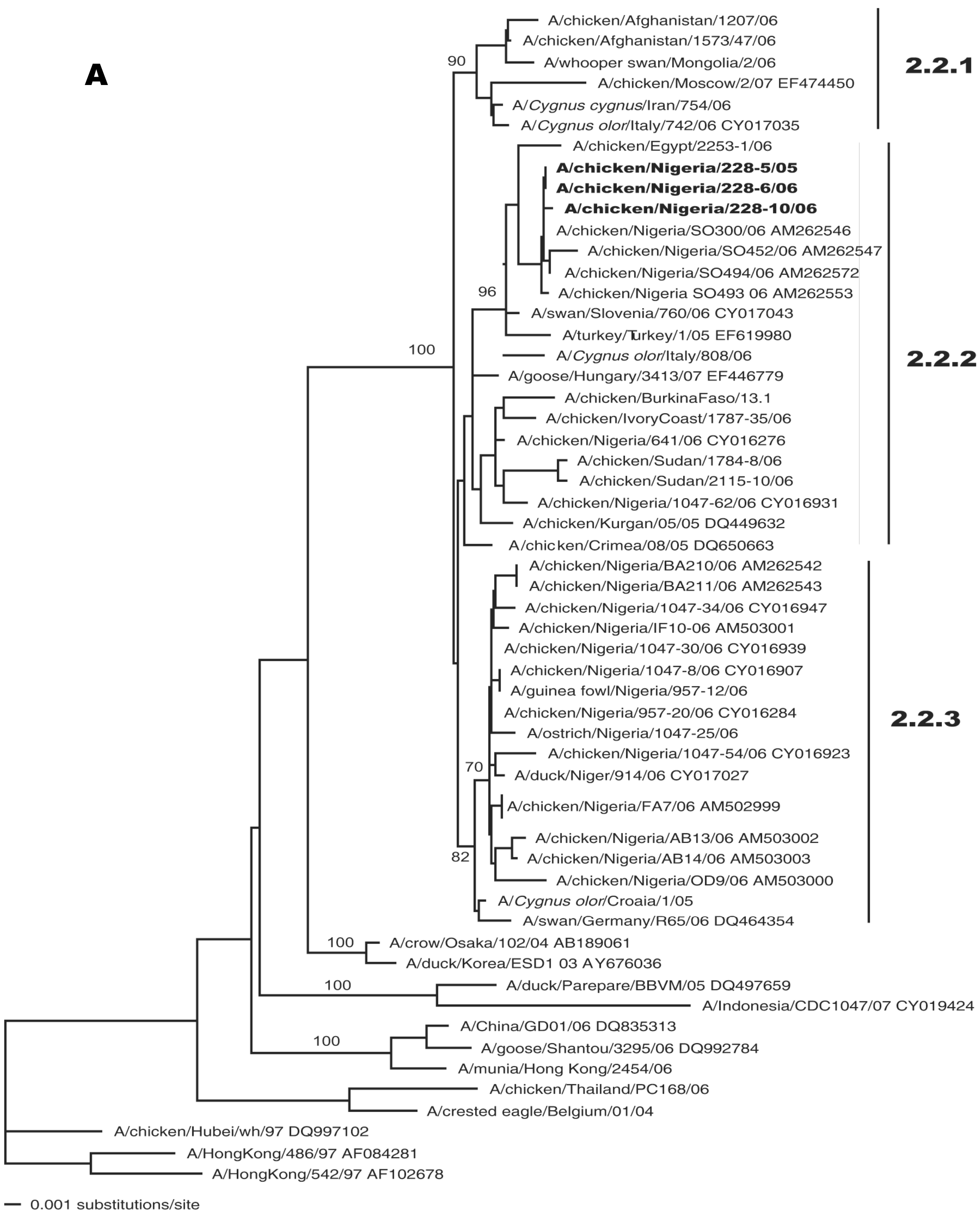
2. Swofford DL. PAUP* (Phylogenetic analysis using parsimony) (* and other methods), version 4. Sunderland (MA): Sinauer Associates; 2002.

3. Felsenstein J. Confidence limits on phylogenies: an approach using the bootstrap. Evolution. 1985;39:783–91. DOI: 10.2307/2408678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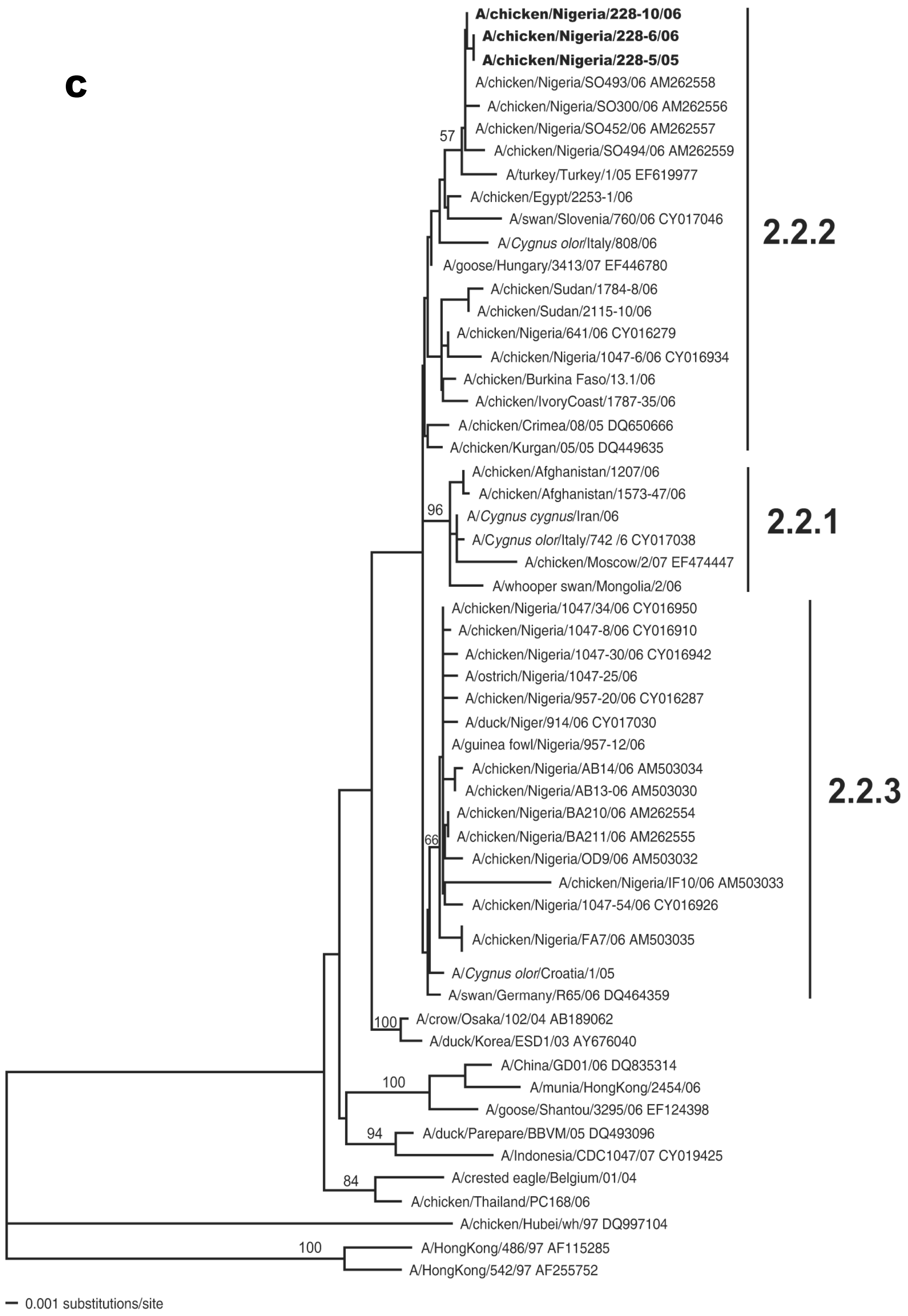
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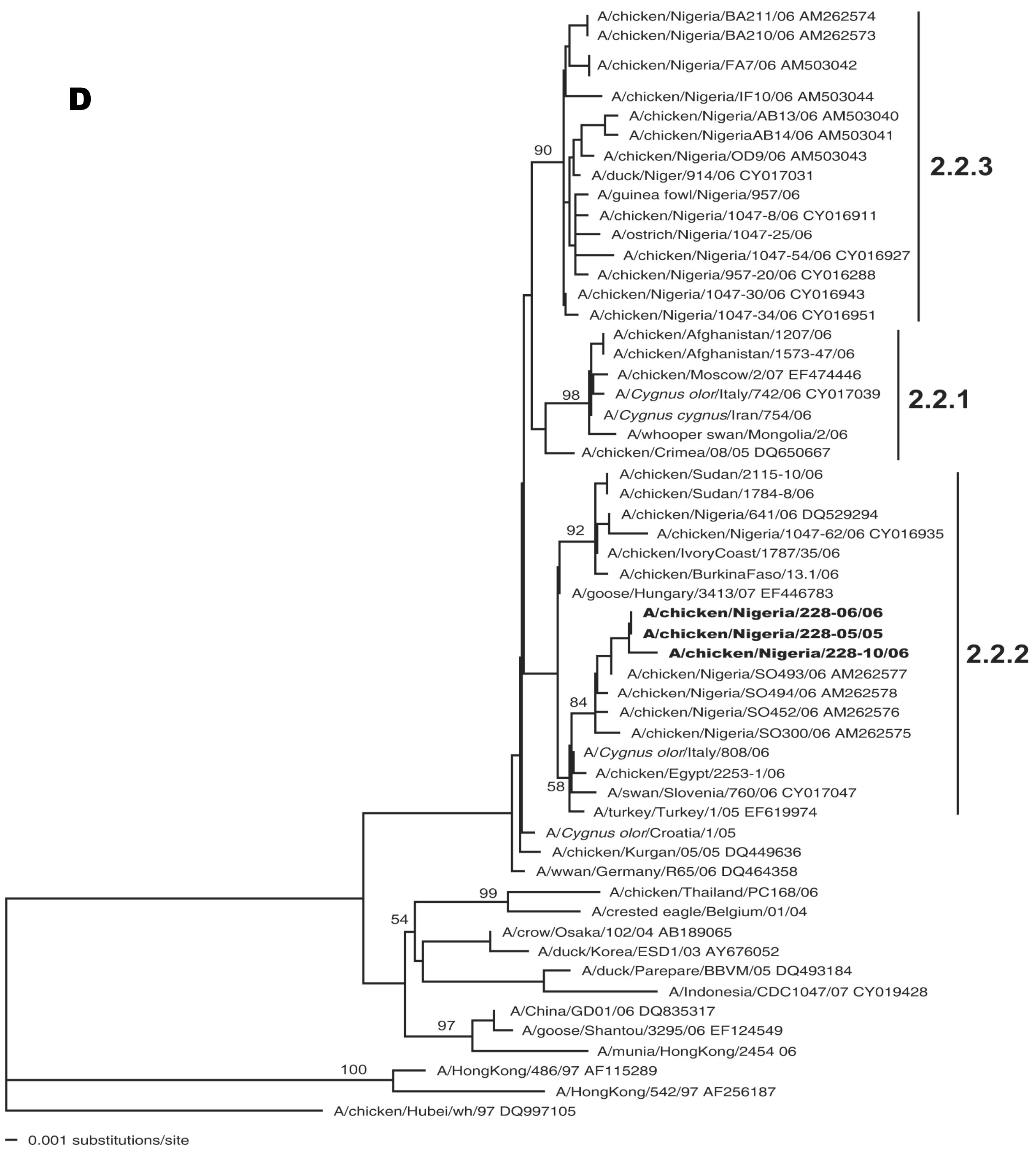
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