

## Electronic Supplementary Material

### Highly pathogenic avian influenza H5N1 Clade 2.3.2.1c virus in migratory birds, 2014–2015

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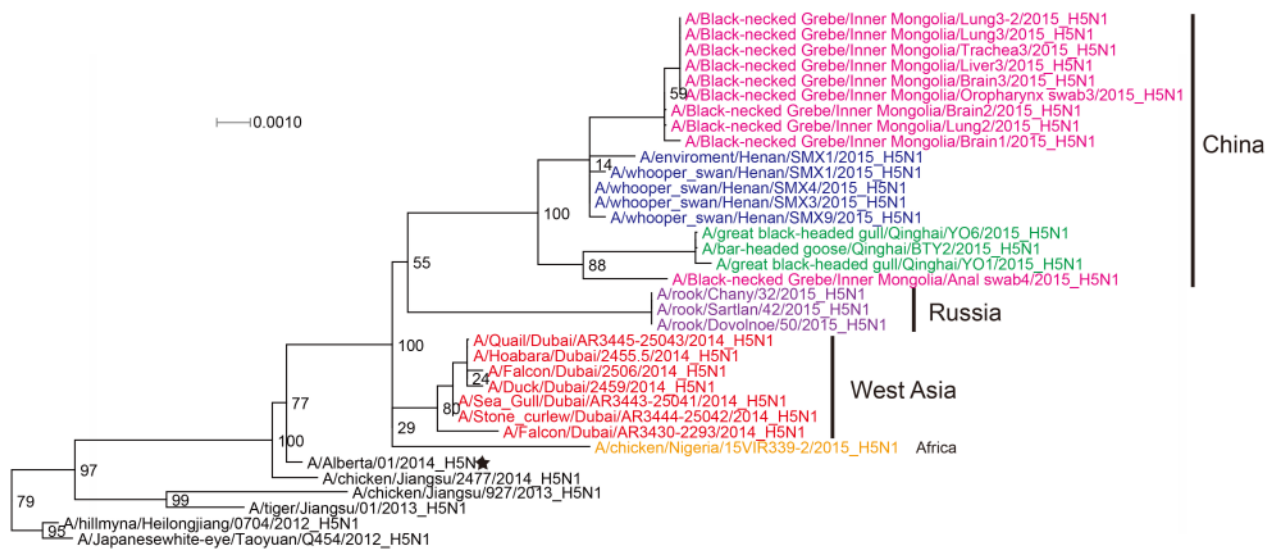


Figure S1. Phylogenetic trees of the PB1 genes of Clade 2.3.2.1c HPAI A (H5N1) viruses. This figure employs the same coloring strategy as for Figure 1.

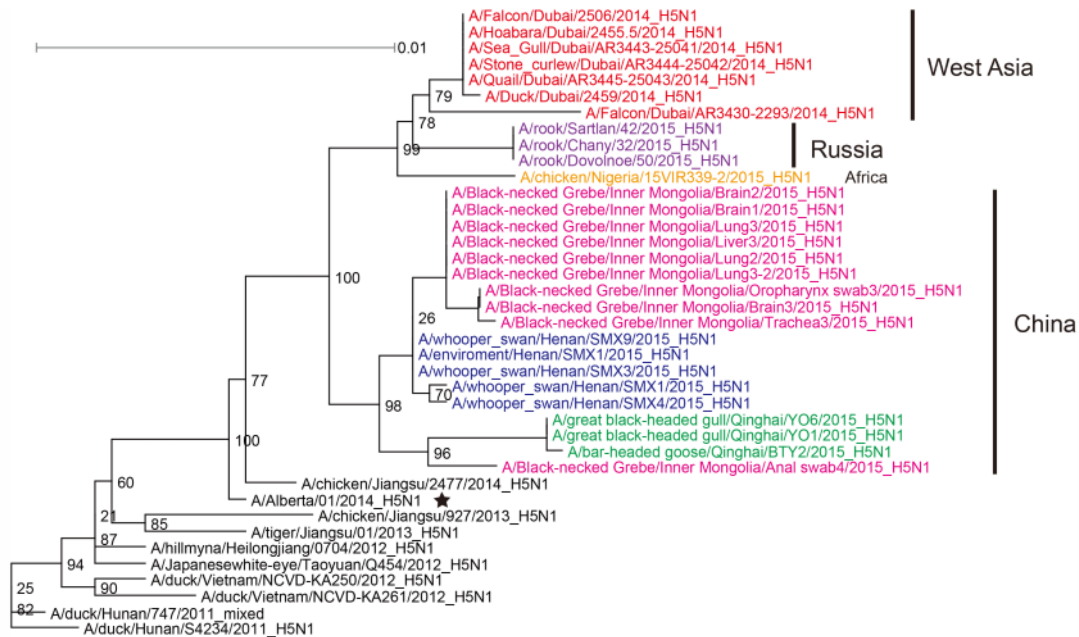


Figure S2. Phylogenetic trees of the PA genes of Clade 2.3.2.1c HPAI A (H5N1) viruses. This figure employs the same coloring strategy as for Figure 1.



Figure S3. Phylogenetic trees of the NP genes of Clade 2.3.2.1c HPAI A (H5N1) viruses. This figure employs the same coloring strategy as for Figure 1.

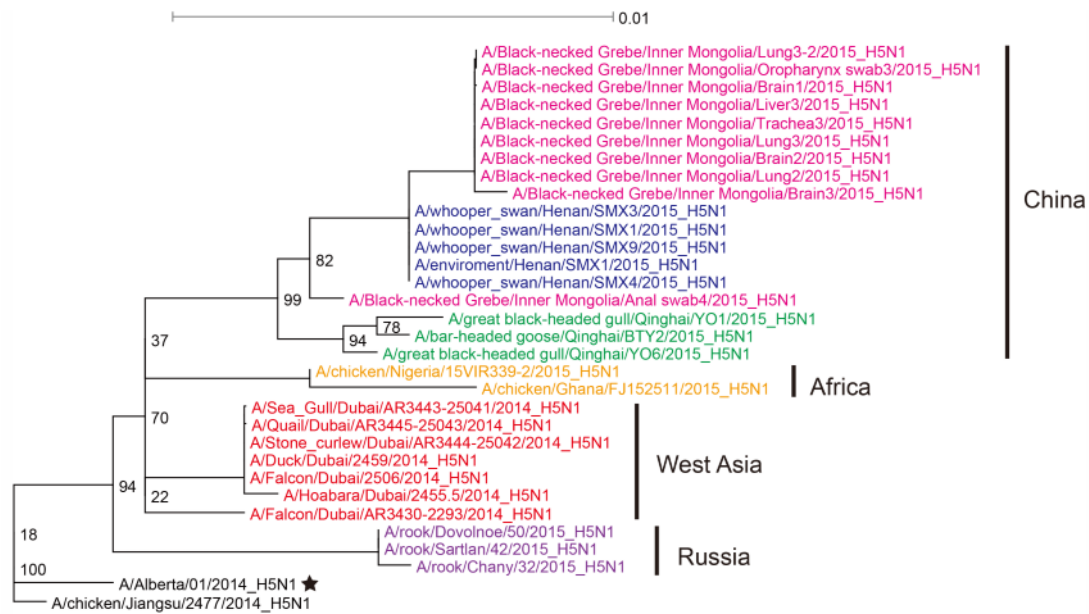


Figure S4. Phylogenetic trees of the NA genes of Clade 2.3.2.1c HPAI A (H5N1) viruses. This figure employs the same coloring strategy as for Figure 1.

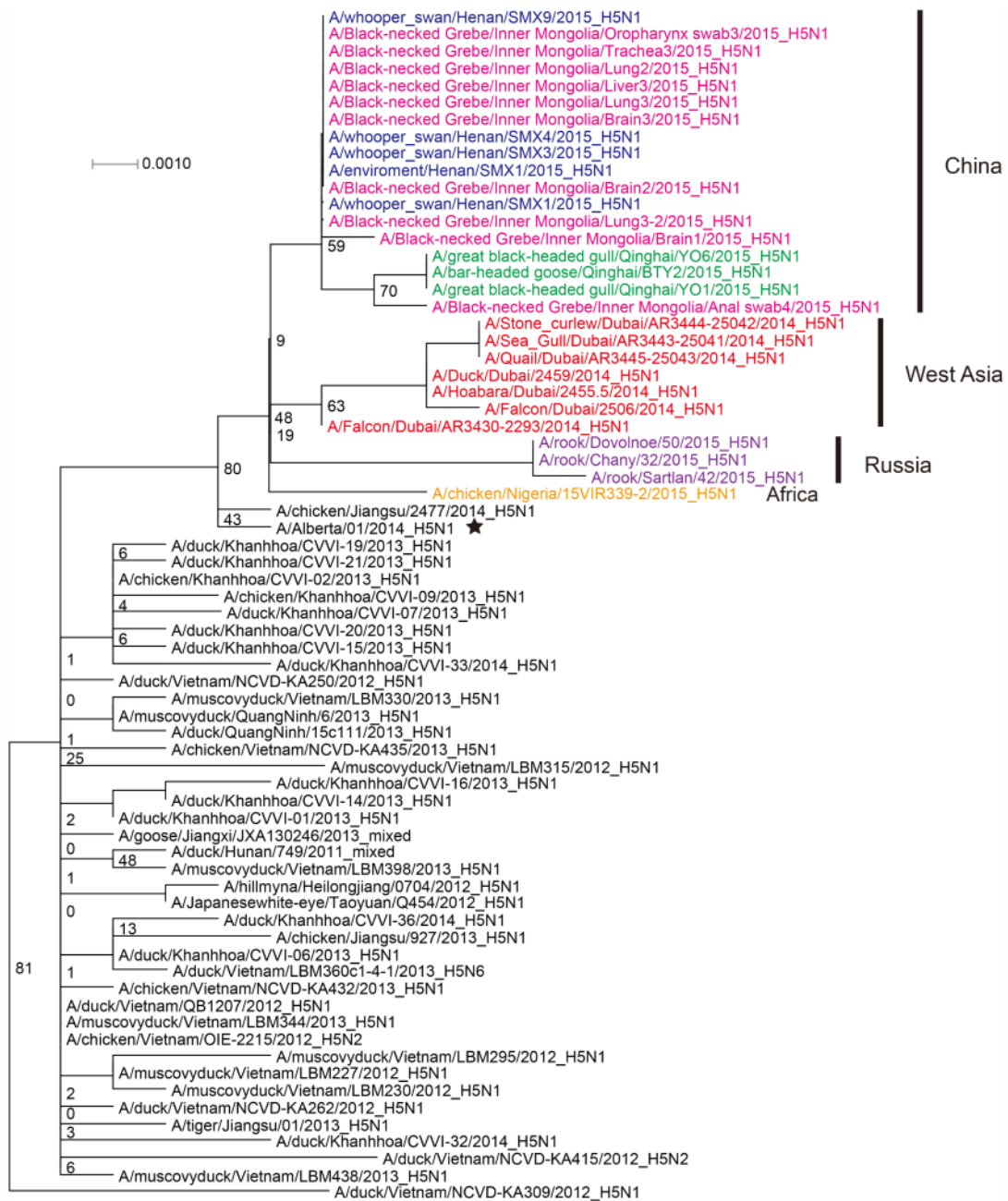


Figure S5. Phylogenetic trees of the M genes of Clade 2.3.2.1c HPAI A (H5N1) viruses. This figure employs the same coloring strategy as for Figure 1.



Supplementary Table 1. Comparison of key amino acid pattern of Clade 2.3.2.1c HPAI A (H5N1) viruses from different geographic regions