Detection of Low Pathogenicity Influenza Virus A(H7N3) during Duck Mortality Event, Cambodia, 2017

Technical Appendix

Technical Appendix Table 1. Segment specific primers used to amplify H7N3 genes

<table>
<thead>
<tr>
<th>Gene Segment and Primer ID</th>
<th>Sequence of Primer Pairs 5’ to 3’</th>
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<tr>
<td>PB2</td>
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<tr>
<td>Pb2f5nc</td>
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<tr>
<td>Pb2r980</td>
<td>GCA TAT ATC CAC AGC TTG TTC</td>
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<td>Pb2r770</td>
<td>CAG AGT YTG ATC ATH GCT GC</td>
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<tr>
<td>Szpb1+</td>
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<tr>
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<td>Pb1r/-5</td>
<td>TTC ACT ATT TTT GCC GTC TGA GTT CTT C</td>
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<td>PAUF</td>
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Technical Appendix Table 2. GenBank accession numbers of Cambodian H7N3 isolates

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<th>Accession Number</th>
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Technical Appendix Figure 1. Phylogenetic analysis (982 nt) of the matrix (MP) gene of viruses isolated from ducks in Kampong Thom province, Cambodia. Trees were generated using the Maximum Likelihood method based on the General Time Reversible model. Scale bars indicate substitutions per site. Bootstrap values (n = 500) >70 are indicated. Cambodian isolates indicated in bold italic. North and South American strains, blue; Eurasian strains, light pink; H7N9 strains from China, red.
Technical Appendix Figure 2. Phylogenetic analysis (2,280 nt) of the polymerase basic protein 2 (PB2) gene of viruses isolated from ducks in Kampong Thom province, Cambodia. Trees were generated using the Maximum Likelihood method based on the General Time Reversible model. Scale bars indicate substitutions per site. Bootstrap values (n = 500) >70 are indicated. Cambodian isolates indicated in bold italic. North and South American strains, blue; Eurasian strains, light pink; H7N9 strains from China, red.
Technical Appendix Figure 3. Phylogenetic analysis (2,274 nt) of the polymerase basic protein 1 (PB1) gene of viruses isolated from ducks in Kampong Thom province, Cambodia. Trees were generated using the Maximum Likelihood method based on the General Time Reversible model. Scale bars indicate substitutions per site. Bootstrap values (n = 500) >70 are indicated. Cambodian isolates indicated in bold italic. North and South American strains, blue; Eurasian strains, light pink; H7N9 strains from China, red.
**Technical Appendix Figure 4.** Phylogenetic analysis (2,151 nt) of the polymerase (PA) gene of viruses isolated from ducks in Kampong Thom province, Cambodia. Trees were generated using the Maximum Likelihood method based on the General Time Reversible model. Scale bars indicate substitutions per site. Bootstrap values (n = 500) >70 are indicated. Cambodian isolates indicated in bold italic. North and South American strains, blue; Eurasian strains, light pink; H7N9 strains from China, red.
Technical Appendix Figure 5. Phylogenetic analysis (838 nt) of the nonstructural (NS) gene of viruses isolated from ducks in Kampong Thom province, Cambodia. Trees were generated using the Maximum Likelihood method based on the General Time Reversible model. Scale bars indicate substitutions per site. Bootstrap values (n = 500) >70 are indicated. Cambodian isolates indicated in bold italic. North and South American strains, blue; Eurasian strains, light pink; H7N9 strains from China, red.
Technical Appendix Figure 6. Phylogenetic analysis (1,497 nt) of the nucleoprotein (NP) gene of viruses isolated from ducks in Kampong Thom province, Cambodia. Trees were generated using the Maximum Likelihood method based on the General Time Reversible model. Scale bars indicate substitutions per site. Bootstrap values (n = 500) >70 are indicated. Cambodian isolates indicated in bold italic. North and South American strains, blue; Eurasian strains, light pink; H7N9 strains from China, red.