

Erratum

Erratum to: Wild Bird’s-Eye View of Influenza Virus A(H1N1) Phylogenetic Evolution

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In EcoHealth Volume 6, 346–350, the article, “Wild Bird’s-eye View of Influenza Virus A(H1N1) Phylogenetic Evolution,” was printed with the figure files in grayscale. The figures should have been printed in color. The figures in question have been reprinted on the following page.

The online version of the original article can be found under
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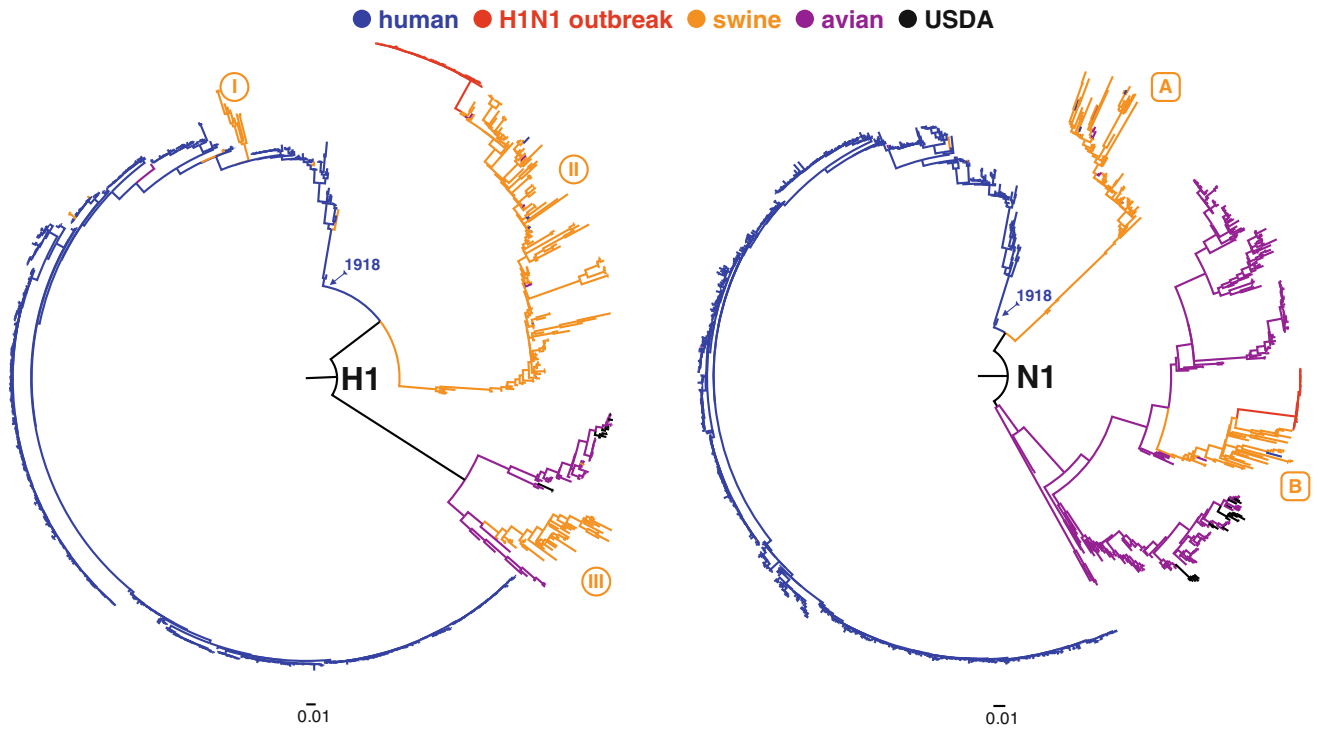


Figure 1. Maximum likelihood tree including H1 and N1 sequences from influenza A viruses from USDA wild bird surveillance samples and publicly available (NCBI database) swine, avian, and human influenza sequences. The sequences produced in this study are shown in black (USDA). Sequences from the 2009 H1N1 outbreak in

humans are shown in red. The 1918 human H1N1 sequence is labeled on each tree. The scale bar denotes 0.01 substitutions per site. All major clades received 100% rapid bootstrap support; I, II, III, A, and B refer to clades discussed in the article.



Figure 2. Map of sampling localities of the USDA H1 and N1 viral sequences for wild birds in the United States.