Supplemental Information

Glycan-Receptor Binding of the Novel Influenza A Virus H7N9 Hemagglutinin

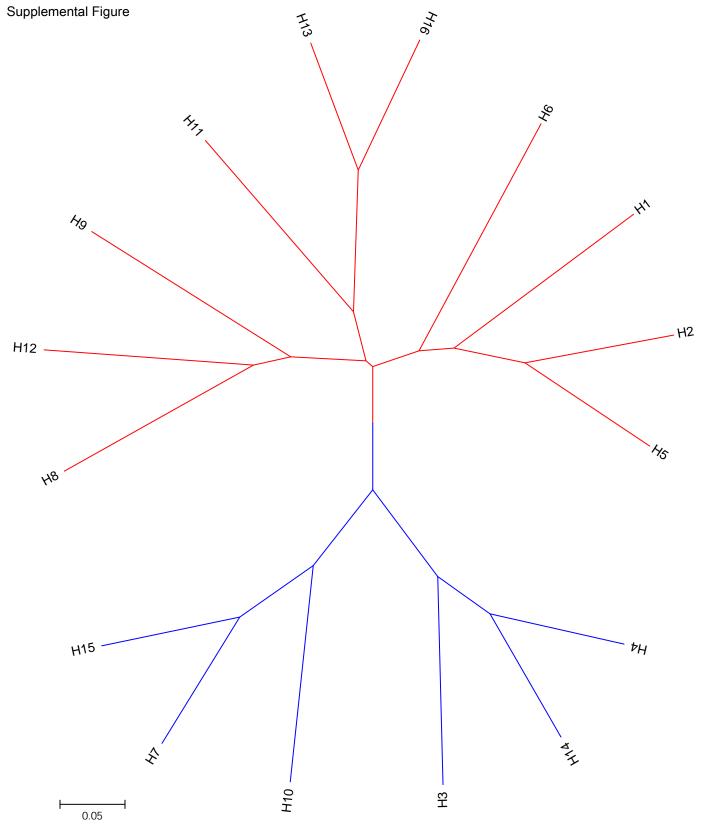
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FIGURE/TABLE LEGEND

Figure S1, related to Table 1 and Figure 1 shows phylogenetic distance between different HA subtypes. Branches leading to group 1 & 2 HAs are labeled and colored in red and blue, respectively. Closely related subtypes are located on branches close to one another

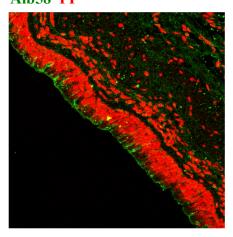
Figure S2, related to Figure 2 has multiple panels. **A.** A/Albany/6/58 (Alb58) pandemic H2N2 HA shows extensive binding to apical surface of tracheal tissue section (predominantly expresses human receptors) even at HA concentration of 10 μ g/ml. **B**, Staining of paraffinized human alveolar section with wild-type and G228S A/Anhui/1/13 hemagglutinin (HA). The wild-type protein did not stain the alveolus as intensely as the G228S mutant HA. This staining pattern is characteristic of avian influenza A viruses. **C.** Staining of paraffinized human receptors. SNA-I showed staining of the apical surface of the human trachea. SNA-I also stained the mucin secreting goblet cells (marked with *) similar to the Anhui 13 G228S mutant HA. The staining by SNA I (*green*) is shown in white arrows. Image was captured at 40X magnification. All tissue sections were counterstained with propidium iodide (PI) shown in red.

Figure S3, related to Figure 1 and Table 1 shows phylogeny tree of H7 HA amino acid sequences. The tree was constructed using 231 full-length, non-redundant amino acid sequences using the Neighbor-Joining method found in the MEGA 5.1 software. The two major H7 lineages are labeled on the right hand side by double-sided arrows. Branches are color-coded according to the number of coevolving residues found in the H7 sequence (red: 5; blue: 4; green: 2; magenta: 1; black: 0). A red rectangular box marks occurrence of the novel H7N9 virus on the tree.



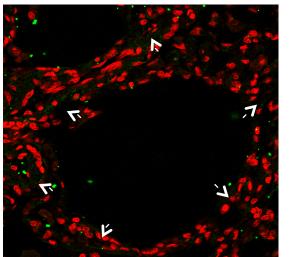


Alb58 PI

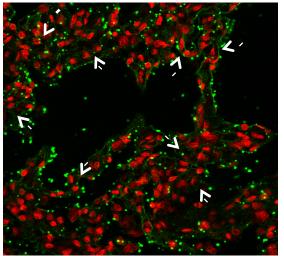


B

WT PI



Mut PI





SNA-I PI

