

Genomic Signatures of Human versus Avian Influenza A Viruses

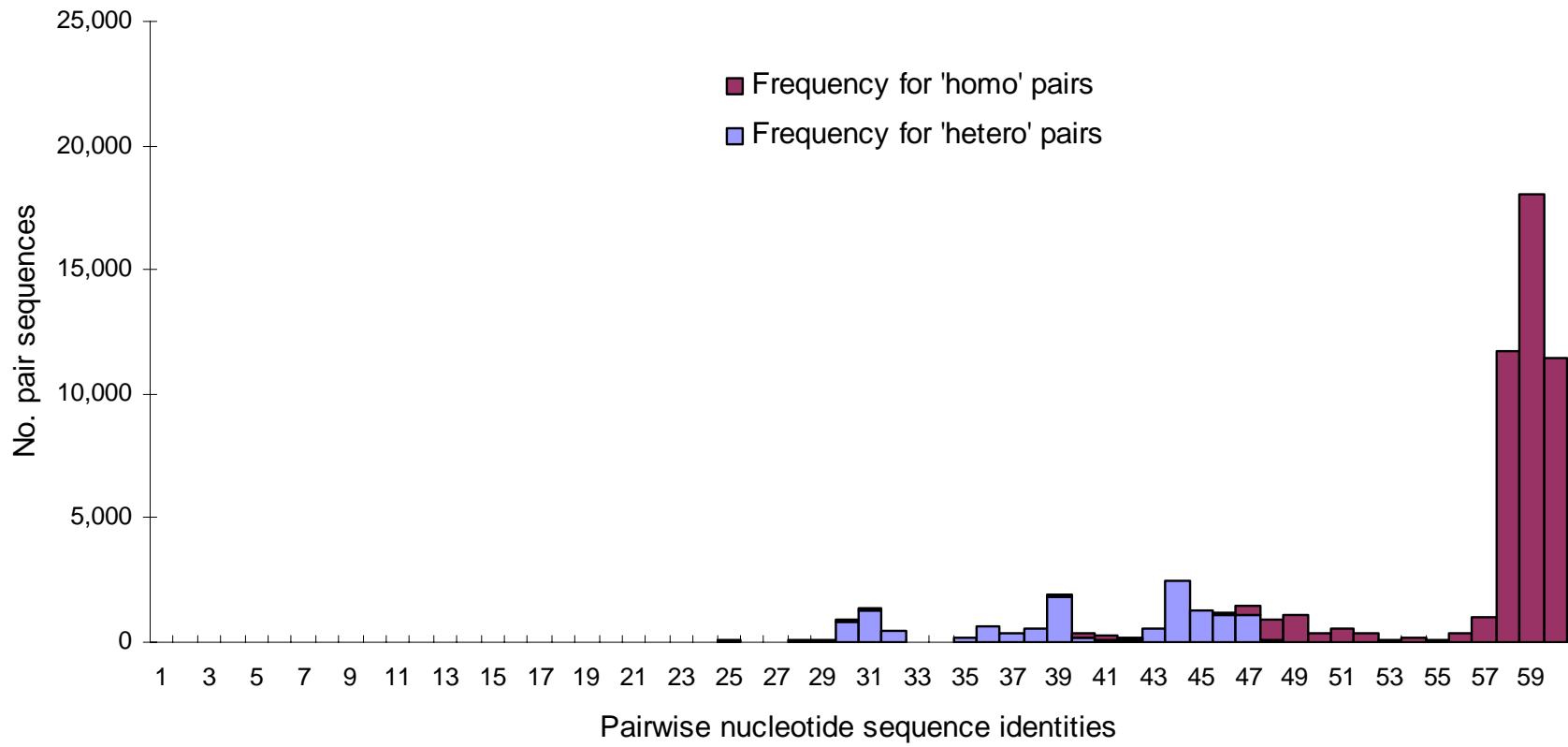
Guang-Wu Chen,^{*1} Shih-Cheng Chang,^{*1} Chee-Keng Mok,* Yu-Luan Lo,* Yu-Nong Kung,* Ji-Hung Huang,* Yun-Han Shih,* Ji-Yi Wang,* Chiayn Chiang,* Chi-Jene Chen,* and Shin-Ru Shih*

*Chang Gung University, Taoyuan, Taiwan

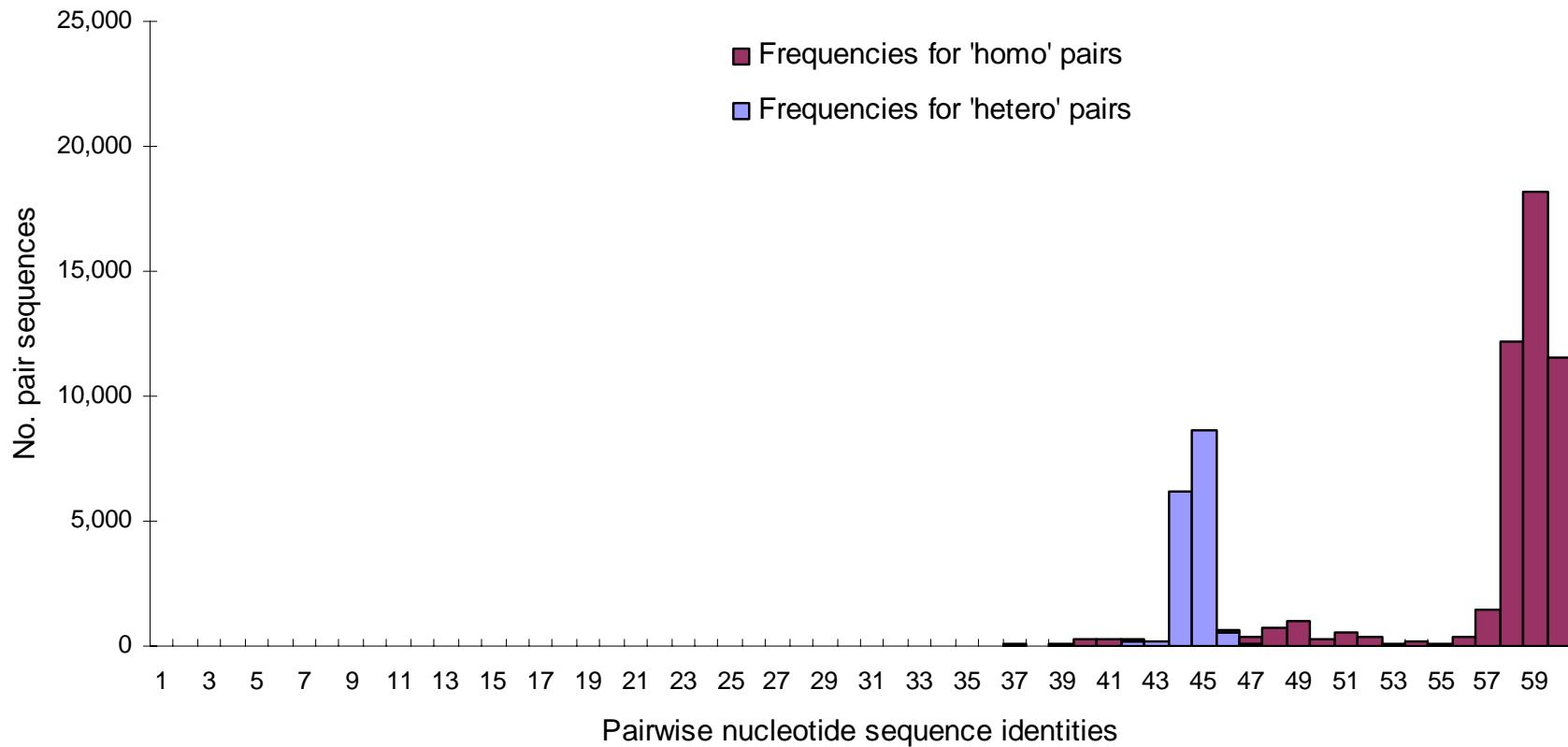
¹These authors contributed equally to this article.

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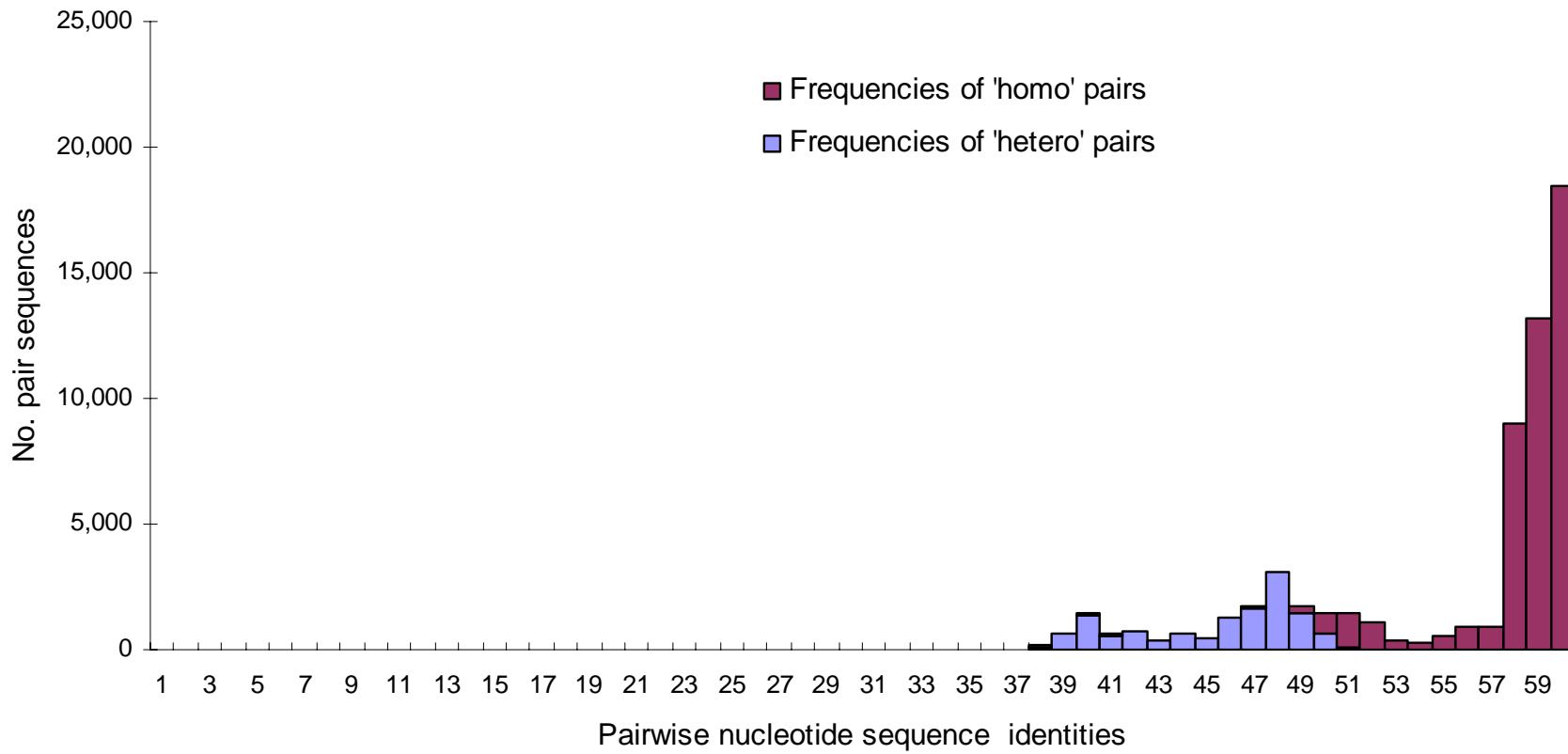
Appendix Figure 3. Histograms compare 43 avian allele A viruses and 306 human viruses (A and C), and 52 avian allele B viruses and 306 human viruses (B and D), based on their NS1 and NS2 genomic segments. Vertical axis shows the count for pairs of sequences with specific percent identity (rounded to integer). Red bars represent frequencies for ‘homo’ pairs – sequences of the same host species (human to human, or avian to avian); blue bars represent frequencies for ‘hetero’ pairs – pairs that cross host species (human to avian, or avian to human).



NS1 – 43 avian allele A viruses vs 306 human viruses

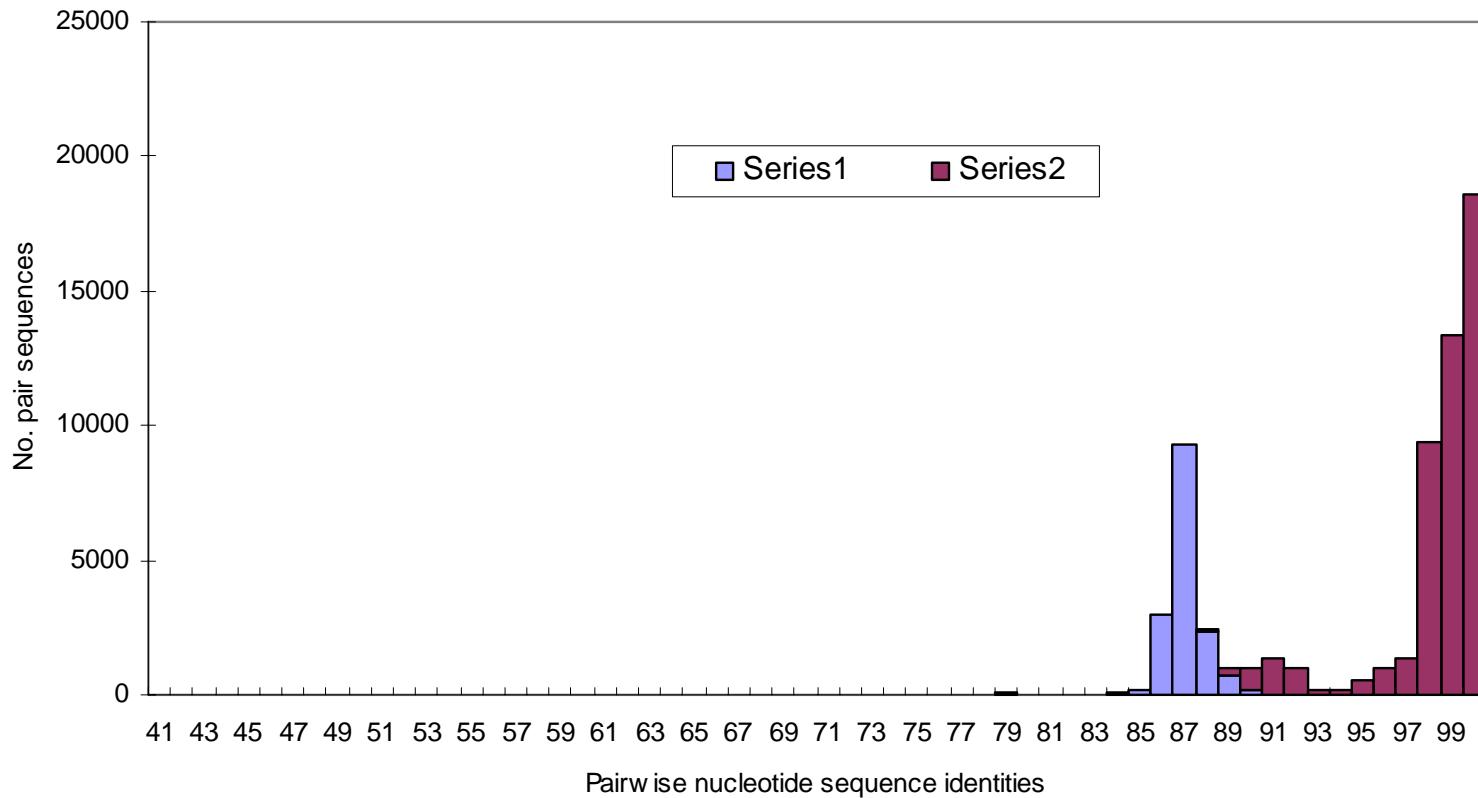


NS1 – 52 avian allele B viruses vs 306 human viruses



NS2 – 43 avian allele A viruses vs 306 human viruses

Chen G-W, Chang S-C, Mok C-K, Lo Y-L, Kung Y-N, Huang J-H, et al. Genomic signatures of human versus avian influenza A viruses. *Emerg Infect Dis* [serial on the Internet]. 2006 Sep. Available from <http://www.cdc.gov/ncidod/EID/vol12no09/06-0276.htm>



NS2 – 43 avian allele B viruses vs 306 human viruses

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