Supplemental Methods

Post-hoc MCC analyses were incorporated for internal gene segments to re-assess inference derived from calculations of genetic similarity regarding hitchhiking of internal gene segments. For these analyses, top BLAST hits [1] for each internal gene segment of A/pheasant/New Jersey/26996-2/2014 (H7N3) and sequences derived for this study incorporated in Bayesian Markov Chain Monte Carlo coalescent analyses performed with BEAST 1.7.4 [2]. The molecular clock (uncorrelated exponential, uncorrelated log-normal or strict clock) was selected following Bayes factors comparison. The SRD06 nucleotide substitution model [3] and a Bayesian skyline coalescent tree prior were used in all simulations [4]. Analyses were performed with chain lengths of 80–160 million generations sampled every 1000 iterations and the first 20–30% trees were discarded as burn-in. For the NS gene segment, sequences that did not share the same allele as A/pheasant/New Jersey/26996-2/2014 (H7N3) were excluded from analysis.

References

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