**Additional Material for Kirkpatrick *et al.***

Summary of evolutionary rates of head and stalk domains of sH1N1, pH1N1, H3N2, B/Yamagata/16/88-like and B/Victoria/2/87-like viruses based on a functional partitioning model. Bayes factor is defined as Pr(Head>Stalk)/Pr(Stalk>Head).

Virus	Mean Whole HA Evolutionary Rate (n/s/y)	Mean STC Evolutionary Rate (n/s/y)	Mean Head Evolutionary Rate (n/s/y)	Mean Stalk Evolutionary Rate (n/s/y)	Bayes Factor
sH1N1	2.46×10^{-3}	2.18×10^{-3}	3.56×10^{-3}	2.42×10^{-3}	infinite
pH1N1	4.35×10^{-3}	4.00×10^{-3}	5.64×10^{-3}	5.18×10^{-3}	7.1
H3N2	4.16×10^{-3}	2.55×10^{-3}	4.76×10^{-3}	3.73×10^{-3}	infinite
B/Vic	2.80×10^{-3}	1.89×10^{-3}	2.98×10^{-3}	2.70×10^{-3}	7.7
B/Yam	2.73×10^{-3}	1.58×10^{-3}	3.20×10^{-3}	2.37×10^{-3}	infinite

Summary of likelihood ratio tests. These tests were conducted on the non-partitioned, whole HA sequences verses the partitioned (STC, head, stalk) HA sequences. The significance indicates the probability of the partitioned model performing better than the non-partitioned model.

			LRT statistics	degrees of freedom	critical value for chi-square with significance level =0.001	P-value for supporting Partitional model
sH1N1	**nucleotide model**					
	Partitioned Log(Likelihood)	Non-partitioned Log(Likelihood)				
	-19409.315	-20214.554	1610.478	2	13.816	P-Value < 0.00001
	codon model					
	Partitioned Log(Likelihood)	Non-partitioned Log(Likelihood)				
	-18845.1	-19656.2	1622.2	2	13.816	P-Value < 0.001
pH1N1	**nucleotide model**					
	Partitioned Log(Likelihood)	Non-partitioned Log(Likelihood)				

		Partitioned Log(Likelihood)	Non-partitioned Log(Likelihood)				
		-13923.459	-14551.487	1256.056	2	13.816	P-Value < 0.00001
	codon model						
	Partitioned Log(Likelihood)	Non-partitioned Log(Likelihood)					
		-13428.9	-14060.8	1263.8	2	13.816	P-Value < 0.001
	Partitioned Log(Likelihood)	Non-partitioned Log(Likelihood)	1383.106	2	13.816	P-Value < 0.00001	
		-19064.542	-19756.095				
	codon model						
	Partitioned Log(Likelihood)	Non-partitioned Log(Likelihood)					
		-18497.1	-19183.5	1372.8	2	13.816	P-Value < 0.001
B/Vic	**nucleotide model**						
	Partitioned Log(Likelihood)	Non-partitioned Log(Likelihood)					
		-10027.183	-10410.123	765.88	2	13.816	P-Value < 0.00001
	codon model						
	Partitioned Log(Likelihood)	Non-partitioned Log(Likelihood)					
		-9527.88	-9912.66	769.56	2	13.816	P-Value < 0.001
B/Yam	**nucleotide model**						
	Partitioned Log(Likelihood)	Non-partitioned Log(Likelihood)					
		-9291.626	-9633.68	684.108	2	13.816	P-Value < 0.00001
	codon model						
	Partitioned Log(Likelihood)	Non-partitioned Log(Likelihood)					
		-8793.41	-9135.43	684.04	2	13.816	P-Value < 0.001
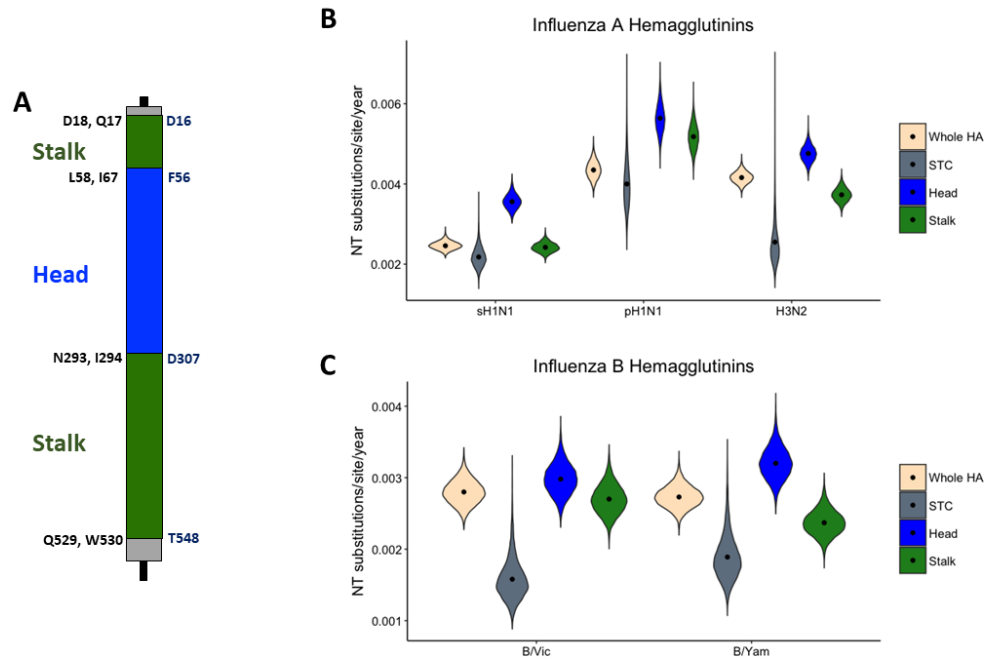
Evolutionary rates of the influenza virus hemagglutinin head and stalk domains. (A) Linear schematic of the HA molecule and partitions used for analysis. The stalk domain amino acid demarcations are shown on the figure for H1 and H3 on the left (black) and influenza B on the right (blue). **(B-C)** Evolutionary rates of influenza A virus or influenza B whole hemagglutinin (peach), stalk/transmembrane/cytoplasmic domains (STC) (grey), head (blue) and, stalk (green) domains. The mean (indicated by black dots) and 95% credible interval of BEAST runs (using a single dataset) are shown in nucleotide substitutions/site/year (n/s/t).