

Subtype	Targets	Non Targets	PD	FP	RP	Pairs
N1	110	578	8.8	97	71	553
N2	241	447	11.7	77	44	234
N3	65	623	8.8	45	61	113
N4	15	673	7.1	370	360	9665
N5	32	656	6.4	355	353	8380
N6	77	611	10.3	29	43	7
N7	22	666	7.23	97	103	480
N8	84	604	6.7	140	211	1785
N9	42	646	6.6	292	305	6310

Table 5
Primers found by PrimerHunter for each subtype of Avian influenza NA. (PD: Percentage of Dis-
similarity; FP: Forward Primers; RP: Reverse Primers)

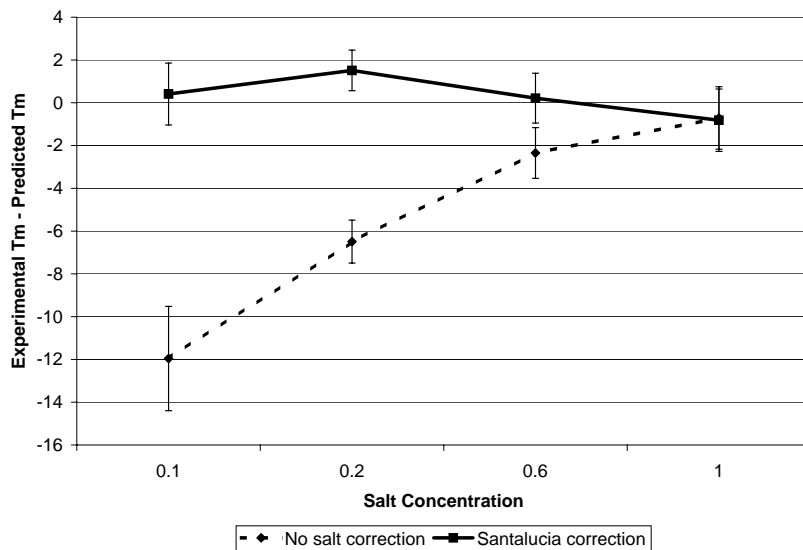


Fig. 6. Average and standard deviation of the difference (in degrees Celsius) between experimental melting temperatures and predictions obtained by fractional programming without salt correction and with salt corrections performed using the SantaLucia model for 376 duplexes of perfectly complementary oligonucleotides with lengths between 20 and 25 base pairs, GC content between 25% and 75%

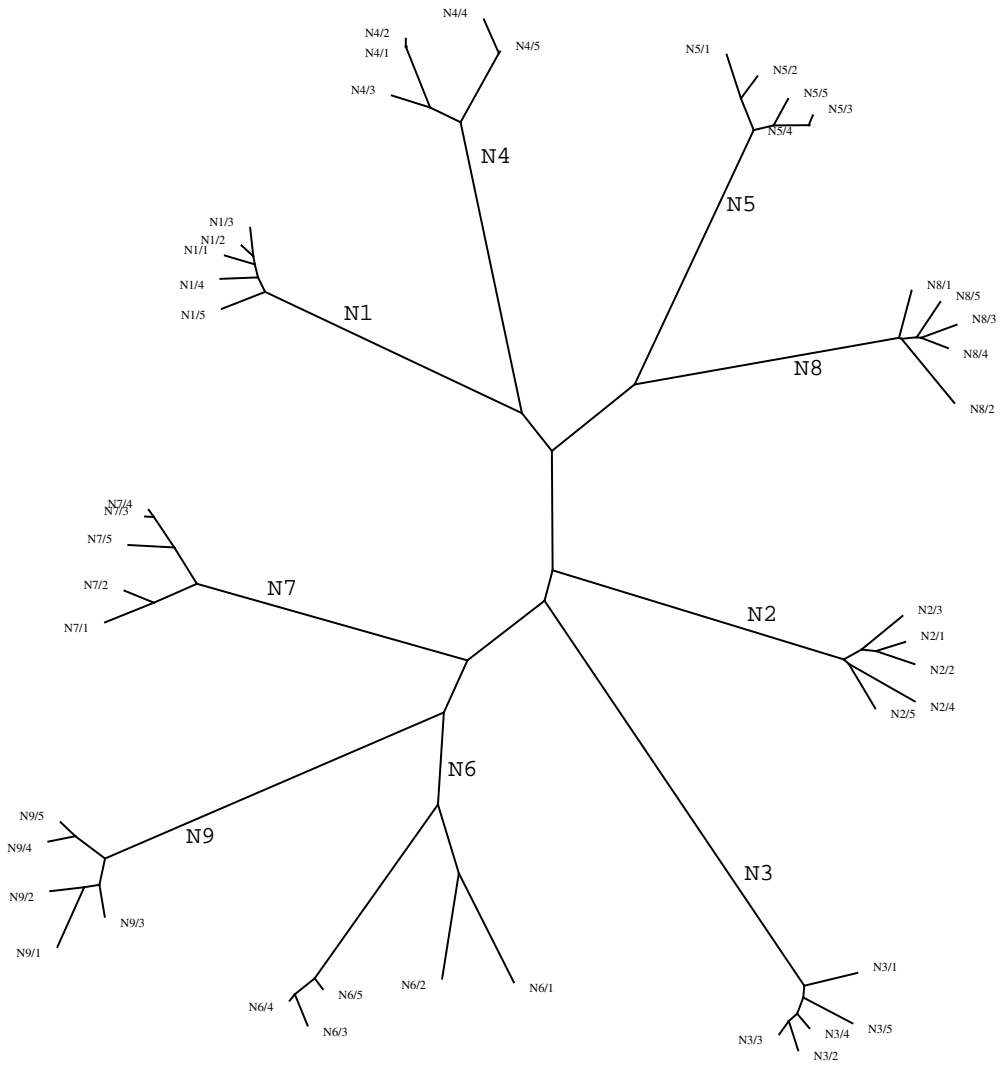


Fig. 7. Phylogenetic tree of avian influenza NA sequences of North American origin from the NCBI flu database (5 complete sequences selected at random for each subtype).