

1918 Influenza Pandemic and Highly Conserved Viruses with Two Receptor-Binding Variants

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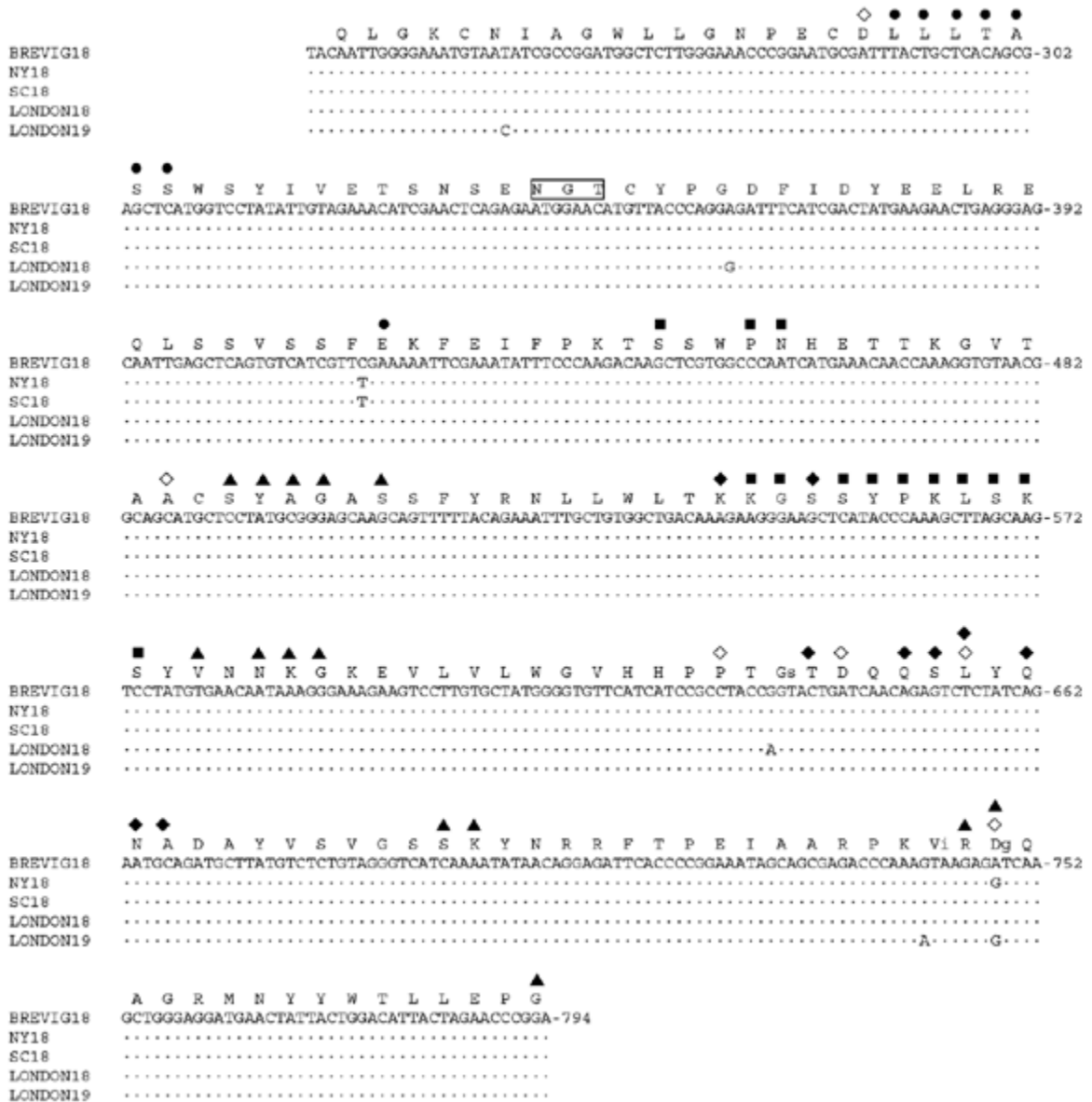


Figure. Partial HA1 domain cDNA sequences from five 1918-19 cases. A 563-bp fragment encoding antigenic (19,20) and receptor-binding (21) sites of the HA1 domain is shown, with the sequences aligned to A/Brevig Mission/1/1918 (BREVIG18) (15). Dots represent sequence identity as compared to BREVIG18. The numbering of the nucleotide sequence is aligned to A/PR/8/1934 (GenBank accession no. NC_002017) and refers to the sequence of the gene in the sense (mRNA) orientation. The partial HA1 translation product for BREVIG18 is shown above its cDNA sequence. Amino acid numbering is aligned to the H3 HA1 domain (15). Boxed amino acids indicate potential glycosylation sites as predicted by the sequence (15). Residues that have been shown experimentally to affect receptor-binding specificity in H1 HAs, D77, A138, P186, D190, L194, and D225 (21–23) are indicated by a white diamond symbol above these six residues. Residues defining four antigenic sites are indicated: C_b (black circle), S_a (black square), S_b (black diamond), and C_a (black triangle) (19,20). Residues that have been mapped to both receptor-binding and antigenic sites (positions 194 and 225) are marked with two symbols. When a nucleotide change as compared to BREVIG18 results in a changed amino acid, the resultant amino acid is shown in lower case to the right of the BREVIG18 residue. Strain abbreviations and GenBank accession numbers: A/Brevig Mission/1/1918 (BREVIG18, # AF116575), A/South Carolina/1/1918 (SC18, # AF117241), A/New York/1/1918 (NY18, # AF116576), A/London/1/1918 (LONDON18, # AY184805), and A/London/1/1919 (LONDON19, # AY184806).

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