

Supplementary material

Tables

Table S1. NCBI Genbank accession numbers for the data set (3211 H1 HA sequences, 1606 N1 and 1406 N2 neuraminidase sequences) of swine influenza A viruses used in the phylogenetic analyses.

Table S2. Hemagglutination inhibition (HI) titers used for the antigenic cartography analyses. Shaded cells indicate homologous titers.

Figures

Figure S1. Phylogenetic relationships of the 3211 H1-HA genes of H1N1/H1N2 swine influenza A viruses. The best-known tree was generated using maximum-likelihood methods, and the branches are colored by HA genetic clade. The scale bar indicates the number of nucleotide substitutions per site.

Figure S2. Phylogenetic relationships of the NA gene of 1606 N1 (A) and 1406 N2 (B) amino acid sequences from H1N1/H1N2 swine influenza A viruses. The best-known tree for each gene was generated using maximum-likelihood methods, and the branches are colored by HA genetic clade. The N1 or N2 lineages are indicated on the right (classical versus N1pdm09; 1998 versus 2002). The scale bar indicates the number of nucleotide substitutions per site.

Figure S3. 3D antigenic map of representative historical and contemporary swine and human H1 influenza viruses. Virus isolates are represented by colored spheres: H1- α (cyan), H1- β (green), H1- γ (dark blue), H1pdm09 (red), H1- δ 1 (yellow), H1- δ 1a (magenta), H1- δ 1b (pink), H1- δ 2 (brown), and human seasonal (gray). Each grid square corresponds to a twofold difference in HI assay titer.

Figure S4. Amino acid sequences alignment of the HA1 protein of H1 viruses used in this study. H1 numbering was used. Dots represent consensus sequences compared to representative strain. Amino acids in the open boxes indicate positions that are different between H1-classical (clusters H1- α , H1- β , H1- γ , and H1-pdm) and H1- δ viruses.

Figure S5. Amino acid sequences alignment of the HA1 protein of H1- δ clade viruses used in this study. Sequences were compared to the antigenic representative (*) in each clade. H1 numbering was used. Dots represent conserved sequences compared to representative strains. Shaded areas represent antigenic sites of H1. Positions that could potentially be associated with antigenic changes are shown in open boxes. Strains displayed in red represent outliers observed in the antigenic analysis (>3AU from cluster representative).

Figure S1

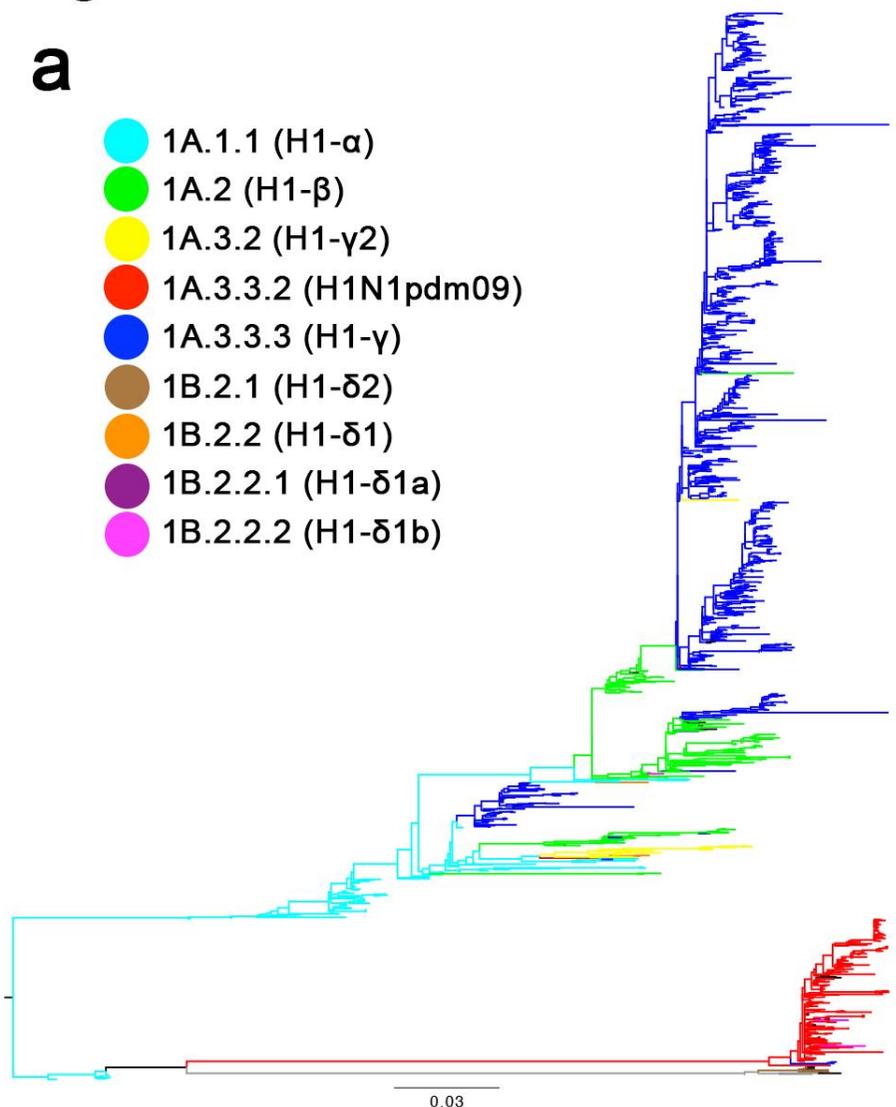
- 1A.1.1 (H1- α)
- 1A.2 (H1- β)
- 1A.3.2 (H1- γ 2)
- 1A.3.3.2 (H1N1pdm09)
- 1A.3.3.3 (H1- γ)
- 1B.2.1 (H1- δ 2)
- 1B.2.2 (H1- δ 1)
- 1B.2.2.1 (H1- δ 1a)
- 1B.2.2.2 (H1- δ 1b)



Figure S2

a

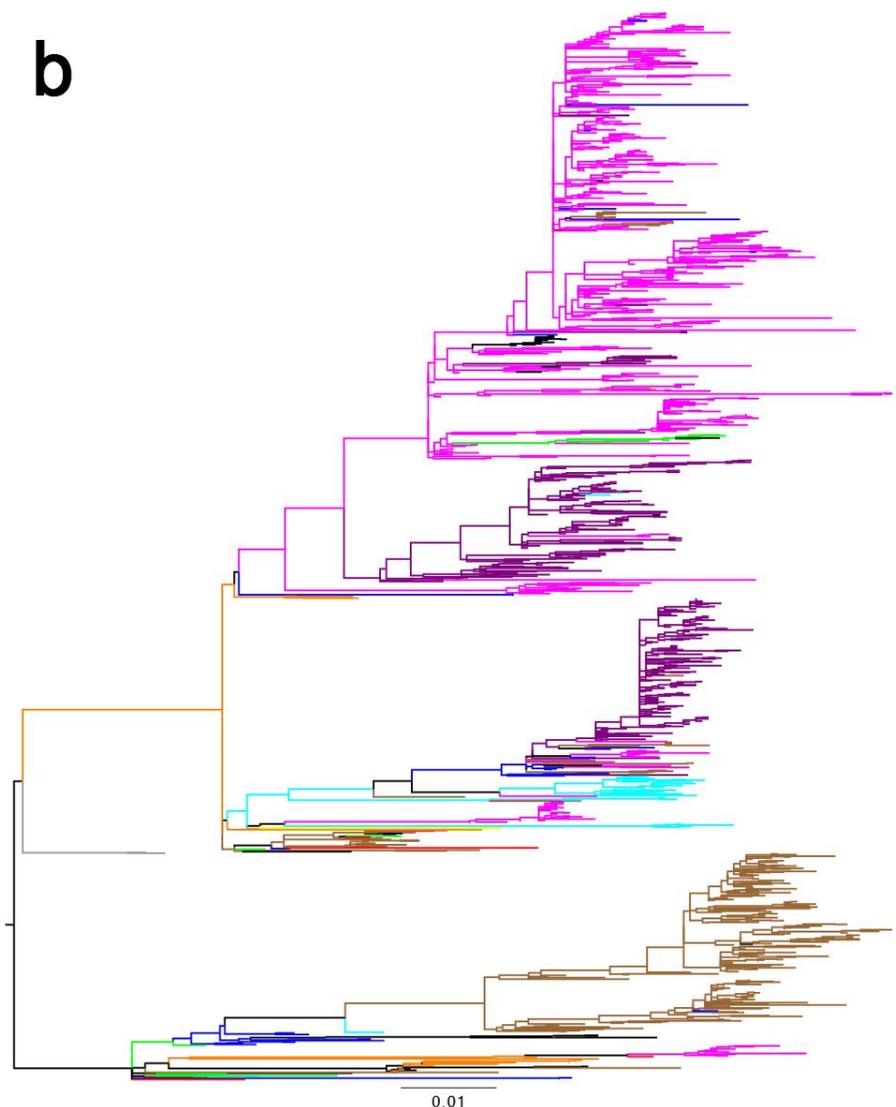
- 1A.1.1 (H1- α)
- 1A.2 (H1- β)
- 1A.3.2 (H1- γ 2)
- 1A.3.3.2 (H1N1pdm09)
- 1A.3.3.3 (H1- γ)
- 1B.2.1 (H1- δ 2)
- 1B.2.2 (H1- δ 1)
- 1B.2.2.1 (H1- δ 1a)
- 1B.2.2.2 (H1- δ 1b)



Classical swine

H1N1pdm09

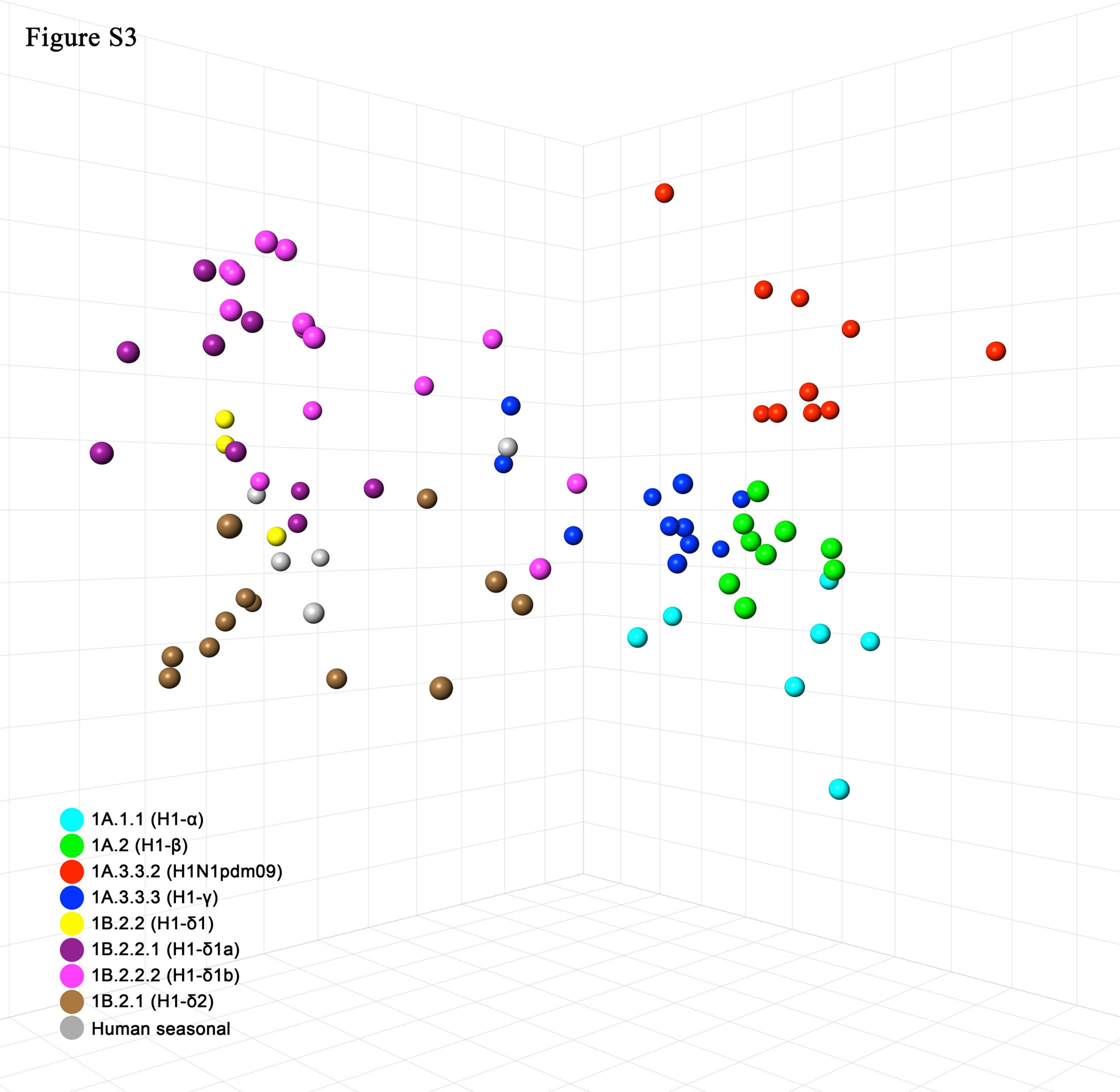
b



2002 swine

1998 swine

Figure S3

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- A 3D scatter plot showing the genetic relationships between various influenza virus sequences. The plot is set within a 3D coordinate system with a light gray grid. The sequences are represented by colored spheres, with their positions indicating their genetic distance from one another. The legend in the bottom-left corner identifies the sequences by color: cyan for 1A.1.1 (H1- α), green for 1A.2 (H1- β), red for 1A.3.3.2 (H1N1pdm09), blue for 1A.3.3.3 (H1- γ), yellow for 1B.2.2 (H1- δ 1), purple for 1B.2.2.1 (H1- δ 1a), magenta for 1B.2.2.2 (H1- δ 1b), brown for 1B.2.1 (H1- δ 2), and gray for Human seasonal. The plot shows distinct clusters for each sequence type, with some overlap between the 1B.2.2.1 and 1B.2.2.2 groups. The 1A.3.3.2 sequence is notably isolated at the top of the plot.
- 1A.1.1 (H1- α)
 - 1A.2 (H1- β)
 - 1A.3.3.2 (H1N1pdm09)
 - 1A.3.3.3 (H1- γ)
 - 1B.2.2 (H1- δ 1)
 - 1B.2.2.1 (H1- δ 1a)
 - 1B.2.2.2 (H1- δ 1b)
 - 1B.2.1 (H1- δ 2)
 - Human seasonal

