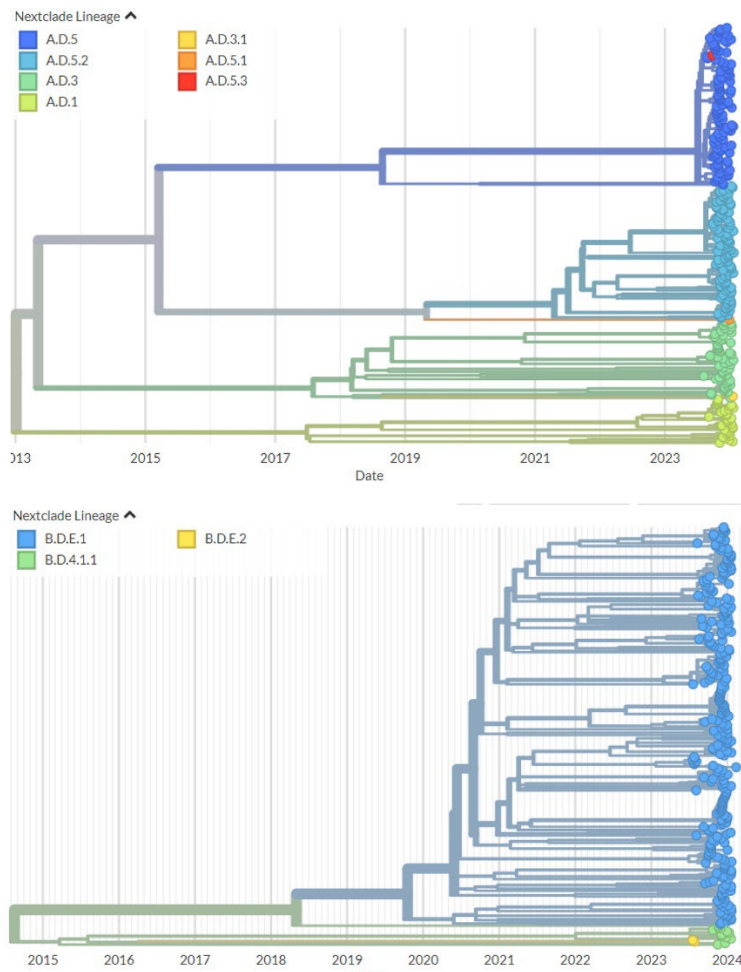


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Appendix



Appendix Figure. Phylogenetic trees shown in Figures 1 and 2 in the main text, annotated in Nextstrain software with a scale of estimated divergence dates by year. Colors denote the lineage classifications of viral genomes as described by Goya et al. (1). Estimated times of lineages' most recent common ancestors (tMRCAs) and corresponding 95% confidence intervals are shown in Table 1 in the main text.

Reference

1. Goya S, Ruis C, Neher RA, Meijer A, Aziz A, Hinrichs AS, et al. Standardized phylogenetic classification of human respiratory syncytial virus below the subgroup level. *Emerg Infect Dis.* 2024;30:1631–41. [PubMed https://doi.org/10.3201/eid3008.240209](https://doi.org/10.3201/eid3008.240209)