

Yellow fever virus resurgence in Sao Paulo State, Brazil, 2024–2025

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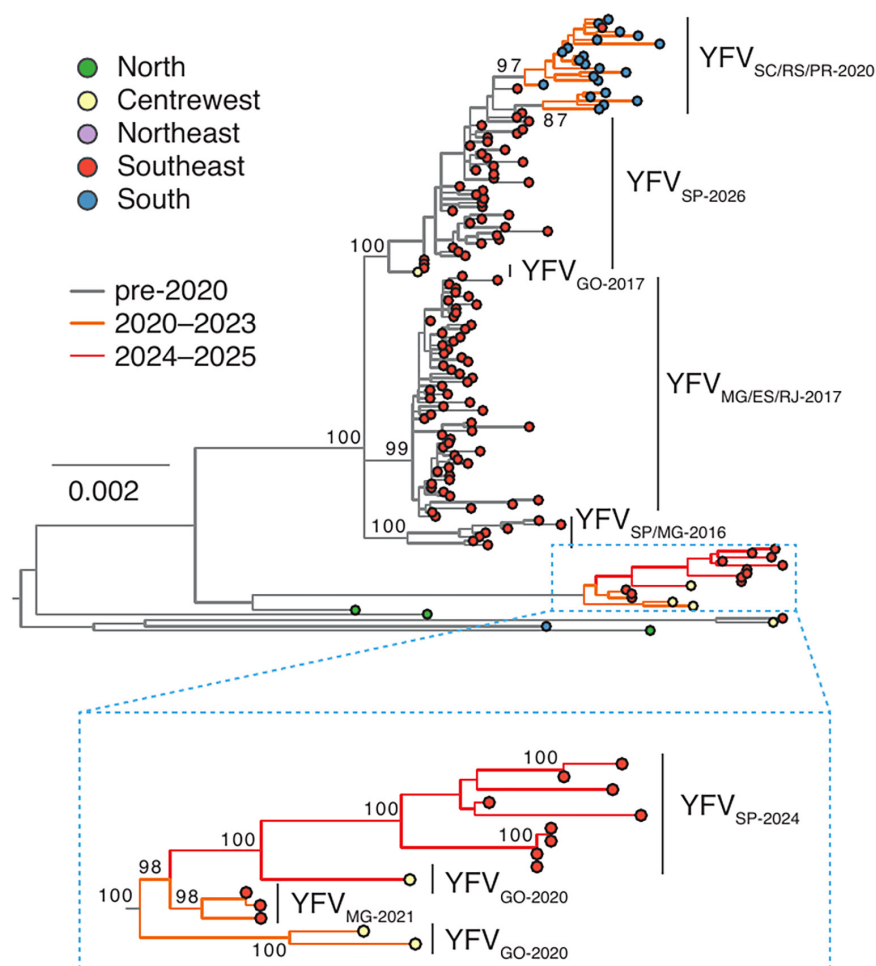
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Supplementary Figure S1 - Maximum likelihood phylogeny of YFV genomes from Brazil. Phylogenetic tree inferred from 151 full-length YFV genomes, showing major spatiotemporal lineages from 2016–2025 (denoted in [Figure 2](#)). Tip colors represent the geographic region of sampling (North, Midwest, Northeast, Southeast, South). Branch colors indicate sampling period: grey (pre-2020), orange (2020–2023), and red (2024–2025). Support values at key nodes indicate ultrafast bootstrap (UFBoot) percentages. The inset at the bottom shows an expanded view of the most recent strains and the clear separation of the SP-2024 sublineage. The scale bar represents substitutions per site.

Supplementary Table S1 – Accession numbers and metadata of sequences in this study, 2024

Accession number	Host	Location	Coordinates	Area	Date of sampling
PQ602526	<i>Alouatta</i> sp.	Pedra Bela	–22.775758; –46.441848*	Car	18 Sep 2024
PQ963937	<i>Alouatta</i> sp.	Pinhalzinho	–22.78642; –46.559196	Car	20 Dec 2024
PQ879115	<i>Alouatta caraya</i>	Ribeirao Preto	–21.16855; –47.86516	RPar	26 Dec 2024
PQ879116	<i>Alouatta caraya</i>	Ribeirao Preto	–21.16855; –47.86516	RPar	26 Dec 2024
PQ879117	<i>Alouatta caraya</i>	Ribeirao Preto	–21.16855; –47.86516	RPar	26 Dec 2024
PQ879118	<i>Alouatta caraya</i>	Ribeirao Preto	–21.16855; –47.86516	RPar	26 Dec 2024

*Coordinates from the municipality centroid.