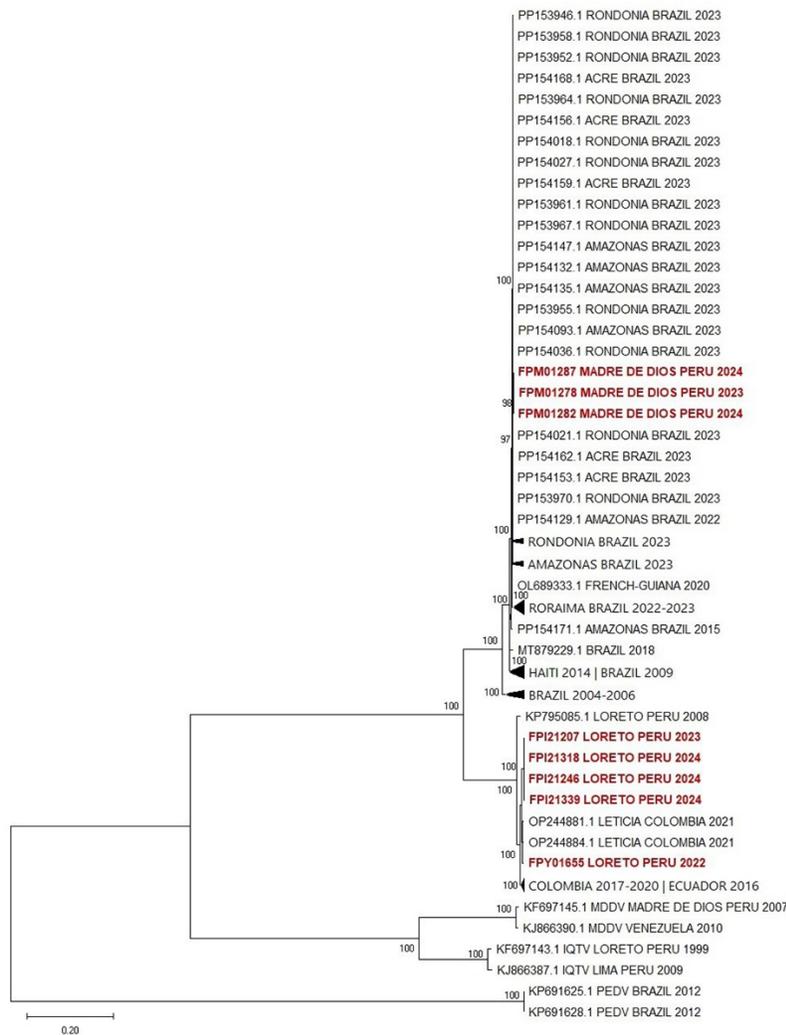


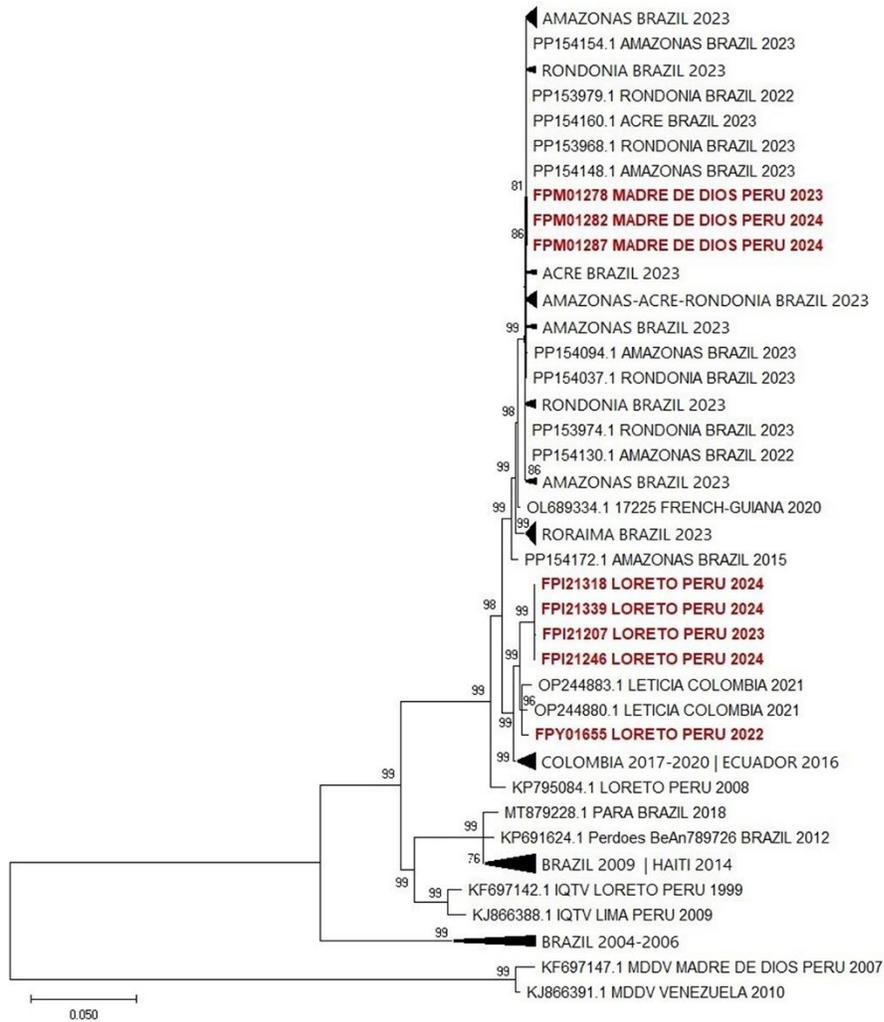
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Co-circulation of Two Oropouche Virus Lineages during Outbreak, Amazon Region of Peru, 2023–2024

Appendix



Appendix Figure 1. Maximum-likelihood phylogeny based on 78 nt sequences of Oropouche virus M segment. Peruvian strains are highlighted in red bold. Only bootstrap values >70% are shown at key nodes. Scale bar indicates nucleotide substitutions per site.



Appendix Figure 2. Maximum-likelihood phylogeny based on 93 nt sequences of Oropouche virus L segment. Peruvian strains are highlighted in red bold. Only bootstrap values >70% are shown at key nodes. Scale bar indicates nucleotide substitutions per site.