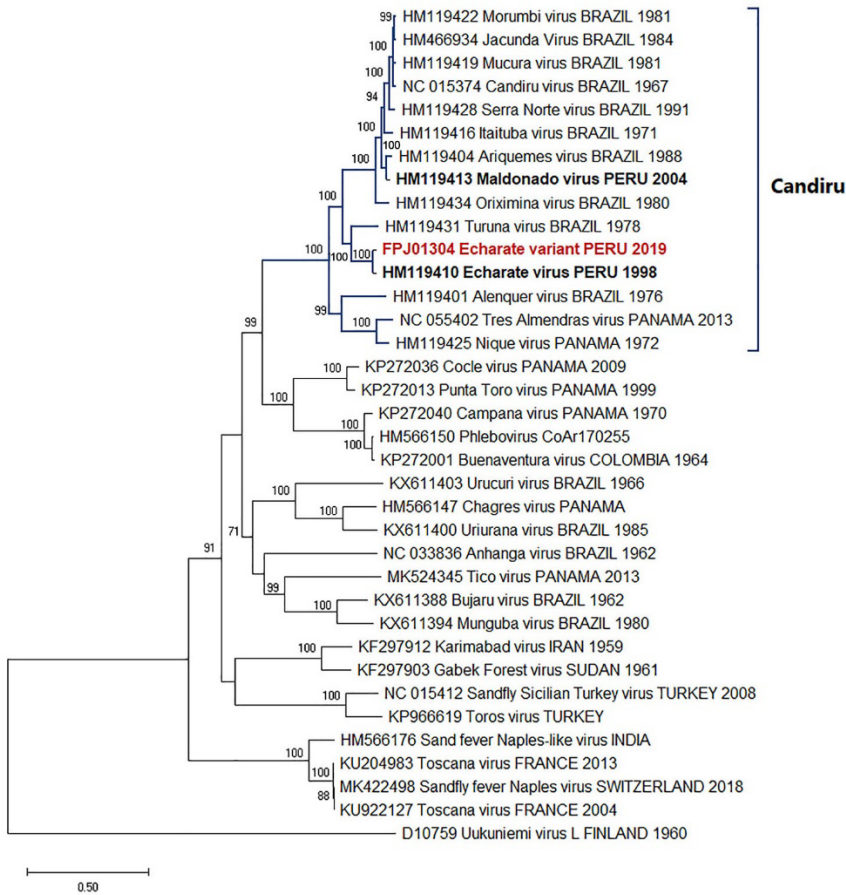


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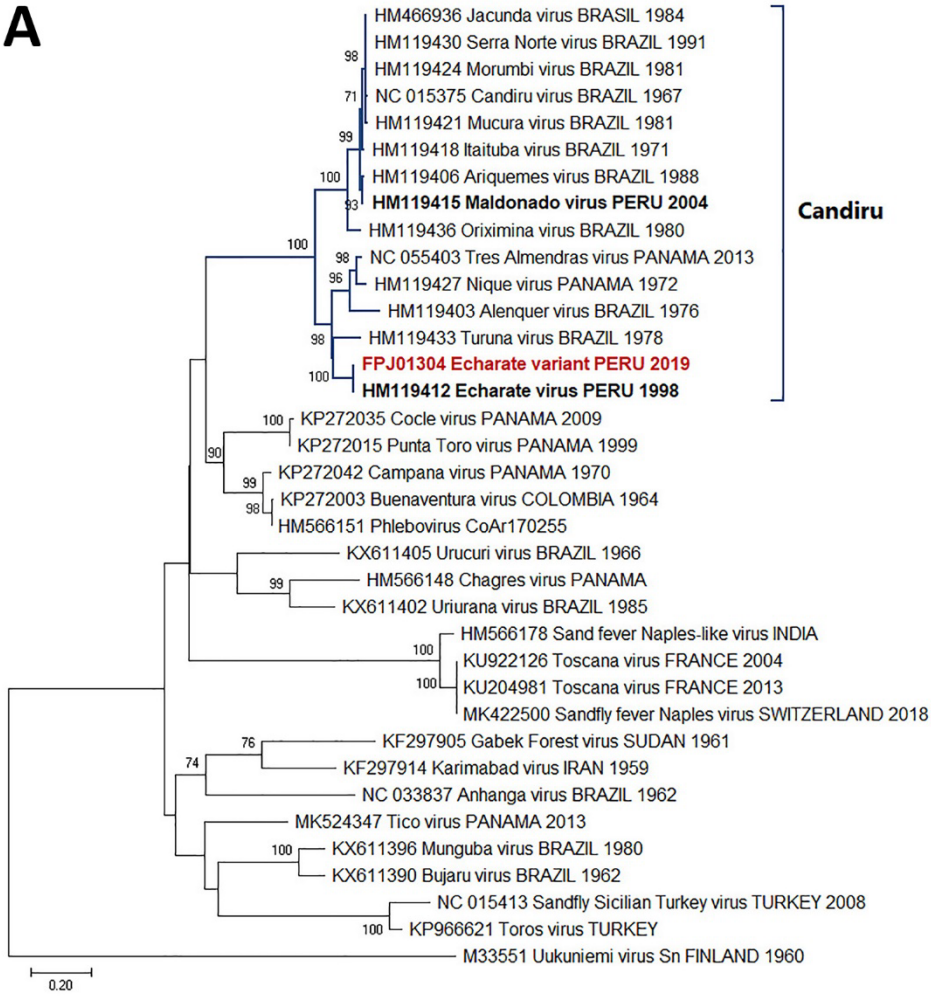
# Novel Echarate Virus Variant Isolated from Patient with Febrile Illness, Chanchamayo, Peru

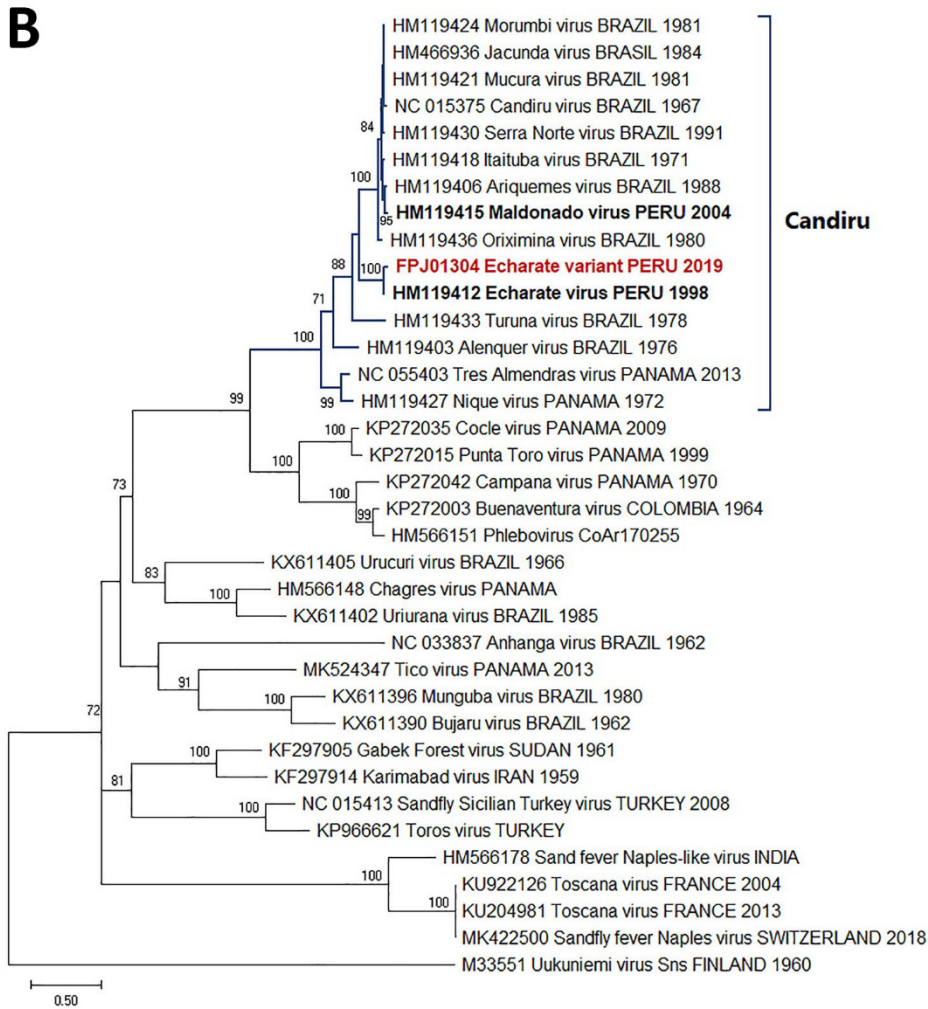
## Appendix 2



**Appendix 2 Figure 1.** Maximum-likelihood phylogeny based on 36 aa sequences of phleboviruses L segment (RdRp). Peruvian strains are in bold and the novel variant is highlighted in red. Only bootstrap values >70% are shown at key nodes. Uukuniemi virus was considered as the outgroup. Scale bar indicates nucleotide substitutions per site. aa, amino acid; L, large segment; RdRp, RNA-dependent RNA polymerase

**A**





**Appendix 2 Figure 2.** Maximum-likelihood phylogeny based on 36 aa sequences of plebioviruses S segment. A) Nucleocapsid protein; B) Nonstructural protein. Peruvian strains are in bold and the novel variant is highlighted in red. Only bootstrap values >70% are shown at key nodes. Uukuniemi virus was considered as the outgroup. Scale bar indicates nucleotide substitutions per site. aa, amino acid; S, small segment.