

Plagued by a cryptic clock

Insight and issues from the global phylogeny of *Yersinia pestis*

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SUPPLEMENTARY FIGURES:

Figure S1: Root to tip regression for clades of *Yersinia pestis* as defined by the global phylogeny

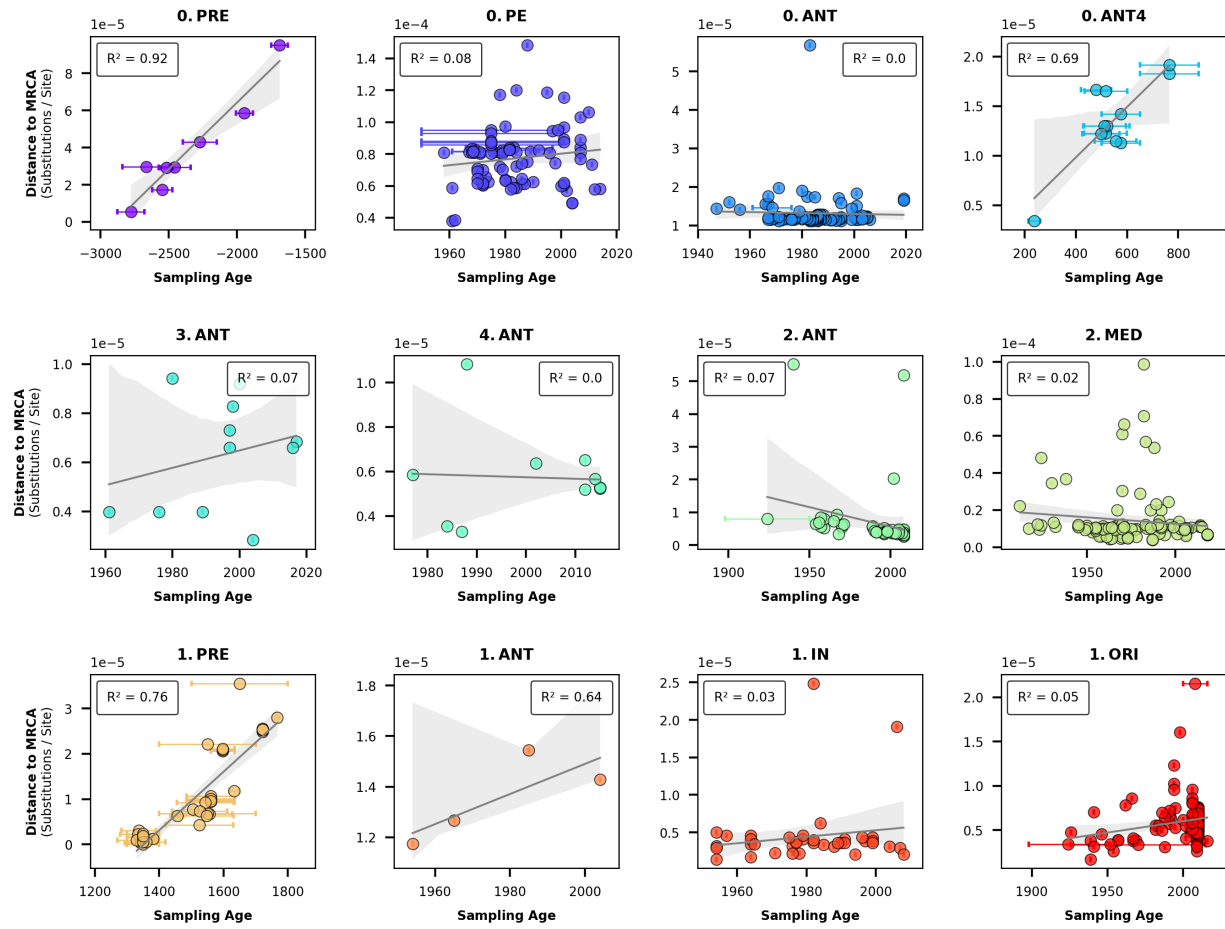
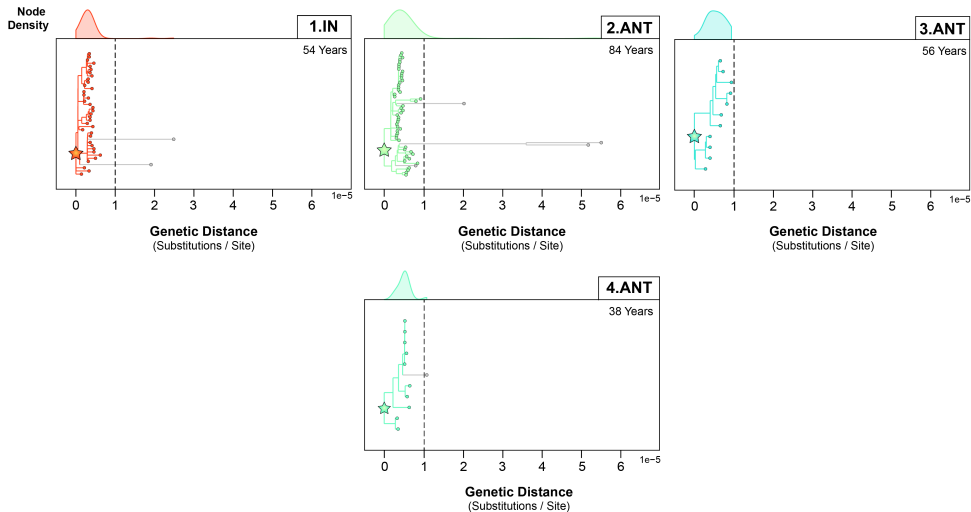
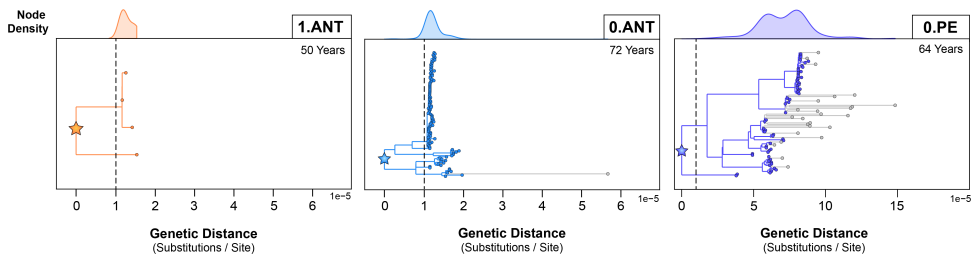


Figure S2: Nodal density vs root nodes for each clade of *Yersinia pestis*

A. No Temporal Signal



B. Insufficient Internal Calibrations



C. Temporal Signal With Informative Dates

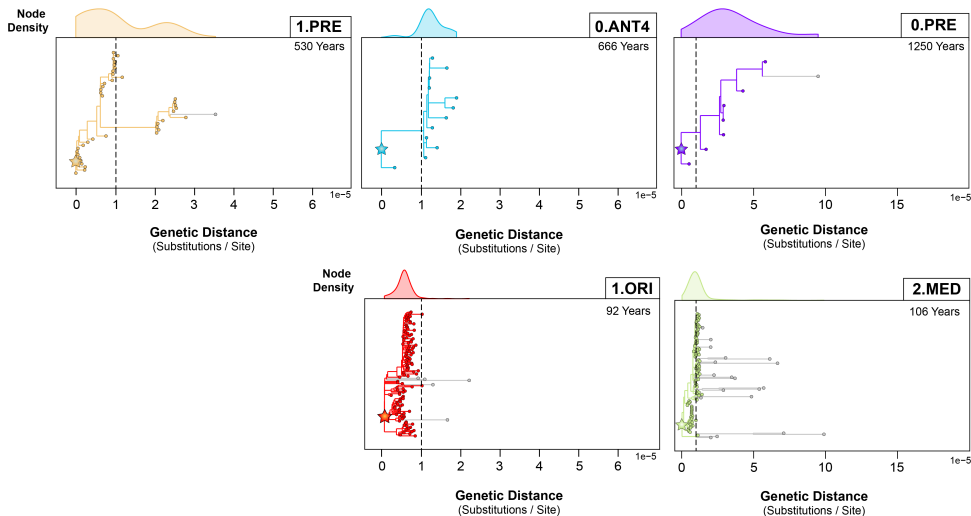


Figure S3: Branch support across MCC Tree of Second Pandemic of Plague

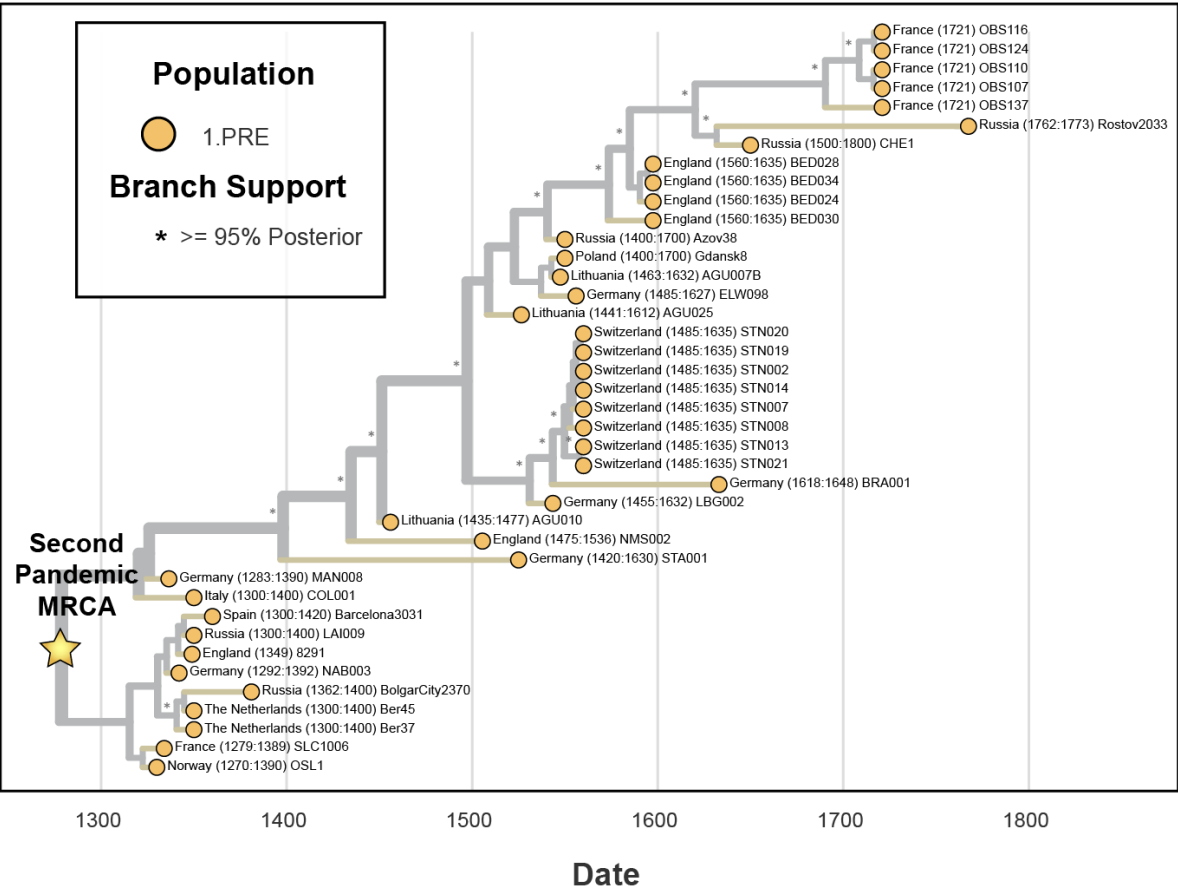


Figure S4: Percent of Samples Collected from the Same Location as their Closest Genetic Relative

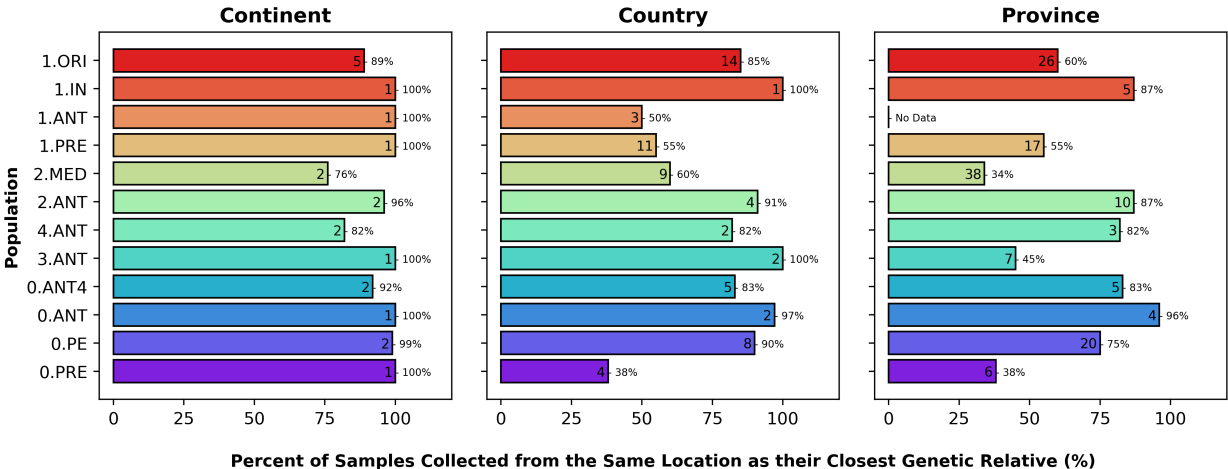


Figure S5: Confidence in Estimating the ancestral location (at varying geographic levels) for the Third Pandemic

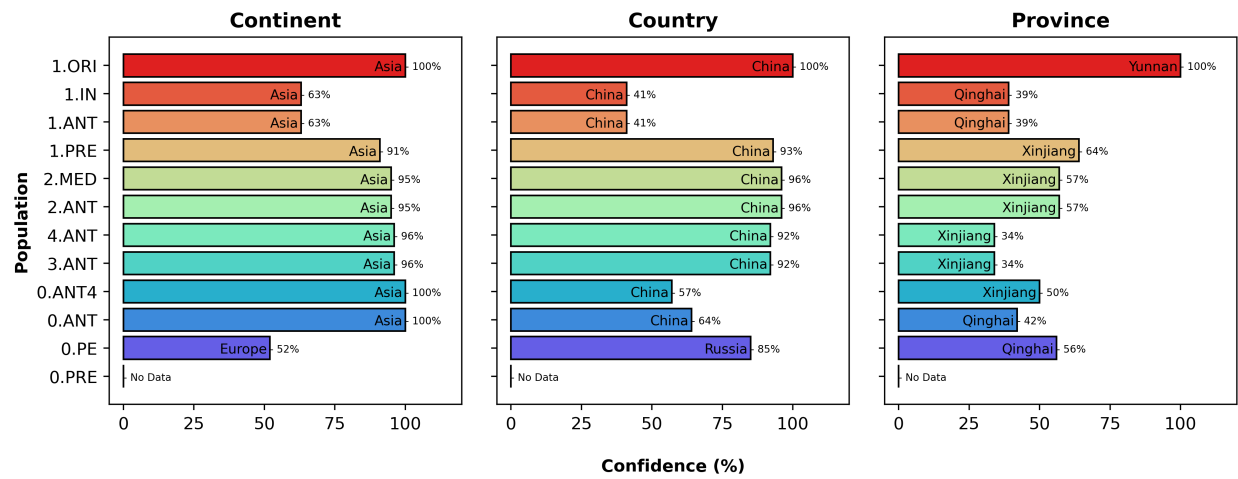


Figure S6: Maximum Likelihood Phylogeny of *Yersinia pestis* of Third Pandemic and the geographic location of phylogenetically closest basal Lineages

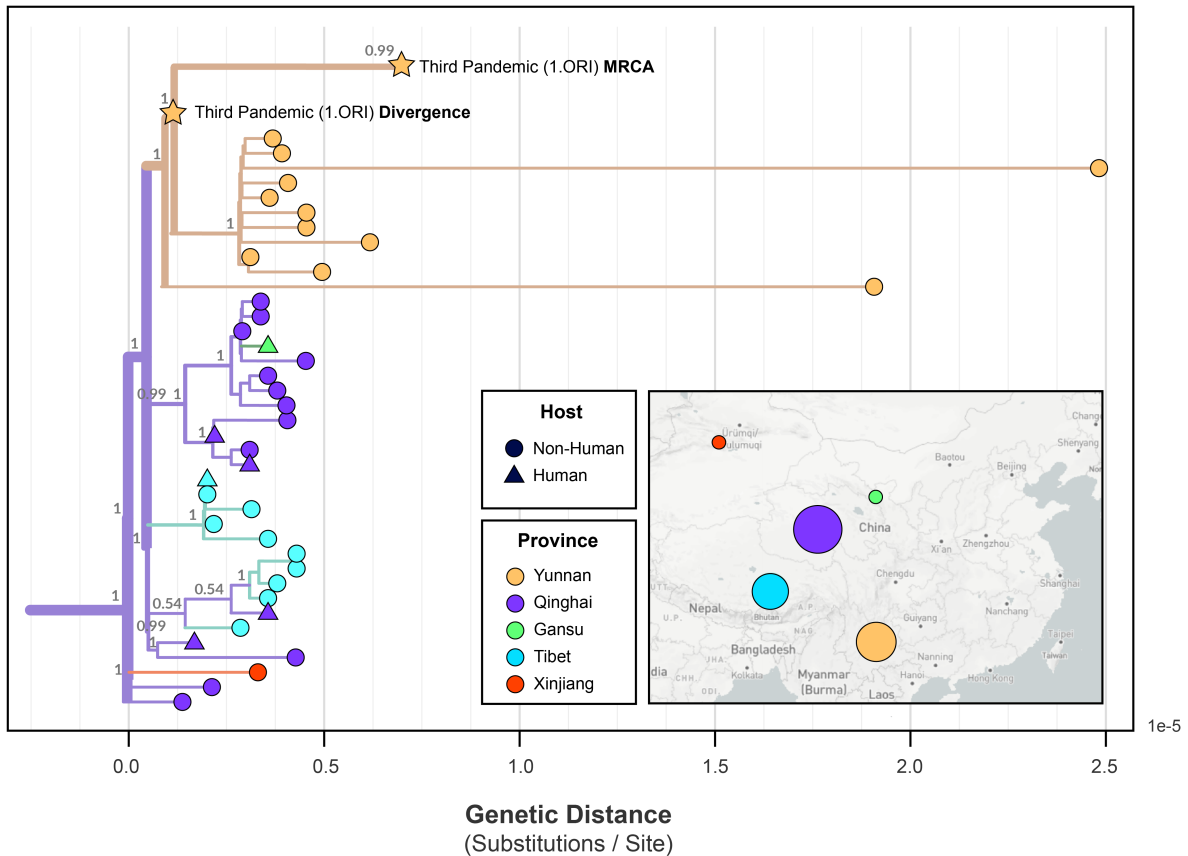


Figure S7: Confidence in Estimating the ancestral location (at varying geographic levels) for all other populations of *Y. pestis*

