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# Plague-Phylogeography:

## Novel Synthesis and Geospatial Analysis

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## Table of Contents

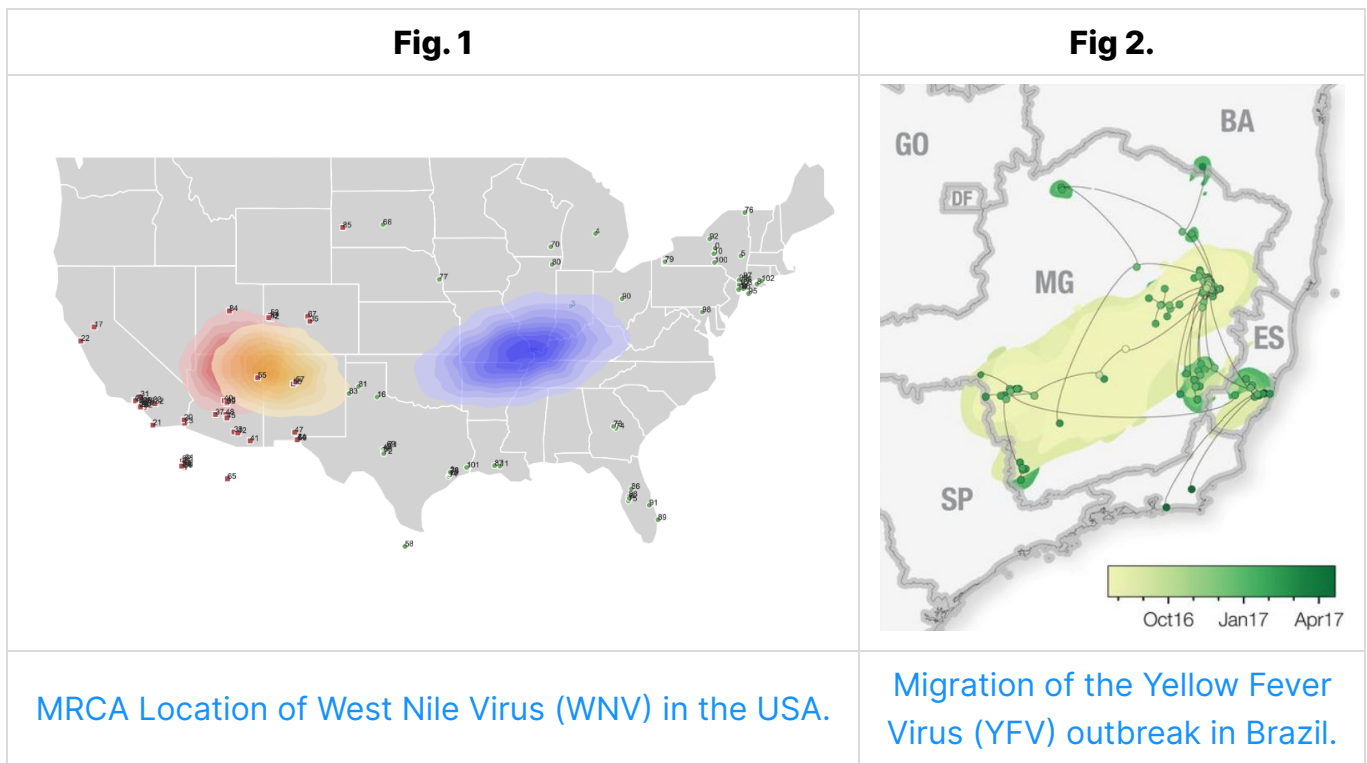
1. Introduction
2. Problem
3. Question
4. Experiment

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## Introduction

- The ancestral location of pathogens can be estimated using **#Phylogeography**.
- **#Geographic-Origin** (s) of an emerging disease (**Fig 1**).
- **#Migration** history of an outbreak (**Fig 2**).

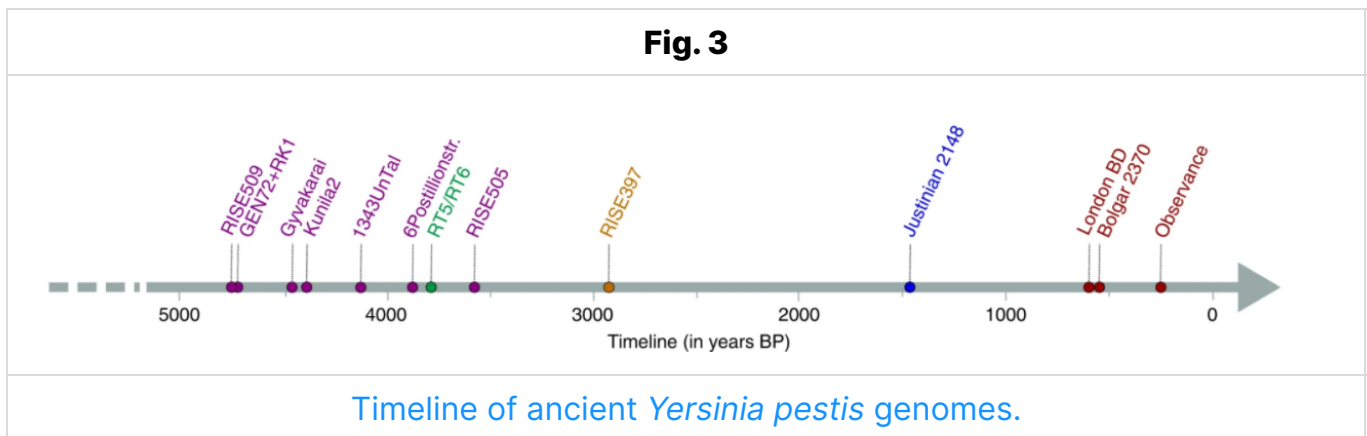
<b>Fig. 1</b>	<b>Fig 2.</b>
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## Why is Plague interesting?

### 1. Breadth and Scope

- Long history with humans (**Fig 3**).
- Huge geographic range (every continent except Antarctica).

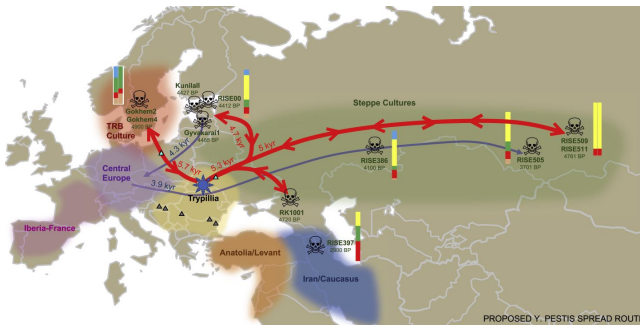


### 2. Hot Debates!

- The **#Geographic-Origin** (s) are contentious (**Fig 4**).
- Multiple **#Reemergences** with distinct spatial patterns (**Fig 5**).

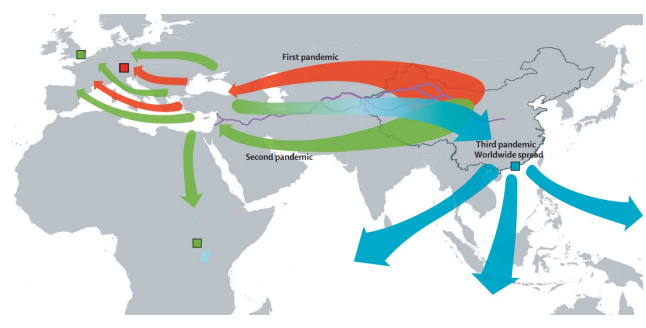


**Fig 4**



Dispersion model during the Late Neolithic Bronze Age.

**Fig 5**



Hypothesized dissemination routes of the major plague pandemics.

### 3. Potential Contributions

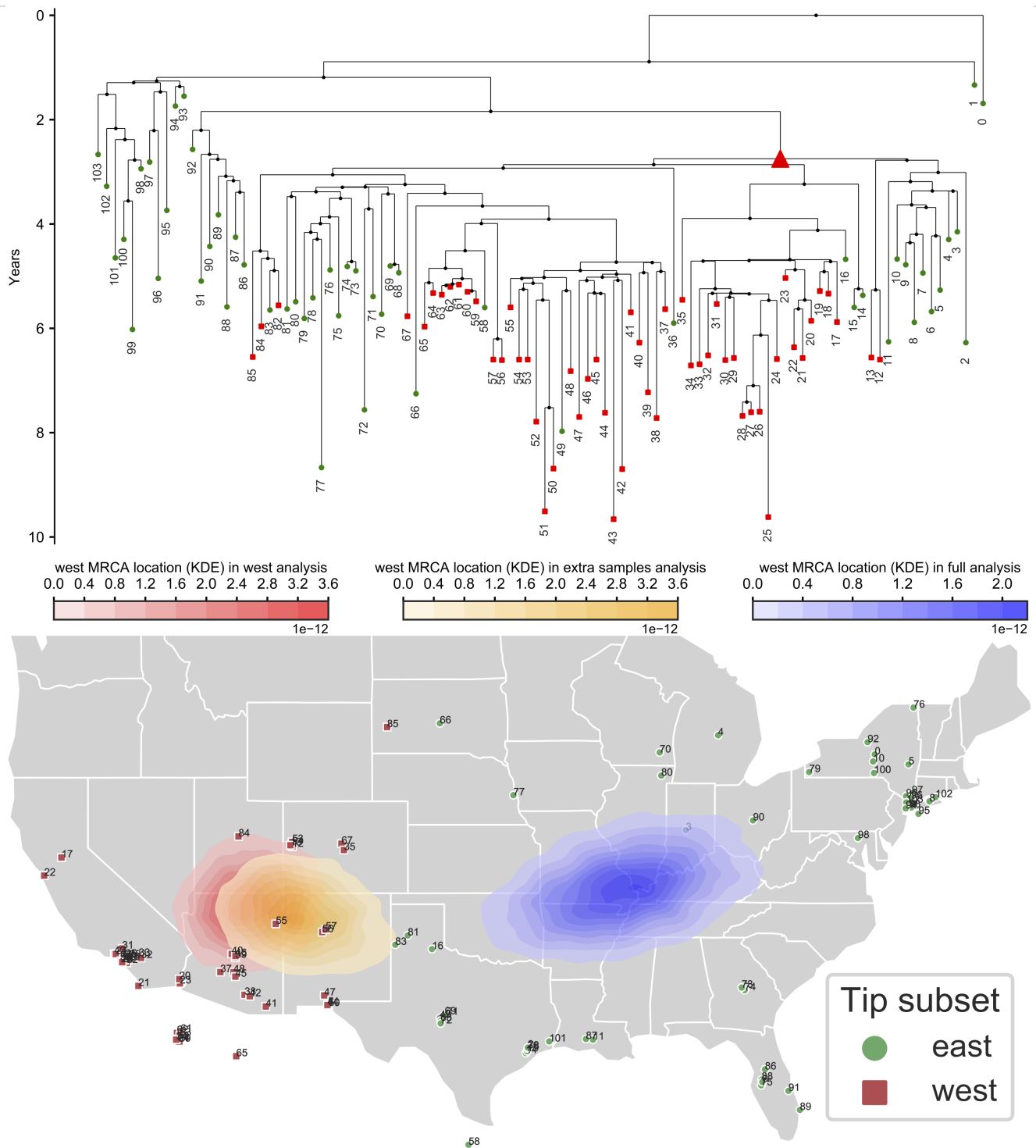
- MOAR data: Triple the sample size of existing **#Yersinia-pestis** phylogenies.
- MOAR stats: Use a statistical approach to mapping the **#Geographic-Origin** (s) and **#Migration**.

## Problem

- **#Phylogeography** is highly sensitive to **#Sampling-Bias**.
- The true distribution is not evenly sampled (under/over-sampling).
- [Kalkauskas et al. 2021](#) demonstrates this looking at West Nile Virus in the USA.

**Fig 6**

**Fig 6**



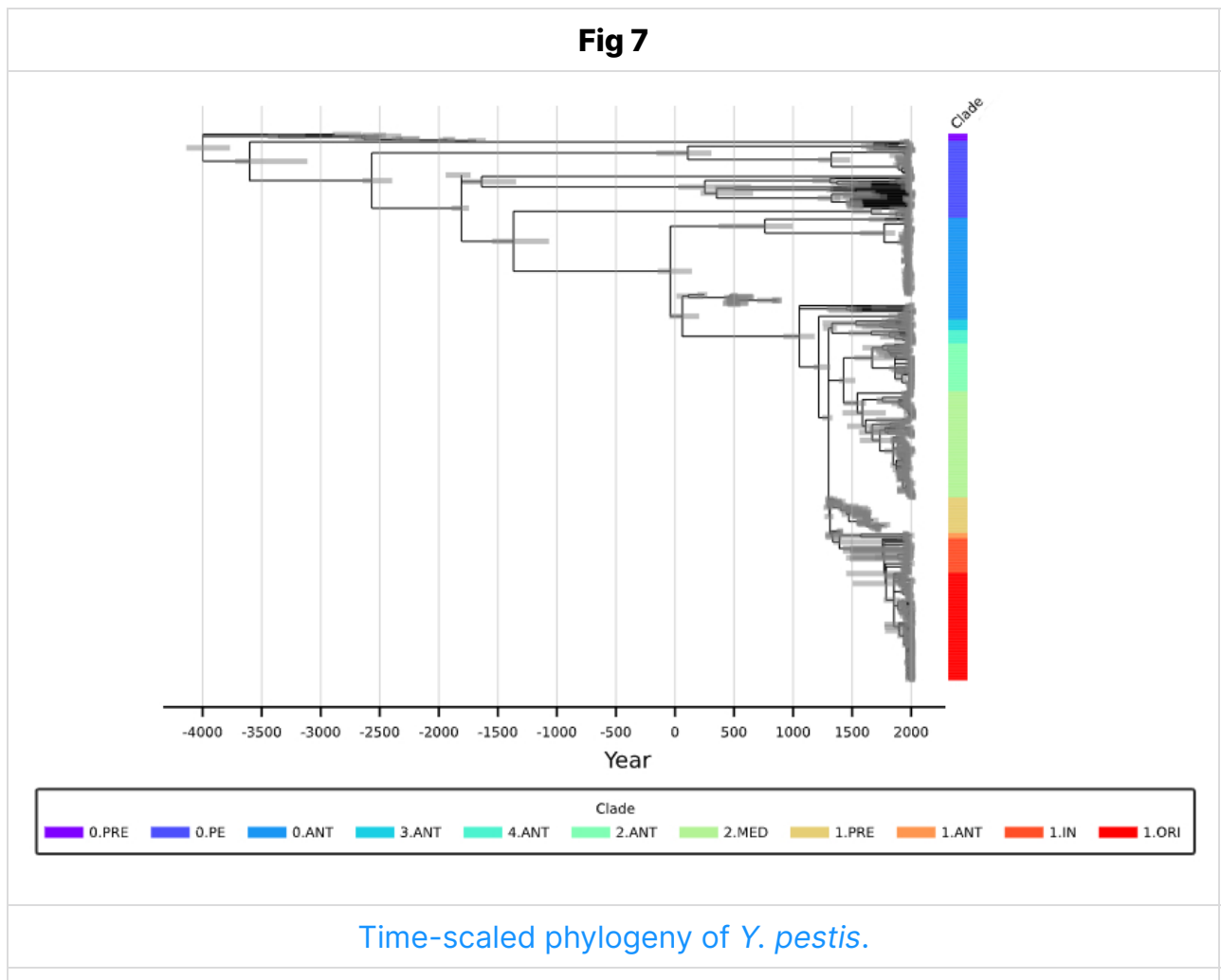
(Top) Maximum Clade Credibility tree of West Nile Virus in the western and eastern USA. (Bottom) MRCA location of all western samples. (Blue: All samples, Red: Only western samples, Orange: western samples and sequence-free eastern samples ).

## Questions

1. What are the **#Geographic-Origin** (s) and **#Migration** patterns of the **#Medieval** **#Plague** **#Pandemic**?
2. To what extent are the results influenced by sampling biases?
  - Over-sampling of East-Asia and the Caucasus.
  - Under-sampling of Africa and the Mediterranean.

## Previous Work

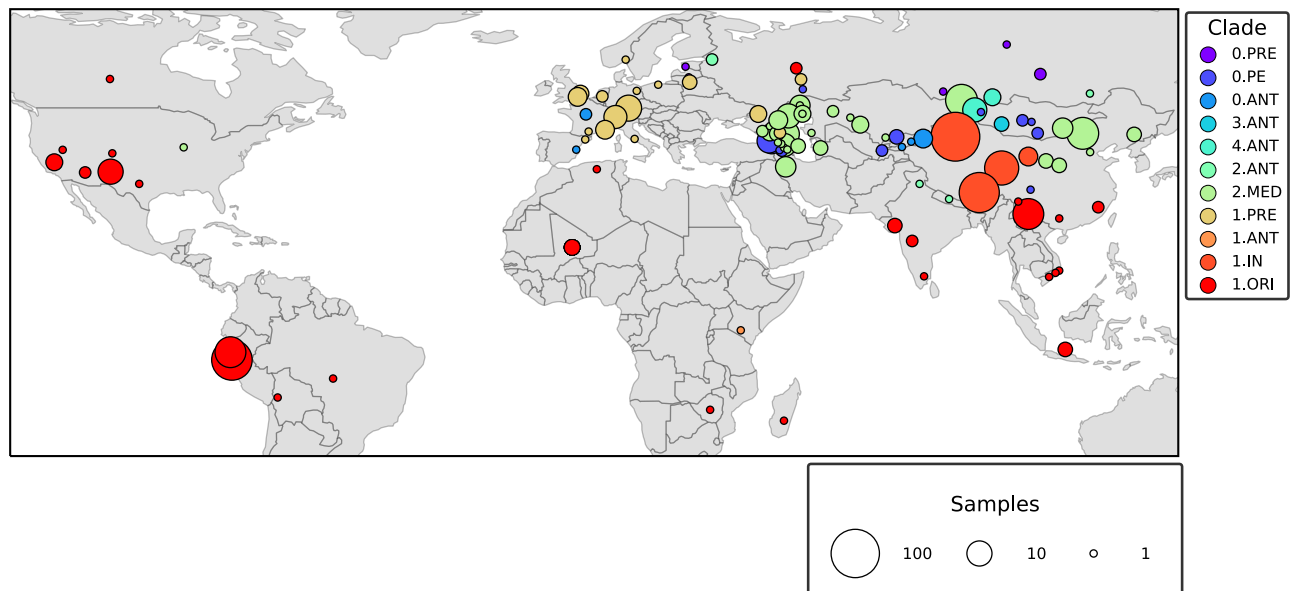
1. Estimated a time-scaled phylogeny of 634 *Y. pestis* genomes.



2. Estimated geographic location for all internal nodes.

**Fig 8**

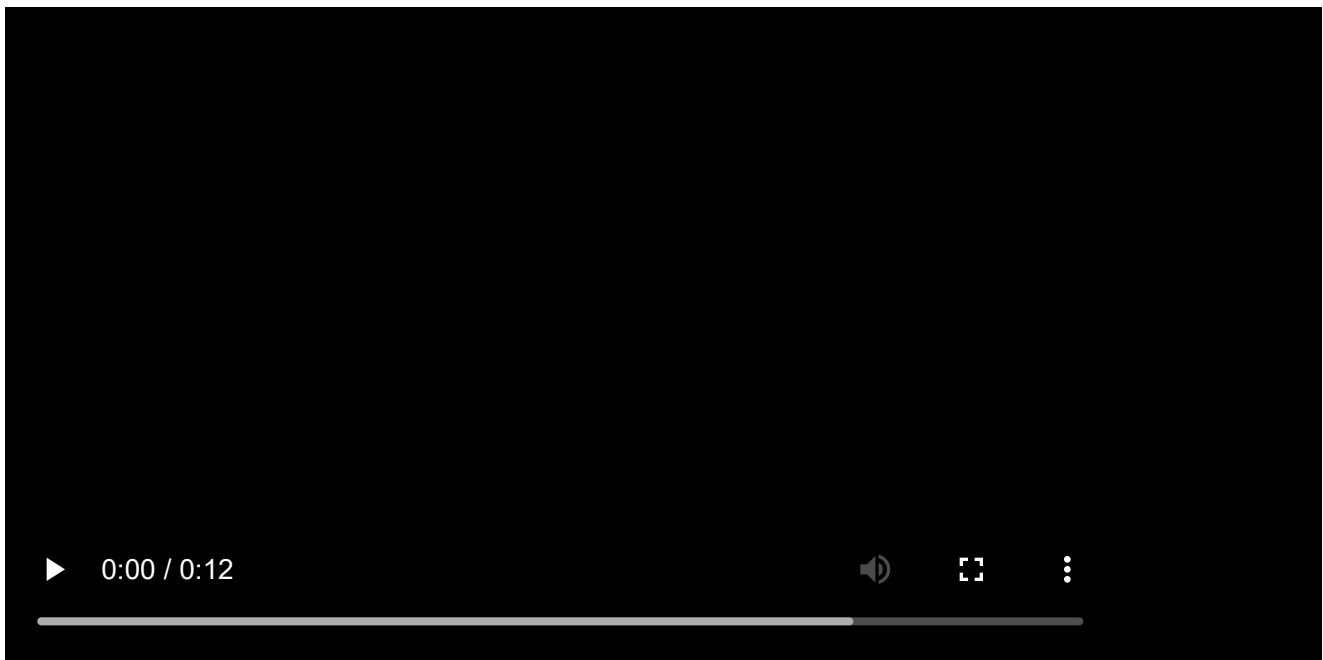
**Fig 8**



Geographic distribution of *Y. pestis* genomes in this study.

3. Plot the arrival of **#Plague** in **#Medieval** **#Europe** and subsequent **#Migration** (s).

**Fig X**

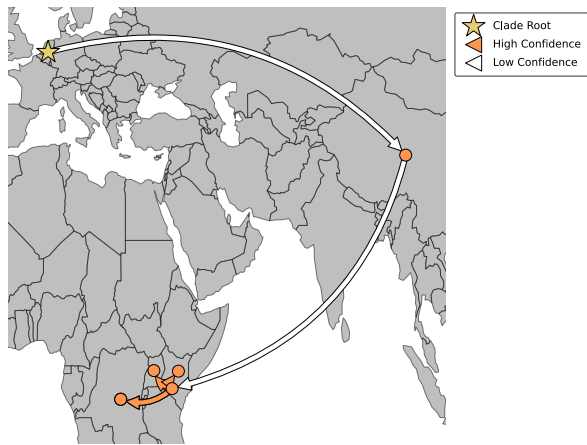


Medieval and Early Modern pandemic clade 1.PRE timetree.

4. Plot the departure of **#Plague** from **#Medieval** **#Europe** .

**Fig 5**

**Fig 5**



African clade 1.ANT spreadmap.