2021-03-23\_Poinar-Lab-Meeting

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## Plague-Phylogeography

#### Novel Synthesis and Geospatial Analysis

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## Introduction

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

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| --- | --- |
| Fig. 1 | Fig 2. |
| [[tmrca\_west\_nile.png]] | [[spread3\_YFV.JPG]] |
| MRCA Location of West Nile Virus (WNV) in the USA | Yellow fever virus (YFV) epidemic in Brazil |

## Plague

##### 1. Breadth and Scope

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

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| Fig. 3 |
| [[spyrou2018Analysis3800yearoldYersinia\_fig2c.jpg]] |
| [Timeline of ancient Yersinia pestis genomes.](https://doi.org/10.1038/s41467-018-04550-9) |

### 2. Hot Debates!

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

[@wagner2014YersiniaPestisPlague]

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| Fig 4 | Fig 5 |
| [[rascovan2019EmergenceSpreadBasal\_fig5d.jpg]] | [[wagner2014YersiniaPestisPlague\_fig4.jpg]] |
| [Dispersion model during the Late Neolithic Bronze Age.](https://doi.org/10.1016/j.cell.2018.11.005) | [Hypothesized dissemination routes of the major plague pandemics.](https://doi.org/10.1016/S1473-3099(13)70323-2) |

## Problem