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Introduction

- TB is the number 1 cause of death due to a single infectious agent
- 10.4M new cases and 1.7M deaths per year (WHO)
- 7 different lineages, each characteristic of particular region(s)
- In 2017, two-thirds of all TB cases were in 8 countries: **India (27%)**, China (9%), Indonesia (8%), the Philippines (6%), **Pakistan (5%)**, Nigeria (4%), **Bangladesh (4%)**, and South Africa (3%)

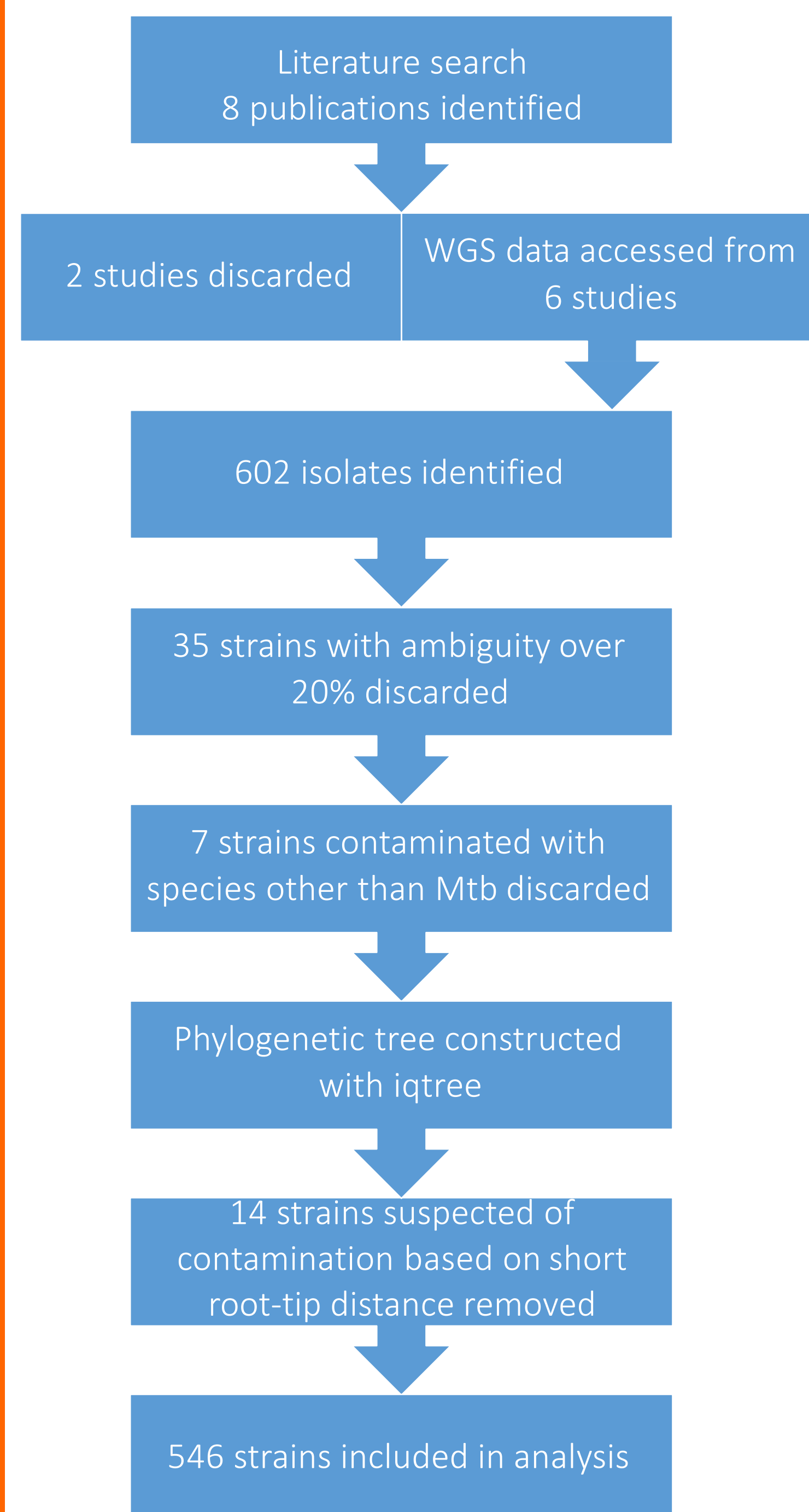
Research Question

How do different historical and geographical factors influence the distribution of Mtb lineages in the Indian Subcontinent (ISC)?

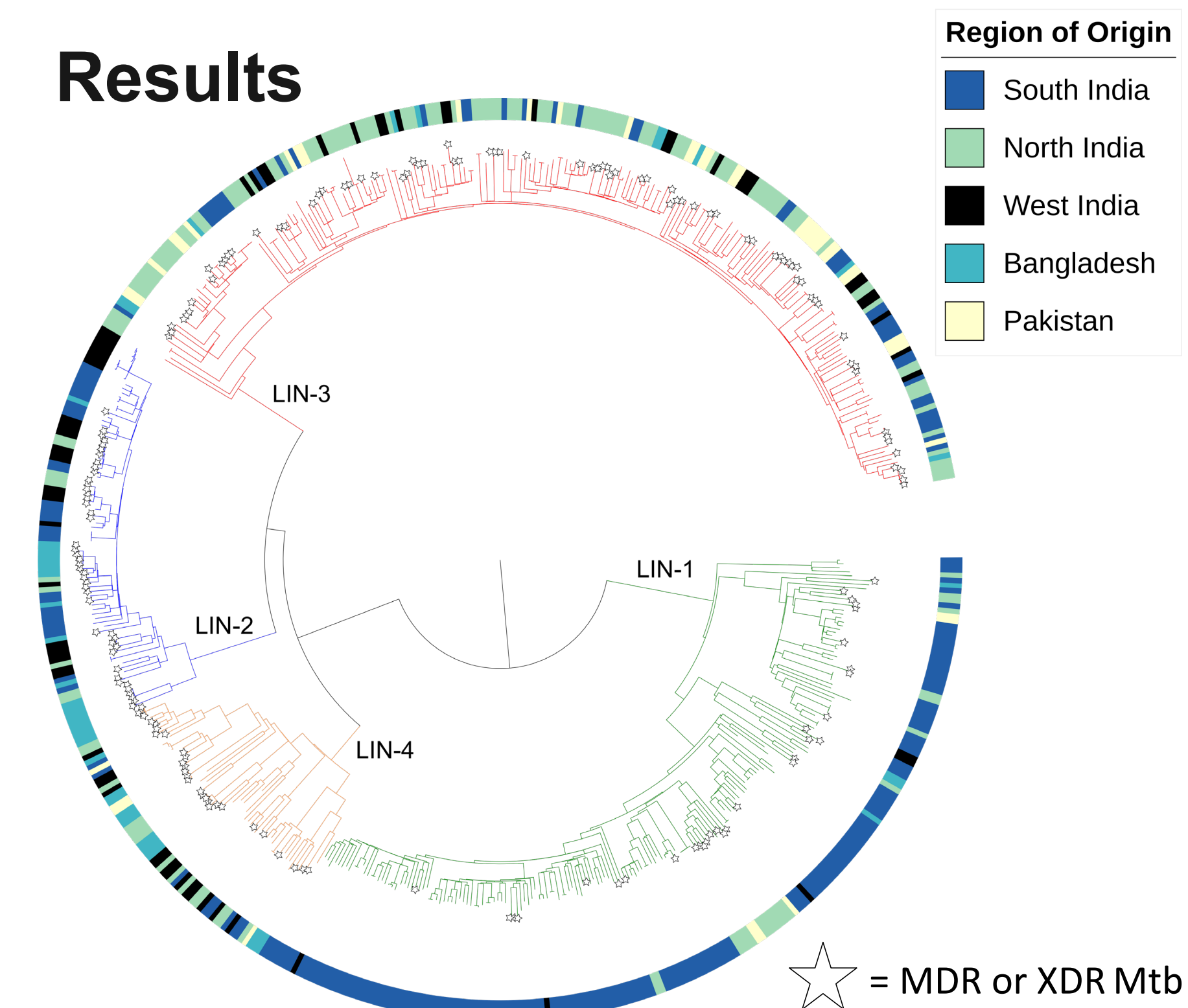
Work profile

- Bioinformatics research intern at the Oxford University Clinical Research Unit (OUCRU), hosted by the Hospital for Tropical Diseases in Vietnam
- Coworkers from all over the world—Vietnamese, British, Australian, Dutch, Thai...
- Part of a larger project to analyze all Mtb in Asia

Methods



Results



Summary of Conclusion:

- LIN-1: characteristic of S. India, not much movement
- LIN-2: external origin (East Asia), hypothesize multiple introductions to ISC, need contextual strains
- LIN-3: originated in N. India, multiple introductions to other countries in ISC, geographically dynamic; hypothesize this is due to N. India's geographical proximity to other countries of ISC, especially compared to S. India
- LIN-4: external origin (Europe), hypothesize many introductions, need contextual strains, geographically dynamic
- Difficult to conclude a relationship between drug resistance and lineage due to heavy selection bias in the sampling for MDR (multi-drug resistance) Mtb

Looking ahead

These 546 strains will be further analyzed along with thousands of other Mtb strains from Asia. In context, we can use phylogenetic trees to more closely examine the epidemiology of TB in Asia. I also worked on a second project, which involved modelling the trends of TB incidence of the 30 highest burden countries. I compared the projected number of cases to the WHO End TB goals until the year 2035. This is an ongoing project. My time at OUCRU was a unique opportunity to become more familiar with various computer languages and apply them to original research.

Acknowledgements

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