

Background

- Brazil has a tuberculosis (TB) incidence in prisoners that is over 25-times greater than in the general population.
- We combined conventional epidemiological methods, detailed contact data, and molecular techniques to understand the transmission network of TB in a high incidence prisoner population and community in the Brazilian state of Mato Grosso do Sul.



Methodology

We performed a population-based study of TB transmission in the state of Mato Grosso do Sul from June 2009 to April 2016.

Study population

- Prisoners and community members in the state with culture-positive TB.

Social contact network of prison

- For each TB positive prisoner, we obtained the date of disease notification and a temporal record for prisoner location, intra-prison movement, and transfer between prisons.

Molecular analysis

- We genotyped the *Mycobacterium tuberculosis* isolates from each person with IS6110 restriction fragment length polymorphism (RFLP) analysis.
- We defined a cluster as a group of individuals with identical RFLP patterns.
- We performed whole genome sequencing on 19 isolates to validate the largest cluster

Inference for potential transmission within prison

- For each identical cluster, we created a longitudinal record with each prisoner's location with relation to other prisoners to infer potential transmission.

Detailed social contact network for prisoners

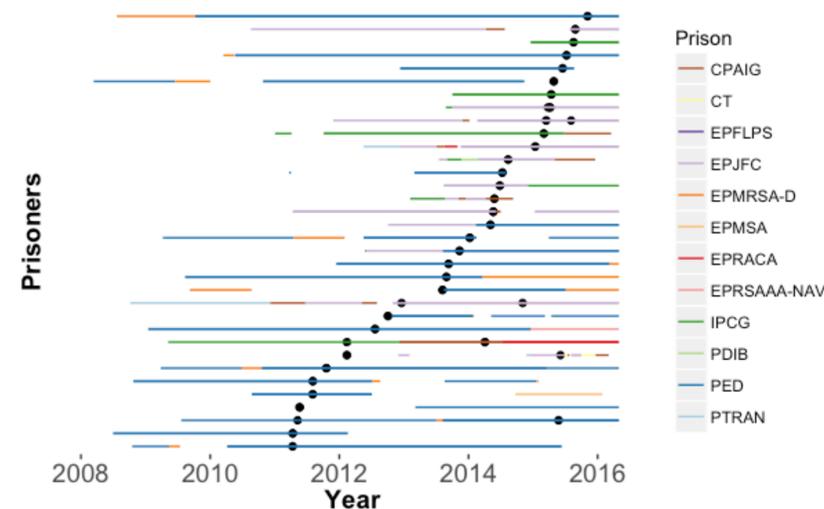


Figure 1: Prison-level temporal record of prisoner movement with date of TB notification. For each prisoner, the horizontal line indicates the time incarcerated with the color corresponding to the prison. The dot indicates date of TB notification. Data on TB diagnosis was collected from five prisons, while prisoner movement records was available for prisons from the entire state.

Molecular analysis of TB in prisoners and community

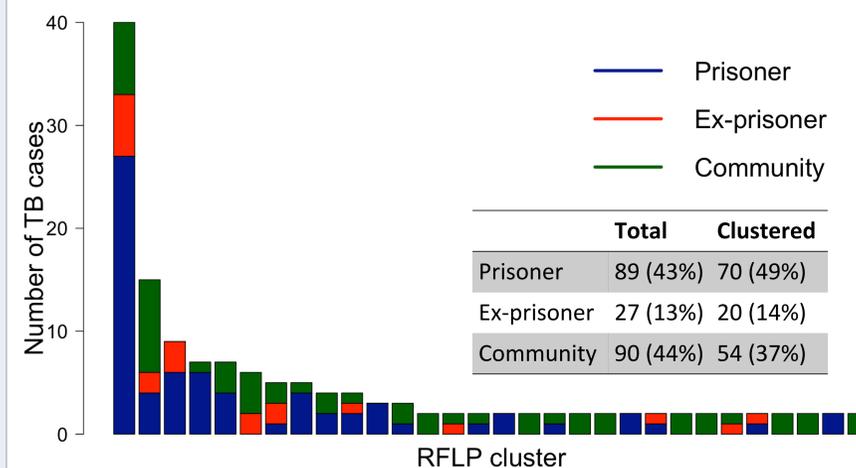


Figure 2: RFLP-defined TB clusters frequently involve prisoners, ex-prisoners and community members, with close phylogenetic relatedness in largest cluster. During the study period, 206 cases of TB were reported and genotyped in the municipality of Dourados. We identified 30 distinct clusters, with 70% of cases being classified within a cluster, suggesting linked transmission. The largest cluster included 40 new TB cases over seven years (28% of all cases), and when examined with whole genome sequencing showed a range of 6-30 single nucleotide variants, suggesting close phylogenetic relationship. **Notably, 40% of community cases were clustered with prisoner or ex-prisoner.**

Inference for potential transmission

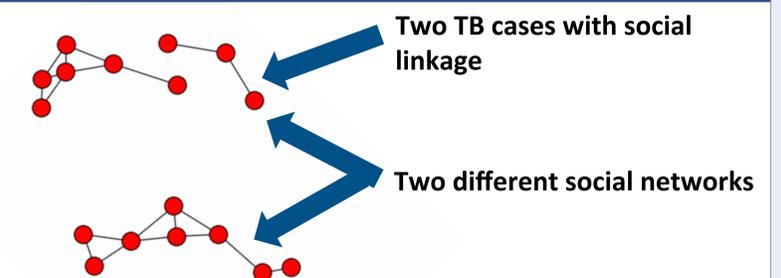


Figure 3: Social contact network within largest cluster. After assembling the full longitudinal record for prisoners from the largest cluster, we found 63% of new TB cases were exposed to a prisoner in the same block who was later diagnosed with TB, and 7.4% were exposed to a prisoner in the same cell who was later diagnosed with TB.

Future Work

- Whole genome sequencing of all TB isolates to perform phylogenetic study, in order to better inform the genomic relationship of the largest cluster.
- Combine genomics data with mathematical model of TB transmission to infer directionality in spread of disease, with a goal of quantifying the attributable fraction of prisons on community TB cases.

Conclusion

- We found sustained transmission of TB over a seven-year period within a Brazilian prisoner population that was **highly interconnected with the community epidemic**, validated by molecular and epidemiological data.
- The majority of cases were clustered, suggesting recent transmission, with a single strain representing 28% of all cases.
- **Efforts to control the TB epidemic in prisons are needed in order to address the TB burden in the community.**

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References

Sacchi FP et al. Prisons as reservoir for community transmission of tuberculosis, Brazil. *Emerg Infect Dis* (2015).