



TARGET TB: Understanding TB transmission dynamics in the context of rapid urbanization of Asia to optimally target interventions and accelerate the End-TB strategy

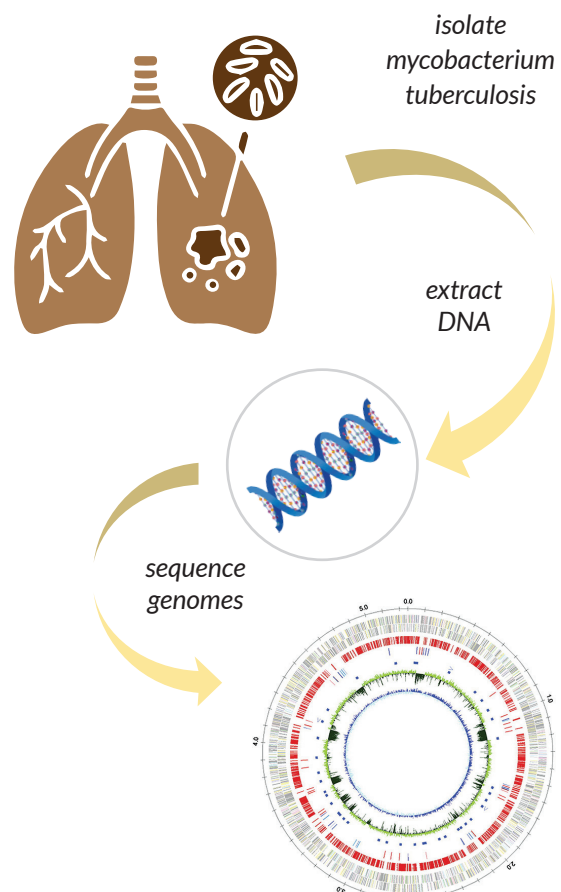


BACKGROUND

TARGET TB will use whole genome sequencing of TB isolates from three contrasting districts of Nepal (Kathmandu, Pyuthan and Banke) to understand how TB transmits within our communities and inform the development of more effective interventions for elimination. These areas represent different urban and rural environments. A better understanding of current TB transmission patterns in these different settings, and the relative contribution of cross border migration, reactivation of latent TB, drug resistance and strain virulence, will inform effective approaches to targeting resources for TB control in these areas, and serve as a model more broadly, in a rapidly urbanizing Asia. The project will be conducted by a consortium including BNMT, GENETUP, TB Nepal and the University of Melbourne (Australia) in collaboration with the NTCC. TARGET TB will collect 1,000 samples for whole genome sequencing to construct a phylogenetic tree of *Mycobacterium tuberculosis* circulating in the three districts and analyse this with international datasets. Target TB will be conducted from March 2021 to December 2023.

OBJECTIVES

1. Understand transmission of *Mycobacterium tuberculosis* in Nepal by characterizing pathogen genomic diversity, population structure, transmission dynamics and drug resistance in urban and rural areas of Nepal with high TB burden.
2. Compare the molecular epidemiology of tuberculosis in three contrasting districts of Nepal.
3. Capacity build resources for molecular epidemiology studies of pathogens including *Mycobacterium tuberculosis* in Nepal.





KEY INTERVENTIONS

- ▶ Active Case Finding for tuberculosis
Recruit patients and collect data, with informed consent, regarding diagnosis, treatment outcome, demographic and migration history.
- ▶ Culture bacterial isolates for DNA extraction
- ▶ Whole genome sequencing of 1,000 *Mycobacterium tuberculosis* isolates collected from patients with tuberculosis
- ▶ Combine patient and genomic data for bioinformatics analysis.
- ▶ Combine sequencing and epidemiology data with NTCC partners to understand detailed genomic epidemiology of TB in Nepal.
- ▶ Evidence briefs and dissemination meetings to translate evidence to policy interventions.

COLLABORATION

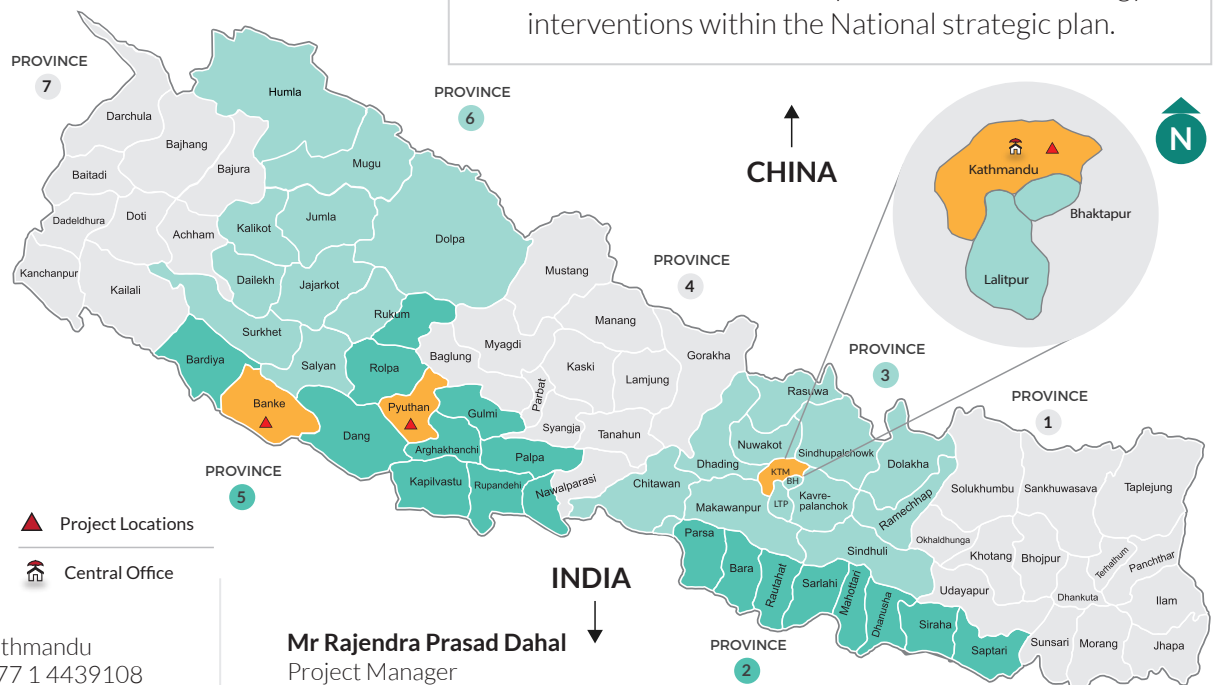
Funded by: Australian Health Medical Research Council (NHMRC)

Collaborator: University of Melbourne
Partners: Ministry of Health, National Tuberculosis Control Center, TB Nepal, NATA GENETUP, health offices, municipalities

EXPECTED OUTCOMES

- 250 additional TB cases identified and enrolled into treatment.
- Genomic structure of *Mycobacterium tuberculosis* population in Nepal determined.
- TB drug resistance mutations and prevalence mapped in three districts.
- Detailed understanding of population transmission of TB in different contexts of Nepal determined
- Strengthened capacity for molecular epidemiology studies within Nepal.
- Evidence to inform and optimize END-TB strategy interventions within the National strategic plan.

PROJECT LOCATIONS



▲ Project Locations

🏠 Central Office

Central Office

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