Oropharyngeal Microbiota and *Mycobacterium tuberculosis* Carriage Among Migrant Workers in Klang Valley, Malaysia

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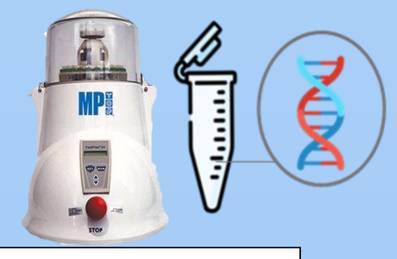
Background

Malaysia receives many economic migrants annually, primarily from Indonesia, Bangladesh, and Nepal (MoHA) - nations with a high incidence of tuberculosis (TB) (WHO, 2024). These migrants often reside in suboptimal accommodations, increasing their vulnerability to respiratory tract infections and TB (Loganathan et al., 2024). This study aimed **to investigate *Mycobacterium tuberculosis* (Mtb) carriage and characterize the oropharyngeal (OP) microbiota of migrant workers working in Klang Valley, Malaysia**.

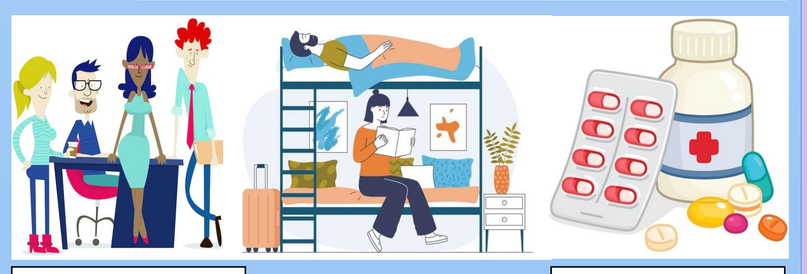
Methods

Sample collection



DNA extraction

Sample stratification based on:

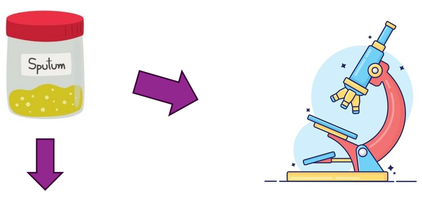


Work environment (domestic vs non-domestic

Room-occupancy (shared vs single)

Antibiotic intake six months prior (no vs yes)

Objective 1

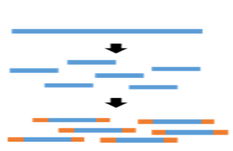


AFB staining and detection

Culture

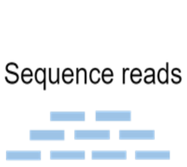
Confirmatory testing by LabLink

Objective 2



Library prep for 16SNGS (16S rRNA next-gen sequencing)

Illumina NovaSeq 6000 (2x150bp)



Bioinformatics and statistical analysis

Results

Out of 258 sputum sample collected, **257** available for AFB staining and culture. **No AFB bacteria detected from sputum samples**.

Sputum colony **culture** of LJ shows **six** different morphologies:

Type 1

Type 2

Type 3

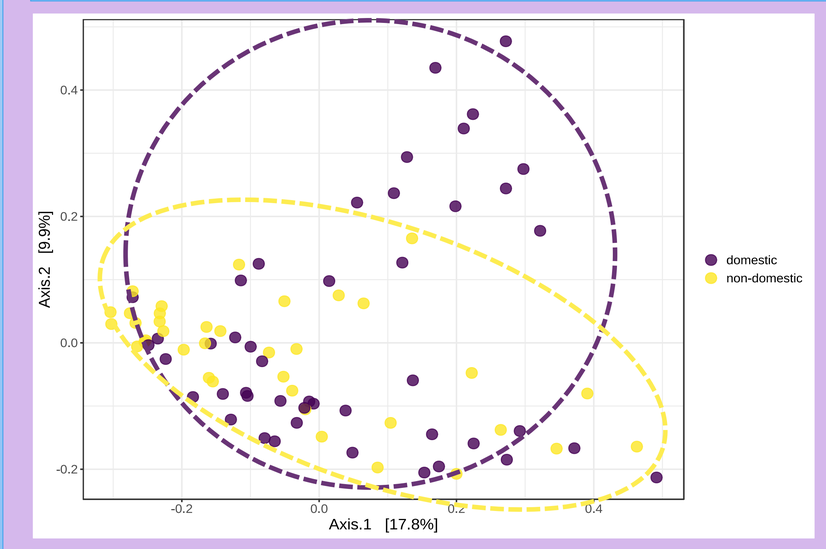
Type 4

Type 5

Type 6

AFB staining shows **Type 2 (light pink)** and **Type 6 (light brown)** positive for AFB. **NTM isolated from Type 6. No Mtb was detected**.

16SNGS revealed **no significance** in **alpha diversity across tested variables**, with *Streptococcus* spp., *Rothia* spp., *Pauljensia* spp., *Granulicatella* spp., and *Neisseria* spp., being the **top five common bacterial genera** found **across variables** – showing remarkable stability in OP microbiome.



Beta-diversity analysis reveals a **statistically significant difference** (p=0.006) **between work environment**; however, the **effect size** is **small** (R^2=0.027).

Most statistically significant abundant bacterial species across variables:
Work environment: *Streptococcus parasanguinis* (p-value: 0.01)
Room-occupancy: *Granulicatella elegans* (p-value: 0.043)
Antibiotic intake: *Porphyromonas pasteri* (p-value: 0.043)

Discussion & Conclusion

- **No active TB detected among study participants**
  - Stringent work pass requirements during annual health screening by the Malaysian government. (Mohd. Dan et al., 2020)
- **OP microbiota shows remarkable stability**
  - **No significant differences** according to room-occupancy and *antibiotic use six months prior*; dominated by commensal species (e.g.: *Streptococcus* spp., *Rothia* spp.) (Bach et al. 2021; Odendaal et al., 2024).
- **Beta-diversity** according to work environment **significantly different (small effect size)**
  - **Occupation might affect OP microbiota** (Zhang et al., 2022; Druzhinin et al., 2022; Wei et al., 2024).
- **No Mtb/NTM at species level (16SNGS)** and **no sign of TB associated microbial dysbiosis**
  - Molecular evidence against active TB carriage within the population (Ticlla et al. 2021).
- **No significant bacterial species abundance change based on room-occupancy alone**
  - **Work place** has **greater impact than shared living quarters** (Enh et al. 2024).

Future recommendations

Research could be expanded to include undocumented migrants and high-risk locations like Sabah, Malaysia. Additional confounders such as participant oral health status and smoking habits could also be added to gain a more comprehensive understanding towards OP microbiota in the migrant population.

Acknowledgements

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Reference