

# Identification of Non-Tuberculosis Mycobacteria as the cause of Pulmonary Disease Using Nanopore Sequencing with MLSTverse Analysis and MALDI-TOF

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## Introduction

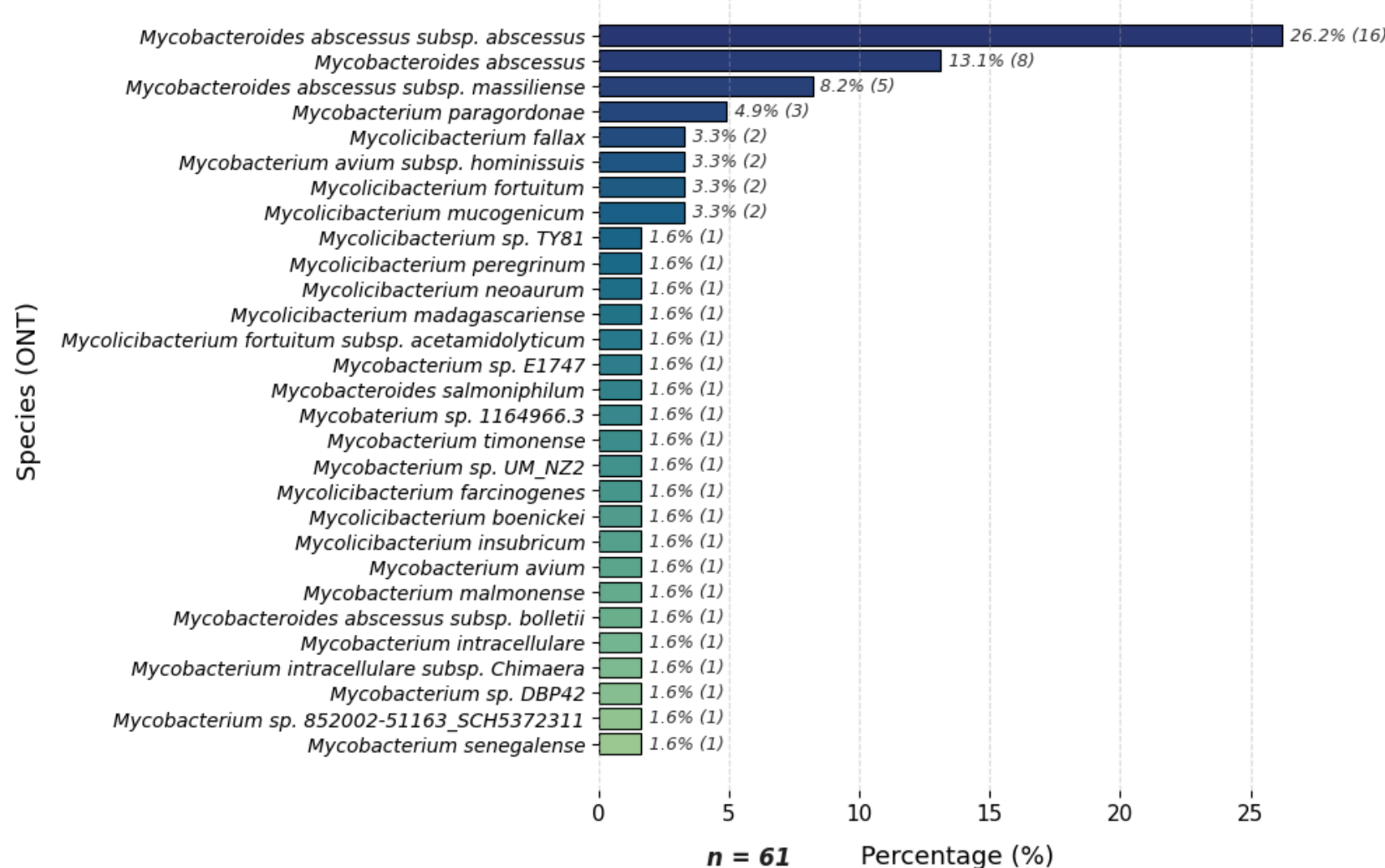
In Indonesia, lung infections caused by nontuberculous mycobacteria (NTM) are increasingly common, particularly among people with lung infections and weak immune systems. These infections are often misdiagnosed as tuberculosis (TB), thus leading to treatment delays that worsen patient outcomes. Species identification of NTM can help clinicians in Indonesia's hospitals start treatment sooner, improving care and reducing the spread of these serious infections. This study aims to identify NTM species causing pulmonary disease using Nanopore sequencing with MLSTverse analysis and to compare the results with MALDI-TOF identification.

## Method

## Results

A total of 61 clinical isolates were analyzed by Nanopore sequencing. Among these, sequencing successfully identified 37 of 61 isolates (60.7%) at the species level and 24 of 61 isolates (39.3%) at the subspecies level. MLSTverse analysis (mlstdb.NTM, 184 genes) revealed *Mycobacteroides abscessus* as the dominant species (30/61; 49.18%), primarily *M. abscessus subsp. abscessus* (16/61; 26.2%) and *subsp. massiliense* (5/61; 8.2%). Identification using MALDI-TOF was performed on 17 isolates, and 16 of them (94.1%) showed results consistent with sequencing, confirming the reliability of both methods.

### Distribution of Species Percentage



## Conclusion

MinION with MLSTverse and MALDI-TOF have significant implications for addressing Indonesia's NTM-PD burden, offering a rapid, scalable diagnostic tool that supports personalized medicine and public health surveillance in resource-limited settings.

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