Metagenomics data of *Mycobacterium* species isolated from soil in Thailand; a possibility for pathogenesis?

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Abstract

*Mycobacterium* species are important groups of bacteria that can be seen worldwide. Some species are documented as pathogens in humans. *Mycobacterium* species are isolatable from clinical specimens. Additionally, they can be isolated from environment. The metagenomics data on *Mycobacterium* species is useful for clinical epidemiological surveillance in each setting. Here, the authors summarize the metagenomics data of *Mycobacterium* species isolated from soil in Thailand. Based on this study, some isolated species are possible pathogenic and might be the cause of new emerging infection in Thailand.

Keywords: Soil, *Mycobacterium*, Metagenomics


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Introduction

*Mycobacterium* species are important groups of bacteria that can be seen worldwide. Some species are documented as pathogens in humans. *Mycobacterium* species are isolatable from clinical specimens. Additionally, they can be isolated from environment (1). The study on *Mycobacterium* species or other bacteria in environment is interesting. The metagenetic and metagenomics are important medical sciences regarding the environmental microbial. Zhang et al detected that the correlation between infectious disease and the modification of the microbiome may lead to better controlling of disease development in the future (2).

For *Mycobacterium*, the metagenomics study is also useful (3). However, the important problem is the lack of big data due to the little interesting on this kind of research (3). In fact, the metagenomics data on *Mycobacterium* species is useful for clinical epidemiological surveillance in each setting.

Objectives

Here, the authors summarize the metagenomics data of *Mycobacterium* species isolated from soil in Thailand.

Materials and Methods

This work is an informatics study. First, the authors performed nucleic acid searching from PubMed for metagenomics nucleotide of *Mycobacterium* species isolated from soil in Thailand. Only the sequences of species confirmed by standard culture are included for further analysis. The derived species are listed, collected and compared with the available data to search for the possibility of pathogenesis. The research followed the Tenets of the Declaration of Helsinki.

Results

According to the literature search, there are at least seven identified metagenomics data of four *Mycobacterium* species (*M. septicum*, *M arupense*, *M. pallens* and *M. neoaurum*) isolated from soil in Thailand as shown in Table 1. The possibility of pathogenesis of each isolated, based on available clinical evidence, is also presented in Table 1.

Discussion

*Mycobacterium* species are important groups of bacteria. Due to the possibility that some species can cause disease, the study on those species is very important. *Mycobacterium tuberculosis* is the most important species that can cause tuberculosis. For other non- tuberculosis species, some are already confirmed for pathogenicity. In general, the bacteria can be seen in environment. The contamination of bacteria in environment is interesting since it might be the source of infection.

In soil, the contamination of *Mycobacterium* species is possible. The study on environmental sample is useful.
This kind of study has been done worldwide for many years. In Thailand, a tropical country where tuberculosis is endemic, this kind of study is also done. In a previous report, *Mycobacterium* species could be isolated from water (4). Due to the advanced molecular microbiology at present, the metagenetic study on environmental sample is possible. Here, the authors analyzed the data on the metagenomics study of *Mycobacterium* species isolated from soil in Thailand. It can be seen that there are many isolated species. Nevertheless, there are no tuberculous species. Of interest, some species are the species that are already confirmed as pathogens for new emerging diseases in several countries around the world (5-7).

### Conclusion

Based on this study, some isolated species are possible pathogenic and might be the cause of new emerging infection in Thailand.

### Table 1. Metagenomics data of *Mycobacterium* species isolated from soil in Thailand

<table>
<thead>
<tr>
<th>Identified nucleotide</th>
<th>Accession number</th>
<th>Pathogenesis possibility</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mycobacterium septicum strain ATCC 700731</td>
<td>JQ899250.1</td>
<td>Yes</td>
</tr>
<tr>
<td>Mycobacterium arupense strain AR30097</td>
<td>JQ899239.1</td>
<td>Yes</td>
</tr>
<tr>
<td>Mycobacterium septicum strain ATCC 700731</td>
<td>JQ899228.1</td>
<td>Yes</td>
</tr>
<tr>
<td>Mycobacterium pallens strain czh-8</td>
<td>JQ899245.1</td>
<td>No</td>
</tr>
<tr>
<td>Mycobacterium arupense strain AR30097</td>
<td>JQ899235.1</td>
<td>Yes</td>
</tr>
<tr>
<td>Mycobacterium pallens strain czh-8</td>
<td>JQ899232.1</td>
<td>No</td>
</tr>
<tr>
<td>Mycobacterium neoaurum strain BAa11</td>
<td>KX897172.1</td>
<td>Yes</td>
</tr>
</tbody>
</table>

### Implication for health policy/practice/research/medical education

Some *Mycobacterium* species might be the cause of new emerging infections in Thailand.

### Authors’ contribution

Both authors wrote the manuscript equally.

### Conflicts of interest

The authors declared no competing interests.

### Ethical considerations

Ethical issues (including plagiarism, misconduct, data fabrication, falsification, double publication or submission, redundancy) have been completely observed by the authors.

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### References