Junior Science Communications
Faculty of Applied Sciences, UiTM Shah Alam
https://journal.uitm.edu.my/ojs/index.php/JSC

E-ISSN 2637-0689
Vol 55, 2025

Colloquium on Applied Sciences 2 2025
20-24 January 2025, Faculty of Applied Sciences, UiTM Shah Alam, Malaysia

In Silico Analysis of Uncharacterized Proteins Expressed in *Mycoplasma pulmonis*

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Structured Abstract

Background: *Mycoplasma pulmonis* is a pathogenic bacterium that causes respiratory disease in rodents and is characterized by its minimal genome and lack of a cell wall. Despite its significance as a model for human respiratory infections, many of its proteins remain uncharacterized. These proteins are of considerable interest for novel drug and vaccine development, as current treatment options are limited. This study aims to analyze the functions and physicochemical properties of uncharacterized proteins in *M. pulmonis* and evaluate their potential as drug or vaccine targets.

Methods: A total of 150 uncharacterized proteins were retrieved from the UniProtKB database for this study. To ensure the reliability of subsequent predictions, only protein sequences longer than 100 amino acid residues were included. Functional annotation was performed using Gene Ontology tools to predict biological pathways and molecular functions. Subcellular localization was predicted with PSORTb, and physicochemical properties were assessed using ProtParam. Transmembrane proteins identified by TMHMM (Transmembrane Helices Hidden Markov Model) were selected for drug target screening. Potential drug targets were evaluated based on criteria of non-homology to host proteins (determined by BLASTp), essentiality (from the Database of Essential Genes), antigenicity (predicted by VaxiJen), and involvement in protein-protein interaction networks (analyzed via the STRING database).

Results: The majority of the retrieved proteins were predicted to be involved in metabolic pathways and binding activities. Thirty-one of these were identified as transmembrane proteins that were non-homologous to the host, essential to the pathogen, and antigenic, making them ideal candidates for drug targeting. The top three candidate proteins (ABC transporter permease protein [Q98RI2], ATP synthase [Q98QT9], and Spermidine/putrescine ABC transporter permease protein [Q98QE3]) were notable for their high number of functional protein-protein interactions.

Conclusion: The findings of this study highlight the potential of uncharacterized proteins as novel drug targets for combating *M. pulmonis* infections. This *in silico* analysis provides a framework for guiding future experimental validation and facilitating drug or vaccine development.

Keywords: *Mycoplasma pulmonis*, Uncharacterized proteins, Drug target

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