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Characterisation of Potential Drug Targets of Mycobacterium Tuberculosis for the Development of Antitubercular Agents

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ABSTRACT

Introduction: Tuberculosis is thought to be the deadliest airborne infectious disease in the world, which vividly ranges from being asymptomatic to a death-causing disease. The treatment landscape has become even more challenging with the emergence of extensive drug resistance and multidrug resistance in tuberculosis.

Aim: Biotin metabolism appears to be an important pathway which plays an essential role in Mtb's survival, persistence and bacterial immunity, providing an alternative anti-TB drug target. Two BioH isoenzymes (BioH1 and BioH2) are reported to be involved in Biotin synthesis in Mycobacterium Tuberculosis as well as other Mycobacterium species.

Materials and Methods: In this study, BioH genes will be isolated from the genomic DNA of Mtb H37RV and cloned into Escherichia coli XLB1 cells using the pET28c vector. The successfully transformed E. coli cells will be cultured in LB media in IPTG at various temperature conditions to check for the protein expression and localisation. A rapid purification procedure for the protein, based on affinity chromatography, will be developed. The purified protein will be judged by SDS/polyacrylamide gel electrophoresis, and all its properties will be depicted by gene sequencing. Mutational analysis of BioH1 and BioH2 genes will be done to identify catalytic residues.

Results: We aim to purify BioH1 and BioH2 proteins for further analysis. The secondary structure of the protein will be developed on the basis of homology modelling, predicting the boundaries of protein domains and provide additional functional annotation of the protein.

Keywords: Affinity chromatography, Drug targets, Tuberculosis treatment

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