

In-Silico Characterization of Rv1477 Gene Product from Mycobacterium Tuberculosis †

Dasari Manoj ¹, Neesar Ahmed ^{1,*}

¹ School of Life Sciences, B S A Crescent Institute of Science and Technology, Vandalur, Chennai-600048, Tamil Nadu, India

* Correspondence: neesar.sls@crescent.education;

† Presented at Virtual symposium to observe World Antimicrobial Awareness week “Applications of biotechnology and microbiology with special emphasis on Antimicrobial resistance”, 18-24 November 2020, Chennai, India

Received: 10.11.2020; Revised: 15.11.2020; Accepted: 17.11.2020; Published: 10.01.2021

Abstract: Mycobacterium tuberculosis is an etiological agent of tuberculosis, which is the leading cause of the top 10 deadly infections. It is estimated that 10 million people fell ill with tuberculosis. One of the sustainable development goals includes ending tuberculosis by 2030. So, there is a need for a better understanding of *Mtb*. When we look deep into the pathogenicity of *Mtb*. after entering the alveolar sac, they invade and replicate in the endosomes of macrophages. Before entering the endosome, bacteria attach to the surface membrane of the macrophage and make necessary modifications using membrane proteins secreted by *Mtb*. bacteria have developed many mechanisms to enter human macrophages in which caveolae-mediated endocytosis is one method. Around 300 membrane genes are found to date in *Mtb* but; many functions of them are unknown. From them, 15 genes are shortlisted based on virulence. Rv1477 (*ripA*) is a gene whose function is unknown. The Present study mainly concentrates on in-silico characterization of Rv1477 gene product.

Keywords: *Mtb*; Caveolae; pEt28a; RV1477; *In-silico* characterization; RV1477.

© 2021 by the authors. This article is an open-access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<https://creativecommons.org/licenses/by/4.0/>).

Funding

This research received no external funding.

Acknowledgments

This research has no acknowledgment.

Conflicts of Interest

The authors declare no conflict of interest.