Chander et al. (2017) Can J Biotech, Volume 1, Special Issue, Page 131
https://doi.org/10.24870/cjb.2017-a117

Canadian Journal of Biotechnology

ISSN 2560-8304

Poster Presentation **OPEN ACCESS**

Category: Metagenomics

Comparative genomic analysis of *Mycobacterium immunogenum* strain CD11_6, a new potential vaccine strain against *Mycobacterium tuberculosis*

Atul Munish Chander[1], Gurpreet Kaur[2], Gurwinder Kaur[3], Sudeep Kumar Maurya[2], Sajid Nadeem[2], Rakesh Kochhar[4], Devinder Kumar Dhawan, Sanjay Kumar Bhadada[5*], Javed N Agrewala[2*] and Shanmugam Mayilraj[3*]

[1]Department of Biophysics, Panjab University, Chandigarh, INDIA

[2]Immunology Laboratory, CSIR-Institute of Microbial Technology, Chandigarh, INDIA

[3]Microbial Type Culture Collection and Gene bank (MTCC), CSIR-Institute of Microbial Technology, Chandigarh, INDIA

[4]Department of Gastroenterology, Post Graduate Institute of Medical Education and Research, Chandigarh, INDIA

[5]Department of Endocrinology, Post Graduate Institute of Medical Education and Research, Chandigarh, INDIA

[*]Corresponding authors: bhadadask@rediffmail.com, javed@imtech.res.in, mayil@imtech.res.in

Abstract

Mycobacterium tuberculosis (*Mtb*) infection is a growing challenge to the scientific world due to drug resistance. In this study, we predicted safety, efficacy and the molecular basis for the potential of strain *Mycobacterium immunognum* (*Mi)* as a vaccine strain against *Mtb* that in some preliminary experiments had reduced the bacterial counts of *Mtb* in infected organs of mice during immunization studies along with generation of memory CD4 T cells and CD8 T cells. *MI* strain CD11_6 was an isolate from duodenal mucosa of a celiac disease patient that was characterized and sequenced. Rapid Annotation using Subsystem Technology (RAST) server was used to annotate, and identify the virulence determinant genes and other features that make it a potential vaccine candidate. Genome of *Mtb* strain H37Rv and its vaccine strain *Mycobacterium bovis* (*Mb*) AFF2122/97 was also retrieved from genome database of NCBI and compared with *Mi*. Virulence determinant genes of *Mi* were mapped and compared with virulent *Mtb* strain H37Rv and strain *Mycobacterium bovis* (*Mb*) AFF2122/97. This comparative analysis revealed that *Mi* is less virulent as compared to *Mb* and *Mtb* whereas *Mi* contains comparable number of genes coding for antigenic surface membrane proteins, membrane transport proteins and cytosolic proteins that predicts its probable vaccination attributes against *Mtb*. Further, sequence alignment results and exploring predicted proteome of the strain CD11_6 also indicates that it has potential candidate vaccine peptides belonging to membrane proteins of *Mtb*.

The study signifies that *Mi* strain CD11_6 has sufficient antigenic repertoire that might have led to activate memory T cells against *Mtb* and causing its eradication. Our further work on this line to validate the role of reported surface membrane proteins may help to know about molecular basis for action of *Mi* that will improve the present vaccination strategies against *Mtb.*

Citation: Chander, A.M., Kaur, G., Kaur, G., Maurya, S.K., Nadeem, S., Kochhar, R., Dhawan, D.K., Bhadada, S.K., Agrewala, J.N. and Mayilraj, S. Comparative genomic analysis of *Mycobacterium immunogenum* strain CD11_6, a new potential vaccine strain against *Mycobacterium tuberculosis* [Abstract]. In: Abstracts of the NGBT conference; Oct 02-04, 2017; Bhubaneswar, Odisha, India: Can J biotech, Volume 1, Special Issue, Page 131. https://doi.org/10.24870/cjb.2017-a117