OPEN ACCESS

Int. Res. J. of Science & Engineering, 2013, Vol. 1(3):90-91 ISSN: 2322-0015

RESEARCH ARTICLE

Computational Genome analysis of Hypothetical Protein in *Mycobacterium laprae* TN For Therapeutic Drug Target Identification

Anjum Sumaira

Department of Zoology, Govt. Vidarbha Institute of Science and Humanities, Amravati – 444604 (MS) India

Address for Correspondence email: sumairaanjum01@gmail.com

ABSTRACT

Mycobacterium laprae Bacteria were selected .In this bacteria hypothetical protein were selected . The present study is aimed at predicting the 3-dimensional structure of Acyl-CoA Synthetase protein in M.leprae, which play a pivotal role in fatty acid metabolism and to find the active site of the protein, which is used as a strategy in drug design. The study was done by using different Bioinformatics tools. In silico differential genomics helps to identify genes that encode for unique metabolism with relation to human. The genomic database provides a vast amount of useful information for the drug target identification. The study revealed that Acyl-CoA Synthetase protein in M.leprae play an important role in fatty acid metabolism whose 3dimensional structure has not yet been solved. By confirming the structure of the modeled protein experimentally and knowing its active site helps in designing of effective Anti-Myobacterial drugs

KEYWORDS

Computational Genome analysis of Hypotetical Protein, homology modeling, *Mycobacterium laprae*

INTRODUCTION

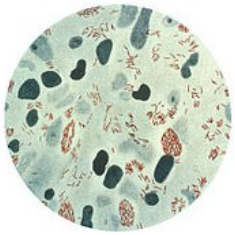
Leprosy, an infection caused by *Mycobacterium leprae*, primarily affects superficial tissues.The infection results in "Leprosy Reactions" characterized by irreversible nerve damage and disabilities. The drug is designed by analogue-based drug design using Dapsone, a widely used drug in leprosy, which creates many side effects during leprosy treatment. The ligand, (the analogue of Dapsone) thus designed has docked well in the active site region of the protein. The result indicates that the designed drug could have better action than the existing Anti-Myobacterial drug for Leprosy and could have lesser side effects.

Sasaki *et al.* (2001) stated that Leprosy, or Hansen's disease, is a chronic infectious disease caused by the bacterium *Mycobacterium leprae.* WHO (1995) suggests that Leprosy is primarily a granulomatous disease of the peripheral nerves and mucosa of the upper respiratory tract; skin lesions are the primary external symptom. Reich (1987) found that left untreated, leprosy can be progressive, causing permanent damage to the skin, nerves, limbs, and eyes. The clinical symptoms of leprosy vary but primarily affect the skin, nerves, and mucous membranes. Rees *et al.,* (1970) found that until the development of dapsone, rifampin, and clofazimine in the 1940s, there was no effective cure for leprosy. The search for more effective anti leprosy drugs to dapsone led to the use of clofazimine and rifampicin in the 1960s and 1970s.

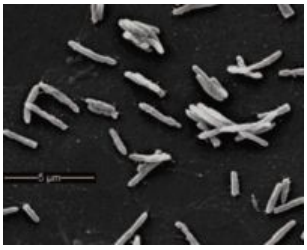
The target identification stage is the first step in the drug discovery process (Terstappen and Reggiani, 2001). Few studies have been reported about identification of drug targets by experimental as well as in *silico* methods from pathogens. Many of the predictions generated in silico by genomics have been validated through functional analysis, led to the identification of essential genes. Knowledge of the latter defines potential targets for new and existing drugs and their specificity can be assessed by comparative genomics with the host or other pathogens (Cole, 2002).

We selected such hypothetical *Mycobactyetium leprae TN* genes for potential therapeutic drug target. Use of bioinformatics approach and comparative analysis of the genome of a pathogenic microbe allows one to identify essential genes necessary for the survival of that pathogen. The proteins encoded by these essential genes, that are not present or are nonhomologous to the host, can be used as drug targets.

The goal of present study is to identify drug target proteins of leprosy bacteria *Mycobacterium leprae TN* .Leprosy is a global social health problem. According to WHO Reports, 228474 leprosy cases are reported in 2011. HIV patients are at high risk. Current treatment for leprosy is of larger duration (MDT). Dapsone, Rifampisin are the most potent drugs used in treatment of lepros. When more than one drug is used in combination, there is a high risk of its side effects.



Microphotographof *Mycobacterium leprae*, the small brick-red rods in clusters, taken from a skin lesion



Mycobacterium leprae

MATERIALS AND METHODS

Sequence retrieval:

The complete genome, genes and protein sequences of *Mycobacterium leprae* TN were retrieved from the NCBI (National Center for Biotechnology Information) The National Center for Biotechnology Information (NCBI) is part of the United States National Library of Medicine (NLM)

Sequence alignment:

The Hypothetical proteins were searched for Essentiality. The selected proteins are subjected to similarity Search against essential proteins of database of essential genes(http://tubic.tju.edu.cu/deg) .) by using E value cut off 0.0001 .The selected essential proteins are subjected to Blastp (http://www.ncbi.nlm.nih.gov /blast) against Human proteins to identify non-homologue . E value cut off .0001(Altschul S 1990).

The sequenced genome database were used to compare every protein coding gene with essential genes of DEG Database.Selected essential genes compared with human genome especially all proteins in *Homo sapiens.*

RESULTS AND DISCUSSION

Analysis of hypothetical proteins by web tools Although experimental & computational methods have been previously employed for the study of essential genes to our knowledge this is the first report identification of essential genes from hypothetical proteins of *Mycobacterium leprae* TN computationally.We identified 496 essential genes from total 604 hypothetical proteins by computational genomic approach.When these genes are searched against human homolog by using BLASTp with e value 0.0001 . By rejecting homolog proteins 108 non human homlog proteins are selected for further study.Proteins with Amino acids greater than 100 are good target, hence from 108 proteins we have selected only 90 proteins as therapeutic target protein.

REFERENCES

1. Altschul SF, Gish W, Miller W et al. Basic Local Alignment Search tool, *J Mol Biol*; 1990; 215(3): 403-410 .
2. Cole ST. Comparative mycobacterial genomics as a tool for drug target and antigen discovery, *Eur Respir:* Suppl. 2002; 36, 78s–86s .
3. Rees RJ, Pearson JM and Waters MFExperimental and clinical studies on rifampicin in treatment of leprosy. *Br Med J.,*1970; 1(5688) : 89-92.
4. Reich CV "Leprosy: cause, transmission, and a new theory of pathogenesis". *Rev. Infect. Dis.*, 1987; 9 (3):590-4.
5. Sasaki S, Takeshita F, Okuda K, Ishii N Mycobacterium leprae and leprosy: a compendium". *Microbiol Immunol.,* 2001; 45 (11): 729-36.
6. Terstappen GC, Reggiani AIn silico research in drug discovery. *Trends Pharmacol Sci* 2001; 22(1):23-6.
7. WHO Leprosy disabilities: magnitude of the problem". *Weekly Epidemiological Record,* 1995; 70 (38): 269-75.

Cite this article as: Anjum Sumaira. Computational Genome analysis of Hypotetical Protein in *Mycobacterium laprae TN* For Therapeutic Drug Target Identification**,** *Int. Res. J. of Sci. & Engg.*, 2013; 1(3): 90-91.

Source of Support: Nil**,** **Conflict of Interest:** None declared