

Draft Genome of *Mycobacterium Leprae* Strain 7935681

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Opinion

Volume 1 Issue 2

Received Date: November 11, 2017

Published Date: November 28, 2017

Abstract

We report the assembled draft genome of *Mycobacterium leprae* strain 7935681 using HiSeq 2000. The genome size obtained was 3.27 Mb. Based on the gene prediction, total genes identified were 5,128, which includes CDS, tRNA and rRNA.

Opinion

Mycobacterium leprae infection causes human leprosy. Leprosy is a chronic disease caused by a slow multiplying bacillus, *Mycobacterium leprae*. This mainly affects skin, damages nerve respiratory tract, eyes and eventually permanent disability [1]. Leprosy is known to occur at all ages ranging from early infancy to very old age. *M. leprae*, has a unique host cell tropism which infects and grows with in Schwann cells surrounding the axons of nerve cells. This tropism is considered to contribute to the pathology of leprosy. The biggest challenge is the fact that *M. leprae* cannot be cultured by normal methods. On a more positive note, the genome of *M. leprae* has been sequenced [2].

Whole genome sequencing of *M.leprae* strain 7935681 was carried out using HiSeq 2000 with 2x100 bp chemistry. The raw data generated was quality filtered using Trimmomatic v 0.35 [3]. High quality reads were assembled using AbySS (Version: 1.5.2) [4] and SSPACE (Version: 3.0) [5] generating 112 scaffolds with an assembly size of 3.27 MB and N50 of 46,192 bp as shown in Table 1. This assembly was found to be the first assembly submitted in NCBI for the strains of *M.leprae* strain 7935681. The genome showed 57.7 % of G+C. The annotation was carried out using RAST server [6]. Total of 5,080 coding genes were predicted with 48 RNA genes which includes, 3 rRNA and 45 tRNA.

Assembly statistics	
Genome assembly size (Mbp)	3.27
Sequencing read coverage depth (fold)	200X
Number of scaffolds	112
avg scaffold	29266
Scaffold N50 (bp)	46192
Max scaffold size (bp)	257291
Min scaffold size (bp)	1508
Annotation statistics	
Number of genes	5128
Average gene length (bp)	434.8
CDS	5046
rRNA	3
tRNA	45

Table 1: *M.leprae* strain 7935681 genome features

Genomics has provided insights into the genes, pseudogenes and genetics of *M. leprae*, and its human host. Our future work is to find the phylogenetic placement of this strain. In order to challenge the phylogenetic model it's important to sequence more *M. leprae* genomes. The availability of a genome sequence may also be informative in terms of further defining the core gene set of a pathogenic mycobacterium and in retracing the proposed common history with *M. leprae* [7].

Accession Number and Availability of the Genome Sequence and the Strain

The Mycobacterium leprae 7935681 whole genome shotgun (WGS) project has the project accession LVXE00000000. This version of the project (01) has the accession number LVXE01000000, and consists of sequences LVXE01000001-LVXE01000107.

Acknowledgement

This work is supported and funded by Eurofins Genomics India Pvt Ltd.

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