

# 2<sup>nd</sup> International Conference on Epidemiology & Evolutionary Genetics

August 18-19, 2014 DoubleTree by Hilton Beijing, China

## Finding mutational sites in drug resistant strain of *Mycobacterium tuberculosis*

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*Mycobacterium tuberculosis* is an acid-fast bacterium that is responsible for causing tuberculosis. The new strains that are evolving with time are resistance to drugs currently being used for tuberculosis treatment. The study was focused on locating mutational sites of a new strain, *Mycobacterium tuberculosis*, using next generation sequencing techniques. *In-silico* genome assembly had been done to find out conserved and divergent regions of reference strains. The sequence data of the new strain was derived from public database, analyzed and assembled using both *de-novo* and mapping methods. The assembled sequence compares reference genome followed by gene prediction and analysis. The newly found genome is aligned with annotated reference genome to retrieve mutational sites in the new strain. The new strain shows several numbers of mutation sites at or nearby exon regions that can cause resistance to drug treatment.

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