

Mycobacterium tuberculosis genomic information through the whole genome sequencing analysis



Background

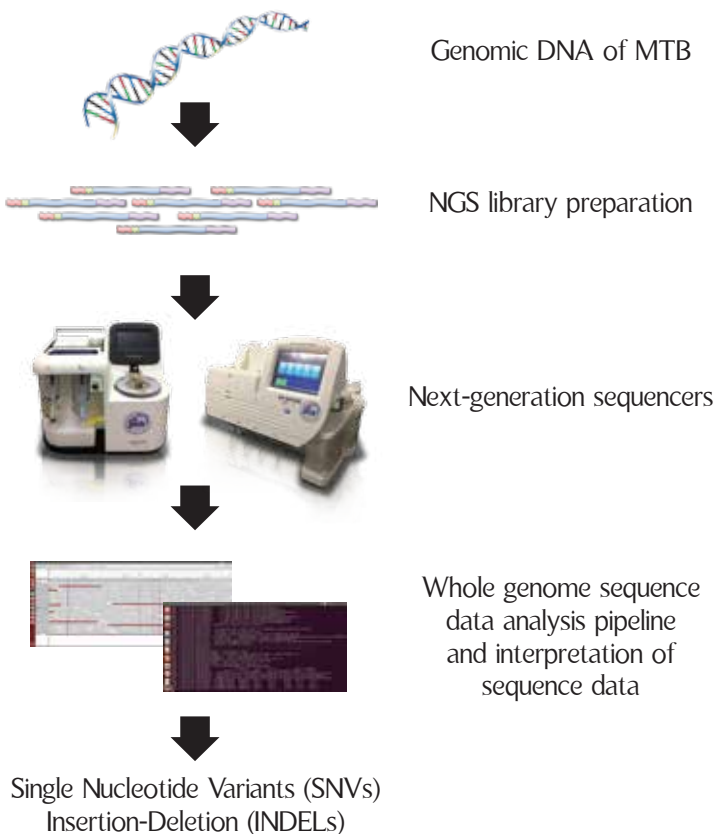
Thailand faced a high burden of tuberculosis with 117 (69-176) thousands tuberculosis patients with 7% mortality rate in 2015 (WHO 2016).

What is a causative agent of tuberculosis?

Mycobacterium tuberculosis (MTB) is a bacterium that causes tuberculosis. There are diversities in strain, drug susceptibility and virulence which can be determined through genomic information.

MTB genome consist of 4.4 million bases pairs. With the available of next-generation sequencing (NGS) technology, the whole genome sequence data of MTB can be obtained within 2 to 3 days.

Methodology



Output

Strains identification:

Genetic diversity information derived from single nucleotide variants (SNVs) and insertion-deletion (INDELs) sequence provide a highest power for strain differentiation of MTB for diagnosis and epidemiology.

Anti-tuberculosis drugs susceptibility:

The SNVs on drug resistance-related genes provide information to identify genetic polymorphisms which are useful for the simultaneous determination of resistance to first-line and second-line anti-tuberculosis drugs.

Virulence-related polymorphisms:

The wide ranges of genetic variants on virulence-related genes provide evidence for further determination of the effect on virulence phenotypes.

Outcome

Established pipeline for laboratory procedures and data analysis of whole genome sequence of MTB is valuable to tuberculosis control in Thailand, in order to effectively monitoring community transmission and outbreak investigation, shorten time to detect extensively drug-resistant tuberculosis and reveal genetic factors that may affect unfavorable treatment outcome.

Impact

The implementation of genomic information of MTB shall strengthen tuberculosis control in Thailand with the early detection of extensively drug-resistant tuberculosis and provide the guidance to pursue outbreak investigation to contain tuberculosis outbreak.