

ABSTRACT

ANALYSIS OF NUCLEOTIDE SEQUENCES OF 16S rRNA *Mycobacterium tuberculosis Complex* (MTBC) FROM SPUTUM OF PULMONARY TB PATIENTS

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Tuberculosis is infectious disease which was caused by the member of pathogenic bacteria group *Mycobacterium tuberculosis Complex* (MTBC). This study was aimed to analyze nucleotide sequence of 16S rRNA gene from MTBC group isolated in pulmonary tuberculosis patient sputums. Sequencing results was compared to sequences of *Mycobacterium tuberculosis* strain H37Rv (wildtype) to determine species homology. MTBC species homology hopefully could be used as information for the benefit of pulmonary tuberculosis molecular epidemiology.

This study used sputum samples of pulmonary TB patients from TB clinic, Dr. Soetomo General Hospital, Surabaya collected from September to November 2016, amounted up to 96 samples. Methods used includes smear BTA staining, microbe culture, rapid test, and molecular method, such as 16S rRNA gene amplification as used in this study to determine bacterial nucleotide sequences from pulmonary TB, in order to analyze bacterial homology to different virulent strain of *Mycobacterium tuberculosis* (strain H37Rv).

The samples with positive PCR and positive culture results were proceeded to the next stage of sequencing. Sequences obtained from genotyping 16S rRNA gene in sputum of pulmonary TB had 70-76% homology to the MTBC strains gene from the Gene Bank. Percentage was caused by considerable variation in the regions suspected as the variable region.

Analysis of *Mycobacterium tuberculosis Complex* using 16S rRNA gene target could not be used yet as basis for determining MTBC group but this gene could be used for identification or phylogenetic analysis and nucleotides variation in variable region.

Keyword: Analysis of sequence, pulmonary tuberculosis, *Mycobacterium tuberculosis Complex*, 16S rRNA