ABSTRACT

Analysis of Nucleotide Sequence of esxA Gene of Mycobacterium tuberculosis from Sputum of Pulmonary RR-TB Patients

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This study aimed to analyze nucleotide sequences of esxA gene from sputum isolates in Rifampicin Resistant (RR-TB) patients and analysis of the severity class in RR-TB patients. Total 98 sputum samples of RR-TB suspect was collected from Dr. Soetomo Hospital, Surabaya from September until December 2016. RR-TB suspect patients with positive and rifampicin resistance result based on GeneXpert test were then tested using PCR and continue with sequencing process. The sequence data was processed using Bioedit program version 7.2.5 and NCBI BLAST. The severity of pulmonary TB patients was assessed using the modified TB Bandim method.

The results showed that average age of patients was 44.42 ± 12.68 years and dominated by male patients. The severity class pattern presented that moderate and severe degree was 62% and mild degree 38%. PCR results showed that all the 24 samples was positive and all samples that sequencing had 100% homolog with wild-type M. tuberculosis H37Rv (NC_000962.3) sequence and MTBC.

Prediction of T cells shows the presence of five T-cell epitopes in IAD Pattern Position and one T cell epitope CD4+ by Rothbard/Taylor Pattern position. From this research, it can be concluded that moderate and severe patient percentage was less than mild degree. Sequence result showed that there is no mutation in esxA gene of RR-TB patients

Keywords: esxA gene, RR-TB, Mycobacterium tuberculosis, Severity Class