ABSTRACT

MULTIPLEX PCR OF 16S rRNA, rv0577, RD9, mtbk_20680, lineage 1-6 GENE IS COMPLEMENTARY WITH PROFILE OF GENOTYPE rpoB GENE OF Mycobacterium tuberculosis PULMONARY TUBERCULOSIS PATIENT ISOLATES ON IDENTIFICATION OF SPECIES, STRAIN, AND RIFAMPICIN RESISTANCE IN JAVA ISLAND

Nastiti Intan Permata Sari

Objective: To classify the bacteria causing tuberculosis infection and also to identify gene mutations related with rifampicin resistance in Indonesia.

Material and Methods: A total of 110 isolates of pulmonary tuberculosis patients from Java Island, Indonesia, were collected from July 2017- October 2018. All samples were examined by molecular methods using specific gene amplification to identify species, strains, and gene mutation in the Mycobacterium isolates, while VNTR and qPCR were also used as methods to confirm species and strains identification.

Results: There were 60,9% Beijing strains and 39,1% non Beijing strains. In addition, identification using lineage analysis exists lineage 1: 0,9%; lineage 2: 57,3%; lineage 4: 37,3%; 3,6% mixed; 0,9% without SNPs; lineage 3, lineage 5, and lineage 6 were not found. The mixed strains and isolate without SNPs were continued to use VNTR and qPCR method for confirmation. Rifampicin resistance was confirmed by sequencing of rpoB gene (13,6%), and Asp435Phe mutations is firstly reported in Java Island.

Conclusion: The Beijing strains and also the rpoB gene mutation in codon 450 were most commonly found in Java Island.

Keywords:
Pulmonary tuberculosis, Mycobacterium tuberculosis complex isolates, species, strains, gene mutation, drug resistance