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Identification of *katG* and *inhA* Genes Mutation in *Mycobacterium Tuberculosis* on MDR TB Patients at Adam Malik General Hospital Medan Indonesia

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Background and Purpose: Multi Drug Resistant Tuberculosis is a major health problem in the world, the occurrence genes mutation of Mycobacterium tuberculosis causes resistance to anti tuberculosis drugs. KatG and inhA genes are the most common mutated genes that play a role in resistant to Isoniazid. In 2016 WHO recommended Shorter Term Regimens of MDR TB, that using high-dose Isoniazid. High-doses Isoniazid cannot be effective to be given if mutation occur in the katG gene. Mutation of inhA gene cause low level resistant, which means high-doses Isoniazid may be effective. The aims of this study are to identify katG and inhA gene mutations in MDR TB patients at H. Adam Malik General Hospital Medan, Indonesia.

Methods: This study was an observational study conducted from July-November 2019 on 30 MDR-TB patients. Samples was taken from the sputum of MDR TB patients that diagnosed by rapid molecular test (Xpert). Identification of *katG and inhA gene mutation on M.tuberculosis* was done by using Multiplex Polymerase Chain Reaction technique.

Results: From 30 MDR-TB patients, 23 (76.67%) mutation occur in only katG gene, single mutation in inhA gene was not found, combination of mutation katG and inhA genes found in 4 (13.33%) isolates.

Keywords: Multi Drug Resistant TB, Isoniazid, katG, inhA, PCR.

Biography:

Ikhsan is Resident of Pulmonology and Respiratory Medicine in Faculty of Medicine, Universitas Sumatera Utara, Medan, Indonesia. The high number of TB cases in Indonesia made him interested in conducting research on TB, especially drug resistant TB.

Speaker Publications:

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