

**Sarwan Adi Kusumo, 2018. Analisis Molekuler Gen *rpoB* *Mycobacterium tuberculosis* pada Pasien *Multidrug Resistant* Tuberkulosis (MDR-TB) di RSUD dr. Soetomo. Skripsi ini di bawah bimbingan Dr. Fatimah, M. Kes. dan M. Hilman Fuadil Amin, M. Si. Program Studi S-1 Biologi, Departemen Biologi, Fakultas Sains dan Teknologi, Universitas Airlangga, Surabaya.**

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### ABSTRAK

Penelitian ini bertujuan untuk mengetahui susunan basa nukleotida gen *rpoB* *Mycobacterium tuberculosis* pasien *multidrug resistant* tuberkulosis (MDR-TB) di RSUD dr. Soetomo, perbedaan urutan basa nukleotida dalam sampel, dan perbedaan urutan basa nukleotida sampel dengan *sequence* gen *rpoB* *M. tuberculosis* H37Rv dari *GenBank*. Sampel yang digunakan adalah sputum pasien terkonfirmasi MDR-TB oleh *GeneXpert* yang didapatkan dari RSUD dr. Soetomo yang didekontaminasi menggunakan metode *Modified Alkali Petroff* dan dilakukan isolasi DNA total dengan *Bacteria DNA Preparation Kit*. Gen *rpoB* *Mycobacterium tuberculosis* diamplifikasi dari DNA total menggunakan primer primer Pol B-5A dan Pol B-5B dan *My Taq™ HS Red Mix*. Produk hasil amplifikasi dielektroforesis untuk memverifikasi keberadaan fragmen gen *rpoB* *M. tuberculosis* sebesar 619 bp. *Sequence* hasil *sequencing* dianalisis menggunakan program *Geneious R11* dan *Basic Local Alignment Search Tool* (BLAST). Hasil *sequence* sampel *post trimming* gen *rpoB* *M. tuberculosis* memiliki ukuran 502-524 bp yang terletak pada basa ke 1281-1804. Keempat sampel *sequence* gen *rpoB* *M. tuberculosis* memiliki persentase kesamaan genetik 100% di dalam populasi sampel. Hasil konsensus *multiple sequence alignment* menunjukkan bahwa *sequence* gen *rpoB* *M. tuberculosis* sampel tidak memiliki urutan basa yang berbeda dengan *sequence* gen *rpoB* *M. tuberculosis* H37Rv, *complete genome* (*accession number* AL 123456.3, CP007027.1, CP009480.1, dan CP003248.2) yang merupakan *strain wild type* dan menjadi *reference sequence* dalam penelitian ini.

Kata kunci: *Multidrug resistant tuberculosis*, *Mycobacterium tuberculosis*, gen *rpoB*, RSUD dr. Soetomo

**Sarwan Adi Kusumo, 2018. Molecular Analysis of *Mycobacterium tuberculosis*' *rpoB* Gene of Multidrug Resistant Tuberculosis Patient in Soetomo Medical Facility. This thesis is under the guidance of Dr. Fatimah, M. Kes. and M. Hilman Fuadil Amin, M. Si. Undergraduate Biology Program, Biology Departement, Faculty of Science and Technology, Airlangga University, Surabaya.**

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***ABSTRACT***

This research aims to find out the base nucleotide sequence of *M. tuberculosis*' *rpoB* gene in multidrug resistant tuberculosis (MDR-TB) patient in Soetomo Medical Facility, the difference of the samples, and difference compared to *M. tuberculosis* H37Rv's *rpoB* gene from *GenBank*. Sample that was used in this research is confirmed as MDR-TB by *GeneXpert* which is acquired from Soetomo Medical Facility. The decontamination is using Modified *Alkali Petroff's* method and the total DNA of the sample was isolated with *Bacteria DNA Preparation Kit*. *rpoB* gene was amplified from the *M. tuberculosis*' total DNA with primer Pol B-5A dan Pol B-5B and *My Taq™ HS Red Mix*. Amplified PCR product was electrophoresized to verify the presence of 619 bp fragment. The result of cycle sequencing was analyzed using *Geneious R11* and *Basic Local Alignment Search Tool* (BLAST). The post trimming sequence of *M. tuberculosis*' *rpoB* gene has the size of 502-524 bp located in base number 1281-1804. All of the sequence of *M. tuberculosis*' *rpoB* gene sample has 100% similarity within the sample. The consensus sequence of *M. tuberculosis*' *rpoB* gene sample has no different nucleotide base sequence compared to the *rpoB* gene sequence of *M. tuberculosis* H37Rv, complete genome (*accession number* AL 123456.3, CP007027.1, CP009480.1, dan CP003248.2) which is the wild type strain and used as reference sequence in this research.

**Keywords:** *Multidrug resistant tuberculosis, Mycobacterium tuberculosis, rpoB* gene, Soetomo Medical Facility