

ABSTRACT

Detection of *gyrA* gene mutation region in Fluoroquinolone resistant *Mycobacterium tuberculosis*

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Background:

Fluoroquinolones are an important class of antibiotics used in the management of bacterial diseases and drug resistance tuberculosis (TB). This study aimed to determine the mechanism of fluoroquinolone resistance in *Mycobacterium tuberculosis* by sequencing of the quinolone resistance determining region (QRDR) of *gyrA*, one of the genes encoding DNA gyrase. Mutations affecting amino acids at positions 74, 90, 91 and 94 have been most commonly associated with resistance.

Methods:

1 Drug susceptibility testing of *Mycobacterium tuberculosis* was performed by the method of proportion, including susceptibility to ofloxacin. Isolates were from sputum specimens of patients treated at the Pulmonary lung Hospital (BP-4) Surabaya East Java (2) DNA was extracted by boiling method. (3) Nucleic acid was amplified by PCR, targeting the region of *gyrA* using primers “: primer *gyrA*-F (5’CAG CTA CAT CGA CTA TGC GA 3’) dan *gyrA*-R(GGG CTT CGG TGT ACC TCA T) and sequenced with ABI 377 sequencer. (4) Sequences were analysed to identify mutations associated with fluoroquinolone resistance.

Result:

9 of 20 isolates tested were ofloxacin resistant *Mycobacterium tuberculosis*. PCR for *gyrA* produced amplicons of 320 bp from five of these isolates. No mutations were identified in *gyrA* (specifically at sites corresponding with codons 90, 91, 94) but all 5 isolates had the mutations S95T.

Conclusion: these findings suggest that the *gyrA* mutation, S95T is polymorphism in Fluoroquinolone resistant *Mycobacterium tuberculosis*, in Surabaya. However, further investigation is required to identify the mechanism of Fluoroquinolone resistance in *Mycobacterium tuberculosis*.

Key word: Fluoroquinolone Resistance, *Mycobacterium tuberculosis*, *gyrA*, gene mutation