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ORAL PRESENTATION

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A novel *gyrB* gene mutation in fluoroquinolone resistant clinical isolates of *Mycobacterium* tuberculosis

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Introduction

Fluoroquinolone (FQ) resistance in *Mycobacterium* tuberculosis can be conferred by mutations in gyrA or gyrB gene. Recent studies suggest that amino acid substitutions in gyrB gene may also play a crucial role in resistance, but genetic studies of these mutations in M. tuberculosis are lacking.

Methods

A total of 100 ofloxacin resistant (OFX r) and 100 OFX sensitive (OFX s) isolates of M.tuberculosis isolates were consecutively selected from routine TB laboratory during 2012-2013. All the isolates were screened for phenotypic OFX r (>2µg/ml) by 1% proportion method and tested for minimal inhibitory concentration by absolute concentration method. Quinolone resistance determining region (QRDR) of gyrA and gyrB genes of 320bp and 428bp respectively were amplified, sequenced and compared with M.tuberculosis H37Rv.

Results

Mutations in the *gyrB* gene were observed in 5 of the 100 OFX r isolates. The single nucleotide mutation sites were in codons 538, 500, 539 (in two isolates) and 592. In one isolate, a substitution at codon 592 (Pro592Ser) was found as novel mutation outside QRDR region of *gyrB* gene. Accession nos. of these isolates include; KF509920-KF509922, KC880086 & KC880101. All the isolates showing mutations in *gyrB* gene also had mutations in *gyrA* gene. Mutations in *gyrA* gene were observed in 79% OFX r isolates. No mutation was observed in *gyrB* gene of OFX s isolates.

Conclusion

No OFX r isolates had shown mutation in the *gyrB* gene in the absence of *gyrA* gene mutation. The role of the *gyrB* gene mutation in conferring resistance to OFX in *M.tuberculosis* needs to be studied further.

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