

Antibiotics and Antibiotic Resistance

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Genomic study of reversion of antibiotic resistance reversion in multidrug resistant *Mycobacterium tuberculosis* SCAID 187.0 by a new drug FS-1

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Reversion of resistance to traditional antibiotics in pathogenic bacteria is just beginning to be realized as a prospective approach to combat the drug resistance in hospitals. Little is known about mechanisms of the drug resistance reversion. In a recent review by Baym et al., several theoretical models were proposed to explain the phenomenon by an active counter-selection of resistant strains from the population. A new nanomolecular anti-tuberculosis drug FS-1 has been registered recently in Kazakhstan. It was found in clinical and *in vitro* studies that FS-1 caused a reversion of sensitivity to traditional antibiotics in multidrug resistant isolates of *M. tuberculosis* (MDR-Mtb). In this study a recently sequenced MDR-Mtb strain SCAID 187.0 (NCBI acc. CP012506) was used in an *in vivo* experiment on Guinea pigs to study changes in the genetic composition of the Mtb population during treatment of the infected animals by different combinations of traditional anti-tuberculosis antibiotics with FS-1. In total, 11 Mtb isolates were fully sequenced by Illumina and aligned against the reference genome for variant calling. Treatment with FS-1 increased the genetic heterogeneity of the Mtb population by counter-selecting from the population of the most virulent MDR clones, which were genetically barcoded in this study. Drug resistance in the remaining clones was seriously compromised by a disruption of the genetic context required for drug resistance. In result, the therapy of a MDR-Mtb infection by traditional antibiotics enforced by FS-1 became effective again. To our best knowledge, this was the first experimental assertion of the drug resistance reversion by the theoretically predicted suppressive drug interaction mechanism.

Biography

Oleg N Reva has completed his PhD from the Institute of Microbiology and Virology in Kyiv, Ukraine. He did his Postdoctoral studies on Bioinformatics in the Medical High School of Hanover, Germany. Currently he is an Associated Professor of Bioinformatics at the University of Pretoria, South Africa. He has published 83 papers and book chapters, cited more than 1500 times.

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