



Strain differentiation of *Mycobacterium tuberculosis* complex isolated from sputum of pulmonary tuberculosis patients

Said Abbadi^{a,*}, G. El Hadid^a, N. Gomaa^a, Robert Cooksey^b

^a Microbiology and Immunology Department, Faculty of Medicine, Suez Canal University, Circuit Road, Ismailia 41111, Egypt, ^bThe Division of AIDS, STD, and TB Laboratory Research, Centers for Disease Control and Prevention, Atlanta, Georgia, USA

Abstract

Objective: This study represents an early attempt to determine the diversity of *Mycobacterium tuberculosis* in Egypt, particularly of drug-resistant strains.

Methods: We characterized 45 *Mycobacterium tuberculosis* complex isolates from sputum samples of Egyptian patients with pulmonary tuberculosis, in order to establish a database of strain types and antimicrobial susceptibility patterns.

Results: One *Mycobacterium bovis* and 44 *Mycobacterium tuberculosis* (MTB) isolates were identified by PCR-restriction fragment length polymorphism (RFLP) analysis of the *oxyR* gene.

Twenty-five (56.8%) of the 44 MTB isolates were susceptible in vitro to all anti-tuberculosis drugs tested; five (11.4%) were mono-resistant to isoniazid or streptomycin (four were resistant to streptomycin and only one was resistant to isoniazid) and 14 (31.8%) were resistant to more than one drug (multidrug-resistant, MDR). Among the 44 MTB isolates tested by RFLP analysis in this study, 40 different RFLP patterns were



obtained. The number of IS6110 copies ranged from 5 to 16. Studying the IS6110 RFLP patterns indicated that the 44 isolates did not cluster together but were generally scattered. None of the 14 MDR isolates were clustered. Twenty-two different spoligotypes were identified among the 44 MTB isolates, of which 13 were unique. The remaining

31 isolates were grouped into nine clusters of strains sharing identical spoligotypes.

Conclusions: We have demonstrated evidence of diversity among the drug-susceptible and resistant MTB strains. Continued surveillance for strains of MTB involved in pulmonary tuberculosis in Egypt, and especially for drug-resistant strains, is warranted.



Molecular identification of mutations associated with anti-tuberculosis drug resistance among strains of *Mycobacterium tuberculosis*

Said H. Abbadi^{a,*}, G. Abdel Sameaa^b, G. Morlock^c, R.C. Cooksey^c

^aMicrobiology Department, Faculty of Medicine, Suez Canal University, Egypt

^bVACSERA, Cairo, Egypt, ^cCenters for Disease Control and Prevention, Atlanta, Georgia, USA

Abstract

Background: Understanding the etiologic organism, antimicrobial resistance mechanisms, and transmission of multidrug-resistant tuberculosis (MDR-TB) can be of great value in optimizing strategies to control and prevent its development and transmission.

Methods: One hundred and fifty-five *Mycobacterium tuberculosis* complex isolates from patients with pulmonary tuberculosis (TB) in Cairo, Egypt were studied. In vitro drug susceptibility testing against rifampin (RIF), isoniazid (INH), streptomycin (SM), ethambutol (EMB), and pyrazinamide (PZA) was performed. Resistance was studied by the standard agar proportion method. Single strand conformation polymorphism (SSCP) and DNA sequence analysis were used to detect mutations in the genes that encode resistance to *rpoB*, *katG*, *rpsL*, and *embB*.

Results: Among 155 consecutive *M. tuberculosis* isolates, 25 (16.1%) were MDR-TB; 13 of these were from newly diagnosed untreated cases, 12 were from re-treated cases, and none of the MDRTB isolates had matching IS6110 fingerprints.



Among the MDR-TB isolates, *rpoB* mutations were found in 76% of RIF-resistant isolates, *katG* mutations were found in 47.1% of INH-resistant isolates, *rpsL* mutations were found in 55.6% of SM-resistant isolates, and *embB* mutations were found in 36.4% of EMB-resistant isolates.

Conclusions: No major differences were found in the frequencies of mutations or types of amino acid substitution between newly diagnosed untreated cases and re-treated cases. The high prevalence of MDR-TB at this hospital underscores the need for continuous monitoring of strains and antimicrobial resistance.



Published Research Articles in International Journals 2008-2009