Abstract

Objective. To compare drug resistance (DR) rates and genetic diversity of Mycobacterium tuberculosis strains from different states of Mexico. Materials and methods. A systematic review of English and Spanish-language articles using MEDLINE and Google Scholar. Search terms included Mycobacterium tuberculosis, Mexico, resistance, mutation and epidemiology. Results. Fifteen studies for phenotypic DR rates (n=2 694), twelve studies for genotypic DR (n=748) and eleven studies for genetic diversity (n=2 044) met our inclusion criteria. Mean DR and multidrug resistance (MDR) rates were 37.5% and 20.6%, respectively. The most frequent mutations were rpoB531 (53.1%), katG315 (50.6%), embB306 (32.1%), rpsL43 (14.6%) and pncA359 (16.7%) in DR strains. Novel mutations were found. Predominant shared types were SIT53 (T1, n=188, 3.9%), SIT119 (X1, n=125, 6.9%), SIT19 (EAI2-Manila, n=80, 6.3%) and SIT42 (LAM9, n=77, 3.0%). SIT1 Beijing genotype has been reported in six states from Mexico. Conclusions. DR and MDR rates continue to increase. Genetic diversity of M. tuberculosis strains in Mexico is high. Reports of Beijing strains are increasing.

Keywords

Mycobacterium tuberculosis; molecular epidemiology; drug resistance; mutation; Mexico