Abstract

In 2003, the incidence of tuberculosis in Argentina showed an increase compared to 2002. The severe national crisis at the end of the 90s has probably strongly contributed to this situation. The goal of this work was to estimate the extent of the spread of the most predominant Mycobacterium tuberculosis strains and to assess the spread of predominant M. tuberculosis clusters as determined by spoligotyping and IS6110 RFLP. The study involved 590 pulmonary, smear-positive TB cases receiving medical attention at health centers and hospitals in Northern Buenos Aires (NBA) suburbs, from October 2001 to December 2002. From a total of 208 clinical isolates belonging to 6 major clusters, 63 (30.2%) isolates had identical spoligotyping and IS6110 RFLP pattern. Only 22.2% were shown to have epidemiological connections with another member of their respective cluster. In these major clusters, 30.2% of the 208 TB cases studied by both molecular techniques and contact tracing could be convincingly attributable to a recently acquired infection. This knowledge may be useful to assess the clonal distribution of predominant M. tuberculosis clusters in Argentina, which may make an impact on TB control strategies.

Keywords

Tuberculosis, Clusters, Predominant clones, Genotyping.