

MOLECULAR EPIDEMIOLOGY OF TUBERCULOSIS IN A CHANGING SCENARIO DUE TO A SHARP INCREASE IN THE NUMBER OF CASES IN IMMIGRANTS

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Purpose of the study: In recent years, the number of cases of tuberculosis (TB) in immigrants in Spain has increased sharply. Our purpose was i) to analyze the patterns of recent transmission of TB involving immigrants in two cities (Madrid and Almería) with different socio-epidemiological features and ii) to apply new epidemiological strategies in identifying the transmission contexts associated with the clusters.

Methods: Analysis by IS6110-RFLP of the TB cases in Madrid (2004-2006) and Almería (2003-2005). Spoligotyping was applied as a second-line typing method. Standardized exhaustive interviews of the clustered cases in Almería supported by photographic recognition of the patients were performed.

Results: In Madrid, among the 1046 TB cases genotyped, 37.4% were clustered (106 clusters, 2-23 cases). 32.8% of immigrant cases and 43.4% of autochthonous cases were clustered. 31 clusters (29.2%) included only immigrant cases, 30 (28.3%) only autochthonous cases and the remaining 45 clusters (42.5%) included both immigrant and autochthonous patients (mixed clusters). In Almería, among the 256 TB cases, 30.5% were clustered (26 clusters; 2-6 cases), 27.0% of immigrants cases and 34.8% of autochthonous cases were clustered ($p=0.176$). Nine clusters (34.6%) included only autochthonous cases, eight (30.8%) only immigrant patients and the remaining 9 clusters (34.6%) were mixed. A pilot study applying standardized interviews in Almería revealed that in 8 clusters (involving > 4 cases) standard contact tracing detected epidemiological links in only one cluster, whereas interviewing the clustered cases succeeded in finding links in six clusters.

Conclusions: In Spain, recent transmission is detected among immigrants and also between the immigrant and autochthonous populations. Identification of the transmission contexts associated with clustering requires novel epidemiological strategies that are more refined than the standard contact tracing.

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