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ABSTRACT

Aims and objectives: Molecular methods in bacteriology showed Mycobacterium tuberculosis (MTB) to have families, such as Beijing, Haarlem, Africa, East-African-Indian, Latin American and T. Each year, tuberculosis (TB) causes more than 2 million deaths in the world. The aim of this study is to determine the prevalence of the MTB T family in different countries using a systematic review and meta-analysis.

Methods: Data sources of this study are comprised of 151 original articles (2000–2012) that were published in the literature databases: PubMed) www.ncbi.nlm.nih.gov/pubmed, the years of coverage of this web site is 1955). The prevalence of MTB T family in different continents, including America, Europe, Asia and Africa, were studied. Inclusion criteria were: research articles with full text, and articles with abstracts in English. Excluded studies were: review articles, congress abstracts, studies that reported in languages other than English and studies that were not available in abstract or full text, studies that their sampling location was uncertain, studies that locations of sampling were performed at the same time, and studies that their data were not clear. These data were analyzed using meta-analysis and random effects models with the software package Meta R, Version 2.13 (p < 0.10) Confidence Interval (CI: 95%).

Results: 44 of 151 articles were applied; the prevalence of MTB T family in different continents was in America (Spain; 80% in 2009), Europe (Sough; 48.7% in 2008), Africa (South Africa; 23% in 2011) and Asia (Iran; 32.3% in 2010). The highest and lowest occurrence rate of MTB T family was Spain 80% in 2009 and in South Korea 2.1% in 2010, respectively. Pooled estimation of MTB T family samples was 19,873. Also, fixed effects for years showed that CI was between 5%–40%.

Conclusion: Different research was studied on the prevalence of MTB T family in various countries. In this study, Spain with 80% in 2009 had more prevalence compared with other countries. The presence of MTB T family in studies indicate effective programs and management are required to control and prevent the spread of MTB, especially the T family.

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