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Source

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Abstract

BACKGROUND:

Genotyping methods are useful tools to provide information on tuberculosis epidemic. They can allow a better response from health authorities and the implementation of measures for tuberculosis control. This study aimed to identify the main lineages and clades of Mycobacterium tuberculosis complex strains circulating in Côte d'Ivoire.

METHODS/MAIN FINDINGS:

Strains isolated from sputum samples of patients ongoing retreatment from all the country were characterized by spoligotyping and by MIRU-VNTR. Profiles obtained by spoligotyping were first compared to the SITVIT/SpoIDB4 database for family assignment. Of 194 strains analysed, 146 (75.3%) belonged to the T lineage. The most predominant spoligotype was the shared international type 53 with 135 strains (69.6%). In contrast with neighbouring countries, LAM (11 strains, 5.7%) and H (9 strains 4.6%) lineages were slightly represented. Only 3 Beijing strains (1.5%) and 4 strains of Mycobacterium africanum (2%) were found. Analysis of the results obtained with MIRU-VNTR revealed also a high level of clustering.

CONCLUSION/SIGNIFICANCE:

The population of Mycobacterium tuberculosis complex strains among retreatment cases in Côte d'Ivoire exhibits a low diversity, allowing to assume recent transmission and locally based infection.