Genetic diversity, transmission dynamics, and drug resistance of Mycobacterium tuberculosis in Luanda, Angola

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ABSTRACT

Objective/background: Despite the important role that the African region plays in a global tuberculosis (TB) epidemiological context, many countries in the region still lack data on the prevalence of specific Mycobacterium tuberculosis strains and drug resistance. This is the case for Angola, which presently lacks any data concerning drug-resistance rates and prevalence of specific M. tuberculosis genotypes and respective population structure. In this study, we made the first characterization of the genetic diversity and drug resistance of M. tuberculosis complex strains circulating in Luanda, Angola’s most important setting concerning TB epidemiology.

Methods: We have analyzed 89 M. tuberculosis isolates recovered from the same number of patients. All clinical isolates were genotyped by spoligotyping and 24-loci mycobacterial interspersed repetitive unit–variable number of tandem repeats (MIRU–VNTRs). First-line drug-susceptibility testing was performed by the standard BACTEC 960 Mycobacteria Growth Indicator Tube (MGIT) procedure.

Results: We have detected 33 different spoligotype profiles corresponding to 24 different shared international types (SITs) and nine orphan profiles. SIT 20 (LAM1) was the most prevalent (n = 16, 18.2%) followed by SIT 42 (LAM9; n = 15, 17.1%). Overall, the M. tuberculosis population structure in this sample was dominated by LAM (64.8%) and T (33.0%) strains. Twenty-four-loci MIRU–VNTR analysis revealed that a total of 13 isolates were grouped into five distinct clusters. Drug-susceptibility testing revealed a worrying situation concerning resistance rates. Drug-susceptibility data showed that 22 (24.7%) of the 89 clinical isolates were resistant to one or more antibacterial drugs of which four (4.5%) were multidrug resistant (MDR). Drug-resistant isolates were found across distinct clades and MIRU–VNTR clusters.

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Conclusion: This first cross-sectional study conducted in Luanda, Angola, provides a framework for future studies and programmatic management of TB in Angola. We provide sufficient evidence for cluster-based transmission with a high predominance of LAM strains, with differential geographic dispersion. The moderate rate of MDR-TB found in this sample has major public health implications and highlights the need for further studies specifically focused on MDR-TB transmission.

Conflicts of interest

The authors have no conflicts of interest to declare.