

Tuberculous Lymphadenitis in Ethiopia Predominantly Caused by Strains Belonging to the Delhi/CAS Lineage and Newly Identified Ethiopian Clades of the Mycobacterium tuberculosis Complex

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Abstract

Recently, newly defined clades of Mycobacterium tuberculosis complex (MTBC) strains, namely Ethiopia 1-3 and Ethiopia H37Rv-like strains, and other clades associated with pulmonary TB (PTB) were identified in Ethiopia. In this study, we investigated whether these new strain types exhibit an increased ability to cause TB lymphadenitis (TBLN) and raised the question, if particular MTBC strains derived from TBLN patients in northern Ethiopia are genetically adapted to their local hosts and/or to the TBLN. Genotyping of 196 MTBC strains isolated from TBLN patients was performed by spoligotyping and 24-loci mycobacterium interspersed repetitive unit-variable number of tandem repeats (MIRU-VNTR) typing. A statistical analysis was carried out to see possible associations between patient characteristics and phylogenetic MTBC strain classification. Among 196 isolates, the majority of strains belonged to the Delhi/CAS (38.8%) lineage, followed by Ethiopia 1 (9.7%), Ethiopia 3 (8.7%), Ethiopia H37RV-like (8.2%), Ethiopia 2 and Haarlem (7.7% each), URAL (3.6%), Uganda 1 and LAM (2% each), S-type (1.5%), X-type (1%), and 0.5% isolates of TUR, EAI, and Beijing genotype, respectively. Overall, 15 strains (7.7%) could not be allocated to a previously

Described phylogenetic lineage. The distribution of MTBC lineages is similar to that found in studies of PTB samples. The cluster rate (35%) in this study is significantly lower ($P = 0.035$) compared to 45% in the study of PTB in northwestern

Ethiopia. In the studied area, lymph node samples are dominated by Delhi/CAS genotype strains and strains of largely not yet defined clades based on MIRU-VNTR 24-loci nomenclature.

We found no indication that strains of particular genotypes are specifically associated with TBLN. However, a detailed analysis of specific genetic variants of the locally contained Ethiopian clades by whole genome sequencing may reveal new insights into the host-pathogen co-evolution and specific features that are related to the local host immune system.



Biography

Fantahun Biadlegne Degenegh is a PhD holder from Medical faculty, University of Leipzig, Germany. He performed studies on molecular epidemiology, resistance mechanisms, and genomic diversity of clinical M. tuberculosis isolates. In addition, he was involved in all aspects of laboratory diagnostics of Mycobacterial infections and has established typing schemes for diagnostic and epidemiologic studies.

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