Ascertaining in vivo virulence of Mycobacterium tuberculosis lineages in patients in Mbeya, Tanzania

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We evaluated the relationship between the degree of immunodeficiency indicated by the number of circulating CD4+ T-cells and Mycobacterium tuberculosis lineages identified by spoligotyping and mycobacterial interspersed repetitive units-variable number of tandem repeats genotyping in human immunodeficiency virus (HIV) infected individuals with pulmonary tuberculosis from Mbeya, Tanzania. Of M. tuberculosis strains from 129 patients, respectively 55 (42.6%) and 37 (28.7%) belonged to Latin American Mediterranean and Delhi/Central-Asian lineages, while 37 (28.7%) patients were infected with other strains. There was no difference in the distribution of M. tuberculosis lineages among patients with early or advanced stages of HIV infection (P = 0.785), indicating that the virulence of strains from these lineages may not be substantially different in vivo.

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