

SECTION 2

Summary

To determine a detailed picture of tuberculosis (TB) epidemiology in Kandy, Sri Lanka, 110 *M.tuberculosis* complex isolates from TB Patients attending the Central Chest Clinic, Kandy, who were positive for acid fast bacilli on direct examination of sputum by Ziehl-Neelsen from 2007 -2009 were analyzed by IS 6110 DNA finger printing and by Spoligotyping. The software GeneDirectory was used to compare the IS 6110 hybridization patterns. Spoligotyping was carried out as previously described and spoligopatterns were analyzed using MS Excel data sheets and grouped together for any similarity. The data was further analyzed by comparing with the SPOTCLUST data base. In RFLP, the majority of the circulating *M.tuberculosis* strains in Kandy belong to a single family, but the degree of IS 6110 DNA polymorphism among strains was high. In total 71 distinct IS 6110 patterns were found with strains clustering into one main family and 10 distinct strains. Within the main family three isolates were grouped into one cluster, with closely related isolates while rest of the bacterial strains was grouped into one. The number of IS 6110 DNA varied between 1 and 17. Strains containing a single copy of IS 6110 were predominant among the study population (15) and except for three, the location of the bands in fingerprints were different. Among the strains tested there were 25 strains that lacked the IS 6110 element. SPOTCLUST incorporates biological information on spoligotype evolution, and in spoligotyping of 110 *M.tuberculosis* isolates revealed a total of 24 families including the nine major families. The most predominant group corresponded to Family33. Strains were distributed among all three principal genetic groups PGG1, PGG 2 and PGG3. Segregation of *M.tuberculosis* into 'ancestral' versus 'modern' lineages based on PGG indicates that isolates from Kandy have originated from both lineages. In spoligotyping high strain diversity was seen and except for two strains 000000000003771 (ST1) and 00000000000031(ST 585) the rest were not defined in the latest spoligotype data bases SpolDB4/SITVIT. This is the first study in Sri Lanka in which the RFLP pattern of *M.tuberculosis* strains and the spoligotyping in a population has been examined. By using the genetic marker of IS 6110 it was possible to differentiate most of the *M.tuberculosis* isolates. The preliminary inferences from this study plead for a more extensive analysis of the data to study the variability of *M.tuberculosis* strains and their transmission dynamics.