

## **DNA finger printing of *Mycobacterium tuberculosis* using restriction fragment length polymorphism (RFLP) with special reference to the prison population**

Restriction Fragment Length Polymorphism (RFLP) analysis has become a very important tool in the epidemiology of tuberculosis (TB). The repetitive Insertion Sequence (IS) 6110 is the most frequently used genetic marker for strain differentiation of *M. tuberculosis* (Mtb).

The aim of this study was to determine the transmission of pulmonary TB among prisoners and their effect on the epidemiology of TB in Sri Lanka, by studying RFLP patterns of isolated strains. Mtb strains were isolated from prisoners and chest clinic attendees. DNA from Mtb was extracted from bacteria using chloroform-isoamyl alcohol (24:1,v/v). Genomic DNA was digested using restriction endonuclease Pvu II and fragments were separated by electrophoresis in a 0.8% agarose gel in 1x TBE (tris-Boric acid -EDTA) at 0.8v/cm overnight. DNA was transferred on to a nitrocellulose membrane by southern transfer. DNA probe (541 bp) was prepared by PCR and purified by sephadex G-50 column. Labeling of the probe, hybridization and detection were carried using the enhanced chemiluminescence detection kit. 151 strains were analysed, 131 isolates were from the general population among which 24 were ex-prisoners. 20 isolates were from prisoners.

Dendrogram analysis showed 41 distinct IS 6110 banding patterns. Bacterial strains were grouped in to three main families, and within each family the isolates were closely related. The occurrence of the Is copies varied from 1 to 7, the majority having 3 to 5 copies. Two strains one each from prisoners and ex-prisoners had identical banding and non were identical among prisoners.

These results confirm that DNA fingerprinting using IS 6110 is a suitable tool for epidemiology of TB. There is little spread among prisoners probably due to high turnover of inmates and late disease manifestation due to the chronicity of the illness. However the prisoners once released may appear to be a source of infection, which can be confirmed by extending the study population. Based on the studies by Soolingen et al, it is recommended that Polymorphic Rich repetitive sequence (PGRS) typing be carried out for further differentiation of strains as the IS copy numbers are low.