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**Title:** Investigation correlation of IS6110-RFLP method and MIRU-VNTR method results in molecular epidemiology studies of Tuberculosis in a regional study in Iran

**Authors:** Mohammad Asgharzadeh1, Hossein Samadi Kafil2

**Abstract:** Background and Objectives: in a study for the genotyping of Mycobacterium tuberculosis isolates in the East Azerbaijan Province of Iran for evaluating the level of risk factors for recent transmission of tuberculosis (TB).

Materials & Methods: we performed both IS6110 and MIRU-VNTR methods in our isolates and we compared this two method for finding correlation of results of these two methods. we performed IS6110-based restriction fragment length polymorphism analysis and MIRU-VNTR PCR- based method in 129 strains.

Results: Among 129 isolates, In IS6110-RFLP method 105 samples was suitable for study and had enough DNA for IS6110 studying and 81 different IS6110 patterns were found, of which 70 were observed only once and 11 were shared by two to eight isolates. Ninety-six isolates (91.4%) were found to have more than five copies of IS6110. In MIRU-VNTR analysis Among 129 isolates, 95 distinct MIRU-VNTR patterns, including 21 clustered patterns and 72 unique patterns were found. The discriminatory power of MIRU-VNTR typing was (HGDI=0.9934) and IS6110 was (HGDI= 0.9928) for our isolates. The minimum estimate for the proportion of tuberculosis that was due to Transmission with IS6110-RFLP was 16.8% and with MIRU-VNTR was 26.4%.

Conclusion: this results together with high patterns polymorphism shows that IS6110-RFLP typing could be useful for studying the epidemiology of TB but in MIRU-VNTR analysis we had more Clustering and source case finding. In the other hand for IS6110 we need a high amount of DNA which caused we lost 24 samples for this study. The minimum estimated rate of recent transmission was 16.8% in IS6110 which is lower than 26.4% in MIRU-VNTR show that IS6110 results can be more reliable than MIRU-VNTR with 12 loci. Clustering was not associated with age, sex or site of infection of TB but drug-resistant isolates were less likely to be clustered than sensitive isolates (p < 0.05). Presence of all IS6110 clustered patients in clusters of MIRU-VNTR suggested that with improving this method with additional locus investigation, we can replace MIRU-VNTR with IS6110 as a standard method for genotyping of M tuberculosis.

**Presentations:** Poster