THREE STEP MI RU-VNTR FOR ROUTINE LABORATORY PRACTICE

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MIRU-VNTR typing with 12 loci, has been efficiently using to discriminate *Mycobacterium tuberculosis* complex isolates epidemiologically. Finding out cross contaminations and nosocomial infections in routine laboratory practice by this method is time and money consuming especially in developing countries. Therefore we suggest a three-step analyzing method instead of performing all 12 loci together.

Totally 475 *Mycobacterium tuberculosis* complex which were isolated from 265 patients in our laboratory in 6 years period. 143 of them which were isolated from different patients were genotyped by using MIRU-VNTR 12, as described by “Supply P et al. Mol Microbiol 2000;762-771”. A retrospective analysis of 143 MIRU data was performed by a computer based program which we created. The program was prepared by using Microsoft QuickBASIC programming language. All of the data were calculated by this program. The best combinations out of 4095 possible results of 12 different primer pairs, to differentiate the clusters and identify unique isolates were determined. According to the results of the loci 10, 16, 23, 26, and 40; 47 unique isolates and 85 isolates in 24 clusters were identified but 11 of the isolates couldn't be identified. Adding the results of the loci 2, 20, 27, and 31; 78 unique isolates and 55 isolates in 20 clusters were identified and 10 of the isolates couldn't be identified. By the results of eleven loci, 54 isolates were in 22 clusters, 79 isolates were unique, and 10 isolates were remained unidentified.

According to our results, to find out cross contaminations and nosocomial infections in routine laboratory practice, it is better to work on loci 10, 16, 23, 26, and 40 initially. Then continue with loci 2, 20, 27, and 31 whether the discrimination is inadequate with first group of loci. If still there are similar results than loci 4, 24, and 39 should be performed. We don't think it is necessary to perform with the locus 39 because we couldn't find any dissimilar results in these 143 samples. The created software is user friendly, fast and able to meet the requirements of different clinical mycobacteriology laboratories.