

**STANDARDIZED MYCOBACTERIAL INTERSPERSED REPETITIVE UNIT-VARIABLE
NUMBER OF TANDEM REPEAT TYPING OF *MYCOBACTERIUM TUBERCULOSIS* IN THE
EUROPEAN CAPITAL**

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A standardized MIRU-VNTR format with significantly improved discriminatory power has recently been proposed. Here, we evaluated this optimized format in a population-based study conducted in the Brussels-Capital Region.

Over 39 months, 852 *M. tuberculosis* isolates (from 807 patients) were genotyped at the Tuberculosis and Mycobacteria Reference Center in Brussels. Resolution power, cluster and lineage identification by the new 15 and 24 MIRU-VNTR sets were compared with those obtained using the previous set of 12 loci, spoligotyping and IS6110-RFLP.

On a subset of 258 isolates, a better resolution was obtained by applying MIRU-VNTR typing in comparison with IS6110-RFLP. Nonetheless, a high mutual correspondence between unique isolates or strain-clusters defined by MIRU-VNTR and IS6110-RFLP (>5 IS6110) was observed. Based on these results, MIRU-VNTR typing was subsequently applied in combination with spoligotyping for screening of the remaining *M. tuberculosis* isolates. In the full population-based sample, all isolates were fully typeable over the 24 MIRU-VNTR loci and all but one by spoligotyping. The recently defined discriminatory subset of 15 loci showed a better resolution than the old set of 12 loci. Moreover, the 9 ancillary loci and/or spoligotyping increase only slightly the numbers of profiles obtained by the 15 loci. Only 10 isolates reproducibly displayed a double allele in a single MIRU-VNTR locus, identifying the simultaneous presence of two closely related clonal variants. Five isolates displayed double alleles in two or more loci, identifying the presence of independent clones. Among the serial isolates, genotypes were conserved over the full MIRU-VNTR set and spoligotypes. Finally, excellent concordance was observed between spoligotype assignments and MIRU-VNTR groupings, except for isolates with T spoligotypes.

MIRU-VNTR typing using the new sets of loci is a powerful genotyping method for epidemiological investigation and for phylogenetical studies. Our results support MIRU-VNTR typing as the new reference genotyping method for *M. tuberculosis* isolates.