

## **MYCOBACTERIA MIRU-VNTRPLUS: ONLINE DATABASE AND ANALYSIS TOOL FOR MIRU, SPOLIGO, AND REGIONS OF DIFFERENCE DATA**

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**Background:** Molecular typing of bacteria from the *Mycobacterium tuberculosis* complex (MTBC) is essential for epidemiological purposes such as investigating the spreading of specific genotypes. Recently, mycobacterial interspersed repetitive units (MIRU) typing has become an important method, as it allows high-throughput, discriminatory and reproducible analysis of clinical isolates. Because of its portable data format, MIRU typing has the potential to be a versatile tool for individual strain identification based on large reference databases. However, so far no public MIRU database with well characterized reference strains is available.

**Methods:** A collection of 177 strains representing the major MTBC lineages was used to build up an internet based database. For each strain epidemiologic and genotype information was stored together with copy numbers of 24 MIRU loci, spoligotyping patterns, regions of difference (RD) profiles, and IS6110 RFLP fingerprint images.

**Results:** Via the freely accessible new service users can compare their strain(s) with the reference strains or analyze their strains without using the database content. Comparisons can be based on single MIRU-, spoligo-, RD-typing data, or by a combination of different datasets. If a combined analysis is performed, weights can be assigned to the different methods. For each comparison, a list of the reference strains most similar to the submitted strain can be displayed, thereby allowing MTBC species and lineage classification. Several distance coefficients are available, including Nei's DA, and categorical. Based upon the respective distance matrix, a dendrogram can be calculated using UPGMA or neighbor-joining clustering algorithms. The resulting trees may be exported in various data formats.

**Conclusion:** The new MIRU-VNTRplus database offers an easy way to compare user strains against a collection of well characterized reference strains. As one additional novel feature, combinations of typing methods can be used for comparison. The open database can be accessed via the internet at <http://www.MIRU-VNTRplus.org>.