Phylogeographical Particularity of the Mycobacterium tuberculosis Beijing Family in South Korea Based on International Comparison with Surrounding Countries

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To understand the domestic population structure of Mycobacterium tuberculosis clinical isolates in the Republic of Korea, we genotypically analysed 80 isolates obtained from various geographical origins in the country. Of these, 64 (80.0 %) isolates were identified as Beijing family strains. It is particularly interesting that their phylogenetic classification, based on the ancient/modern separation and the presence/absence of the genomic region RD181, revealed a majority of the ancient (RD181+) subfamily in the population. The 15 loci of variable number of tandem repeat(s) of mycobacterial interspersed repetitive units (15–MIRU–VNTR) were also analysed. Combination with the previous VNTR data reported from surrounding countries revealed that the topology of the minimum spanning tree was linked tightly not to the geographical origins of the patients but to the phylogenetic characteristics of the isolates. These results show that the phylogeographical distribution of the M. tuberculosis Beijing family around far-eastern Asia could be estimated using international accumulation and comparison of VNTR genotyping data.