

学位論文の要旨

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<p>主論文の題名</p> <p>Molecular Genotyping of <i>Mycobacterium tuberculosis</i> in Mie Prefecture, Japan, Using Variable Numbers of Tandem Repeats Analysis.</p> <p>主論文の要旨</p> <p>Tuberculosis(TB) remains a major public health problem in Japan. In recent years, molecular typing methods have become useful tools for the control of TB and help to indicate possible epidemiological links between TB patients. The variable numbers of tandem repeats (VNTR) analysis is a method frequently employed as a molecular epidemiological tool for <i>M. tuberculosis</i> genetic fingerprinting. In this study, we characterized the population of <i>M. tuberculosis</i> circulating in Mie prefecture, Japan, and assessed the utility of proposed (Japan Anti-Tuberculosis Association) JATA12 and 15-VNTR analyses of 158 <i>M. tuberculosis</i> clinical isolates using 25 VNTR loci. The results revealed that the ancient Beijing sublineage is the most prevalent <i>M. tuberculosis</i> in Mie prefecture, accounting for 85.0% of 113 Beijing lineage isolates. Our experimental results also showed that JATA-VNTR by using well-selected loci is reliable method compared with standardized 15-locus (mycobacterial interspersed repetitive unit) MIRU-VNTR, and that JATA15-VNTR analysis reliably improved the discriminatory power compared with basic JATA12-VNTR analysis. In summary, our data suggest that JATA-VNTR is useful tool for discrimination of <i>M.tuberculosis</i> in areas where ancient Beijing strains are frequently isolated. This study is the first report of the molecular genotyping of <i>M. tuberculosis</i> in this region of Japan, and this information is expected to improve our understanding of TB transmission in this region.</p>			