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## **Genetic diversity of Mycobacterium tuberculosis isolates from Tochigi prefecture, a local region of Japan.**

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### **Abstract**

**BACKGROUND:** Foreign-born patients with tuberculosis (TB) may introduce globally disseminated isolates of *Mycobacterium tuberculosis* into large cities in Japan. The risk of dissemination of these isolates into local regions, however, has not been determined. This study analyzed the molecular epidemiology of *M. tuberculosis* isolates obtained from TB patients living in a local region of Japan.

**METHODS:** Whole genome sequences of 169 *M. tuberculosis* isolates, obtained from 148 Japanese-born and 21 foreign-born patients living in Tochigi, Japan, were analyzed using the Comprehensive analysis server for the *Mycobacterium tuberculosis* complex (CASTB).

**RESULTS:** The 169 isolates were clustered into four clades; Lineage 2 (111 isolates 65.7%), Lineage 4 (43 isolates, 25.4%), Lineage 1 (13 isolates, 7.7%), and Lineage 3 (2 isolates, 1.2%). Of the 111 isolates belonging to Lineage 2, 79 (71.2%) were of the atypical Beijing sub-genotype. Of the 13 Lineage 1 isolates, nine (69.2%) were from foreign-born patients. The isolates belonging to Lineage 4 were further clustered into three clades, two containing isolates shared by both Japanese- and foreign-born patients. The two isolates belonging to Lineage 3 were obtained from foreign-born patients.

**CONCLUSIONS:** The genotypic diversity of *M. tuberculosis* in a local region of Japan is increased primarily by the presence of isolates obtained from foreign-born patients.

**KEYWORDS:** CASTB; Foreign-born; Japan; Lineage; Whole genome sequencing

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