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# STUDY ON THE ASSOCIATION BETWEEN BEIJING GENOTYPE *MYCOBACTERIUM TUBERCULOSIS* AND DRUG-RESISTANCE

Yi Liu<sup>1</sup>, Xuxia Zhang<sup>1</sup>, Yuqing Zhang<sup>1</sup>, Cong Yao<sup>1</sup>, Wei Wang<sup>1</sup>  
Qing Xing<sup>2</sup>, Suming Wang<sup>2</sup> and Chuanyou Li<sup>1</sup>

<sup>1</sup>Capital Medical University, China

<sup>2</sup>Beijing Research Institute for Tuberculosis Control, China

**A**lthough there were some molecular epidemiology studies of *Mycobacterium tuberculosis* (Mtb) in Beijing, however, the study on revealing the association between drug resistance and Beijing genotype was still lack. As a retrospective study, isolates from patients with smear-positive tuberculosis were subjected to drug susceptibility testing (DST) and analyzed by spoligotyping and variable number of tandem repeats (VNTR) typing. We analyzed association relationship by statistics methods. Among the 1189 Mtb strains Beijing genotype family was the dominated genotype. We found a significant difference between Beijing and non-Beijing genotype strains when considering risk factors sex, age and registered residence. 849 (71.4%) strains were fully sensitive to first-line drugs, while 340 (28.6%) strains were resistant to at least one of the drugs. Meanwhile, 9% (107/1189) was MDR-TB. Statistics analysis results indicated that the frequencies of INH-resistance of Beijing genotype strains were significantly lower than that of non-Beijing genotype strains. Our results indicated that there was a correlation relationship between Beijing genotype and drug resistance only in INH. This study provided a broader profile of drug resistance levels and the distribution of Mtb genotypes in Beijing.

liuyilotus@hotmail.com