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Abstract (oral session)

**A study on the correlation between polymorphisms of the SLC11A1 gene and tuberculosis and drug-resistant tuberculosis in Chinese Han population**

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**Objective:** To investigate the distribution of polymorphisms of SLC11A1 gene with susceptibility to tuberculosis (TB) in Chinese Han population suffering from TB and drug-resistant TB so as to approach the correlation between gene polymorphisms and the development of TB and drug-resistant TB. **Methods:** Single nucleotide polymorphisms (SNP) of SLC11A1 gene were typed and analyzed by pyrosequencing, real-time Probe and SNaPshot among 459 patients with pulmonary tuberculosis (229 patients with drug-sensitive TB, 230 patients with drug-resistant TB) and 30 healthy controls in Chinese Han population. Logistic regression analysis and chi-square test were used. **Results:** SLC11A1 gene 3' UTR TGTG+/del genotype occurred more frequently in patients with pulmonary tuberculosis than in controls ( $P=0.038$ ). No significant difference was observed in the distribution of INT4 and D543N genotypes between patients with pulmonary tuberculosis and controls. Combined analysis of D543N and 3' UTR variants demonstrated that GG+/del and GA+/del genotypes occurred more frequently in patients with pulmonary tuberculosis than in controls ( $P=0.048$  &  $P=0.034$ ). The genotype of INT4 site and allelic frequency of SLC11A1 gene for drug-sensitive TB group were significantly different from those for drug-resistant TB group ( $P=0.031$ ,  $0.046$ ). If recessive inheritance was assumed, the genotypes of INT4 site from the two groups were significantly different (OR=5.756, 95% CI: 1.261 - 26.269,  $P=0.011$ ). Taken together with the relationship between OR values using various combinations, it confirmed that the genetic mode of INT4 site was in accordance with recessive inheritance. **Conclusion:** SLC11A1 gene polymorphisms in 3' UTR and heterozygosity of D543N and 3' UTR variants might be susceptibility to tuberculosis in Chinese Han population. INT4 site on SLC11A1 gene are probably associated with the development of drug-resistant TB in Chinese Han population. Further study on this issue will help us to predict population with high risk of drug-resistant TB and explore effective intervention to decrease the incidence of this disease. drug-resistant TB and explore effective intervention to decrease the incidence of this disease.