



Correlation between natriuretic peptide receptor C (*NPR3*) gene polymorphisms and hypertension in the Dai people of China

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ABSTRACT. Hypertension affects one-fifth of the world population. Genome-wide association studies (GWAS) have identified several single nucleotide polymorphisms (SNPs) that correlated with hypertension in large samples. However, the genetic mutations leading to hypertension might differ among various populations, as they have different origins and are subjected to different environmental pressures. Therefore, additional studies are urgently needed to verify the GWAS findings across different populations. This study focused on the natriuretic peptide receptor C gene (*NPR3*), one of the hypertension-positive genes identified in a GWAS of an East Asian population. The correlation analysis between *NPR3* and hypertension was replicated in 450 Chinese Dai (235 patients vs 215 controls) and 484 Chinese Mongolian (211 patients vs 273 controls) individuals. The positive SNP identified by GWAS analysis and three other tag SNPs representing the *NPR3* linkage disequilibrium (LD) block regions were selected for genotyp-

ing. The results revealed that the rs1173766 polymorphism was associated with the occurrence of hypertension ($\chi^2 = 6.87$, $P = 0.0088$), and that the T allele should be protective in the Dai ethnic group. Considering a close LD block at the 3' end of the *NPR3* gene in the East Asian population, we speculate that there might be a mutation in the last five exons or the 3' untranslated region of *NPR3* that could change the structure or expression of the *NPR3* gene. However, in the Mongolian ethnic group, these SNPs were not associated with the incidence of hypertension, suggesting population heterogeneity for the genetic factors that contribute to hypertension.

Key words: Population diversity; Hypertension; GWAS; Genetics; NPR3