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Genetic polymorphisms of pharmacogenomic VIP variants in the various ethnic minority from China

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Background: It is well-established that the differences among ethnic groups in drug response mainly lie in the genetic diversity of pharmacogenes. A number of genes or variants which play a crucial role in drug response have been summarized as the Very Important Pharmacogenes(VIP) by PharmGKB database. And to clarify the polymorphic distribution of the VIP genes in different ethnic groups will aid to the personalized medicine in specific populations.

Methods: In the present study, we genotyped 85 pharmacogenomic VIP variants in the Kyrgyz population, Lhoba population, Uygur population, Deng people, Mongol nationality, Sherpa population, and Tibetanin Northwestern China and compared our data with other four major human populations including Han Chinese in Beijing, China (CHB), the Japanese in Tokyo, Japan (JPT), a northern and western Europe population (CEU), and the Yoruba in Ibadan, Nigeria (YRI). 85 pharmacogenomic VIP variants were genotypedin 700 Chinese subjects consisting of 100 Kyrgyz, 100 Lhoba, 100 Uygur, 100 Deng, 100 Mongol, 100 Sherpa and 100 Tibetan by Mass ARRAY platform. Genetic frequencies of these variants, haplotype distribution and comparison with those in four Hap Map populations including Han Chinese in Beijing, China (CHB), the Japanese in Tokyo, Japan (JPT), a northern and western Europe population (CEU), and the Yoruba in Ibadan, Nigeria (YRI) were analyzed.

Results: We found there were three the selected VIP variant genotype frequencies in these ethnic minorities which differed from thoseof the CHB, JPT and CEU, respectively ($p < 0.05/85$), particularly differed from the YRI.These three sites located in the PTGS2 gene, ADH family ADH1B genes, VDR gene.VDR encodes the nuclear hormone receptor for vitamin D3 and secondarybile acid lithocholic acid. Mutations in this gene are associatedwith type II vitamin D-resistant rickets.The *PTGS2*(prostaglandin-endoperoxide synthase 2)gene is located on chromosome 1andencodes prostaglandin G/H synthase-2, whichcatalyses the first two steps in the metabolism of arachadonic acid. The -765G > C promoter SNP (rs20417) is the best-studied variant in *PTGS2*.NR1I2 is a key regulator for the expression of genes involvedin all stages of drug metabolism and transport. Phase I drugmetabolizing enzymes regulated by PXR/NR1I2 include several CYPs, carboxylesterases, and dehydrogenases. Haplotype analyses also showed differences among the ethnic minoritiesin China and the four Hap Map populations.

Conclusion: Our data complement the pharmacogenomics information of ethnic minorities in China provided by the existing database worldwide, and provide a template for the study of pharmacogenomics in various ethnic minority groups in China. These information would provide a theoretical basis for safer drug administration and individualized treatment plans for the ethnic minorities in China.

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