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Genetic polymorphisms of pharmacogenomic VIP variants in seven national minorities from different regions of China

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Pharmacogenomic variant information is well known for major human populations; however, this information is less commonly studied in minorities. We genotyped 85 very important pharmacogenetic (VIP) variants (selected from the PharmGKB database) in the Tibetan, Uygur, Miao, Li, Deng, Kyrgyz, Ihoba populations and compared our data with other major eleven populations from the HapMap data set, including ASW, CEU, CHB, CHD, GIH, JPT, LWK, MEX, MKK, TSI and YRI. We also downloaded SNP allele frequencies from the Allele Frequency Database to observe the global genetic variation distribution for these specific loci. Through statistical analysis, we found that genotype frequencies of A*DH1B, AHR, CYP3A5, PTGS2, VDR, MTHFR* and *VKORC1* in our study populations differed widely from those in the 11 HapMap populations. Population structure and F-statistics (Fst) analysis also showed significant differences between these seven minorities and other HapMap populations. Our results complement the information provided by the database of pharmacogenomics on Tibetan, Uygur, Miao, Li, Deng, Kyrgyz, Ihoba populations. We provide a theoretical basis for safer drug administration and individualized treatment plans for these seven populations. We also provide a template for the study of pharmacogenomics in various ethnic minority groups in China.

Biography

Tianbo Jin has completed his PhD from Xi'an Jiaotong University and Postdoctoral studies from Brown University, School of Medicine. He is the Deputy Director of Key Laboratory for Molecular Genetic Mechanisms and Intervention Research on High Altitude Disease of Tibet Autonomous Region. He has dedicated to Pharmacogenomics for several years and published more than 100 papers in SCI journals.

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