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Genetic polymorphisms in very important pharmacogenomic (VIP) variants in the Tibetan population

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ABSTRACT. Genetic polymorphisms of very important pharmacogenomic (VIP) variants are important for personalized medicine. However, these have not been extensively studied in the Tibetan population. In this study, 82 VIP variants were detected in the Tibetan and Han (HAN) populations from northwestern China. Subsequently, we compared the differences between the Tibetan population and ten populations, including the HAN, Japanese in Tokyo (JPT), Mexican ancestry in Los Angeles (MEX), Toscans in Italy (TSI), African ancestry in Southwest USA (ASW), Luhya in California Webuye, Kenya (LWK), Gujarati Indians in Houston, Texas (GIH), Maasai in Kinyawa, Kenya (MKK), Yoruba in Ibadan, Nigeria (YRI),

and Utah residents with Northern and Western European ancestry from the CEPH collection (CEU). Using the χ^2 test, we identified differences in the frequency distribution of 4, 4, 7, 10, 11, 11, 13, 15, 19, and 20 loci in the Tibetan population, compared to the HAN, JPT, MEX, TSI, ASW, LWK, GIH, MKK, YRI, and CEU populations, respectively [$P < 0.05/(82*10)$]. rs2115819, rs9934438, and rs689466, located in the *ALOX5* (arachidonate 5-lipoxygenase), *VKORC1* (vitamin K epoxide reductase complex, subunit 1) and *PTGS2* (prostaglandin-endoperoxide synthase 2) genes, respectively, in the Tibetan population were different from those in most of the populations. Our results complement the information provided by the database of pharmacogenomics on Tibetan people, and provide an avenue for personalized treatment in the Tibetan population.

Key words: *ALOX5*; *VKORC1; PTGS2*; Pharmacogenomics; SNP

