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Detection of the Polymorphism of 19 SNPs Associated with the Metabolism of Anti-CVD Drugs by Multiplex PCR-LDR in CVD Patients

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ABSTRACT Cardiovascular diseases (CVD) are worldwide threat to human health, resulting in the highest mortality among all causes of death. The effect of therapeutic medicines for CVD varies greatly among people because of their different genetic background. In order to evaluate the necessity of having genetic testing before taking medicines in CVD patients, 19 SNPs influencing the metabolism of frequently-used anti-CVD drugs were selected and detected in 237 CVD patients by PCR-LDR method. The results showed that the genotypic distribution of most SNPs met the Hardy–Weinberg principle. The allelic distribution of the SNPs in the tested samples was similar to that in Chinese population. 78 percent of these patients carried at least one allele that affected the efficacy of the medicines. The accuracy of the PCR-LDR detection for the clinical samples was comparable to that of Sanger sequencing, and with higher multiplexity and lower cost.