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Interference of Homologous Sequences on the SNP Study of CYP2A13 Gene

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摘要

Background and objective It has been proven that cytochrome P450 enzyme 2A13 (CYP2A13) played an important role in the association between single nucleotide polymorphisms (SNP) and human diseases. Cytochrome P450 enzymes are a group of isoenzymes, whose sequence homology may interfere with the study for SNP. The aim of this study is to explore the interference on the SNP study of CYP2A13 caused by homologous sequences. Methods Taqman probe was applied to detect distribution of rs8192789 sites in 573 subjects, and BLAST method was used to analyze the amplified sequences. Partial sequences of CYP2A13 were emplified by PCR from 60 cases. The emplified sequences were TA cloned and sequenced. Results For rs8192789 loci in 573 cases, only 3 cases were TT, while the rest were CT heterozygotes, which was caused by homologous sequences. There are a large number of overlapping peaks in identical sequences of 60 cases, and the SNP of 101 amino acid site reported in the SNP database is not found. The cloned sequences are 247 bp, 235 bp fragments. Conclusion The homologous sequences may interfere the study for SNP of CYP2A13, and some SNP may not exist.

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