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Blood clot as a DNA source for studying genetic polymorphism of human carcinogen-metabolizing enzymes

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Abstract

AIM: Genetic polymorphism of human carcinogen-metabolizing enzymes such as cytochromes p450 (CYP) and glutathione S-transferases (GST), may cause alterations of enzyme activity and affect an individuals ability to metabolize environmental carcinogens. In cancer epidemiological and interventional studies, serum from cancer patients and non-cancer subjects are often discarded. The present study was undertaken to investigate the possibility of using blood clots as a DNA source for PCR-based genetic polymorphism analysis on carcinogen- metabolizing enzymes.

METHODS: Twenty blood samples were obtained from healthy subjects in Henan, China. The blood clots were stored in -80 ℃ prior to use. PCR-bas ed identification was performed in comparison to the use of purified DNA.

RESULTS: The DNA yield from 4 clot samples ranged from 13 to 9 6 μg/mL clots. Successful polymorphism analysis of CYP2E1 (Pst 1, Rsa 1, and Dra 1), GSTM1, and GSTT1 was demonstrated for all 20 samples examined. The concordance rate of PCR-based identification was 100% for direct use of clot lysate in comparison to the use of purified DNA.

CONCLUSION: We conclude that the blood clot is a valuable DNA source for genetic polymorphism analysis. Concerning with the existing cancer epidemiological studies, this convenient DNA source provides a good opportunity to determine the relationship between genetic polymorphism and cancer susceptibility.

Key words: Cytochromes p450; Glutathione S-transferase; Genetic polymorphism; DNA; Carcinogen metabolizing enzymes

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