TP53 mutations and polymorphisms in hepatomas in South-Korea

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Background TP53 is the most frequently mutated gene in human cancers arising from a wide spectrum of tissues. Mutations in TP53 gene have been identified in all exons and virtually all introns. However in Korea, TP53 mutation studies have been conducted either at the protein level by immunohistochemical methods or by analysis of a limited part of the TP53 gene, i.e., the hot spot region.

Methods We have initiated a large-scale molecular epidemiological approach to determine complete spectra of TP53 mutations and polymorphisms in one of the most common human cancers in South-Korea, the hepatoma, by using Two-Dimensional Gene Scanning (TDGS).

Results TDGS is a cost effective, expedient, and accurate technology based on multiplex PCR and two-dimensional DNA electrophoresis. In a two-step multiplex PCR, the p53 coding region (exons 2–11) was first amplified as a single 8.9 kb fragment by long distance PCR, which then served as a template for the subsequent co-amplification of the individual exons in three multiplex groups. The PCR products were combined and then separated on the basis of both size and base pair sequence in a denaturing gradient gel, using an automated 2-D electrophoresis system. We analyzed the 88 genomic DNA samples from tumors.

Conclusion We have identified heterozygote DNA variants present throughout the p53 exons. The spectrum of these mutations together with clinicopathologic features are presented.