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Analysis Of DNAs In Normal And Tumor Tissues Of Hepatocellular Carcinoma Using Whole Genome Sequencing

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Background : Primary liver cancer is the second leading cause of cancer-related deaths in Korea. Hepatocellular carcinoma (HCC) is one of the most common types of primary liver cancer, and infection with hepatitis B virus (HBV) and hepatitis C virus (HCV) is one of the important causes of the development of HCC. However, the mechanisms of the development of HBV and HCV-infected related HCC are not clear. The aim of this study is to examine the genes involved in the development of HBV and HCV-infected related HCC.

Methods : 4 HBV-infected HCC and adjacent normal liver tissue and 2 HCV-infected hepatocellular carcinoma and adjacent normal liver tissue were included in this study. Single point mutation (single nucleotide polymorphisms, SNP) and insertion/deletion (indel) mutations were analyzed using whole genome sequencing.

Results : Indel mutation of DNMT3A gene was commonly observed in 4 samples. Single point mutations of SIRT1, ZDHHC8P1, FGF18-SMIM23, and KRT73-KRT2 were observed in common in 3 samples. rs148398571 SNP of DPP9 gene was found only in HCV samples, and rs140405310 of ANGPTL6 was found only in recurred sample.

Conclusions : The mutations between HCC and adjacent normal liver tissue were not consistent in all samples. However, indel mutations in the DNMT3A gene and SNPs of SIRT1, ZDHHC8P1, FGF18-SMIM23, and KRT73-KRT2 might contribute to the development of HCC. These results could provide evidence for the development of diagnostic and therapeutic tools for HCC.

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