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# Hepatitis C virus core gene polymorphism in cases of hepatocellular carcinoma

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**Introduction:** Hepatocellular carcinoma (HCC) is one of the common sequelae of hepatitis C virus (HCV) infection. It remains controversial, however, whether HCV itself plays a direct role in the development of HCC. Although HCV core protein was reported to display tumorigenic activities in cell culture and experimental animal systems, its clinical impact on HCC development in humans is still unclear.

**Aim:** We mapped sequence differences in the viral core gene which is strongly implicated in cellular transformation and the development of liver cancer to test the hypothesis that core gene sequences from HCC patients differ from those of patients without HCC.

**Methods:** HCV core sequences from HCC patients and controls were obtained and compared with each other. A logistic regression model was developed to predict the HCC risk of individual mutations and other sequence features.

**Results:** Study showed that sequences of HCV in patients with hepatocellular carcinoma differ from those of patients with early-stage liver disease. One polymorphism was particularly strongly associated with liver cancer. Specifically, core amino acid position 71 was present in 33.3% of the full length sequences from patients with HCC but only 6.7% of patients without HCC. Multivariate analysis identified core amino acid polymorphism, elevated α-fetoprotein (AFP) levels, elevated ALT level, elevated alkaline phosphatase level and liver fibrosis as independent factors associated with HCC.

**Conclusions:** HCV core genes from patients with and without HCC differ at several positions. Our findings suggest that HCV core gene sequence data might provide useful information about HCC risk. Prospective investigation is needed to establish the temporal relationship between appearance of the viral mutations and development of HCC.

## Biography

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