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Somatic mutations, hepatitis B virus integration and epigenetic modification during the evolution process of hepatocellular carcinoma

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Hepatocellular carcinoma (HCC) is the third leading cause of cancer mortality worldwide. Chronic infection with hepatitis B virus (HBV) and/or hepatitis C virus (HCV) is the major cause of this malignancy. Recently, advanced sequencing technologies such as whole genome sequencing, exome sequencing, and RNA sequencing have provided opportunities to understand the insight of how somatic mutations, structure variations, HBV integrations and epigenetic modifications contribute to HCC development. Chronic inflammation provides “fertile field” for somatic mutation, selection, and adaptation, the so called evolutionary process during HCC development. Genomic variations of HCC caused by various etiological factors might be different, but the common genomic variations should be important to elucidate the HCC evolutionary process. Genome-wide analysis of HBV integrations may help clarifying the mechanisms of HBV-induced hepatocarcinogenesis and disease progression. RNA sequencing presents additional evidences of epigenetic modifications during HCC evolution. In this review, the current findings of next generation sequencing of HCC caused by various etiological factors to interpret the potential mechanisms of HCC evolution is summarized. Understanding the key genomic variations during HCC evolution is essential for accurate prognosis prediction and efficient targeted treatment of this fatal malignancy.

Biography

Xiaowei Ji is now pursuing her graduate degree in the Department of Epidemiology from Second Military Medical University. She has one paper revised in a reputed journal.

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