

Identification of Ankyrin Repeat and RNASE Domain Mutations of RNASE-L in HCC and its correlation with HCV Viral Load



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Biography

Anum Liaquat Ali is a researcher working in Dow University Pakistan whose research interest lies in Microbiology and genetic engineering.



Abstract

Hepatocellular carcinoma (HCC) is the 5th commonest malignancy and leading second most common cause of cancer associated deaths worldwide and each year the death ratio is about 662,000 people across the globe. The WHO has provided the statistics and registries of cancer, which claims the estimation of about 564,000 new cases of HCC identification every year. The highest risks have been reported in accordance to people found living in Eastern Asia, central Africa, and Western Africa. HCC is a form of liver cancer and about 80% of cases are correlated with chronic viruses infections. In 80%–90% patients of HCC it has been observed that the initiation of cirrhosis is due to HBV and HCV. Different types of gene mutations are also involved HCC pathogenesis. RNASE L has one of the most significant role in antiviral response. Which is regulated by interferon and involved in the cleavage of viral RNA therefore the aim of this study is to identify RNASE L ANK and RNASE domain mutation/s in patients and correlate it with viral load of HCV.

ii. Objectives:

- (1) To undertake mutational analyses of RNASE L 2,5A binding site in ANK and RNASE L RNASE domains.
- (2) To determination of HCV viral load in HCC.

Methodology: In this study a total of 120 whole blood samples will be investigated. DNA will be extracted followed by the PCR. To analyze RNASE-L amplified PCR product gel-electrophoresis will also be performed. The amplified samples of RNASE-L would be directed to Macrogen, Korea for the sequencing while mutation analysis will be done by BioEdit and MEGA 7 software. All the RNASE-L mutations will be co-related with HCV viral load.



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