

## Identification of Ankyrin Repeat, RNASE Domain of RNASE L Gene Mutation in Hepatocellular Carcinoma and its Association with HCV Viral Load

**Background:** Hepatocellular Carcinoma (HCC) is the most common primary malignant tumour of the liver. This is multiple risk factors are associated with its pathogenesis. Chronic liver infection via Hepatitis is by far most common cause of HCC worldwide. It is a viral infection by Hepatitis C virus (HCV), Hepatitis B virus (HBV) and Hepatitis D virus (HD). Pathogenesis of HCC is a combination of multiple genetic factors. Certain gene mutations are directly involved in the development of carcinoma; one that stands out most are RNASE-L. We assume that mutation of this gene also co-relates with viral load of hepatitis which in turn increases the severity of HCC.

**Methodology:** This study was conducted in Dow University of Health Sciences, department of Molecular Pathology DDRRL and National Institute of Liver & GI Diseases (NILGID), We investigated 80 whole blood samples, from which we extracted DNA and then PCR performed. The amplified PCR products were sent to Macrogen, Korea for analysis and sequencing of RNASE-L gene mutation followed by sequence analysis via BioEdit and MEGA 7 software. After which HCV viral load was correlated with those sequences.

**Result:** The categories of our sample were; 1) HCV positive patients, 2) HCV positive patients with HCC and 3) HCC diagnosed patients. Out of the 80 blood samples, 5% are of HCC, 50% are of HCC along with HCV, and the remaining blood samples are of HCV positive individuals. Out of which 57.5% are males and 42.5% are females. Sequence analysis revealed, only one sample to have SNV G>A in RNASE domain, and none of the samples have SNV in ARD

**Conclusion:** In this study we tried analyze the genetic aspect of HCC, so that it can help us therapeutically. Our health care system is in dire need of some immediate reforms that are necessary to control the prevalence of HCC.

### Biography

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