Environmental Microbiology 2022 &

17th International Conference on Virology, Emerging Diseases & vaccine

&

6th International Conference on Microbes and Beneficial Microbes

ISSN: 2472-1212

November 03, 2022 | Webinar

Determination of ankyrin repeats domain (ANK) of rnase l gene in hepatitis c patients and its effects in viral load

Hepatitis C virus is the major globally cause of death. Different types of gene are involved as Ankyrin repeat domains of RNASEL gene it perform a significant role in antiviral response, regulated by interferon, and involved in cleavage of viral RNA. Therefore, aim of this study was to identify Ankyrin repeat domain expression in Hepatitis C positive patients and correlate it with viral load of **Hepatitis** C. Objectives were to determine expression analyses Ankyrin repeat domains in hepatitis C patients and to correlate HCV Viral load with expressions of Ankyrin repeat domains.

Methods:

In this study, a total of 80 Hepatitis C RNA positive patient's whole blood samples were investigated.

RNA was extracted from plasma followed by Real Time PCR for quantization of HCV viral load and genotypic analyses. DNA was extracted from these samples followed by PCR amplification of ARK domain.

Results:

Out of the total 80 patients who were included in study, all had HCV infection. Among them, 48 (63.8%) were males and 32 (36.1%) were females. All patients infected with HCV were found to have genotype 3.ANK domain in HCV patients' sample mean range 17.000 \pm 15.187. Majority of patients were males and belonged to age group 58-73 years age. Mean age of patients was 50.86 \pm 14.84 years. All the HCV infected individuals had HCV genotype 3 and had viral loads mean range 837404.21 \pm 1302318 therefore all high HCV viral loads shown Ankyrin repeats domain of RNASE Gene expression mean rang 17.00 \pm 15.187.

Conclusion:

Further, in understanding about HCV disease result suggest which is an **individualized** therapy that is account for the gene factors, such as gene ankyrin repeat domain of Rnasel gene in conjunction with therapeutic effect are required to establish better strategies for controlling infection with HCV.

Keywords:

HCV, ANK, RNASE L, PCR.

Biography:

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Received: August 03, 2022; Accepted: May 20, 2022; Published: November 03, 2022

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