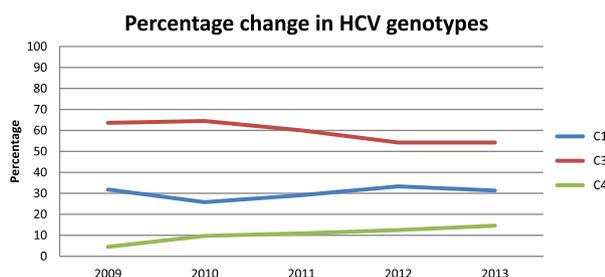
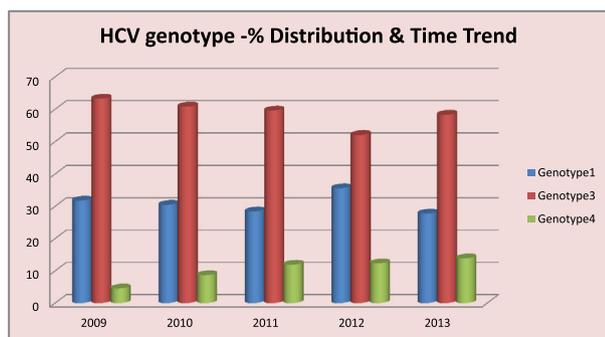


percentage of genotype 4 is 4.54% in 2009, 8.69% in 2010, 11.92 % in 2011, 12.32% in 2012 and 13.88 % in 2013. This rising trend of genotype 4 is statistically significant (P = 0.014).

Conclusion: Genotype 3 is the most prevalent HCV genotype in South India (with maximum of 3b followed by 3a) followed by genotype 1 (commonest is 1b followed by 1a and 1c) and then genotype 4 (commonest are 4a and 4d, with 4b as least common). A rising trend of Genotype 4 is noted from 2009 to 2013.

Discussion: HCV genotype 4, which is resistant to therapy, traditionally considered to be confined to the Middle East and Africa, now shows a rise in trend in South India.



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AN INCREASING TREND OF HEPATITIS C VIRUS GENOTYPE 1 AMONG HIGH RISK GROUP POPULATIONS IN EASTERN INDIA

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Background: Hepatitis C Virus (HCV) is increasingly a huge burden on health care systems throughout the world with large number of infected people worldwide. Genotyping and evaluation of viral load in HCV infected patients is important for clinical evaluation and therapeutic interventions. Thus, the present study was designed to determine the distribution pattern of HCV genotypes in high risk

group patients and establish their relationship with viral load.

Objectives: The major aims of this study were to ascertain the predominant circulating strain from eastern India among the high risk group populations and to correlate the viral load within these HCV patients.

Methods: A total of 444 HCV sero-positive samples from different high risk population groups like history of blood transfusion (HBT), dialysis (D), hemophilia (H), intra venous drug users (IVDUs) and thalassemia (T) patients were included in this study. The detection of HCV RNA was performed using nested RT-PCR assay of the 5' untranslated region. For genotyping, five prime untranslated region (5' UTR) positive samples were subjected to core region amplification by nested RT-PCR assay. The HCV viral load was measured based on 5' UTR of HCV genome using AgPath-ID™ One Step RT-PCR kit.

Results: Of the total 444 sero-positive samples 315 (70.94%) were RNA positive among them 228 were genotyped. Genotype 3 was found to be 52.24% (3a: 62.5%, 3b: 36.72%, 3k: 0.78%) followed by 47.34% genotype 1 (1a: 34.48%, 1b: 63.8%, 1c: 1.72%), genotype 6h was 0.42% of our study population. Genotype 1b was the predominant genotype within the population groups of HBT (33.34%), D (35.71%) and IVDUs (38.46%) and genotype 3a was significantly high only in the populations comprising of T (63.43%) individuals. The mean viral load among the different patients groups were $6.28 \pm 0.89 \log_{10}$ IU/ml. The viral load observed among the three genotypes were $6.43 \pm 0.75 \log_{10}$ IU/ml, $6.31 \pm 0.77 \log_{10}$ IU/ml and $5.12 \pm 0.87 \log_{10}$ IU/ml for genotype 1, 3 and 6 respectively. Genotype 1 was associated with significantly higher (P < 0.0001) viral load compared to genotype 3 and 6.

Conclusion: The major circulating strain prevalent within the high risk group of eastern region is found to be genotype 3 closely followed by genotype 1 and with a small fraction of genotype 6. Increase in overall percentage of genotype 1 is being observed among high-risk group population. The viral loads were also significantly associated with the genotypes and genotype 1 showing statistically higher viral load compared to that of genotype 3 and 6.

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ELEVATED LEVEL OF LIVER ENZYMES IS NOT A SERUM MARKER FOR HEPATITIS C VIRUS INFECTION AMONG β-THALASSEMIC INDIVIDUALS

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