Prevalence of hepatitis C virus and its genotypes among a cohort of drug users in Kenya

Abstract:

Prevalence of hepatitis C virus and that of its main genotypes varies between the worlds geographic regions. The risk factors for infection with HCV include blood transfusion, tattoing and injecting drug use. To examine the prevalence of HCV and determine its main genotypes among a cohort of drug users in Kenya. A laboratory based study. Hepatitis research laboratory in the Centre for Virus Research at the Kenya Medical Research Institute, Nairobi. Three hundred and fourteen male and 19 female intravenous and non-intravenous drug users aged between 15-55 years. Seventy four (22.2%) out of 333 samples tested positive for anti-HCV. Sixty nine out of the 74 serum samples were assayed for HCV RNA and 38 (55.5%) were positive. The RNA positive samples were further subjected to sequencing and 19 (73%) of the samples were classified as genotype 1a, while seven (27%) samples were classified as genotype 4. Genotypes 2, 3, 5 and 6 were not identified in this study. These results demonstrate a high HCV infection prevalence among this cohort of drug users (22.2%) as compared to that of the general population, which is estimated to be 0.2-0.9%. The study also confirms the presence of at least two major genotypes among Kenyan drug users (genotypes 1 and 4).