Introduction
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During the late 1970s, despite the introduction of screening tests for the detection of hepatitis B surface antigen (HBsAg), 7-10 % of blood transfusion recipients in the United States of America developed post-transfusion hepatitis (PTH). Serological tests for the diagnosis of hepatitis A and hepatitis B were negative in 90 % of these cases and the term Non-A, Non-B (NANB) hepatitis was used to describe the condition.

Two different agents were thought to be responsible for NANB hepatitis, one parenterally-transmitted (PT-NANB) and other enterically-transmitted (ET-NANB). These two agents were distinguishable by their incubation periods, lack of cross immunity, physiochemical properties and histopathological changes in chimpanzees. Infection with one of the agents was associated with the appearance of cytoplasmic tubules within infected hepatocytes and the other with nuclear aggregates. Buoyant density studies and prevention of transmission to chimpanzees by heat, β-propiolactone, formalin or organic solvent inactivation of the infectious fraction with the tubule-forming agent suggested it to be a small, enveloped, RNA virus. This particular agent after successful cloning in 1989 came to be known as the "hepatitis C virus" (HCV).
HCV infection is found in 0.02 to 27 % of blood donors worldwide. Because the infection is chronic in more than 60 % of infected persons, the disease is an important public health and economic problem. The management of patients with chronic hepatitis C is complex—the disease is often only mildly symptomatic and slowly progressive, about 20 % of patients develop cirrhosis after 20 years of infection and perhaps 10 % of those with cirrhosis develop hepatocellular carcinoma (HCC).

Transmission of HCV is primarily through parenteral, vertical and sexual route and hence the high-risk group consists of recipients of blood transfusions, haemophiliacs, haemodialysis patients, infants of HCV-positive mothers, intravenous drug abusers and health care workers exposed to needle-stick injuries. Transmission has also been reported through tattooing, bites and intrafamilial mode.

The HCV genome has certain conserved regions and certain hypervariable regions. The diversity of this virus, in the variable regions, has lead to its classification into "genotypes" that differ substantially in nucleotide sequence. Currently there are 11 genotypes with more than 70 subtypes. These genotypes have a characteristic geographic distribution and are important in the prognosis of the disease.

Since its discovery a lot of work has been going on in the field of developing better diagnostic systems for HCV. As a result we have the Enzyme-linked immunosorbent assays (ELISA) and Recombinant immunoblot assays (RIBA) in the third-generation. With every newer generation assay
there is an increase in specificity and sensitivity and there is also an effort to minimise the time in diagnosis.

As there is no antigen detection system available commercially for the diagnosis of HCV infection, the Reverse transcriptase- Polymerase Chain Reaction (RT-PCR) is the only assay which indicates ongoing viral replication or viraemia and it has proven to be a very useful diagnostic tool in detecting HCV-RNA from serum, liver biopsies, urine, tear and oral fluid.

Currently the treatment for hepatitis C is alpha-interferon (α-IFN) and Ribavarin given singly or in combination. There is a fall in Alanine aminotransferase levels and HCV-RNA levels in serum in the responders. The treatment regimen could last for 6 to 12 months. It has been shown that treatment is effective when combination therapy is followed and that too for a longer duration.

Disease prognosis is influenced by a number of factors. Co-infection with other hepatitis viruses, consumption of alcohol, and increasing age are all associated with poorer prognosis. Infection with type 1b and 4 have the worst prognosis, proceeding much faster to severe forms of chronic hepatitis, cirrhosis and HCC.

Prevention is the only way to tackle this problem as there is no vaccine available for HCV at present. The impending blocks for the development of a successful vaccine are the absence of neutralising antibodies and the heterogeneity of the HCV genome. Currently, the approach is to develop a vaccine based on HCV proteins expressed by recombinant DNA technology.
In the background of all these findings, the present pilot study was taken up to analyse the baseline prevalence pattern of HCV infection and its molecular characterisation in Tamilnadu, South India.