

Sequencing hepatitis C virus

In India, scientists have sequenced the genome of an Indian isolate of hepatitis C virus (HCV), opening up new vistas for the development of better diagnostics and therapies. The three-year project, sponsored by the Department of Biotechnology, was carried out at the Deccan College of Medical Sciences and Allied Hospital at Hyderabad, in collaboration with industries like Shantha and Sudarshan Biotech and an NRI scientist, Prof. Ramareddy V. Guntaka from the University of Tennessee, the United States. Data obtained from this significant development would help identify specific genetic sequences for developing better diagnostics, new drug targets, anti-viral compounds and vaccines. There are at least 20 different strains of HCV across the world and most of them have been sequenced. The Indian strain had not been sequenced so far.

Hepatitis C is the major cause of liver diseases like chronic hepatitis, liver cirrhosis and hepatocellular carcinoma throughout the world. It is the most dreaded among the entire hepatitis virus group, with 85 per cent of infected cases resulting in severe complications like liver cancer. In India, over 25 million people are estimated to be carrying this virus described as 'stealth virus' as it silently affects the patients. Of them, about 4.5 million run the risk of developing liver cirrhosis or cancer.

Globally, there are 11 genotypes and several subtypes of HCV. The only approved anti-HCV agents are compounds like interferon alpha and ribavirin. The HCV genome is a single-stranded RNA molecule which codes for a single protein of about 3,000 amino acids. The sequenced Indian strain, which has since been submitted to the United States-based GenBank, resembles the Japanese strain and it would take at least six more months to determine the extent of genetic variation of the strain among Indians. (Chemical Weekly, 25 September 2001)