Development of a Hepatitis C Virus (HCV) Vaccine

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Technology description

HCV is a major causative agent of post-transfusion and community-acquired non-A, non-B hepatitis world-wide. About 4 million people in the US and probably more than 100 million worldwide are infected with HCV. The majority of HCV infected individuals become persistently infected and many develop chronic hepatitis which progresses eventually to liver cirrhosis and hepatocellular carcinoma. HCV is a member of the flavivirus family. The HCV viron contains a positive-strand RNA genome of 9.5 kilobases including a highly conserved 5' non-coding region followed by a long open reading frame of 9030 to 9099 nucleotides that is translated into a single polyprotein about 3,010 to 3030 amino acids long. Although the viral genomic organization has been characterized in detail, morphologic analysis of hepatitis C virus has been hampered by low levels of HCV particles in infected patients and the inability to propagate efficiently the virus in cultured cells. The levels of the viral particles present in infected patient plasma and/or liver tissues are very low, making it difficult to visualize the virus. Studies of HCV infection in chimpanzees, a reliable animal model for hepatitis C, have provided evidence that HCV is inactivated by chloroform, indicating that it contains lipids and therefore is probably enveloped. Filtration studies have estimated the viron particle size to be about 30-60 nm in diameter. The National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK) of the National Institutes of Health (NIH) is seeking licensees and/or capability statements from parties interested in entering into a Cooperative Research and Development Agreement (CRADA) to develop a hepatitis C virus (HCV) vaccine based on the synthesis, large-scale production, and purification of non-infectious HCV-like particles containing HCV structural proteins

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