



## The Discovery of Hepatitis C Virus

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Hepatitis, or the inflammation of the liver, is primarily caused by viral infection. Other significant factors to it include alcohol abuse, environmental contaminants, and autoimmune diseases. It became apparent in the 1940s that there were two major forms of contagious hepatitis. In the 1960s, Hepatitis B and A vaccines were being made but according to Harvey J. Alter, large cases of transfusion-related hepatitis still remained. This led to the identification of an unknown infectious agent that caused the “non-A, non-B” Hepatitis which is the untreated transfusion-related hepatitis cases. For more than a decade, the unknown infectious agent was then identified. The phenomenal discovery that resulted in the 2020 Nobel Prize in Physiology or Medicine was awarded to the three scientists: Harvey J. Alter, Michael Houghton, and Charles M. Rice. Their landmark studies revealed that it was the Hepatitis C that was the culprit in the remaining blood-borne hepatitis. Harvey J. Alter’s analytical research of transfusion-associated hepatitis confirmed that a common cause of chronic hepatitis was an unknown virus. In order to separate the genome of a new virus called the Hepatitis C virus, Michael Houghton used an unestablished method. Charles M. Rice offered the final proof that the hepatitis C virus itself could develop hepatitis. The discovery of the Hepatitis C virus identified the cause of the remaining cases of chronic blood transfusion-related hepatitis and made it possible for thousands of lives to be saved by blood testing and new treatments.

### Detecting HCV through sequencing

The hepatitis C virus (HCV) has infected over 170 million people worldwide and is a globally relevant blood-borne agent that causes liver diseases. HCV is a

diverse group of RNA viruses that are currently split into both genotypes 1-7 and subtypes. HCV infection can be treated with antiviral drugs, but it is important to establish the HCV genotype for optimal treatment strategy selection.

### PacBio sequencing

Recently, newly developed novel sequencing technologies have been capable of producing exceptionally long reads. Single-Molecule Real-Time (SMRT) sequencing using the PacBio RSII or Sequel sequencers (Pacific Biosciences) is among the main third-generation sequencing technologies. SMRT sequencing is a system for sequencing-by-synthesis focused on real-time visualization of fluorescently tagged nucleotides along with the production of specific DNA model molecules. SMRT sequencing has been applicable to numerous scientific issues, such as identifying the full-length genome sequences of bacteria, metagenomic analysis of viruses or bacteria, haplotype gene determination, transcriptomic analysis of splicing variations, and determination of the full-length human genome sequence, taking the benefit of ultra-long read length into account.

### Nanopore sequencing

Nanopore sequencing is another technique for single-molecule real-time sequencing. Nanopore sequencing does not use base synthesis reaction, which radically varies from other sequencing technologies. Instead, it specifically detects the sequence of the nucleotides that make up single-stranded DNA molecules by changing the electrical voltage as it moves through a protein pore.