**Hepatitis C Virus Typing**

The Hepatitis C Virus (HCV) is highly variable and diversified worldwide. The genotype/subtype of HCV has great clinical significance in that the selection of the most appropriate antiviral regimen is based on the HCV genotype/subtype. According to the International Committee on Taxonomy of Viruses (ICTV), as of June 2017, HCV is classified into 7 genotypes and 86 subtypes. To support the ICTV classification scheme, the ViPR team has developed a robust HCV typing pipeline based on phylogenetic inference.

A complete description of the method is described in the SOP document on the ViPR website.

This typing tool is also available for annotating user-provided sequences. Go to [https://www.viprbrc.org > Hepatitis C Virus > Analyze & Visualize > Genotype-Recombination Detection](https://www.viprbrc.org).

Users can easily search for sequences based on genotype/subtype annotations via the sequence search page ([https://www.viprbrc.org > Search Data > Search Sequences](https://www.viprbrc.org)).

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<th>Strain Information</th>
<th>HCV Genotyping/Subtyping Report (Beta) (SOP)</th>
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An HCV typing report provides genotype/subtype assignment and the corresponding support value. Report files include an alignment of query sequence with the reference alignment, an output tree where the query sequence is placed within a fixed reference alignment and a subtype assignment report from cladiator.

In addition to providing the HCV typing tool via the ViPR website, all HCV genomes >400 nt in the ViPR resource have been annotated using the tool. Compared with GenBank, this method provides genotype/subtype annotations in ViPR for 22943 (27%) sequences with no genotype information in GenBank records, and subtype annotations in ViPR for 3533 (4%) sequences with only genotype information in GenBank.

The November 2017 release of ViPR is now available, visit [www.viprbrc.org](http://www.viprbrc.org)

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**Outreach Events**

- **December 5-8, 2017:** Bioinformatics Workshop on Applications of Genomics & Bioinformatics to Infectious Diseases, Lyon, France

The GABRIEL Network and J. Craig Venter Institute co-organized this workshop. Twelve attendees from seven countries (Bangladesh, Brazil, Cambodia, France, India, Laos and Paraguay) attended the workshop. The IRD/ViPR team taught next generation sequencing technologies, sequences and sequence annotations in public databases, evolutionary analysis and comparative genomics analysis.