

Scientists Model Hepatitis C Virus

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One of the most common life-threatening viral infections in the United States today is hepatitis C virus (HCV). The standard treatment is successful in only about 50 percent of treated HCV chronic patients, with no effective alternative treatment for those who fail to clear the virus.

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Source: Los Alamos National Laboratory

Recently, scientists at Los Alamos National Laboratory, in collaboration with researchers from the Center for HCV Research at Rockefeller University, developed the first mathematical model of intracellular HCV replication. The model is designed to help scientists and medical researchers develop a better understanding of the dynamics of replication, as well as the mechanisms of drugs currently being used to treat HCV. This new understanding may eventually lead researchers to a more successful treatment for the virus.

In research published recently in the *Journal of Virology*, Los Alamos theoretical biophysicist Harel Dahari and his colleagues describe how they leveraged recent advances in HCV cell culture replication to provide the quantitative data necessary for creating a computer model of the dynamic interplay between host and virus during replication of the virus in Huh-7 (human liver) cells.

"With more than 200 million people in the world infected with HCV and half of those not responding to treatments," said Dahari, "our model can be an important tool for understanding the HCV replication mechanisms. Perhaps more importantly, it may prove useful in designing and evaluating new antivirals for use in combating the virus."

According to the researchers, the next step will be to incorporate virus production and infection into one comprehensive model of the complete HCV life cycle.

Dahari, Ruy Ribeiro and Alan Perelson from Los Alamos and Charles Rice from Rockefeller University collaborated in this research, which was

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