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## How to tell if a hepatitis-C-virus-infected patient will respond to therapy

Hepatitis C virus (HCV) causes hepatitis and increased risk of developing liver cancer. Current treatments are expensive, have severe side effects, and fail in about half the patients treated. However, the Virahep-C Study Group, at Saint Louis University, has now developed an approach that predicted the outcome of therapy, raising the possibility of a test to predict treatment response and reduce treatment failures, something that could save a great deal of pain and expense for HCV-infected patients.

The research team, led by John Tavis and Rajeev Aurora, used a method known as covariation analysis to analyze variation in the genome-wide amino-acid sequence of viruses isolated from HCV-infected patients before they underwent treatment. Using this approach, networks of covariation were found to associate with specific responses of the patients to treatment. The authors suggest that the data has implications for the development of a test to predict how an individual infected with HCV will respond to treatment and might help identify targets for new antiviral drugs. In an accompanying commentary, Thomas Oh and Charles Rice, at Rockefeller University, New York, discuss further the therapeutic implications of these data.

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TITLE: Genome-wide hepatitis C virus amino acid covariance networks can predict response to antiviral therapy in humans

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ACCOMPANYING COMMENTARY TITLE: Predicting response to hepatitis C therapy

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