Discovery could improve hepatitis C treatment

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Dr. Melanie Bahlo from the Walter and Eliza Hall Institute is part of an international team that has discovered a genetic variation that could identify those people infected with hepatitis C who are most likely to benefit from current treatments. Credit: Walter and Eliza Hall Institute

Walter and Eliza Hall Institute researchers are part of an international team that has discovered a genetic variation that could identify those people infected with hepatitis C who are most likely to benefit from current treatments.

Dr Melanie Bahlo and Dr Max Moldovan from the institute's Bioinformatics division worked with researchers from the University of Sydney and elsewhere to analyse the genomes of more than 800 people, including more than 300 Australians, who were receiving treatment for chronic hepatitis C infection.

Their genome-wide association study of people receiving hepatitis C treatment revealed that genetic variants near the interferon gene IL28B were associated with people's response to treatment.

Three per cent of the world's people are infected with hepatitis C and few are able to clear the virus without treatment.

The standard treatment is a combination of pegylated interferon-alpha and ribavirin (PEG-IFN-alpha/RBV). However this treatment is expensive ($20,000 per person in Australia), can have serious adverse effects and is unsuccessful in 50-60 per cent of cases.

At present it is not possible to identify the 40-50 per cent of people who will respond well to treatment.

To address this problem, Dr Moldovan and Dr Bahlo are building and evaluating statistical models that incorporate genetic variants, in combination with clinical and baseline factors, to best predict treatment outcome.

Through this approach the research team found that people having a specific genetic profile at a genetic variant called rs8099917 showed the strongest virological response when undergoing treatment.

The research results were published online last week in the international journal *Nature Genetics*. Two other research papers validating the same finding have been published in the past month.

Dr Bahlo said with the knowledge of the gene variants it would be possible to develop a diagnostic test, based on a person's genetic profile, to identify those who are likely to respond to treatment with PEG-IFN-alpha/RBV.

Further, the location of the newly-discovered genetic variant opens the way for development of a more effective hepatitis C treatment, which is likely to result in fewer adverse effects than PEG-IFN-alpha/RBV.

Finding effective treatments is essential as many people infected with hepatitis C become chronic carriers of the disease and may develop liver cirrhosis or liver cancer.

Source: Walter and Eliza Hall Institute