

Diagnostics

Biomarker to predict the risk of being infected with hepatitis C virus

A research group of the Andalusian Public Health System, in collaboration with the University of Jaén, has identified an allelic variant of the LDLRAP1 gene associated with a low susceptibility to hepatitis C infection and which, thus, can be used as a biomarker to predict the risk of an individual to be infected by this virus.

Oficina de
**TRANSFERENCIA
DE TECNOLOGÍA**
Sistema Sanitario Público de Andalucía



Description

A small proportion of individuals exposed to the hepatitis C virus (HCV) do not become infected. It has been observed that the lipidomic profile of individuals infected with HCV is different from those that eliminate viremia, either spontaneously or after antiviral therapy. Despite this, few genetic studies have been carried out in this context. Specifically, the association of the polymorphisms rs5925 and rs1042034, within the LDLR and APOB genes respectively, with resistance to HCV infection, has been reported, but none of them has been validated so far.

Currently the treatments against HCV are very effective, however, their cost and duration are barriers to the implementation of global measures for the elimination of this infectious agent. In addition, total eradication will only be possible if preventive measures of infection are adopted. Therefore, the development of new strategies for the management of HCV should be based on both preventive and therapeutic measures that replace or complement current treatments.

In this context, our group has evaluated genetic markers of genes involved in lipid metabolism. Specifically, an allele of the LDLRAP1 gene associated with low susceptibility to HCV infection and low expression of LDLRAP1 mRNA has been identified. A case-control study has been carried out in 1,006 patients chronically infected with HCV and 2,153 control subjects and 30 subjects exposed to the virus who do not become infected. Thus, identification of said allele by conventional techniques would allow predicting the risk of an individual exposed to HCV virus infection, which would help to establish adequate preventive and/or therapeutic strategies.



Advantages

1. It allows to stratify and classify subjects according to their risk to be infected by HCV, which helps to design new therapeutic and preventive strategies against this disease.
2. This biomarker could be used as a possible therapeutic target. The fact that there are naturally mutations in this gene that block their function without seriously affecting the live of the carriers, indicates that the protein product thereof can be transiently inhibited pharmacologically without danger for the subject.



Intellectual property

This technology is covered by a Spanish patent application with the possibility of international extension.



Aims

We are looking for a partner interested in a license and/or a collaboration agreement to further develop and exploit this innovative technology.



Classification

Area: Diagnostics

Pathology: Infectious diseases and Microbiology