**Diagnostics**

Combined genetic polymorphisms for predicting the response to treatment in patients infected with hepatitis c virus

A research group of the Andalusian Public Health System, in collaboration with the University of Jaén, has developed a method for predicting the response to treatment with pegylated interferon and ribavirin in patients infected with hepatitis C virus (HCV).

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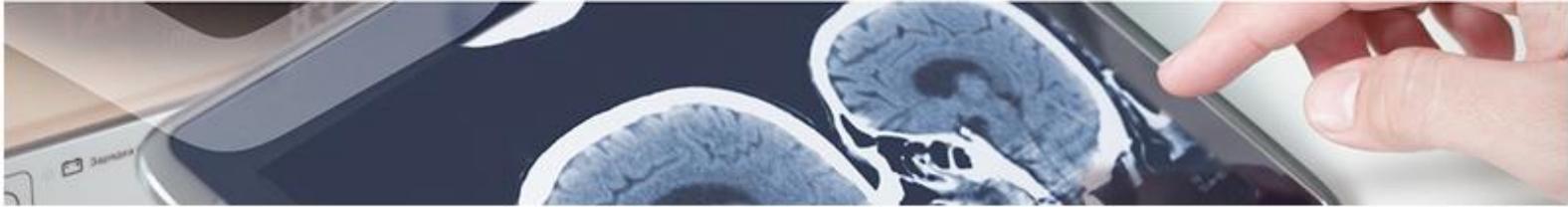
Description

Hepatitis C virus (HCV) infection increases lipidic biosynthesis and lipid storage in hepatocytes, contributing to HCV-associated hepatic steatosis, hypobetalipoproteinemia and insulin resistance. The assembly of the HCV virus is closely linked to the synthesis of very low density lipoproteins (VLDL) and the secretory pathway.

On the other hand, combined treatments based on pegylated interferon and ribavirin present strong adverse events and have a high cost per patient. However, the average efficacy rate reaches only 50-60% of patients. Therefore, a preliminary prediction based on genetic data would allow a more accurate selection of patients with a better prognosis.

Therefore, there is an unmet medical need of developing a new predictive method and kit for patients infected with hepatitis C virus (HCV), which could lead physicians to identify those patients more likely to respond to a combined therapy with pegylated interferon and ribavirin.

The present technology is based on a depth genetic analysis of more essential genes involved in cholesterol transport routes, a complete coverage of single nucleotide polymorphisms (SNPs) of LDLR genes and the fact that there are no previous studies which have established an association between LDLR and the pre-treatment with viral load (VL).

Advantanges

1. Univariate genotypic analysis performed in 442 patients infected with HCV allowed the identification of several predictive biomarkers of SVR.

2. The identification of the host critical factors that modulate the replication and spread of HCV has the potential to become a new target for antiviral drugs.
3. The genetic polymorphisms of LDLR genes are useful as predictive biomarkers for HCV genotype 1, 2, 3 and 4 infections, or any one of their combinations.

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: Diagnostic / Vaccines & Infectious diseases

Hospital Universitario Virgen del Rocío. Edificio de Laboratorios, 6ª Planta. Avda. Manuel Siurot, s/n 41013 Sevilla. ESPAÑA ☎+34 955 013 647 MÓVIL: +34 671 597 574
☞ pablo.hervas.exts@juntadeandalucia.es

JUNTA DE ANDALUCIA
CONSEJERÍA DE IGUALDAD, SALUD Y POLÍTICAS SOCIALES

IBIS
INSTITUTO DE BIOMEDICINA DE SEVILLA

FISEVI
Fundación Pública Andaluza para la Gestión de la Investigación en Salud de Sevilla