

ORAL PRESENTATION

Open Access

O312. Host genetics of HCV disease — *IL28B*

J Fellay

From Tenth International Congress on Drug Therapy in HIV Infection
Glasgow, UK. 7-11 November 2010

Co-infections with HCV and HIV are common, because both viruses share routes of transmission and establish chronic infections. The standard treatment for chronic hepatitis C, a combination of peginterferon- α and ribavirin, is poorly tolerated and only successful in about half of the treated patients. Thus, identification of accurate predictors of treatment response is highly desirable.

Several independent genome-wide association studies have recently identified human genetic variants around the *IL28B* gene (coding for IFN- λ 3) that strongly associate with spontaneous clearance of HCV and with treatment success, both in HCV mono-infected and in co-infected patients. I will put these findings in perspective and discuss their practical and theoretical implications with regard to drug development, clinical trial design and clinical management of chronic HCV infection. Results of detailed genetic and functional analyses of the *IL28B* gene region will also be presented.

Published: 8 November 2010

doi:10.1186/1758-2652-13-S4-O30

Cite this article as: Fellay: O312. Host genetics of HCV disease — *IL28B*.
Journal of the International AIDS Society 2010 **13**(Suppl 4):O30.

Submit your next manuscript to BioMed Central
and take full advantage of:

- Convenient online submission
- Thorough peer review
- No space constraints or color figure charges
- Immediate publication on acceptance
- Inclusion in PubMed, CAS, Scopus and Google Scholar
- Research which is freely available for redistribution

Submit your manuscript at
www.biomedcentral.com/submit



Institute of Microbiology and Service of Infectious Diseases, University of
Lausanne, Geneva, Switzerland



© 2010 Fellay; licensee BioMed Central Ltd. This is an open access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/2.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.