Hochschulbibliographie

Dokumenttyp: Zeitschriftenaufsatz

Autor(en) des Beitrags:
Mueller, Tobias; Fischer, Janett; Gessner, Reinhard; Rosendahl, Jonas; Böhm, Stephan; van Bömmel, Florian; Knop, Viola; Sarrazin, Christoph; Witt, Heiko; Marques, Andreas Mas; Kovacs, Peter; Schleinitz, Dorit; Stumvoll, Michael; Blüher, Matthias; Bugert, Peter; Schott, Eckart; Berg, Thomas

Titel des Beitrags:
Apolipoprotein E allele frequencies in chronic and self-limited hepatitis C suggest a protective effect of APOE4 in the course of hepatitis C virus infection.

Abstract:
Infectious hepatitis C virus (HCV) particles bind to host lipoproteins such as low-density lipoproteins (LDLs). Low-density lipoprotein receptors (LDLR) have been termed candidate receptors for HCV-LDL complexes. Functional host genetic single nucleotide polymorphisms (SNPs) in the apolipoprotein E (APOE) gene encoding apolipoprotein E (apoE) - a major structural LDL component and natural ligand of LDLR - likely influence the course of HCV infection. We investigated the prevalence of APOE SNPs in two large and independent cohorts of patients with chronic HCV infection compared to respective controls. We genotyped 996 chronically HCV-infected patients; 179 patients with spontaneous HCV clearance; 283 individuals with non-HCV-associated liver disease; and 2234 healthy controls. APOE genotype proportions in patients with persistent HCV infection significantly differed from healthy controls (P = 0.007) primarily because of a substantial under-representation of APOE4 alleles in chronically HCV-infected patients (10.2%) compared to 13.0% in healthy
controls (P = 0.001). The distribution of APOE4 allele positive genotypes (?2?4, ?3?4, ?4?4) also significantly differed between chronically HCV-infected patients and healthy controls (1.4%, 17%, 1% vs. 2.4%, 20.5%, 1.7%; P = 0.001), suggesting a protective effect of the APOE4 allele in HCV infection. This was confirmed by a significant over-representation of the APOE4 allele in patients with spontaneous HCV clearance (17.6%; P = 0.00008). The APOE4 allele distribution in patients with non-HCV-associated liver disease (14.0%) was very similar to healthy controls and also differed from chronically HCV-infected patients (P = 0.012), suggesting HCV specificity. Our findings suggest that the APOE4 allele may confer a protective effect in the course of HCV infection.