Abstract

Solid organ transplantation (SOT) represents a life-saving procedure and a future perspective for patients suffering from organ failure. On the other hand, SOT recipients are burdened with numerous complications, including infections or lifelong administration of immunosuppressive medication. There are several well-known factors related to graft and patient survival, including general health status, age at the time of SOT, diagnosis leading to SOT, acute or antibody-mediated rejection, development of the metabolic syndrome and complications including viral diseases. Viral infections in SOT recipients may present with a very distinct natural history compared with the healthy population. Several can cause immune activation leading to graft rejection; others can be associated more likely with immune tolerance. We aimed to identify the impact of variants of selected genes on the natural history of various viral diseases in SOT recipients and thus their overall outcome, morbidity and graft survival.

Cytomegalovirus (CMV) infection is the most common viral infection in SOT recipients. We focused on the role of the *IL28B* rs12979860 locus genotype in the risk of CMV disease occurrence. We proved the T allele is associated with a more frequent occurrence of CMV disease in liver transplant (LTx) recipients after cessation of antiviral prophylaxis. Subsequently, we analysed the impact of SNP rs738409 C/G (I148M) in *PNPLA3* on the viral load before LTx and hepatocellular carcinoma (HCC) incidence in patients with liver cirrhosis caused by genotype 1b HCV infection. We demonstrated that patients transplanted for chronic liver failure (CLF) were significantly younger and had more severe dysfunction than patients transplanted for HCC. Allele G increased the risk of LTx for CLF in both the allelic and the recessive models. Genotype GG carriers had lower HCV viral load than those carrying at least one allele C. Ultimately, we evaluated expression of transcripts associated with operational tolerance (OT) in kidney transplant recipients with or without HBV infection. Patients with HBV infection had higher expression of *GATA3, TCL1A, IL-10* and *TNF-α* and lower expression of *SENP-6*. The above-described transcription profile was compatible with OT and concordant with excellent survival of kidney recipients with HBV infection and renal grafts in these recipients.

Keywords: CMV, HCV, HBV, viral infections, gene variants, organ transplantations.