O180

Abstract (oral session)

Cytokine gene polymorphism and cytomegalovirus reactivation in paediatric liver transplant recipients

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Objective: Cytomegalovirus (CMV) is one of the most frequent opportunistic pathogens and a substantial cause of morbidity and mortality in immunosuppressed patients (pts). Polymorphism within cytokine genes may influence the susceptibility and the clinical course of infectious diseases. The immunogenetic factors influencing outcome of CMV infection in paediatric liver transplant recipients (LTx) have been little investigated. The aim of this study was to assess the polymorphisms in selected cytokine genes that my impact on CMV reactivation in children after LTx. Methods: One hundred twenty six paediatric pts after LTx (median age at LTx 1.3 years, range 0.1 -18.0) were included in this study. All pts were CMV seropositive prior to LTx and 105/126 pts received graft from a positive donor (in 21 pts - donor was negative). All children were followed up for at least 12 months after LTx (median 29, range 12-111 months). CMV reactivation (defined as positive CMV DNA in blood) was detected in 91/126 pt within 1st year post-LTx. The remaining 35 pts had undetectable CMV DNA for at least 12 months. Polymorphisms of: TNF- alpha -1031 T/C (rs1799964), TNF-alpha -308 G/A (rs1800629), TNFRI -201 C/A (rs4149570) IL-1 beta -511 C/T (rs16944), IL-1 beta +3954 C/T (rs1143634), IL-10 -1082 A/G (rs1800896), IL-10RA +5964 C/T (rs4252270), IL-12p40 3'UTR (rs3212227), IFN- gamma +874 A/T (rs2430561) MCP1 -2518 A/G (rs1024611) MCP1 +1543 C/T (rs13900), CCR5del32 and IL-1RN VNTR, were analysed in all pts. The association between cytokine polymorphisms and CMV reactivation after LTx was assessed by multivariable logistic regression adjusting for potential confounders. Results: Significantly decreased frequencies of IL-1beta -511 CT and TT genotypes were found in pts with CMV reactivation compared to pts without CMV DNAemia after LTx (43% vs 70%, OR = 0.34, 95% CI:0.13 - 0.88, p = 0.02). In addition, significantly overrepresented heterozygous TNFRI -201 CA genotype was detected in children who experienced CMV reactivation compared to CMV DNA-negative pts (53% vs 23%, OR = 4.1, 95% CI: 1.4 - 11.6, p = 0.005). The rest of the polymorphisms analysed showed no significant association with virus reactivation. Conclusion: Genetic polymorphism within IL-1beta and TNFRI genes may contribute to CMV reactivation in children after LTx. In addition, carriers of IL-1beta-511 CC and/or heterozygous TNFRI -201 genotype may especially benefit from anti-viral prophylaxis.