



Category: Clinical Genomics

CMV genotyping using different samples in post renal transplant recipients with CMV disease

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Abstract

CMV is the most common viral infection which occurs in post renal transplant recipients (PTR). There are four different gB genotypes (gB1 to gB4) which exist in CMV. Studies have reported that mixed infection with different genotypes will cause severe clinical manifestations as well as co-infection with other herpesvirus including Epstein-Barr virus (EBV) [1]. CMV can cause compartmentalized disease involving different organs with different genotypes. There are reports in immuno compromised individuals with different genotypes [2, 3]. Institutional ethics committee approval was obtained prior to conduct of the study (IEC-NI/08/DEC/07/46). Whole blood, saliva and urine were collected from PTR. DNA were extracted (Qiagen DNA mini kit) and CMV quantitative PCR targeting ppUL83 gene was performed with CMV R-geneTM using an ABI 7900 Fast real time PCR (SDS Version: 2.4). PTR who had high viral load (>1000 copies/ml) in any three or two samples were included for CMV genotyping PCR targeting gB region (410-bp) [2]. DNA sequencing was performed in ABI 3730 GA platform by Sanger method and sequences were analysed by reference strains. A total of 24 samples were collected from 9 PTR. Among these four PTR had high viral load in all three samples (whole blood, urine & saliva) and those with high viral load (n=5) in 2 samples (Whole blood & urine/saliva) were screened for CMV genotyping. Majority of the strains belonged to genotype B1 and only one PTR was infected with genotype B2 in three samples. In PTR with genotype B1, gastro intestinal infection (GI) was predominantly found in 78% (n=7) followed by graft dysfunction (GDF) in 56% (n=5) of the PTR. PTR who detected with genotype B2 was associated with fever, leukopenia (CMV syndrome), GDF and also found with EBV infection. Co-infection with EBV was observed in 44% (n=4); VZV and HSV type 1 was also observed. Genotypes are associated with the severity of the disease and co-infection with other herpes virus infections. In our study subjects, genotype B1 predominantly noted as reported in western countries. Study on distribution of genotypes among PTR may help to determine the specific strains for vaccine development.

References

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