MOLECULAR CHARACTERIZATION OF HUMAN CYTOMEGALOVIRUS (HCMV) IN SOME HCMV INFECTED RENAL TRANSPLANT PATIENTS IN SRI LANKA

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MOLECULAR CHARACTERIZATION OF HUMAN CYTOMEGALOVIRUS (HCMV) IN SOME HCMV INFECTED RENAL TRANSPLANT PATIENTS IN SRI LANKA

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Cytomegalovirus (CMV) is one of the most common viruses that can be observed in immunocompromised patients such as organ transplant patients, HIV patients and neonates. HCMV infections are frequently associated with salivary glands, though they may be found throughout the body. It is a leading cause of virus-associated birth defects, including mental retardation and deafness. In Sri Lanka, HCMV infection has become a major health problem among immunocompromised patients who have undergone transplantation of organs such as kidneys.

The main objective of this study was to establish a methodology for amplifying and sequencing a part of the UL139 gene region to determine HCMV strains in a cohort of immunocompromised patients in Sri Lanka and to determine the genetic relatedness of HCMV strains using phylogenetic analysis. DNA sequences of Sri Lankan HCMV isolates were compared with data from Genbank in order to compare the relatedness of Sri Lankan HCMV isolates with other global HCMV strains.

Whole blood samples were collected from patients who had undergone kidney transplantation at Nephrology and Transplant Unit, General Hospital (Teaching), Kandy. The whole blood samples have been collected from patients those who were confirmed for the presence of the HCMV by a PCR assay or serological tests.

Twenty eight serum samples were processed and DNA was extracted by using a Guanidium thiocyanate viral DNA extraction method. A 224bp region of the viral DNA was amplified by PCR using primers specific for the UL139 gene.

The amplified PCR products were purified and sequenced using an ABI Prism 310 genetic analyzer. Cycle sequencing was performed in order to confirm the sequences. The sequences were aligned, analyzed and compared with global strains in the ICVTdB to

determine the phylogenetic relationships between the global strains and Sri Lankan isolates. Sri Lankan isolates showed a high degree of homogeneity and clustered in to a single branch of the phylogenetic tree.

Therefore, no distinctive genetic diversity could be observed among sequenced Sri Lankan HCMV isolates. The low diversity may be a result of the virus proliferating relatively recently, with less time for accumulating new mutations. The reason for having very low genetic diversity also could be that the virus is mainly locally transmitted and circulating within the country with very little importation of the virus from outside Sri Lanka. The low degree of genetic diversity observed in this study will have implications on the epidemiology and patient management of this disease.