



Molecular characterization of JC virus (JCV) from HIV-infected Indian patients with progressive multifocal leukoencephalopathy (PML)

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PML, which is caused by the polyomavirus JC, is underreported in Asian and African countries. The transcriptional control region (TCR) located between the origin of DNA replication and agnoprotein coding region exhibits significant sequence heterogeneity among JCV variants isolated from PML patients. JCV (Mad1) and some other rearranged variants grow efficiently in primary human fetal glial (PHFG) cells and produce infectious virions, whereas archetype JCV is incapable of growing in PHFG, suggesting that rearrangements in the TCR region are essential for JCV replication in these cells. The objective of this project was to molecularly characterize JCV from HIV-infected PML cases diagnosed at postmortem. DNA was extracted from paraffin embedded tissues from three patients with clinical and histological diagnosis of PML. Frontal cortex (FC), kidney and spleen tissue was available from one patient whereas parietal cortex (PC), tissue was available from other patients. The JCV TCR and V-T intergenic regions were amplified using nested PCR and sequences were aligned using DNASTAR Lasergene software. The TCR region from FC, PC and kidney was identical to the JCV (Mad1) strain whereas the spleen derived TCR region was similar to the CY archetype strain. Based on the sequence variations detected in the V-T intergenic coding region, two patients were found to be infected with JCV genotype 1A. Our data concur with previous studies that indicate deletion and duplication of the TCR of JCV in plasma and brain is associated with poor PML prognosis. To our knowledge these data represent the first JCV sequences reported in PML patients from India.