PREVALENCE AND GENOTYPES OF JOHN CUNNINGHAM VIRUS FROM ORGAN TRANSPLANT RECIPIENTS AT A HOSPITAL IN THAILAND (2014-2015)

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Abstract. John Cunningham virus (JCV) mainly causes asymptomatic infection and remains latent in kidneys and B lymphocyte, leading to progressive multifocal leukoencephalopathy (PML) in immune-compromised hosts and nephropathy in post-transplant recipients. Prevalence and genotypes of JCV infection in Thailand were determined from JCV viral load and nucleotide sequence of post-kidney and -bone marrow transplant recipients' urine samples (n = 108) during 2014-2015. Prevalence was 28% and genotypes identified by phylogenetic analysis of VP1 gene from 25 strains indicated predominance of genotype 7A, with genotype 7C1 identified in one sample from a bone marrow recipient. JCV non-coding control region (NCCR) presented non-archetypal structure in 80% of viral specimens and in 100% of nephropathy recipients' samples, the first such report in Thailand. The findings should provide useful evidence leading to further investigations into the association of JCV with PML, nephropathy and other opportunistic diseases in HIV / AIDS and long-term immune-suppressive drug treated patients in Thailand.

Keywords: John Cunningham virus, JCV genotype, JCV prevalence, transplant recipient, Thailand

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