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Diversity of BK polyomavirus genomes in correlation with BKPyV-associated diseases in Australian and Vietnamese transplant recipients

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BK polyomavirus (*BK virus* or BKPyV) is a circular double-stranded DNA virus with an approximately 5100 bp genome. BKPyV is opportunistic pathogen related to several human diseases under immunosuppressed status. It affects mostly renal and bone marrow transplant patients and may cause BKPyV-associated nephropathy (BKVAN) occurring in 1-10% of renal transplant recipients. It is divided into four major genotypes (BKPyV I-IV). However, there are limitations of a 287-bp VP1 region to sub-classify genotype subgroups. The aim of this study was to detect the distribution of BKPyV genotypes and subgroups in Australian and Vietnamese Transplant Recipients (TRs) and to compare the improvement of phylogenetic analysis based on Whole Genome Sequencing (WGS) rather than 287-bp VP1 region sequencing. BKPyV DNA-positive blood and urine samples were analyzed from Australian and Vietnamese TRs. Primer-directed rolling circle amplification method was used to enable sufficient polyomavirus-specific WGS whole genome sequencing reads for accurate assessment of the BKPyV whole genome. Advances in Next-Generation Sequencing (NGS) technologies, is an effective approach to explore genetic diversity over the BKPyV complete genome. NGS was performed on a BKPyV DNA-enriched WGS directly from clinical samples. Phylogenetic analysis of BKPyV based on WGS and VP1 region, four major genotypes I, II, III and IV were detected in Australia, whereas only genotypes I and IV were found in Vietnam. Genotype I was classified into four subgroups I-a, I-b1, I-b2 and I-c in Australia, while subgroup I-b1 was detected in Vietnam. Within genotype IV, it was classified into IV-a2 and IV-c2 subgroups in Australian TRs and three subgroups IV-a1, IV-a2 and IV-c1 in Vietnamese RTRs. However, the 287-bp VP1 region poorly differentiated subgroups in genotype IV, particularly subgroups IV-c1 and IV-c2 compared to WGS phylogeny. Phylogenetic analysis based on the WGS is more accurate than the 287-bp VP1 region in classifying BKPyV genotypes/subgroups.

Biography

Van Dinh Trang has his expertise in clinical medical microbiology. He has been studying BK polyomavirus in the University of Sydney since 2015.

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