

# New JC Virus (JCV) Genotypes From Papua New Guinea and Micronesia (Type 8 and Type 2E) and Evolutionary Analysis of 32 Complete JCV Genomes

[D V Jobe](#)<sup>1</sup>, [J S Friedlaender](#), [C S Mgone](#), [H T Agostini](#), [G Koki](#), [R Yanagihara](#), [Ng TCN](#), [S C Chima](#), [C F Ryschkewitsch](#), [G L Stoner](#)

## Affiliation

- <sup>1</sup> Neurotoxicology Section, National Institute of Neurological Disorders and Stroke, National Institutes of Health, Bethesda, Maryland 20892-4126, USA.
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## Abstract

The JC virus (JCV) is a ubiquitous human polyomavirus that frequently resides in the kidneys of healthy individuals and is excreted in the urine of a large percentage of the population. Geographic-specific JCV variants, isolated from urine and from brain of progressive multifocal leukoencephalopathy (PML) patients, have been grouped into seven distinct genotypes based on whole genome analysis and by individual polymorphic nucleotides (typing sites) in the VP1 coding region. Mutations in the archetypal regulatory region, sometimes consisting of deletions and/or duplications, are also useful taxonomic characters for further characterizing and subdividing genotypes. Investigation of JCV variation in Papua New Guinea (PNG) revealed three distinct variants called PNG- 1, PNG-2, and PNG-3. These variants exhibited consistent coding region and regulatory region mutations. Evolutionary analysis of 32 complete JCV genomes including six new viral genomes from the western Pacific suggests that the new PNG JCV variants are closely associated with the broad group of Type 2 strains of JCV found throughout Asia, forming a monophyletic group with the Northeast Asian strains (Type 2A). Within the Type 2 clade, however, the PNG JCV variants cluster as two distinct groups and are therefore described here as new JCV genotypes designated Type 2E and Type 8.