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A novel JC virus variant found in the Highlands of Papua New Guinea has a 21-base pair deletion in the agnoprotein gene.

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Abstract

OBJECTIVES: This paper describes a unique JC virus (JCV) variant recovered from the Highlands of Papua New Guinea that contains an inframe 21-bp deletion in the agnoprotein gene. We characterize the mutation and suggest possible roles for the deletion in JCV evolution.

STUDY DESIGN/METHODS: JCV DNA was extracted from urine and polymerase chain reaction (PCR) amplified using whole genome primers. PCR products were cloned, and multiple clones were sequenced. The JCV agnogene was PCR amplified to verify the presence of the agnogene deletion.

RESULTS: This mutation creates a 21-bp deletion near the 3' end, which alters the predicted secondary structure of the messenger RNA and changes local codon usage at the 3' end of the agnogene. Protein secondary structure predictions suggest the deleted portion of the agnoprotein may be a flexible surface feature.

CONCLUSIONS: We describe the first stable coding region deletion in JCV that presumably signifies a single evolutionary event that led to the split from other Highlands viral groups and occurred well after the human expansions that led to the peopling of the Southwest Pacific.