

Human polyomavirus JC variants in Papua New Guinea and Guam reflect ancient population settlement and viral evolution

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Abstract

The peopling of the Pacific was a complex sequence of events that is best reconstructed by reconciling insights from various disciplines. Here we analyze the [human polyomavirus JC](#) (JCV) in Highlanders of Papua New Guinea (PNG), in Austronesian-speaking Tolai people on the island of New Britain, and in nearby non-Austronesian-speaking Baining people. We also characterize JCV from the Chamorro of Guam, a Micronesian population. All JCV strains from PNG and Guam fall within the broad Asian group previously defined in the *VP1* gene as Type 2 or Type 7, but the PNG strains were distinct from both genotypes. Among the Chamorro JCV samples, 8 strains (Guam-1) were like the Type 7 strains found in Southeast Asia, while nine strains (Guam-2) were distinct from both the mainland strains and most PNG strains. We identified three JCV variants within Papua New Guinea (PNG-1, PNG-2 and PNG-3), but none of the Southeast Asian (Type 7) strains. PNG-1 strains were present in all three populations (Highlanders and the Baining and Tolai of New Britain), but PNG-2 strains were restricted to the Highlanders. Their relative lack of [DNA sequence](#) variation suggests that they arose comparatively recently. The single PNG-3 strain, identified in an Austronesian-speaking Tolai individual, was closely related to the Chamorro variants (Guam-2), consistent with a common Austronesian ancestor. In PNG-2 variants a complex regulatory region mutation inserts a duplication into a nearby deletion, a change reminiscent of those seen in the brains of [progressive multifocal leukoencephalopathy](#) patients. This is the first instance of a complex JCV rearrangement circulating in a human population.

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