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GENOME ANNOUNCEMENT

Complete Genome Sequence of a Tenth Human Polyomavirus

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Nine polyomavirus (PyV) species are known to productively infect humans. The circular DNA genomes of PyVs are readily detectable using rolling circle amplification (RCA). RCA-based analysis of condyloma specimens from a patient with warts, hypogammaglobulinemia, infections, and myelokathexis (WHIM) syndrome demonstrated the presence of a tenth apparently human-tropic polyomavirus species, which we name HPyV10.

Members of the viral families *Papillomaviridae* and *Polyomaviridae* are nonenveloped double-stranded circular DNA viruses that infect vertebrates, including humans. Human papillomaviruses (HPVs) are exclusively tropic for differentiating keratinocytes (1). Emerging evidence suggests that a subset of polyomavirus (PyV) species also infect human skin (3).

In an effort to identify previously unknown viruses, we purified virions out of skin specimens from a patient with a rare genetic disorder known as warts, hypogammaglobulinemia, infections, and myelokathexis (WHIM) syndrome. The syndrome is marked by patients' relative inability to effectively control HPV infections (2). Five pedunculated condylomas (warts) from buttock skin >4 cm from the anus were surgically excised for therapeutic reasons. The surgical field was prepped by scrubbing with povidone-iodine solution. Surgical discard material not needed for pathological analysis was minced and treated with a nuclease cocktail, followed by collagenase digestion. Virions were purified by ultracentrifugation through Optiprep, as previously reported (3).

DNA was extracted from Optiprep-purified virions and subjected to random-primed rolling circle amplification (RCA; GE). RCA products were digested with restriction enzyme BstYI (NEB) and resolved by agarose gel electrophoresis. Separated restriction fragments were ligated into plasmid pZero2 (Invitrogen). Sequencing of several cloned restriction fragments revealed close homology to HPV6, which commonly causes anogenital condylomas. Clones of a different, relatively faint pair of BstYI fragments showed partial homology to HPV124.

Surprisingly, several cloned restriction fragments showed no homology to papillomaviruses but were instead homologous to various human and animal PyVs. Using a primer walking approach, we sequenced the entire genome of a previously unknown polyomavirus present in the RCA mixture. The sequence of a full-length BamHI clone of the viral genome was identical to that resulting from direct sequencing of the RCA mixture.

Densitometric analysis of restriction-digested RCA products showed that bands derived from the novel polyomavirus were roughly one-third as intense as comparably sized HPV6-derived bands. The relatively high apparent abundance of the novel polyomavirus strongly suggests that human cells (as opposed to environmental contamination) were the ultimate source of the virus. We suggest that the new polyomavirus is human-tropic and can therefore be named human polyomavirus 10 (HPyV10).

While we were completing our sequencing of HPyV10, we learned of a manuscript in press (4) reporting a novel polyomavirus isolated from human stool specimens. Although Wang and colleagues did not acquire data to conclusively resolve the question of whether their novel Malawi polyomavirus (MWPyV) is human-tropic or derived from dietary sources, analysis of the nucleotide sequences of the MWPyV isolates (accession numbers JQ898291 and JQ898292) shows that they are 95% to 99% identical to that of the HPyV10 isolate reported here. Thus, MWPyV is presumably human-tropic as well.

Our results raise the possibility that WHIM patients exert equally poor control over both HPV and cutaneous HPyV infections. Future RCA-based studies of patients suffering from this rare genetic disease may therefore be helpful in revealing additional new HPV and HPyV species.

Nucleotide sequence accession number. The genome sequence of HPyV10 isolate 10ww has been deposited in GenBank under accession number JX262162.

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