Complete Genome Sequence of a Novel Human WU Polyomavirus Isolate Associated with Acute Respiratory Infection

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We report here the complete genome sequence of a WU polyomavirus (WUPyV) isolate, NM040708, collected from a patient with an acute respiratory infection in New Mexico. The double-stranded DNA (dsDNA) genome of NM040708 is 5,229 bp in length and differs from the WUPyV reference with accession no. NC_009539 by 6 nucleotides and 2 amino acids.

To obtain a complete genome sequence, we conducted both alignment-guided consensus sequence generation and de novo assembly. Both methods produced a genome of 5,229 bp, with 100% agreement. Previous complete genome sequencing of WUPyV has revealed a highly conserved genome with minimal genomic variation (2). In our sample, alignment to NC_009539 revealed a total of 6 variants, of which 2 were nonsynonymous. We detected a single-amino-acid-changing variant in the large T antigen, Ile594Leu (accession no. YP_001285488.1), and one in the VP2 protein, Glu250Gln (accession no. YP_001285485.1). Phylogenetic analysis was conducted using neighbor joining with 1,000 bootstraps to 64 compete WUPyV genomes using CLC Genomics Workbench. Isolate NM040708 grouped most closely with genotype 1A isolates B3571, B3655, and B4932 (NCBI nucleotide accession numbers GU296372, GU296373, and GU296376, respectively), which were all collected from Australia in 2003, and strain T38 (NCBI accession no. GU296399), which was collected in 2003 from Canada (2). At the nucleotide level, NM040708 and B3571 differed by a single base pair at genomic position 2146 (ADD50976.1: G477C). The substitution of a cytosine for a guanine at position 477 was not predicted to cause an amino acid change in the VP1 protein, suggesting that the two isolates encode identical proteins.

Nucleotide sequence accession number. The whole-genome sequence of isolate NM040708 has been deposited in GenBank under the accession no. KU672381.

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