

Complete Genome Sequences of Two Novel Isolates of Human Parainfluenza Virus 1 Associated with Acute Respiratory Infection

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Using target capture of viral nucleic acid and next-generation sequencing, we generated the complete genomes of two novel human parainfluenza virus 1 isolates. Isolates AR001 (accession no. KX570602) and NM001 (accession no. KX639498) were collected 3 months apart from pediatric patients with acute respiratory infection from Arkansas and New Mexico, respectively.

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Acute respiratory infections (ARI) are one of the leading causes of morbidity and mortality in young children, accounting for ~25% of hospital admissions (1) and almost 2 million deaths worldwide per year (2, 3). Human parainfluenza viruses (hPIV) are one of the leading causes of ARI and pediatric hospitalizations in the United States (4, 5). The hPIVs are enveloped viruses with a single-stranded negative-sense RNA genome of ~15,300 to 17,400 nucleotides that belong to the subfamily *Paramyxovirinae* of the *Paramyxoviridae* family (6). There are four distinct serotypes of hPIVs (hPIV-1, -2, -3, and -4a/b) (7).

Here, we present the complete genome sequences of two novel hPIV1 isolates collected 3 months apart from two pediatric patients with differing clinical courses. Patient 1 (AR001) was a 5-year-old male with no significant past medical history seen at Arkansas Children's Hospital in Little Rock, AR, on 9 September 2015 after having a nonproductive cough for 6 days with rhinorrhea. The patient was afebrile and had an oxygen saturation in arterial blood (SaO₂) of 98%. A chest X ray revealed cardiopulmonary disease. He required only supportive care and was discharged home after evaluation. Patient 2 (NM001) was a 6-year-old otherwise-healthy female who presented on 16 December 2015 to the University of New Mexico Hospital in Albuquerque, NM, with 10 days of productive cough, intermittent fevers up to 104°F, and a SaO₂ of 89%. Her chest X ray documented bronchial wall thickening and hyperinflation consistent with a viral infection. She was hospitalized for one day on the general pediatric floor and required 5 h of supplemental oxygen.

An Illumina stranded-RNA sequencing library was created from RNA isolated from swab samples, and hybridization-based enrichment was performed using the University of New Mexico (UNM) ResVir respiratory viral panel probe set. The UNM ResVir panel contains 5,683 hybridization probes designed to be complementary to coding sequence (CDS) regions of 24 human respiratory viruses. Next-generation sequencing was performed on an Illumina MiSeq using v3 chemistry and paired 75-bp reads. Sequencing of AR001 and

NM001 resulted in 83,471 and 919,050 sequencing reads aligning to the hPIV 1 RefSeq reference NC_003461, respectively. No other viruses were detected. Consensus genome sequences were generated by reference-guided alignment to NC_003461 and annotated using the VIPR Genome Annotator (8).

The genome of AR001 is 15,572 nucleotides in length and differs from the hPIV1 RefSeq reference NC_003461 by 647 nucleotides and 137 amino acids. Isolate NM001 is 15,580 nucleotides in length and differs from the hPIV1 RefSeq reference NC_003461 by 688 nucleotides and 133 amino acids. The two isolates differ from each other by 118 nucleotides and 23 amino acids. Phylogenetic analysis of the two isolates through nearest-neighbor joining (CLC Genomics Workbench version 9) revealed that both AR001 and NM001 grouped with two strains isolated in France in 2010 to 2011 (accession numbers KF530218 and KF530224) and a 2011 strain from the United States (accession no. KF530213). Taken together, these data indicate that although related, these two hPIV1 isolates, obtained from Arkansas and New Mexico 3 months apart, exhibit significant genomic differences, which may underlie the patients' different clinical phenotypes.

Accession number(s). The whole-genome sequence of isolates AR001 and NM001 have been deposited in GenBank under the accession numbers [KX570602](https://www.ncbi.nlm.nih.gov/nuclink/KX570602) and [KX639498](https://www.ncbi.nlm.nih.gov/nuclink/KX639498), respectively.

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