



# Complete Genome Sequence of a Porcine Polyomavirus from Nasal Swabs of Pigs with Respiratory Disease

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**ABSTRACT** Metagenomic sequencing of pooled nasal swabs from pigs with unexplained respiratory disease identified a large number of reads mapping to a previously uncharacterized porcine polyomavirus. *Sus scrofa* polyomavirus 2 was most closely related to betapolyomaviruses frequently detected in mammalian respiratory samples.

A group of preweaned pigs approximately 2 to 3 weeks of age on a farm in Minnesota presented with clinical signs of respiratory disease, mainly sneezing. Despite a history of influenza virus and porcine reproductive and respiratory syndrome virus infections, nasal swabs were collected for metagenomic sequencing to eliminate the presence of other potential pathogens.

A pool of five nasal swabs were centrifuged to remove large debris, and the supernatant was treated with a nuclease cocktail to enrich for viral nucleic acids. Barcoded random primers were used for reverse transcription and second-strand synthesis followed by amplification using a barcode primer. Sequencing libraries were prepared using an Illumina Nextera XT kit and sequenced on an Illumina MiniSeq system using paired 150-bp reads. The resulting 3.1 million reads were mapped to the host *Sus scrofa* genome, with the unmapped 2.5 million reads next assembled *de novo* into 550 contigs at least 1,000 bp in length, which were analyzed by BLASTn.

A 4,978-bp contig consisting of over 20% of the reads showed sequence similarity to a recently described alpaca polyomavirus (1) (GenBank accession number KU879245). Additional viruses associated with porcine respiratory disease identified in the pooled nasal swabs included porcine cytomegalovirus (2), porcine astrovirus 4 (3), and porcine parainfluenza virus 1 (4). The presence of multiple respiratory viruses and lack of additional diagnostic testing preclude assignment of an etiologic role to any of these viruses for the observed respiratory disease.

BLASTp analysis of the putative large T antigen found 66% identity to alpaca polyomavirus, indicating that this virus represents a novel species, *Sus scrofa* polyomavirus 2 (5). Likewise, predicted proteins for the small T antigen and VP1 and VP2 capsid proteins were most similar to alpaca polyomavirus (49 to 68% identity). In addition to sequence similarity, phylogenetic analysis supports *Sus scrofa* polyomavirus 2 as a new species in the genus *Betapolyomavirus*.

*Betapolyomavirus* includes 26 recognized species that infect mammals (5). Interestingly, the highest observed sequence similarity was to alpaca polyomavirus and human polyomavirus 3 and 4 (KI and WU polyomaviruses, respectively), all of which have been associated with respiratory disease (1, 6–9). Further research is needed to determine the clinical significance of *Sus scrofa* polyomavirus 2 infection of pigs.

**Accession number(s).** The complete genome sequence of *Sus scrofa* polyomavirus 2 (strain 180230) was deposited in GenBank under accession number [MG976810](https://www.ncbi.nlm.nih.gov/nuccore/MG976810).

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## REFERENCES

1. Dela Cruz FN, Jr., Li L, Delwart E, Pesavento PA. 2017. A novel pulmonary polyomavirus in alpacas (*Vicugna pacos*). *Vet Microbiol* 201:49–55. <https://doi.org/10.1016/j.vetmic.2017.01.005>.
2. Plowright W, Edington N, Watt RG. 1976. The behaviour of porcine cytomegalovirus in commercial pig herds. *J Hyg* 76:125–135. <https://doi.org/10.1017/S0022172400055017>.
3. Padmanabhan A, Hause BM. 2016. Detection and characterization of a novel genotype of porcine astrovirus 4 from nasal swabs from pigs with acute respiratory disease. *Arch Virol* 161:2575–2579. <https://doi.org/10.1007/s00705-016-2937-1>.
4. Palinski RM, Chen Z, Henningson JN, Lang Y, Rowland RR, Fang Y, Prickett J, Gauger PC, Hause BM. 2016. Widespread detection and characterization of porcine parainfluenza virus 1 in pigs in the USA. *J Gen Virol* 97:281–286. <https://doi.org/10.1099/jgv.0.000343>.
5. Polyomaviridae Study Group of the International Committee on Taxonomy of Viruses, Calvignac-Spencer S, Feltkamp MC, Daugherty MD, Moens U, Ramqvist T, Johne R, Ehlers B. 2016. A taxonomy update for the family *Polyomaviridae*. *Arch Virol* 161:1739–1750. <https://doi.org/10.1007/s00705-016-2794-y>.
6. Dinwiddie DL, Dehority WN, Schwalm KC, Young JM, Gross SM, Schroth GP, Young SA. 2016. Complete genome sequence of a novel human WU polyomavirus isolate associated with acute respiratory infection. *Genome Announc* 4:e00177-16. <https://doi.org/10.1128/genomeA.00177-16>.
7. Gaynor AM, Nissen MD, Whiley DM, Mackay IM, Lambert SB, Wu G, Brennan DC, Storch GA, Sloots TP, Wang D. 2007. Identification of a novel polyomavirus from patients with acute respiratory tract infections. *PLoS Pathog* 3:e64. <https://doi.org/10.1371/journal.ppat.0030064>.
8. Rao S, Lucero MG, Nohynek H, Tallo V, Lupisan SP, Garcea RL, Simoes EAF; ARIVAC Consortium. 2016. WU and KI polyomavirus infections in Filipino children with lower respiratory tract disease. *J Clin Virol* 82:112–118. <https://doi.org/10.1016/j.jcv.2016.07.013>.
9. Kennedy JL, Denson JL, Schwalm KS, Stoner AN, Kincaid JC, Abramo TJ, Thompson TM, Ulloa EM, Burchiel SW, Dinwiddie EL. 2017. Complete genome sequence of a novel WU polyomavirus isolate from Arkansas, USA, associated with acute respiratory infection. *Genome Announc* 5:e01452-16. <https://doi.org/10.1128/genomeA.01452-16>.