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Genome sequence of *Equine Erythroparvovirus 1*, identified in the United States

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ABSTRACT *Equine Erythroparvovirus 1* is a parvovirus that was identified in the blood of four horses in the United States. Here, we report one genome from a horse in New York State. This genome may represent a new species within the genus *Erythroparvovirus*.

KEYWORDS genomes, parvovirus, taxonomy, veterinary clinical studies

Parvoviruses contain a linear single-stranded DNA genome of ~5 kb (1). *Erythroparvovirus*, a genus within the family *Parvoviridae*, has been reported primarily in the sera of primates, seals, bovines, and rodents, but not in equines (2). The viral genome contains two open reading frames: NS and VP. The NS1 gene is largely responsible for DNA replication, DNA damage response, and apoptosis pathways. According to Cotmore et al.'s proposal (3), viruses within the family *Parvoviridae* are considered the same species if the NS1 proteins share >85% amino acid sequence identity while diverging by >15% from other virus species of the same genus. Many parvoviruses are considered to be nonpathogenic (4).

Through metagenomic sequencing, an *Erythroparvovirus* was detected in a blood sample from an observational study on equine fevers in November 2012 (Y. Sun, submitted for publication). The horse (150458) was a 13-year-old gelding with a fever of 101.5°F and no other clinical signs.

A blood sample was collected as part of routine clinical care, and 200 µL was treated with ZAP-OGLOBIN II Lytic Reagent at 37°C for 15 min (NC0098316, Beckman Coulter), then extracted using the MagMAX CORE Nucleic Acid Purification Kit (A32700, Thermo-Fisher). Library preparation was performed using the Illumina DNA Prep kit and sequenced using Illumina MiSeq paired-end 2*250 setting on v3 chemistry. The raw data contained 1,315,288 total reads. Sequences were then quality-checked and cleaned using trimmomatic v.0.39 (5), retaining trimmed sequences above 100 nucleotides long. Paired-end sequences retained after trimming and removing low-quality reads were used for assembly using SPAdes version 3.15.5 (6) with—meta (7) with default options. Other contigs containing non-parvovirus sequences were removed from the resulting file, and a fasta file with solely the putative parvovirus genome contig was created using awk. Prokka (8) v.1.14.5-r9 was used with option—kingdom set to "Viruses" to annotate the putative parvovirus genome. The genome showed 76.1% similarity to Primate Erythroparvovirus 1 (*Human parvovirus B19*) and 75.2% similarity to Ungulate Erythroparvovirus 1 (*Bovine parvovirus 3*), which, despite having a lower *e*-value (2e−32 compared to 8e−18 for Human B19), showed a slightly lower percentage identity of 75.2%.

The genome has a GC content of 56.6% and size of 5,115 bp. The putative NS1 gene is identified as spanning from nucleotides 2,736 to 4,967, and the putative VP gene from nucleotides 53 to 2,731. The missing number of bases at the 5′ and 3′ ends of the

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genome could be due to limitations of read length of short-read untargeted sequencing, making the ends of the genome less represented, leading to gaps in the region. The closest relative for the full NS1 gene is *Bovine parvovirus 3*/*Erythroparvovirus ungulate 1* (MG745680) with 75.3% nucleotide identity. The closest viral NS1 amino acid match was *Chipmunk parvovirus* (YP_009507375.1) with 49.25% identity, 61% query coverage based on a BLASTP search of the refseq_protein database. Expanding the search to the nr protein database resulted in a match to a metagenome-assembled genome of *Parvovirus panthera NS1* (DBA48951.1) with a better query coverage (83%) and 45.5% identity. Our findings suggest that the constructed *Erythroparvovirus* genome is very likely a new *Erythroparvovirus* species.

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AUTHOR CONTRIBUTIONS

Y. Tina Yu, Conceptualization, Formal analysis, Investigation, Writing – original draft | Ximena Olarte Castillo, Investigation, Supervision, Writing – review and editing | Guillaume Reboul, Conceptualization, Formal analysis, Investigation, Writing – original draft | Jordan Zehr, Formal analysis, Writing – review and editing | Yining Sun, Investigation, Writing – review and editing | Renee Anderson, Data curation, Methodology, Writing – review and editing | Minghui Wang, Formal analysis, Writing – review and editing | Qi Sun, Methodology, Supervision, Writing – review and editing | Rebecca Tallmadge, Data curation, Investigation, Writing – review and editing | Kelly Sams, Data curation, Investigation, Supervision, Writing – review and editing | Joel Brown, Investigation, Writing – review and editing | Nicholas Marra, Formal analysis, Investigation, Writing – review and editing | Bryce Stanhope, Data curation, Investigation, Writing – review and

editing | Jennifer Grenier, Methodology, Writing – review and editing | Colin R. Parrish, Investigation, Writing – review and editing | Nicola Pusterla, Investigation, Methodology, Writing – review and editing | Thomas Divers, Conceptualization, Writing – review and editing | Linda Mittel, Conceptualization, Funding acquisition, Writing – review and editing | Laura B. Goodman, Conceptualization, Resources, Supervision, Writing – original draft

DATA AVAILABILITY

The assembled genome is deposited in GenBank under accession PP681139. The raw reads are deposited in SRA under accession SRX23874400.

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