

Complete Genome Sequence of Equine Herpesvirus Type 9

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Equine herpesvirus type 9 (EHV-9), which we isolated from a case of epizootic encephalitis in a herd of Thomson's gazelles (*Gazella thomsoni*) in 1993, has been known to cause fatal encephalitis in Thomson's gazelle, giraffe, and polar bear in natural infections. Our previous report indicated that EHV-9 was similar to the equine pathogen equine herpesvirus type 1 (EHV-1), which mainly causes abortion, respiratory infection, and equine herpesvirus myeloencephalopathy. We determined the genome sequence of EHV-9. The genome has a length of 148,371 bp and all 80 of the open reading frames (ORFs) found in the genome of EHV-1. The nucleotide sequences of the ORFs in EHV-9 were 86 to 95% identical to those in EHV-1. The whole genome sequence should help to reveal the neuropathogenicity of EHV-9.

Equine herpesvirus type 9 (EHV-9) is the newest member of the equine herpesviruses. We isolated EHV-9 from a Thomson's gazelle (*Gazella thomsoni*) that died in an outbreak of epizootic acute encephalitis at a zoological garden in 1993 (3). EHV-9 was originally designated gazelle herpesvirus type 1 (GHV-1). GHV-1 showed serological cross-reactivity with EHV-1 in neutralization tests, although the DNA fingerprinting and Southern hybridization patterns of GHV-1 differ from those of EHV-1. These data indicated that GHV-1 is an equine herpesvirus. Therefore, GHV-1 has been redesignated EHV-9.

Experimental infection in various animals, including hamster, mouse, horse, and goat, showed that EHV-9 possesses a wide host range and strong neurotropism (4, 8, 9, 10, 11, 12, 13). Natural EHV-9 infection has been reported to cause lethal encephalitis in a giraffe (6) and polar bear (2, 10). Thus, EHV-9 has the potential to spread other hosts.

To sequence the genome, DNA of the EHV-9 strain P19 was purified from the culture supernatant of the fifth passage in embryonic equine kidney cells. The genome was sequenced by shotgun Sanger sequencing with an average coverage of 18.4X. The reads were *de novo* assembled with the Consed assembler (5).

The complete sequence of EHV-9 is 148,371 bp. The genome has all 80 of the open reading frames (ORFs) in EHV-1 strain Ab4p (GenBank accession number [AY665713](#)). ORFs 42, 52, and 53 showed the highest degrees of identity to those in EHV-1 (95%), while ORF71 showed the lowest degree of identity (86%). All but one of the insertions and deletions (indels) of the ORFs with respect to those in EHV-1 strain Ab4p were in-frame additions and deletions of codons only. Only one frameshift was found, and that was in ORF68.

EHV-9 is strongly neuropathogenic in various animals. However, EHV-1 usually infects only horses, causing abortion and respiratory infections, although it has been identified in several cattle cases, where the cattle showed various symptoms (9). EHV-1 is also known to cause equine herpesvirus myeloencephalopathy, which has recently been increasing (7). Because EHV-9 and EHV-1 are genetically close to each other but have different host ranges and pathogenicities, comparison of their genomes should help to explain their differences in host range and neuropathogenicity.

Nucleotide sequence accession number. The EHV-9 strain P21 genome sequence has been deposited in GenBank under accession number [AP010838](#).

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