Peste des petits ruminants virus (PPRV) is a highly contagious viral pathogen of small ruminants (8) that is found in areas of endemicity across much of Africa, the Middle East, and Asia and has recently emerged in Tibet, China (3, 5, 10–13). PPRV is regarded as a significant hurdle to the development of sustainable agriculture and causes economically significant mortalities (13). Importantly, in addition to its pathogenicity with respect to small ruminants, PPRV also affects wildlife species, although the relationship between virus isolate and clinical outcome is poorly understood. Reports of PPRV infection in wildlife species include infection of small-ruminant species (4, 6, 7) and subclinical infections of cattle and buffalo (1, 9).

As with all morbilliviruses, serologically, only one serotype of PPRV exists, although, genetically, isolates can be grouped into four lineages. Currently, full-genome sequence data are available for two isolates within lineage I, Nigeria/76/1 (EU267274), a mild field isolate, and Nigeria/75/1 (X74443), a vaccine strain; one isolate from lineage II, Côte d’Ivoire/89, a virulent field isolate (ICV/89-EU267273); and three pathogenic isolates from lineage IV, Turkey/2000 (NC-006383) and two Tibetan isolates, Tibet/30/2007 (FJ905304) and Tibet/2007 (JF939201). A further, nearly complete lineage IV genome exists, that of Sungri/96, an Indian vaccine strain, although the 3′ terminus remains undefined (AY560591). The Tibet/Bharal/2008 isolate (JX217850) reported here belongs to lineage IV and is the first genome to be characterized that has been derived from wild small ruminants (4).

Fourteen pairs of oligonucleotide primers were designed based on the full-length genome sequences of previously derived lineage IV viruses. These primers were then used to amplify 14 overlapping fragments of the Tibet/Bharal/2008 isolate. PCR products were purified and sequenced with an ABI 3730xl genome sequencer (Applied Biosystems). The genome termini were determined using 3′/5′ rapid amplification of cDNA ends (RACE) (2). A total of 111 sequences were assembled (DNAStar Inc.) into overlapping contigs that represented the full genome, with an average of 5.2-fold coverage at each nucleotide position. The total genome size of Tibet/Bharal/2008 was identical to that of previously published PPRV isolates, 15,948 nucleotides with identical genome organization characteristics, including the nucleocapsid protein (N), phosphoprotein (P/C/V), matrix protein (M), fusion protein (F), hemagglutinin (H), and the large polymerase protein (L). Genome and antigenome promoter regions, gene start and stop sequences, and intergenic trinucleotides were present as expected. At the nucleotide level, Tibet/Bharal/2008 shared 99.8% homology with Tibet/30/2007 and Tibet/2007; 97.2% homology with Turkey/2000; 97.5% homology with Sungri/96; 92.6% and 92.7% homology with Nigeria/75/1 and Nigeria/76/1, respectively; and 89.6% homology with ICV/89. Direct comparison of Tibet/Bharal/2008 with Tib/30/2007 and Tib/2007 demonstrated one mutation in H (K176E); one mutation in N (A441V); two mutations in P and V (D51G/K101R), which share NH2 terminal homology; three mutations in L (G133R/V1201I/F1483L); and two mutations in C (I44V/K94E). The mutations in the P and associated accessory proteins may be important for immune modulation, while substitutions in L may affect polymerase processivity. Further studies are essential to understand the mechanism of transmission of PPRV between wild bharals and domesticated sheep and goats in the Himalayan region.

**Nucleotide sequence accession number.** The full-genome sequence of Tibet/Bharal/2008 has been deposited in GenBank under accession number JX217850.

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