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Complete Genome Sequence of Bovine Polyomavirus Type 1 from Aborted Cattle, Isolated in Belgium in 2014

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The complete and fully annotated genome sequence of a bovine polyomavirus type 1 (BPyV/BEL/1/2014) from aborted cattle was assembled from a metagenomics data set. The 4,697-bp circular dsDNA genome contains 6 protein-coding genes. Bovine polyomavirus is unlikely to be causally related to the abortion cases.

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From July until November 2014, an increase in the number of bovine abortions showing atypical icteric appearance and splenomegaly was observed in Belgium (1). In addition to specific diagnostic efforts to diagnose pathogens known to be associated with bovine abortion, a viral metagenomics workflow was applied to samples (liver, spleen, placenta, abomasal fluid) from 5 aborted fetuses. Briefly, samples were homogenized in phosphate-buffered saline (10% wt/vol) and prepped with 0.4-μM selective filtration and nuclease treatment, and DNA was extracted as previously described (2, 3). Sequencing libraries were prepared using the NexteraXT kit (Illumina) according to the manufacturer's instructions and quantified with the Kapa library quantification kit for Illumina platforms (Kapa Biosystems), and fragment length distribution was verified using the Bioanalyzer with the High Sensitivity DNA kit (Agilent Technologies). Sequencing was performed on a MiSeq sequencer using a MiSeq reagent kit version 3 (Illumina) with 2 × 300-bp paired-end sequencing. Eighteen libraries were multiplexed using standard Illumina indexing primers.

The quality of the sequences was checked with the FastQC tool version 0.10.1 (http://www.bioinformatics.babraham.ac.uk/projects/fastqc). Stretches containing unidentified nucleotides ("N") were trimmed using Cutadapt version 1.3 (4) prior to quality-trimming using Sickle version 1.210 (Q score <30, length <50 bp) (5).

For the metagenomics analysis, rRNA reads and host reads were removed using the SortMeRNA tool version 1.7 (6) and mapping against the bovine reference genome (GenBank accession nos. AC_000158.1 to AC_000187.1, NC_006853.1) using BWA-MEM version 0.7.5a-r405 (7). Remaining reads were subjected to a megablast sequence alignment analysis against the NCBI nucleotide database using blast-2/2/27+ software (8), with an E value threshold of 0.001, followed by taxonomy assignment using MN version 4.70.4 (9, 10). Bovine polyomavirus type 1 (BPyV-1) sequences were present in all samples and could be confirmed in 5 out of 18 tested samples using real-time RT-PCR (11).

Members of the family *Polyomaviridae* are small, nonenveloped, double-stranded DNA viruses, which are widely distributed among vertebrates (12). They share a genome structure consisting of a 4.8- to 5.5-kbp circular double-stranded DNA. A BPyV-1 is unlikely to be causally involved in the abortion cases, as it is a known persistent contaminant of cattle that has been detected in bovine sera (13, 14), meat products (15, 16), and even waste and surface water (17–19).

A total of 50,230 quality-trimmed sequences from a highly positive liver sample were mapped against a reference genome (GenBank accession no. KM496323) using GS Mapper version 2.9 (Roche), resulting in a 4,697-nucleotide contig corresponding to the complete genome length. The protein-coding genes were predicted relative to reference sequence NC_001442 by GATU (20) and supplemented with manual annotation for spliced genes.

The complete genome of this bovine polyomavirus type 1 (BPyV/BEL/1/2014) is characterized as a double-stranded circular DNA comprising 4,697 bp, with an average GC content of 41.41%, and containing 6 protein-coding genes.

Nucleotide sequence accession number. The complete genome sequence of BPyV/BEL/1/2014 was deposited in DDBJ/EMBL/GenBank under the accession number KU200259.

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