A Spontaneous Deletion of the US1.67/US2 Genomic Region on the Bovine Herpesvirus 1 Strain Cooper

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Bovine herpesvirus 1 (BoHV-1) is an alphaherpesvirus with a genome of 135 kb. Some BoHV-1 genes are nonessential and may be deleted from the viral genome. Here, a spontaneous gene deletion was identified in the BoHV-1 strain Cooper. Genes of the US1.67/US2 region were absent, as determined by next-generation sequencing.

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Viruses are continuously undergoing genetic adaptations, where mutations and recombination are major players (1). These can be exemplified by genome rearrangements detected in laboratory-adapted strains of human cytomegalovirus (HCMV) (2). This may be of particular relevance for vaccine strains, which are often subjected to undefined number of passages in vitro. In the worst scenario, genetic alterations may lead to changes in genomic composition that may alter the immunizing capacity of a particular vaccine virus.

Here, the detection of a spontaneous deletion of two genes of the genome of a “classical” bovine herpesvirus type 1 (BoHV-1) vaccine strain (NVSL BoHV-1.1 Cooper reference strain) (3) is reported. The virus had been submitted to 12 successive passages in cell culture in our laboratory before sequencing. Virus multiplication was carried out in Madin-Darby bovine kidney cells and concentrated by ultracentrifugation, and DNA was extracted by usual methods (4). Sequencing of the whole viral genome was performed by next-generation sequencing in a MiSeq (Illumina) platform. A total of 645,622 raw reads were generated, with an average length of 139 bp, i.e., a coverage of 674 average length of 139 bp, i.e., a coverage of 674

Nucleotide sequence accession number. The GenBank accession number is KU198480.

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