Complete Genome Sequences of Two Novel European Clade Bovine Foamy Viruses from Germany and Poland

Torsten Hechler, a Magdalena Materniak, b Timo Kehl, a Jacek Kuzmak, b and Martin Löchelt b

German Cancer Research Center, Research Program Infection and Cancer, Heidelberg, Germany, a and National Veterinary Research Institute, Department of Biochemistry, Pulawy, Poland b

Bovine foamy virus (BFV), or bovine spumaretrovirus, is an infectious agent of cattle with no obvious disease association but high prevalence in its host. Here, we report two complete BFV sequences, BFV-Riems, isolated in 1978 in East Germany, and BFV100, isolated in 2005 in Poland. Both new BFV isolates share the overall genetic makeup of other foamy viruses (FV). Although isolated almost 25 years apart and propagated in either bovine (BFV-Riems) or nonbovine (BFV100) cells, both viruses are highly related, forming the European BFV clade. Despite clear differences, BFV-Riems and BFV100 are still very similar to BFV isolates from China and the United States, comprising the non-European BFV clade. The genomic sequences presented here confirm the concept of high sequence conservation across most of the FV genome. Analyses of cell culture-derived genomes reveal that proviral DNA may specifically lack introns in the env-bel coding region. The spacing of the splice sites in this region suggests that BFV has developed a novel mode to express a secretory but nonfunctional Env protein.

REFERENCES

tide sequence and spliced pol mRNA levels of the nonprimate spumavirus bovine foamy virus. J. Virol. 72:2177–2182.


