

Bovine viral diarrhea virus and camelids: adaptation of a viral pathogen to a new host species.

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Bovine viral diarrhea virus (BVDV) is a major viral pathogen of ruminants worldwide. Disease caused by BVDV ranges from clinically unapparent to severe acute hemorrhagic syndrome. The severity of the disease is strain dependent. Generally, infected animals have fever, nasal secretions, anorexia, sometimes diarrhea, and almost always show some degree of leukopenia or decline in circulating leukocytes. The latter is associated with some degree of immunosuppression.

BVDV-1 and BVDV-2 are species within the pestivirus genus of the *Flaviviridae*. These viruses possess a single-stranded, plus-sense RNA genome of approximately 12.3 kilobases in length. The viral proteins are encoded as a single large ‘polyprotein’ that is processed to the mature proteins following translation by both viral and cellular proteases. BVDV can be divided into two groups, the cytopathic and the noncytopathic biotypes. As these names imply, the cytopathic viruses kill infected cells while the noncytopathic viruses do not; these viruses establish persistent, unapparent infections. The cytopathic biotype arises from a noncytopathic virus by insertions, duplications or other changes in the NS2/3 protein of the virus.

The noncytopathic viruses can cause persistent infections in both cell cultures and in animals if the fetus is infected during the first trimester of pregnancy. The infection must occur before the developing immune system become functional. If this occurs the new immune system recognizes the virus as ‘self’ and raises no immune response against it. Thus, the animal is born persistently infected (PI) and spreads virus for the rest of its life. This is considered the major means of spread of BVDV in livestock herds. Many young PI animals show signs of the infection, termed poor doers, but many appear completely normal and there is no indication of infection. The PI animal has been characterized best in cattle, but PI animals have been found in other species, such as white-tailed deer, sheep, camels and New World camelids.

BVDV in camelids has only gained recognition in the last few years. Early reports found isolated cases but BVDV was not considered a concern for camelids. Roughly ten years ago, reports began to be published showing that BVDV could be isolated from camelids and that some were found to persistently infected. Further, almost all strains isolated from camelids were BVDV-1b. Two surveys of alpaca owners were published that looked at prevalence of the virus in alpaca herds. The first by Topliff [1] showed that in the 63 herds used in the study 25.4% had anti-BVDV antibodies and 6.3% had PI crias. In the study by Kim [2], over 12,000 alpacas were screened to identify PI animals. Of these, 46 viruses were isolated from PI alpaca or from diagnostic samples. All were determined to be BVDV-1b viruses. These studies demonstrated the presence of BVDV in alpaca populations in the US and Canada. Interestingly, when the open

reading frames of many of the viruses from the Kim study were sequenced, almost all were found to be >99.5% identical at the nucleotide level and appear to represent a single strain that is circulating through alpaca herds. Additionally, this sequence analysis revealed 4 amino acid residues in the E2 protein that may be involved in adaptation to alpaca.

- [1] Topliff CL, Smith DR, Clowser SL, *et al.* Prevalence of bovine viral diarrhea virus infections in alpacas in the United States. *J Am Vet Med Assoc* 2009; 234:519-29.
- [2] Kim SG, Anderson RR, Yu JZ, *et al.* Genotyping and phylogenetic analysis of bovine viral diarrhea virus isolates from BVDV infected alpacas in North America. *Vet Microbiol* 2009; 136:209-16.