

Envelope glycoprotein nucleotide sequence and genetic characterization of North American ovine lentiviruses

Abstract:

Ovine lentiviruses (OvLV) resemble human immunodeficiency viruses in genomic organization, viral heterogeneity, and spectrum of cytophenotypic expression. To gain a better understanding of the relationship of North American OvLV isolates with other characterized OvLV strains, the complete DNA nucleotide sequence of the env region of a highly lytic (rapid/high) OvLV strain (85/34) was determined and compared with the sequence of amplicons within env of three other OvLV strains of varying cytophenotype and isolated from the same flock of sheep. LTR and pol regions also were compared among these strains. The env region of 85/34 was 986 codons in length and the reported nucleotide sequence showed features shared by other OvLV including heavy glycosylation and conserved and hypervariable regions within the surface membrane protein region. Phylogenetic analyses of regions within LTR, reverse transcriptase, and env grouped the four virus strains together and similar to the maedi-visna OvLV strains, including visna virus, South African ovine maedi visna virus, and EV1 (British OvLV isolate), but they were distinct from caprine arthritis encephalitis virus.