BOVINE LEUKEMIA VIRUS: CHROMOSOMAL INTEGRATION AND MOLECULAR CLONING OF THE INTEGRATED PROVIRUS DNA

Yasuki OGAWA

Department of Epizootiology,
Faculty of Veterinary Medicine,
Hokkaido University, Sapporo 060, Japan

Integration of bovine leukemia virus (BLV) in the genomes of bovine lymphosarcoma cells from cattle with enzootic bovine leukosis (EBL) was investigated. To characterize the BLV provirus in the lymphosarcoma cell DNA, molecular cloning of the integrated provirus DNA was performed.

The results obtained were as follows:

1. Southern blot hybridization of BLV cDNA to *Eco* RI, *Xba* I, or *Kpn* I restriction fragments of EBL tumor DNAs showed that: 1) one to four of the provirus DNA were integrated per genome; and 2) in most cases, the restriction pattern of the integrated provirus DNA was the same in each of the two or three different tumors from the same animals, but different in the tumors from four different animals. These findings suggest the monoclonal or sometimes polyclonal origin of different tumors in an individual animals, and the existense of multiple chromosomal integration sites for the provirus.
2. The BLV clone was isolated from a library, which was constructed from genomic DNA of EBL tumor cells using λ vector Charon 4A. Restriction mapping and hybridization studies on the clone revealed that: 1) the restriction map of the provirus in this clone was similar to that of linear unintegrated BLV provirus DNA, but dissimilar to that of the integrated provirus DNA reported previously; 2) the size of the cloned provirus DNA was slightly shorter than that of these DNAs; 3) the clone contained provirus DNA of 9 kilobases (kb) with cellular flanking DNA of 6.8 kb; and 4) the orientation of the cloned provirus DNA from the 5' to 3' ends and its long terminal repeats were identified. These findings suggest that the clone contained the total viral genome.

The characterization of the clone will be of great value to analyze leukemogenesis by BLV.