

Molecular Phylogenetic Analysis of PERVs from Domestic Pigs in Korea

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The use of nonhuman species as source of organs for human transplantation, xenotransplantation, is considered a potential solution to the shortage of human organs and tissues for transplantation. However, the discovery of porcine endogenous retrovirus (PERV) has strengthened objection to the clinical use of pig xenografts. In our study, to control of PERV transmission from pig to human, *gag* and *env* gene of PERV were studied. Genomic DNAs of domestic pigs (Berkshire, Duroc, Landrace and Yorkshire) and 2 types of miniature pigs were prepared from PBMCs. About 1.5 kb fragments of covering full *gag* gene and about 1.5 kb fragments of partial *env* gene were amplified by PCR. Total 60 and 115 clones were obtained each using Topo ligation system. The clones were sequenced and sequence analysis was carried out. In analysis of *env*, three classes of PERVs have been identified with type AC and B. Type AC clones and type B clones were composed of 57% and 43%, respectively. Among them, 15 clones had correct open reading frame. Base on the reference strains, molecular phylogenetic analysis was performed by program of Clustral X and Treecon. These data suggest that proviral PERVs have a potential to make an infectious viruses through xenotransplantation.