

Endogenous retroviruses (ERVs) originate by germline infection and subsequent mendelian inheritance of their exogenous counterparts. With notable exceptions, all mammalian ERVs are evolutionarily old and fixed in the population of its host species.

Some groups of retroviruses were believed not to be able to form endogenous copies. We discovered an additional endogenous Lentivirus and a first endogenous Deltaretrovirus. Both of these groups were previously considered unable to form endogenous copies. Endogenous lentiviruses were discovered only recently and are still quite rare. These are still just small pieces of evidence insufficient to give a broader picture about the history of virus endogenization. We described a novel endogenous Lentivirus in the genome of Malayan colugo (*Galeopterus variegatus*) denoted ELVgv (endogenous Lentivirus of *G. variegatus*). Based on several analyses we proved that this is the oldest Lentivirus discovered up to date and confirmed its presence in the only other extant species of Dermoptera - *Cynocephalus volans*.

Endogenous deltaretroviruses were the last group without a single endogenous member. We detected the remnants of endogenous Deltaretrovirus in the genome of Natal Long-fingered bat (*Miniopterus natalensis*). However, this sequence was present in the genome only in one copy. We subsequently amplified and sequenced the provirus remnants from other related Miniopteridae bats.

Besides filling in the gaps of missing types of endogenous retroviral copies in genomes, we tried to add to current knowledge about the process of endogenization. The processes accompanying endogenization and the features of viruses capable of endogenization are still not well elucidated.

This might be owed to absence of a suitable model of endogenization. We propose such a model. Besides endogenous retrovirus in koalas, ERV in mule deer (*Odocoileus hemionus*) forms new germ line insertions in the natural host population in the present evolutionary time and might serve as an important model of the retrovirus endogenization process. We have determined complete genome sequence of the deer ERV, denoted cervid endogenous retrovirus (CrERV). In the previous studies, thousands of highly polymorphic CrERV integrations in approximately 50 animals were characterized. Notable polymorphism within the population

of mule deer with CrERV integration sites allocated to specific area verify the predicted young age of the virus as well as the current process of endogenization.

We performed experiments to characterize CrERV from virological perspective and explain the inefficiencies in virus replication cycle, for CrERV exhibits xenotropic behavior despite being efficient in creating new germ line copies. Experiments tackling this question were only partially successful and several questions remained unanswered. Besides these experiments, we tried to assemble retrovirus restriction factors from Cervidae species' genomes and perform analyses to estimate possible presence of their positive selection.

We also came across of concept, which could elucidate the occurrence of a replication block of viruses with amphotropic envelope in Chinese hamster ovary cells (CHOK1). We propose that these cells (widely used in biotechnology applications) bear an endogenous retrovirus unable to produce infectious particles, but able to produce defective Env protein. This protein might inhibit infection by exogenous retrovirus by competitive inhibition at the receptor.