

Z 107     **Phylogenetic Relationships among *Haliotis* spp. Based on Nuclear Ribosomal DNA Internal Transcribed Spacer 1 Sequences**

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Phylogenetic relationships among genus *Haliotis* (Gastropoda) were analyzed by comparing the DNA fragments of the PCR-amplified internal transcribed spacer (ITS) 1. In our previous molecular studies using RAPD and allozyme patterns were shown unequal results on classification of the sea abalone based on the shell characters. In addition, there were reported various kinds of hybrids and variants by spontaneous interspecific hybridization and by artificial breeding. We performed molecular genetic studies on the ITS 1 of the nuclear ribosomal DNA (nrDNA) in 5 *Haliotis* species (*H. discus hannii*, *H. discus*, *H. gigantea*, *H. sieboldii* and *H. diversicolor aquatilis*). The fragments of the PCR-amplified ITS 1 were sequenced and compared each other with restriction endonuclease digestion pattern. The results suggest that this molecular studying method can be contributed in discrimination the species among the sea abalone.

Z 108     **Identification and Phylogeny of Endogenous Retrovirus Sequence Belonging to the HERV-F Family in Hominoid Primate**

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Several family of endogenous retrovirus (ERV) elements exist in the genome of primates. An investigation was undertaken of primate pol gene sequence from an endogenous retrovirus family, ERV-F, related to a new human endogenous retrovirus family (HERV-F) that was isolated from a human glioma cDNA library. By using polymerase chain reaction (PCR) and with primers derived from HERV-F (XA34) sequence, we detected the pol gene sequence of the ERV-F family in hominoids and Old World monkeys, but not in New World monkeys. The data indicates that HERV-F family may be integrated in the primate germ cell lines approximately 40-45 million years ago. Twenty-four pol gene sequences from hominoid primates were isolated. Nucleotide sequence revealed a high degree of similarity with that of HERV-F. A phylogenetic tree obtained by the neighbor-joining method indicated close relationships of pol gene sequences across hominoid primate. This result suggests that the HERV-F family have evolved independently during primate evolution.