

evolutionary cause of sociality. Matrophagous young of the subsocial spider *Amaurobius ferox* (Araneae, Amaurobiidae) exhibit the collective predation during their post-maternal social period. We examined functional mechanism implicated in the collective prey capturing of the young. Efficiency of the predation increased with the number of individuals in a group while one individual was not able to achieve the task by itself. This cooperation was not indirectly intervened by the production of silk but directly by individual predatory acts. In the course of the social period the body mass of the young that cooperatively captured the big preys caught up with that of the young individually captured only the small preys of the same weight. This result suggests that the young of this subsocial animal profit from living together even after mother's death by their cooperative hunting.

A111 Observation of Collective Hunting in a Subsocial Spide

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Young of the subsocial spider *Amaurobius ferox* (Araneae, Amaurobiidae), after cannibalizing their mother, remain together through several instars and feed communally. We video-analyzed the collective prey capturing behavior of the spiderlings. The predation sequences showed great similarities between clutches (latency-orientation-moving-touching-seizing-feeding) and constant patterns in the attacks and holding the prey, which suggest a behavioral organization among the individuals participating in the capture. This collective behavior might involve cooperative mechanism which is one of the most important criterion in the permanent-social spider where siblings successively prolong their stay in the natal nest, hunt for prey collectively and often feed together on prey items.

A112 Geographical Variation of mtDNA ND 6 gene of *Littorina brevicula* (Littorinidae, Gastropods) in Korea

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The geographical variation on 11 populations (107 individuals) of the planktonic-developing periwinkle *Littorina brevicula* was analysed in terms of three regions and polluted environments by mtDNA ND6 gene. The sequence (500 bp) and 22 haplotypes were determined by the autosequencer (ABI 310). One main haplotype (*LbndA*) with frequencies from 0.44 to 1.0 was predominated in all populations. Genetic analysis of *L. brevicula* (60 ind.) from the polluted and unpolluted sites yielded 14 distinct haplotypes. Moreover, *LbndA* was most common and shared by 78% of them. In *LbndA* frequency, polluted site (0.872) was significantly higher than unpolluted sites (0.694, $p < 0.005$). And also, 70% of other 13 haplotypes was detected at populations of unpolluted sites ($p < 0.001$).

A113 Phylogeny of SINE-R Retroposons in Asian Apes

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The SINE-R retroposon family was derived from the long terminal repeats (LTRs) of human endogenous retrovirus K (HERV-K) that had been active during the hominoid evolution. The retroposons and HERV-K

LTR elements have potential relevance to structural change and genetic variation of the hominoid genome. In our previous study, we found that the SINE-R retroposons were hominoid specific. Here we identified seventeen new SINE-R retroposons (14 from orangutan and 3 from gibbon) from Asian apes and phylogenetically analysed them in comparison with those of the humans and African great apes. None of the retroposons from Asian apes were closely related to SINE-R.C2 that is human specific, originally identified in the gene for the C2 component of complement, whereas some retroposons (Ch-M10, Ch-M16, Gor-M, Gor-F1, Gor-M6, Gor-F9) from African great apes showed very close relationship with that of the SINE-R.C2 retroposon. The phylogenetic tree based on the SINE-R retroposons revealed wide overlap of the retroposons across species, suggesting that the SINE-R retroposons have been evolved parallel pattern in the course of hominoid evolution.

A114 Molecular Cloning and Phylogeny of the Human Endogenous Retrovirus HERV-W in cDNA Library of the Human Fetal Brain

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A new human endogenous retroviral family (HERV-W) has recently been described that is related to multiple sclerosis-associated retrovirus (MSRV) sequences that have been identified in particles recovered from monocyte cultures from patients with multiple sclerosis. Using the PCR approach with cDNA library of human fetal brain, two pol fragments (HWP-FB10 and HWP-FB12) of HERV-W family were identified and analyzed. They showed 89 percent sequence similarity with that of the

HERV-W. Translation of the pol fragments from human fetal brain showed frameshift and termination codon by deletion/insertion or point mutation. Phylogenetic analysis of the HERV-W family from GenBank database indicates that the HWP-FB10 is very closely related to the AC000064 derived from human chromosome 7q21-q22. Further studies on the genetic relationship with neighbouring genes and functional role of this sequence are indicated.

A115 A Theoretical Model-building for Intraspecific Taxa Base on Morphometric Analyses the *Ixeris chinensis* plex (Asteraceae, Lactuceae)

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Morphological discrete plays a prime role in the superficial recognition of microspecies within the species. However, most morphological characters scoring in the species complex usually show considerable overlap in each, And the separation of microspecies and their hierarchical arrangements are then usually intractable. In order to have a biosystematic study for the *Ixeris chinensis* complex as well as to establish a theoretical model-building for microspecies, morphometric procedures were used with 40 morphological characters from each of 110 individuals. Of them, 20 individuals of *I. tamagawaensis*, known to a nearest relative to the complex were included as an outgroup. After the huge amount of original data measured was firstly reduced by a factor analyzed, implied data values newly produced by factor score were continuously analyzed by a series of statistic methods. We will not only discuss taxonomic categories at the levels of both species with the result of these analyses but test taxonomic schemes proposed for the complex.