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Phylogenetic Implications of V4 and V7 Expansion Segments of SSU rDNAs in Insects

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The putative SSU rRNA secondary structure of a collembolan species, *Hypogastrura dolsana*, was constructed. We compared primary and secondary structures of V4 and V7 regions in insects and other arthropod groups. Among SSU rDNAs of arthropods deposited to EMBL, SSU rDNAs of pterygote insects emerged during the Carboniferous approximately 300 MYA by a first major radiation have an unique, long insertion of 22-59 nucleotides length in V4 region and SSU rDNAs of holometabolous insects emerged synchronously in the early Permian about 280 MYA have an unique, long insertion of 44 - 103 nucleotides length in V7 region as well as V4 insertion. The V4 regions of pterygote insects have one more stem and loop motif and the V7 regions of holometabolous insects have much longer stem due to the insertion compared to those of other major arthropod groups. Despite its structural conservation, expanded fragments differ strongly in primary sequence. The results support that pterygote insects and holometabolous insects are monophyletic groups and indicate that V4 and V7 insertions occurred prior to the acquisitions of flying system and complete metamorphosis in insect groups, respectively. We suggest that primary and secondary structures of SSU rDNA V4 and V7 expansion segments have unique and distinctive pattern enough to elucidate phylogenetic relationships in insect groups.

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PHYLOGENY AND NEW FAMILY GULGASTRURIDAE OF COLLEMBOLA(INSECTA) BASED ON MORPHOLOGICAL, ALLOZYME AND 18S rDNA DATA

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The present proposal of the new taxon, Gulgastruridae, is based on *Gulgastrura reticulosa*, first described by Yosii as monotypic new genus from a Korean limestone cave (Yosii, 1966). Its systematic position, however, was not so clear, having been put in Hypogastruridae but also considered close to Onychiuridae. In order to characterize it further we checked the external morphology by scanning electron microscopy and confirmed the absence of 3rd antennal organ (III AO), postantennal organ (PAO) and ocelli in contrast to outstanding development of "apical organ" which has never been observed elsewhere in any Collembola group. Our investigation of the moulting cycle, in addition, revealed 110 days in average of intermoulting period, the longest of and almost doubles that on record (Lee & Thibaud, 1987).

The great extent of divergence, apparently undertaken by this form from any existing Collembola groups made it necessary to confirm it further by applying new methodology of cladistics, allozyme analysis and DNA sequence alignment. By cladistics and allozyme study it turned out to be allied to Onychiuridae rather than to Hypogastruridae to which it had been originally assigned (Lee *et al.*, 1995b; Park *et al.*, 1996). Its polymorphism and heterozygosity were revealed extremely low as are usually the case with troglolobionts (Park *et al.*, 1986). Further study of 18S rDNA sequencing was performed which demonstrated its affinity with Onychiuridae with showing, however, low bootstrap value which justifies the independent familial category of the *Gulgastrura reticulosa* (Lee *et al.*, 1995a).