
The discrepancy between host crayfish phylogeny and ectosymbiotic branchiobdellidan distribution in Japan; insights into historical co-dispersal from a molecular phylogeny perspective

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Abstract

Genetically the Japanese crayfish, *Cambaroides japonicus*, show clear differentiations between populations of the western and eastern Hokkaido, while those in southern Hokkaido and Honshu Islands sometimes share the same haplotype. In contrast, the species composition of the ectosymbiotic branchiobdellidans found on Hokkaido and Honshu is different. Generally, the phylogeny and distribution patterns of a host and its symbionts are expected to be congruent, however, we found discrepancies between the distribution of branchiobdellidan species and that based on crayfish phylogeny. We hypothesize two possible reasons for this discrepancy: 1) branchiobdellidans may have unknown long-distance dispersal mechanism, and 2) random species extinction of branchiobdellidans may have occurred at each site after the co-dispersal with its host, while maintaining high species diversity.

We conducted a comprehensive sampling for branchiobdellidans on Hokkaido and northern Honshu Islands. Specimens were sequenced for mitochondrial COI and 16S rRNA and the results compared with host phylogenies and distribution. Phylogenetic analysis of the branchiobdellidans revealed the presence of independent clusters at the species level and suggest that the divergence age among species estimated from the COI was earlier than Japanese crayfish immigration to Japan. The phylogenetic relationship, within the *Cirrodriulus cirratus* complex sampled from Hokkaido, indicated significant localization in either eastern or western Hokkaido, and is consistent with the phylogenetic relationship and distribution of the host crayfish lineage. In addition, the estimated divergence age of the two major branchiobdellidan groups was consistent with the divergence age of the host. These results were the same for *C. sapporensis*, having been collected in various regions along with the *C. cirratus* complex.

Results support hypothesis 2 and suggest that Japanese branchiobdellidan species had already speciated to the current level before Japanese crayfish immigrated to Japan and co-dispersion with the host is a major factor in defining the current distribution of Japanese branchiobdellidans.

Keywords: Branchiobdellida, Crayfish, Biogeography, Phylogeography, Japan

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