

博士論文（要約）

論文題目 Phylogeny and population structure of bamboo worms (Annelida: Maldanidae)
(タケフシゴカイ科環形動物の系統進化と遺伝的集団構造)

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Abstract

Biodiversity is a critical factor in the maintenance of ecosystem functioning and services. Loss of biodiversity impairs ecosystem functioning. Biodiversity conservation is therefore vital in facilitating the sustainable use of ecosystem services. Members of phylum Annelida often dominate macrobenthic communities in marine sediment. The Maldanidae (bamboo worms) comprise more than 280 described species that belong to 40 genera and six subfamilies. Maldanids occur in various environments ranging from intertidal to hadal zones. The Maldanidae often aggregate and influence other benthic organisms by altering sediment conditions through tube construction and deposit feeding. Consequently, they sometimes play important roles in community structuring. Although maldanids offer an opportunity to explore evolutionary processes, inter- and intraspecific diversity in maldanids, for example morphology and life histories, molecular phylogenetic and population structure analyses on Maldanidae are yet to be conducted. The present study aimed to enhance our understanding of maldanid diversity by conducting phylogenetic and population structure analyses. The results obtained may not only yield information on the basic biology of maldanids but also have implications for associated conservation activities.

In Chapter 1, I reconstruct a molecular phylogeny using 52 maldanids in all six subfamilies based on two nuclear genes (18S rDNA and 28S rDNA) and two mitochondrial genes (16S rDNA and cytochrome *c* oxidase subunit I, COI). The present study confirmed the monophyly of the subfamilies Rhodininae, Maldaninae, Lumbriclymeninae, and Nicomachinae. Euclymeninae was recovered as paraphyletic; Nicomachinae was clustered within Euclymeninae. Ancestral state reconstruction suggested that the plate-like structures on the heads (cephalic plates) of some members were lost at least three times despite their functional importance of capping tubes while the plates on tails (anal plates) were lost once. Mapping habitat depths on the

phylogenetic tree suggested that shifts among depth zones frequently occurred in distinct maldanid lineages. In the present study, the diversity in the Japanese maldanid species was revealed for the first time based on molecular phylogenetic analyses. At least 23 species were genetically and/or morphologically proposed as new records from Japan, other than the 42 previously reported species. The results suggest that even some common coastal species represent new records in Japan and/or are undescribed species.

In Chapter 2, contrasting patterns of genetic diversity in two maldanid species, which differ in their geographical distributions, were revealed based on population structure analyses using the mitochondrial COI and nuclear SNPs. *Praxillella* cf. *pacifica* showed a clear population structure, a haplotype network with several star-shape clusters and each of them corresponded to local populations of the species. This network characteristic is shared with other Japanese coastal species with low dispersal ability, such as the intertidal mud snail *Batillaria attramentaria*. On the other hand, “*Clymenella*” *collaris* showed a unique population structure with low haplotype and nucleotide diversities in Iwate, northeastern Japan. The population structure of “*C.*” *collaris* in Iwate may have been influenced by changes in the extension of the Kuroshio Current or warm water masses during past interglacial periods. Its population structure is not consistent with other recognized patterns in coastal species in Sanriku region, northeastern Japan. Preliminary analyses, however, revealed a similar population structure in an ocypodid crab *Macrophthalmus japonicus*. The population structure exhibiting isolated local populations in northern Japan may therefore be common but could have been overlooked in Japanese coastal species that do not inhabit the Sea of Japan.

The present study provides novel information on both species and genetic level diversity in Japanese maldanids. The results are essential for applied studies e.g., conservation ecology, and could contribute to elucidating evolution in Maldanidae at both inter- and intraspecific levels.