

博士論文（要約）

論文題目 Phylogeographic study of the Asian horn snail
Batillaria attramentaria (Mollusca, Gastropoda)

（ホソウミニナの系統地理学的研究）

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Chapter 1 General introduction

1-1. Phylogeography and environmental fluctuations in the Quaternary

Populations of many species are not genetically homogenous and show some kinds of geographical structure for genetic characteristics. Current patterns of the geographic distribution of genetic as well as morphological intraspecific diversity have been formed by historical events such as climatic and geomorphological changes as well as biotic and abiotic selection processes (Ruzzante et al. 2011).

1-2. Phylogeography of marine species around Japan

The Japanese waters are divided into six climate regimes between the sub-boreal (the Sea of Okhotsk and the Pacific east of Hokkaido Island) and tropical (the Ryukyu and Izu-Ogasawara (Bonin) Islands) zones where various and unique ecosystems are associated with each type of environments (Fujikura et al. 2010). In addition, fluctuations in the marine environments surrounding Japan were noticeable during the Quaternary. The Japan Sea (East Sea) is a semi-enclosed sea in the northwestern Pacific, which is connected with adjacent marginal seas and the Pacific Ocean only by shallow and narrow straits with sill depths of < 130 m. A large variation of the divergence time has been indicated to be related with species-specific characteristics in the life history and distributional ranges, genetic differentiation associated with the historical events has been reported between the Pacific Ocean side and the Japan Sea (East Sea) side of the Japanese Islands for many coastal marine organisms (e.g. Kojima et al. 1997, 2004; Akihito et al. 2008, Kokita & Nohara 2011; Hirase et al. 2012).

1-3. *Batillaria attramentaria*

Intertidal snails of the genus *Batillaria* belonging to the family Batillariidae are a dominant group of benthic animals in coastal areas around Japan. They play an important role in maintaining healthy environments of coastal areas (Kamimura & Tsuchiya 2006). Among them, the Asian horn snail *Batillaria attramentaria* (G. B. Sowerby II, 1855) is a species with the highest cold-resistance and distributed from Sakhalin, throughout the Japanese waters to the China Seas (Hasegawa 2000). For this species, the scientific name *B. cumingi* (Crosse, 1862) has been frequently used especially in papers by Japanese researchers. However, Ozawa et al. (2009) stated that *B. cumingi* is a junior synonym of *B. attramentaria* on the basis of the geographical distribution, taxonomic references, and molecular phylogenetic analysis. In this thesis, I use the latter according to their recommendation. In the previous study based on partial nucleotide sequences of mitochondrial cytochrome *c* oxidase subunit I (COI) gene, individuals of *B. attramentaria* were divided into two phylogenetically distinct groups, which are distributed along two warm currents (Kojima et al. 2004). They are referred to the Tsushima group and the Kuroshio group after the names of the currents. Individuals in the Tsushima group inhabit coasts along the Tsushima Current and its branches, while the individuals belonging to the Kuroshio group mainly inhabit coasts along the Kuroshio Current.

1-4. Human-mediated transport of *B. attramentaria*

Since the early days of the last century, the human-mediated transport of *B. attramentaria* has been reported. It had been introduced to the Pacific coast of the North America with the importation of seedlings of the Pacific (Japanese) oyster *Crassostrea gigas* from Japan (Bonnot 1935). The seedlings had been transported for the purpose of aquaculture and introduced to the bays and estuaries of the Pacific coast of the USA from the 1900s to the 1970s, until sufficient natural resources were established and domestic aquaculture operations started to supply adequate amounts of seeds (Carlton 1992). Indeed, Miura et al. (2006) reported that nucleotide sequences of mitochondrial DNA obtained from all individuals of this species collected in the USA are identical to those of individuals of Miyagi Prefecture. In recent years, great efforts to eradicate *B. attramentaria* have been made in San Francisco Bay by volunteers under the initiative of environmental protection organization, the Bay Institute (see the site <http://www.bay.org/>). Accidental release of marine organisms transported with commercial marine products such as the short-necked clam *Ruditapes philippinarum* has been reported within Japan (Okoshi 2004; Koike et al. 2006).

1-5. Aim of this study

As mentioned above, it is thought that the geographical distribution of *B. attramentaria* has been determined by historical major environmental changes associated with the glacial-interglacial cycle and been altered by the human activities. The aim of this study is to reveal the detailed population genetic structure of *B. attramentaria* and gene flow among its local populations. Such information is important to conserve not only local populations of this species but also coastal ecosystems in Japan. It is also helpful to understand the effects of the past environmental fluctuations on populations of coastal species and to foresee those in the future.

Chapter 2

Elucidation of population structure of *Batillaria attramentaria* based on mitochondrial gene sequences

(5 年以内に出版予定)

Chapter 3

Development of microsatellite markers for *Batillaria attramentaria*

(本章の内容は **Molecular Ecology Resources, Volume 13, Issue 4, p 760–762, July 2013** に掲載, 契約内容によりインターネット公表に対する許諾が得られていない)

Chapter 4

Elucidation of population structure of *Batillaria attramentaria* using 14 microsatellite markers

(5 年以内に出版予定)

Chapter 5. General discussion

5-5. Conclusion

By using two distinct genetic markers which are different in the hereditary mode and the resolution, the detailed phylogeographic structure, histories of local populations, and connectivity among local populations were revealed for *B. attramentaria* covering a large proportion of its distributional range. As expected in the general introduction (Chapter 1), the present genetic structure of this species has been formed by both historical major environmental changes and contemporary human activities. In addition, in spite of its low dispersal ability, the unexpected long-distance dispersion was also clarified. This study will greatly contribute to understand the influences of environmental changes and human activities on coastal species around Japan.

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