

琉球大学学術リポジトリ

Phylogenetic Relationships among the Species of Meretrix (Mollusca: Veneridae) in the Western Pacific and Indian Ocean

メタデータ	言語: 出版者: 琉球大学21世紀COEプログラム 公開日: 2008-10-07 キーワード (Ja): キーワード (En): 作成者: Yashiki, Ayako, Yamaguchi, Masashi, Imai, Hideyuki メールアドレス: 所属:
URL	http://hdl.handle.net/20.500.12000/7403

Phylogenetic Relationships among the Species of *Meretrix* (Mollusca: Veneridae)
in the Western Pacific and Indian Ocean

Ayako Yashiki¹⁾, Masashi Yamaguchi²⁾ and Hideyuki Imai²⁾

¹⁾Graduate School of Engineering and Science, University of the Ryukyus, Nishihara, Okinawa 903-0213, Japan.

²⁾Faculty of Science, University of the Ryukyus, Nishihara, Okinawa 903-0213, Japan.

Asian hard clams in the genus *Meretrix* (Veneridae) are commercially important bivalves in Asia and East Africa. These clams inhabit tidal flats, estuary and sandy beaches in the Indian Ocean, Southeast Asia, Chinese mainland, Korean Peninsula and Japanese Archipelago. In this genus, there are at least nine recognized species, i.e., *M. meretrix*, *M. casta*, *M. lusoria*, *M. petechialis*, *M. ovum*, *M. planisulcata*, *M. lyrata*, *M. lamarckii* and *M. attenuata*. Previous work on the *Meretrix* has mainly focused on aquacultural and fishery study because of their economical importance. For taxonomical research, only the shell morphologies were used, although their shape and color often showed marked intraspecific and individual variability. For that reason, species identification of *Meretrix* has frequently been confused in the literature. This genus has been recognized as a taxonomically difficult group and is one of poorly studied in spite of economical importance.

In this study, allozyme analysis was carried out to find inter- and intraspecific genetic variability in the *Meretrix*. Allozymes from a total of twelve populations in six species, *M. lusoria* (Japan, Korea and Taiwan), *M. lamarckii* (Japan), *M. petechialis* (China and Korea), *M. lyrata* (China), *M. ovum* (Thailand and Mozambique) and *Meretrix* sp. (Ryukyus) were examined at thirteen loci. *Meretrix* sp. from the Ryukyus was genetically distant from all other species examined (Nei's genetic distance $D=0.96$), although it showed similar shell characters to *M. lamarckii*. The genetic distance between the Taiwanese and Japanese populations of *M. lusoria* showed a high degree of genetic differentiation ($D=0.39$). In Taiwan, seedlings of *M. lusoria* were introduced from Japan and China during the 1920's, and their descendants have formed an intensively cultured stock in Taiwan. Our results suggested that the Taiwanese population might represent a different species from *M. lusoria*. These results may suggest that the current morphology-based species identification for the genus *Meretrix* is in need of reexamination.