

Allozyme and Morphometric Analysis of Two Common Mussel Species of the Genus *Mytilus* (Mollusca, Mytilidae) in Korean, Japanese and Russian Waters

In-Seok Park⁺, Yuri ph. Kartavtsev*, Anton Y. Chichvarkhin*,
Akihiro Kijima** and Naoto Hanzawa***

⁺Korea Maritime University, Busan 606-791, Korea, *Institute of Marine Biology, Vladivostok 690041, Russia, **Tohoku University, Ongawa 986-2242, Japan, and
***Yamagata University, Yamagata 990-8560, Japan

Introduction

Investigations of the population genetics of the common mussel (*Mytilus*) have a long history. This group of mollusks has attracted worldwide attention (Gilg and Hilbish, 2003) In this study, we introduce allozyme and morphometric research and discuss the relatively new situation created by the introduction of the 'galloprovincialis' form to Peter the Great Bay and other locations in the East Sea.

The main goal of the current study was to answer the following questions: Is this zone stable and where are its borders? How closely related are the indigenous form 'trossulus' and the introduced 'galloprovincialis' in the region? Has any introgression occurred, and if so, in which direction?

Materials and Methods

We investigated ten allozyme and ten morphometric traits in nine collections of *Mytilus galloprovincialis* and one collection of *M. trossulus* from the East Sea and surrounding waters.

Results and Conclusions

In summary, (i) the genetic Discreteness of the *Mytilus* ex. gr. *edulis* taxa is supported by both earlier markers and new species-specific markers—*MPI*^{*}, *GLU-5'*, *GLU-3'*, *ITS*, *PLII α* ; (ii) ecological diversification of these three taxa is well developed (Seed, 1992); (iii) there are morphological criteria to discriminate between *M. trossulus* and *M. galloprovincialis*, although they are somewhat ambiguous, i.e., the variation overlap, especially for direct traits that can be used in the field. There is no real genetic evidence supporting that they are ecological forms through selection across contrasting salinities, as claimed previously (Tedelgren et al., 1990).

How can we explain the existence of fixed species-specific markers in this case? If we do not follow the strict BSC, we may conclude that the three *Mytilus* ex. gr. *edulis* taxa, *M. trossulus*, *M. edulis*, and *M. galloprovincialis*, do not have fewer reasons to be accepted as separate species (sibling species) than those in many other animal groups. If the orthodox BSC is followed, then only *M. trossulus* should be accepted as a species-level taxon, with *M. edulis* and *M. galloprovincialis* as semispecies or, in formal zoological nomenclature, subspecies. The future evolutionary fate of the group depends on two major factors, both of which may impact hybridization: (1) the stability of global and local ecological systems and (2) the stability or decrease in the frequency of introductions by ship transportation.

References

- Gilg M.R. and T.J. Hilbish. 2003. Spatio-temporal patterns in the genetic structure of recently settled blue mussels (*Mytilus* spp.) across a hybrid zone. *Marine Biol.* 134: 679~690.
- Seed R. 1992. Systematics, evolution and distribution of mussels belonging to the genus *Mytilus*: an overview. *Amer. Malac. Bull.* 9: 123~137.
- Tedelgren M., G. Andre, K. Johanesson and N. Kautsky. 1990. Genotypic and phenotypic differences between Baltic and North Sea populations of *Mytilus edulis* evaluated through reciprocal transplantations III. *Physiology. Mar. Ecol. Prog. Ser.* 59: 221~227.

*Corresponding author: In-Seok Park, Tel: 051-410-5321; Fax: 051-405-4322;

E-mail: ispark@hhu.ac.kr