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PS-11 Genetic diversity and population genetic structure of *Macrobrachium lar* and *M. formosense* in the Ryukyu archipelago

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[Purpose]

Freshwater shrimp of *Macrobrachium lar* and *M. formosense* are distributed mostly in the Ryukyu archipelago in Japan and edible species of inland waters resources. In order for appropriate management of these species, the scarce information of population structure and genetic diversity need to be studied. This research focused on genetic diversity and population structure of the above two species that differ in pelagic larval period.

[Materials and Methods]

A total of 177 individuals of *M. lar* were collected in Taiwan and five sites in the Ryukyu archipelago. A total of 337 individuals of *M. formosense* were collected in Taiwan and five sites in the Ryukyu archipelago, and three sites of mainland and Kyusyu, Japan. Polymerase chain reaction and sequence analysis were conducted after designing the species specific primers to amplify mitochondrial DNA control region. Genetic variation and population structure were analyzed using Arlequin and analysis of molecular variance (AMOVA).

[Results]

Macrobrachium lar and *M. formosense* showed high genetic diversity. Pairwise *Fst* did not show genetic differentiation of *M. lar*. On the other hand, three groups of *M. formosense* (one is from Taiwan, another is from Yaeyama Islands to Amami Island and the other is from mainland and Kyusyu) were genetically different. The UPGMA tree derived from pairwise *Fst* value did not show geographical cline in *M. lar*, while the value of *M. formosense* showed genetically close relationship between Taiwan group and mainland-Kyusyu group than Taiwan and Yaeyama Islands. These results and biological difference as well as Kuroshio-current factor were discussed for larval distribution.

Keywords: *Macrobrachium*, population genetics, genetic diversity, Ryukyu