

琉球大学学術リポジトリ

High levels of genetic diversity and differentiation between Japanese and Taiwanese populations of sakura shrimp (*Sergia lucens*) based on sequence of the mitochondrial DNA control region

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: 2008-03-07 キーワード (Ja): キーワード (En): 作成者: Imai, Hideyuki, Chang, Jin-Hua, 今井, 秀行 メールアドレス: 所属:
URL	http://hdl.handle.net/20.500.12000/4941

PS-10 High levels of genetic diversity and differentiation between Japanese and Taiwanese populations of sakura shrimp (*Sergia lucens*) based on sequence analyses of the mitochondrial DNA control region

Hideyuki IMAI* and Jin-Hua Cheng**

*Faculty of Science, University of the Ryukyus

**Tungkang Biotechnology Research Center, Taiwan Fisheries Research Institute

A nucleotide sequence analysis of the mitochondrial DNA control region was conducted to investigate the level of genetic variability and differentiation between Japanese and Taiwanese populations of sakura shrimp (*Sergia lucens*). The latter half of the control region, which contained 589 nucleotide sites, was sequenced using DNA extracted from 131 individuals collected from Japanese and Taiwanese populations, yielding 124 haplotypes. The amount of genetic variability within the populations as shown by the level of haplotype and nucleotide diversity indicates that the populations included in this study have higher levels of diversity than other crustaceans. Our AMOVA, *F_{st}*, and exact test results indicate the existence of significant genetic differences between Japanese and Taiwanese sakura shrimp, suggesting that widespread dispersal of larvae and oceanographic effects may not be sufficiently stable to restrict gene flow between distinct areas.