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Environmental Effects on the Morphology and Population Genetic Structure of *Littorina brevicula* around Korean Waters

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Widespread marine gastropod and planktonic developer, *Littorina brevicula*, is one of the most common snails found in the tidal zone along southeast Asian coast. This periwinkle, *L. brevicula*, has variation of shell morphs and colorations along two habitats affected by wave or not, and they are widely distributed in Korean waters influenced by four different ocean currents. And also, the species is partly exposed to air and reported more tolerant to wide range of pollutant, temperature and other factors affected by tidal changes. To investigate these properties, the environment effects (habitats, currents and heavy metal pollution) on morphology and population genetic structure of the periwinkle around Korean waters were performed. Firstly, morphological variation has often been explained as adaptation, in other words as the result of natural selection pressure such as predators or wave action. Usually genetic differentiation among populations within morphological variation was detected in uniplanktonic development species. However, this study surveyed genetic differentiation among distinct shell morphs within planktonic developing *L. brevicula* using mtDNA markers, 12S rRNA and ND6. Sequencing analyses of 329bp fragment of the 12S rRNA and 486bp of the ND6 mtDNA revealed the existence of 1 and 3 haplotypes, respectively. Morphotypic association with population genetic variability were tested using a nested clade analysis (NCA) and analysis of molecular variance (AMOVA). No significant association in NCA and AMOVA were found between haplotypes distribution and morphology ($p > 0.05$). These results mean that the lack of genetic structure (i.e. homogenization of allelic variation among populations) and populations are genetically connected ($p > 0.05$). It suggests the existence of a high level of gene flow of the species. Secondly, because Korean waters are influenced by different minor current systems, this may lead me to expect certain genetic differentiation among populations of marine invertebrates around Korean coastlines. To test this idea, the genetic differentiation of 14 populations of the periwinkle, using mtDNA markers, cyt b and ND6 was examined. Sequencing analyses of 500 bp fragment of the cyt b and 501 bp of the ND6 mtDNA revealed the existence of 14 and 24 haplotypes, respectively. Geographic association with population genetic variability was tested using a nested clade analysis (NCA). However, no significant association between geography and haplotype distribution was found ($p > 0.05$), which suggests the existence of a high level of gene flow of the species around Korean waters. The lack of genetic structure and likely high gene flow among these populations, even under influences of different minor current systems, may be accounted for long periods of dispersal of the planktonic larvae from this gastropod species within major currents on the northwestern Pacific Ocean. Finally, changes in genetic variability and allele frequency can be response from natural populations by effect of heavy metal pollution. The genetic diversity and population structuring of natural populations of the periwinkle from heavy metal polluted and unpolluted environments along the southeast coast of Korea were examined using COII and combined (COII+ cyt b + ND6) mtDNA markers. Sequencing analyses of 626 bp fragment of the COII and 1627 bp of the combined mtDNA revealed the existence of 9 and 18 haplotypes, respectively. This study applied AMOVA to test existence of structuring association of haplotype distribution with environments (polluted and unpolluted). No genetic differences within combined (COII+cyt b+ ND6) mtDNA were detected between environments. On the other hand, differences in population haplotype diversity and structuring were found within COII mtDNA between polluted and unpolluted environments ($p < 0.05$). The COII mtDNA haplotype (=genetic)diversity was significantly higher in polluted environments ($p < 0.05$). This increased genetic diversity within heavy-metal polluted environments compared to unpolluted ones stands out as emergent effects from pollution at a population level. By the results, the genetic diversity of populations within COII mtDNA can be ecological indicator.