

Genetic diversity and population structure of Korean eelgrass, *Zostera mirina*

Man Kyu Huh, Jin Zi Cui*, Hak Young Lee**, Kun Seop Lee* and Bok Kyu Lee

Donggeui University · *Pusan National University · **Cheonnam National University

Introduction

The Korean populations of *Z. marina* are typically distributed in patches. Although molecular and biochemical approaches are now increasingly being applied to address the taxonomic and phylogenetic relationships within the animals, plants, and other algal species in Korea (Huh 1998; Hwang *et al.* 1998; Huh 2001), no population genetic studies of this species have been conducted. The objectives of this study are to estimate the level of genetic diversity in the species, and to describe its genetic variation pattern within and among populations.

Materials and methods

Materials were collected from eight populations of *Z. marina* in Korea. Electrophoresis was performed using 12.0% starch gels according to the methods by Soltis *et al.* (1983). Fourteen enzyme systems (*Mdh-1*, *Mdh-2*, *Mdh-3*, *Got*, *Me-1*, *Me-2*, *Per-1*, *Per-2*, *Per-3*, *Pgd-1*, *Pgd-2*, *Idh*, *Skd*, and *Pgi*) were assayed in this study.

Percentage polymorphic loci (P), mean number of alleles per locus (A), effective number of alleles per locus (A_e), and gene diversity (H_e) were calculated using a computer program. Nei's gene diversity formulae (H_t ,

Hs, *Dst*, and *Gst*) were used to evaluate the distribution of genetic diversity within and among populations.

Result & Abstract

The study of genetic diversity was carried out in the eelgrass, *Zostera marina* L. Although this species has been regarded as ecologically important one, there is no report on population structure in Korea. Starch gel electrophoresis was used to investigate the allozyme variation and genetic structure of ten Korean populations of this species. Of the 14 genetic loci surveyed, eight (57.1%) was polymorphic in at least one population. Genetic diversity was high at the species level (*Hes* = 0.237), whereas, that of the population level was relatively low (*Hep* = 0.211). Nearly 79% of the total genetic diversity in *Z. marina* was apportioned within populations. The sexual reproduction, high fecundity, and colonization process are proposed as possible factors contributing to high genetic diversity. The indirect estimated of gene flow based on *Gst* was 8.38.

References

- Huh M.K. 1999. Genetic diversity and population structure of Korean alder (*Alnus japonica*: Betulaceae). *Can. J. For. Res.* **29**: 1311-1316.
- Huh M.K. 2001. Allozyme variation and population structure of *Carex humilis* var. *nana* (Cyperaceae) in Korea. *Can. J. Bot.* **79**: 457-463.