

Genetic diversity and population structure  
between natural and cultivated populations of  
sea lettuce, *Enteromorpha prolifera*, in Korea  
revealed by RAPD markers

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### Introduction

Although it has been known through many morphological and physiological studies, its genetic diversity and population structure have not yet been investigated in this species. Therefore, detailed studies, in particular at the DNA level, on genetic diversity of natural populations of wild sea lettuce, and genetic relationships between natural sea lettuce and cultivated sea lettuce are necessary from the viewpoint of plant evolution. Seaweeds have not been studied extensively and population genetics of marine species is virtually unknown. Such lack of information limits understanding of speciation, adaptation, or genetic change, which requires knowledge of genetic patterns and process by which they are modified. This knowledge is crucial for developing program to protect and preserve the genetic resources of plant species.

### Materials and methods

Five cultivated and six natural populations, which represent the geographical range of sea lettuce in Korea, were provided for this study.

DNA was extracted using the plant DNA Zol Reagent (Life Technologies Inc., Grand Island, New York, U.S.A.) according to the manufacturer's protocol. Forty

arbitrarily chosen 10-mer primers, the kit C (OPC-01 to 20) and the kit D (OPD-01 to 20) of Operon Technologies (Alameda, Co.) were used. All the reactions were repeated twice and only reproducible bands were scored for analyses.

## Result & Abstract

RAPD analysis was conducted to estimate genetic diversity and population structure of the wild (natural) and cultivated sea lettuce, *Enteromorpha prolifera*. Compared with other ecologically and ecologically significant green seaweed, population structure of this species has not been studied. The objectives of this study were to estimate the levels of genetic diversity in the wild and cultivated populations and to describe how its genetic variation is distributed within and among its populations. In natural sea lettuce, 93.2% at the species level showed detected of polymorphism. The cultivated populations were found to have fewer alleles per locus (1.20 vs. 1.23), fewer effective alleles per locus (1.37 vs. 1.39), lower percent polymorphic locus (37.0 vs. 39.2), and lower gene diversity (0.119 vs. 0.136) than wild populations. These genetic diversity parameters indicated that the cultivated populations were genetically depauperate relative to its presumptive progenitor and the domestication process has eroded the level of genetic variation of this species. Nevertheless, genetic diversity of this species was higher than average values for species with similar life history traits. The sexual reproduction, perennial, high fecundity, and colonization process are proposed as possible factors contributing to high genetic diversity.

## References

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