

Variations of RAPD and Chemical Composition of *Capsosiphon fulvescens* Culturing in Korea

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Introduction

The green marine algae, *Capsosiphon fulvescens* has been cultivated in south coast of southern Korea for many years on a commercial scale. This species is very popular in Korean as a food supplement because of its attractive flavor and flexible taste. It is, therefore, necessary to isolate and utilize qualified germplasms for mass production of this economic seaweed. Several reports have been published on phylogenetic applications of RAPDs including the characterization of interspecific genetic variation, the identification of isolates and hybrids, and the study of phylogenetic relationships. However few authors have used RAPDs to assess the genetic variability among populations of a seaweed species (van Oppen et al., 1994; Alberto et al., 1997). The present study was undertaken for characterizing the identities of *Capsosiphon fulvescens* populations cultivating in Korea through the analysis of PCR based random amplified polymorphic DNAs (Welsh and MacClelland, 1990; Williams et al., 1990) and chemical composition aimed to isolate the useful strains for aquaculture.

Materials and Methods

Thalli of *Capsosiphon fulvescens* were collected from Janghung, Wando, and Jindo of southern Korea during December 1998 to February 1999. Selected clean samples for RAPD analysis were washed thoroughly with autoclaved distilled water twice and washed again with autoclaved double distilled water twice. About 100mg fresh weight thalli was ground in liquid nitrogen in a sterile mortar with a pestle, and extracted DNAs by following earlier three methods (Cenis, 1992; Hong et al., 1992; Mayes et al., 1992). The extracted 3ng DNA in 25 μ l reaction volume was amplified by 36 cycles of the polymerase chain reaction with 10-mer arbitrary primers. Amplification products were resolved by 1% agarose gel electrophoresis, and the similarity matrix using the Jaccard's coefficient was calculated based on resulted

banding patterns. Proximate composition, total and free amino acids of the three samples were analysed and compared to the above results.

Results and Summary

DNAs were effectively extracted from the *Capsosiphon fulvescens* thalli by three methods applied. There were no inhibitory activity when PCR was performed, that is, good amplification bands were obtained. Furthermore, the banding patterns obtained showed high reproducibility of the samples. Of the 90 primers screened, 50 produced bands and 19 revealed polymorphisms. Genetic similarities among three populations were high as 0.797~0.812. Populations that are further away from each other, Janghung and Jindo, had the lowest similarity coefficient 0.797, whereas the intermediate population of Wando showed a higher similarity with Jindo than Janghung. These results suggest a higher genetic flow among the populations. Variations in the chemical composition among the three samples were observed in nearly accordance with the variation found in RAPD analysis.

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