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Genetic Difference in Two Species of Laver Conchocelis analyzed by RAPD-PCR

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Introduction

One species of laver (*Porphyra tenera* Kjellman) is an economically important aquacultural species belonging to the family Bangiaceae. Under the natural ecosystem, this laver is widely distributed in the western sea, southern sea and Jeju Island in the Korean Peninsula as well as in Japan. Especially, the other species of saw-toothed stone laver (*Porphyra dendatae*) is cultured along the western to south coast of Korea. The laver dried in a rectangular paper-like sheet in size is the most commonly eaten alga in Korea. Nowadays, laver is one of the most delicious algal species among the algae during the four seasons. Basically, the color of the laver is reddish-purple, brownish-red and very dark purple but varies widely according to their environment conditions and locality. The color, size and the shape of the laver blade vary according to their habitat such as the depth of the water, the salinity, the temperature, the photoperiod and the nutrition etc. As the laver culture industry is increasing considerably, the understanding of the genetics of this alga speciesto evaluate exactly the patent genetic effects induced by laver production operations. Particularly, the clustering analysis of the genetic distance between genera/species/populations of various fishes and invertebrates from the different geographic sites has been performed using RAPD-PCR is of small number (Klinbunga et al., 2000 Yoon and Kim, 2003). Here, we performed the genetic diversity and the clustering analysis of two species of lavers (*Porphyra* spp.) growing in the South Sea of Korea.

Materials and methods

Two species of lavers were obtained from Wando in the vicinity of the South Sea in Korea. The conchocelis of laver was collected, placed the sterile tubes on ice immediately, and stored at -40? until needed. The RAPD-PCR analysis was performed on the conchocelis extract of 22 individuals using eight arbitrarily selected primers of different decamer primers. We used the primers to identify the genetic variations, DNA polymorphisms, genetic diversity, and similarity of these lavers. RAPD-PCR was performed using two Programmable DNA Thermal Cyclers (Perkin Elmer Cetus, USA). DNA amplification was performed in a 25 l sample, containing 10 ng of template DNA, 20 lpremix (Super-Bio Co., Korea), and the 1.0 unit primer. Amplification products were generated via electrophoresis on 1.4% agarose (VentechBio, Korea) gel containing TBE. The 100 bp DNA Ladder (Bioneer Co., Korea) was used as DNA molecular weight marker. The average of

within-population similarity is calculated by pairwise comparison between individuals within a population. Using similarity matrices to generate a dendrogram, facilitated by the PC-package program Systat version 10 (SPSS Inc., USA), a hierarchical clustering tree was constructed. Systat version 10 was also used to obtain other statistical results, including means, standard errors, and t-test scores.

Results and summary

Genomic DNA isolated from two species of lavers obtained from Wando in the vicinity of the South Sea was amplified at several times by PCR reactions. The eight arbitrarily selected primers OPA-04, OPA-06, OPB-01, OPB-08, OPB-10, OPB-11, OPB-14 and OPC-10 generated the identical, polymorphic and specific fragments. The size of DNA fragments varies from 100 bp to 2,200 bp. 528 fragments were identified in the laver species and 443 in the saw-toothed stone laver species: 22 polymorphic fragments (4.2%) in the laver species and 30 (6.8%) in the saw-toothed stone laver species. The oligonucleotide decamer primer OPA-04 generated the identical DNA fragments, approximately 900 bp, in the laver species as well as in the saw-toothed stone laver species.The average bandsharing value was 0.623 0.008 within the laver species and 0.560 0.009 within the saw-toothed stone laver species. The genetic distance between two geographical laver species ranged from 0.076 to 0.627 (Fig. 1). RAPD-PCR analysis has revealed the significant genetic distance between two laver species pairs ($P<0.001$).

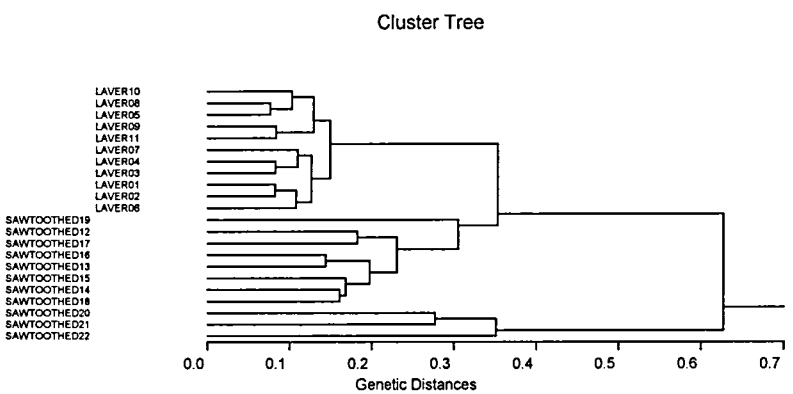

Fig. 1. Hierarchical dendrogram of genetic distances obtained from two geographical species of laver.

References

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