

Phylogenetic Relationships of *Ulva* and *Enteromorpha* Inferred from nrDNA Internal Transcribed Spacer2 Sequences

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Introduction

The family Ulvaceae species are difficult to distinguish from one another on the basis of morphological and cytological criteria alone. ITS2 sequences are known to evolve quickly and have been reported to be useful for the study of intraspecific and interspecific variation and biogeography in algae (Bakker et al., 1992). We will here describe the basic characteristics of the ITS2 sequences in *Ulva* and *Enteromorpha* to compare our result with the above previous studies.

Materials and Methods

Ulva and *Enteromorpha* thalli were collected from five sites in Jeju including eleven purported individuals, four species within these two genera in the Ulvaceae. Total DNA was extracted with DNeasy[®]Plant Mini Kit (QIAGEN inc.). PCR amplification, Cloning of the PCR product and Sequencing were conducted by a modified Malta' method (1999). Initial sequence alignments were constructed using the Clustral X program. Sequences from GenBank (18samples) were aligned with those of this study for data analysis.

Distance analyses were conducted by the tree-building algorithm of Neighbor-Joining and Minimum Evolution methods with Kimura' two parameters , Jukes-Cantor and Tamura and Nei's distances within the program MEGA (version

2b3) (Kumar et al., 2001), respectively. In the parsimony analysis, the phylogenetic tree was constructed by the Maximum Parsimony (Fitch, 1971) method with the program PAUP (version 4.0b8) (Swofford, 1998).

Results and Summary

In this study for Ulvaecae, the length of ITS2 varied between 167 and 203 bp. The results of this investigation showed that two genera, *Ulva* and *Enteromorpha* grouped in a monophyletic assemblage with 100% bootstrap support in all phylogenetic trees. However, a thorough examination of these characters from representatives does not provided to identify any unique morphological features for clades in this tree.

This study revealed that *Ulva conglobata* and *Ulva pertusa* belongs to one clade in phylogenetic tree. Also, *Enteromorpha* and *Ulva* are not distinct evolutionary entities, and can result in a plant with either a blade or a tube morphology. This data, which was resulted from this investigation could be applied to interspecific and population variation, beside of fouling research in green algae.

Selected References

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