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Investigation of the Molecular and Morphological Variability in *Batrachospermum Arcuatum* (Batrachospermales, Rhodophyta) from Geographically Distant Locations

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Abstract

Phylogeographic patterns in *Batrachospermum arcuatum* were investigated using the mitochondrial intergenic spacer between the cytochrome oxidase subunit 2 and 3 (cox2-3 spacer) from locations worldwide. Sixteen locations were sampled in six regions as follows: three locations in Bulgaria, two in China, three in the northwestern United States, one in New Zealand, six in Hawaii and one in Taiwan. Sequencing of 107 individuals resulted in 12 haplotypes. In the United States and Bulgaria, there was considerable sequence divergence among haplotypes. Likewise in the Hawaiian Islands, there was variation among haplotypes, and each island appeared to have a single haplotype represented. Three closely related haplotypes were present at the Taiwan location. The New Zealand sample was identical to one of the haplotypes from the northwestern United States. Individuals representing the 12 cox2-3 spacer haplotypes were sequenced for the rbcL gene. In the combined analysis, the Hawaii and Taiwan samples were a well-supported clade as were two Bulgaria samples. The US and New Zealand haplotypes formed a well-supported clade and likewise the China samples, but the relationship of the third Bulgaria haplotype to these others was unresolved. The specimens showed morphological variation among localities and regions, but no morphological features appeared to be diagnostic of the molecular results. *Batrachospermum arcuatum* appears to be a widespread taxon with considerable morphological plasticity that does not coincide with the substantial molecular variation. Alternatively, *B. arcuatum* may harbour cryptic species. There appears to be a temperate origin of the taxon and a derived group of haplotypes from tropical regions.

Key words : *Batrachospermum arcuatum*; Cox2-3 spacer; Freshwater; Phylogeny; Phylogeography; RbcL gene; Rhodophyta