

Hierarchical Spatial Structure and Discriminant Analysis of Genetic Diversity in the Red Alga *Mazzaella laminarioides* (Gigartinales, Rhodophyta)

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Abstract

Our study of the genetic structure of *Mazzaella laminarioides* (Bory) Fredericq (Gigartinales) in the central Chilean region documented a high level of genetic diversity based on random amplified polymorphic DNA (RAPD) markers and indicated the occurrence of significant genetic structure at different spatial scales. A total of 288 haploid gametophytes was analyzed with 17 polymorphic RAPD bands, which produced 202 distinct multilocus genotypes. Within stands, mean gene diversity ranged from 0.210 to 0.249 and no significant linkage disequilibrium could be detected among pairs of alleles, revealing that recombination (sexual reproduction) regularly shuffles the genes at that scale. Analysis of molecular variance within stands (less than 30 m) showed that the structure was very low, only marginally significant, and did not increase with increasing hierarchical levels at this lowest spatial scale. In contrast, at a larger spatial scale (among stands, from 5 to 60 km), increasing geographical distance seemed to account for increasing isolation between populations even if natural barriers, such as sandy beaches or river estuaries, may play a role in such isolation. Moreover, the strong genetic differentiation occurring between locations separated by 60 km allowed the assignment of individuals to their original population through a canonical discriminant analysis. This approach further allowed the identification of potential recent migrants from one population to the other. Thus, in species like *M. laminarioides* for which the dominance of RAPD markers can be avoided by selecting haploid individuals, RAPD analysis appeared to be specially appropriate for the study of genetic differentiation.