

Hierarchical analysis of the population genetic structure in *Concholepas concholepas*, a marine mollusk with long-lived dispersive larva

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Abstract

For most marine invertebrate species, dispersal is achieved mainly or exclusively by pelagic larvae. When the duration of the pelagic larval stage is long, genetic homogeneity over large geographic scales is expected. However, genetic structure has often been reported over small spatial scales, suggesting that more complex processes occur than a simple positive relationship between pelagic larval duration and gene flow. *Concholepas concholepas* has a larval stage that can last up to 3 months in the water column with a wide distributional range covering from 6°S to 56°S. We used a hierarchical sampling technique to test if the genetic homogeneity of this highly dispersive species is maintained throughout its total geographic range in spite of environmental heterogeneity. In the three studied regions (Antofagasta Bay, Valdivia and Patagonia), a spatial pattern of isolation by distance in conjunction with a spatial genetic structure was observed. Within each region, different spatial genetic patterns were detected. In Antofagasta Bay and Valdivia there was evidence of substantial gene flow among populations, whereas in Patagonia, populations showed genetic structure and a unique, genetically isolated location was identified. These results revealed the existence of spatial differences in the genetic patterns among regions with different coastal topographies in *C. concholepas*, and give us new insights into the interrelationships of larval dispersal potential, actual larval dispersal and physical processes. Regarding the sustainable management of *C. concholepas*, two important issues are derived from this study: (i) to highlight the need for a regional context in the management of *C. concholepas*, (ii) to determine the distinctiveness of the most austral population and to focus on the conservation efforts due to the relevance of this area.

Keywords

Concholepas concholepas, Long larval dispersal, Population genetics.