




# Population structure in high shore littorinids: a contrast between riprap and rocky shores



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today, but due to the occurrence of sex change was considered an appropriate model for investigating the consequences of predation by humans upon the sex change phenomenon. Limpet populations were exploited by systematic removal for 18 months, during which records were kept of limpet density, size frequency and sex ratios, and shore macro-community structure. The hypothesis tested was that selective removal through time of largest limpets would influence the timing and magnitude of several biological processes, including sex change, growth, migration and density regulation. There was strong evidence that the size at sex change ( $L_{50}$ ) decreased in response to the exploitation treatment, given by analysis of the averaged  $L_{50}$  extracted from the logistic regression on each treatment plot. The observed  $L_{50}$  at controls ( $50.54 \pm 6.38$  mm) suggested that sex change was occurring at a bigger size than expected from the overlap in male and female size classes. The study sites located in the south-west of England had considerable differences in community structure: Trevone was a moderately exposed shore with barnacles and *Fucus* spp. dominated community while Constantine can be considered an exposed shore with a *Mytilus* spp. dominated shore community. Thus the sex change response could be context-dependent and influenced by the community on the rest of the shore. To further understand the sex change in *P. vulgata* it is essential to design experiments that consider differences among patches. The knowledge of sex change dynamics in exploited sex changing limpet populations would allow management procedures to counter population decline being essential to rocky shore conservation and resource management.

**T22.O3****POPULATION STRUCTURE IN HIGH SHORE LITTORINIDS:  
A CONTRAST BETWEEN RIPRAP AND ROCKY SHORES**

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The number of anthropogenic structures deployed in coastal areas has increased markedly in recent times and many studies have now shown that these structures seldom mimic the natural habitats they replace. To date, however, most such studies have focused on the numbers and relative abundance of species and little is known about how these structures affect the patterns of species aggregation and size structure, despite the fact that variations in these parameters may have important ecological consequences at population and community levels. Here we compare the relative abundance, patterns of aggregation and size structure of two high shore gastropod littorinids (*Tectarius striatus* and *Melarhappe neritoides*) on riprap and adjacent rocky shores. While the relative abundance of *T. striatus* was similar on riprap and natural rocky shores, *M. neritoides* was significantly more abundant on rocky shores. At small spatial scales (cm's) both littorinids species showed more aggregated distributions on riprap. At larger scales (m's), both littorinids were also more aggregated on riprap although this was only significant for *T. striatus*. Habitat type influenced the size structure with both species attaining a significantly larger size on riprap. Here we add to the wider literature by showing that anthropogenic structures can affect intertidal assemblages in ways other than richness or the relative abundance of organisms alone.

The here documented variation in patterns of aggregation and size structure between habitats likely influence the population dynamics of these species and may have wider community level consequences.

#### T22.O4

##### mtDNA SUGGESTS STRONG GENETIC DIFFERENTIATION AT UNEXPECTEDLY FINE-SCALES IN A HIGH-DISPERSAL MARINE PERIWINKLE

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Marine invertebrates with long-lived planktonic larvae are assumed to have high dispersal potential and broad-scale gene flow. They are thought to disperse over long distances and to be genetically homogeneous over large areas. The periwinkle *Melarhaphé neritoides* which ranges along much of the European coastline, is such a species. Its long-lived planktonic larval phase lasts 4-8 weeks and previous allozyme studies have shown very little to no population genetic differentiation along the European coast, even over distances of thousands of kilometers. However, a growing number of studies based on DNA markers suggest that there is a poor correlation between pelagic larval duration (PLD) and the level of population genetic differentiation ( $r^2 = 0.29$ ). Nevertheless, recent work reaffirms that PLD might still be a good predictor of population genetic differentiation as a function of geographic scale, if based on unbiased  $F_{ST}$  estimates and appropriate sampling sizes. We explored these conflicting views by assessing mtDNA (COI, 16S, Cytb) differentiation among five intensively-sampled populations of *M. neritoides* in the Azores. In contrast with previous allozyme data, our mtDNA data reveal remarkably high genetic diversity and differentiation among *M. neritoides* populations, even those as close as 50 km. Even at this scale, populations do not seem to share haplotypes, despite the assumed high potential of broad-scale gene flow in *M. neritoides*. Hence, the relationship between PLD and dispersal potential or the level of population genetic differentiation, is indeed not straightforward.

#### T22.O5

##### INDIVIDUAL AND POPULATION LEVEL DIETARY BREADTH OF *CONUS MILLIARIS* AT EASTER ISLAND

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Understanding the processes associated with changes in resource utilization can illuminate the factors affecting niche expansion. *Conus miliaris* is a broadly distributed Indo-West Pacific predatory marine snail that was previously found to exhibit ecological

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SUPLEMENTO 8

JULHO DE 2013

WORLD CONFRESS OF MALACOLOGY 2013

*Book of Abstracts*

*Ponta Delgada, São Miguel, Açores  
July 22-28, 2013*

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