

Wandering Mussels; Using natural tags to identify connectivity matrices amongst Marine Protected Areas

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Summary

Understanding connectivity in the marine environment is crucial to describe population dynamics and to develop spatial management strategies. We studied the mussel *Mytilus galloprovincialis* as a model-species to investigate connectivity patterns within two Portuguese Marine Protected Areas (Berlengas and Arrábida MPAs). By investigating the microchemistry of bivalve larval shells (using laser ablation inductively coupled plasma mass spectrometry LA-ICPMS) we generated a reference map of location-specific-chemical signatures. This atlas was then employed to trace back natal origins of newly settled mussels and build connectivity matrices between populations. According to our results, 3 distinctive chemical signatures were identified, corresponding to 3 regions: Arrábida, Baía de Cascais and Promontório da Estremadura (PERMANOVA; $p < 0.001$). Linear discriminant analyses allowed for a high reclassification success (74%-81% of jackknifed cross-validated cases correctly classified) based on the analysis of 8 trace-elements (B, P, Co, Cu, Zn, Ce, Pb and U). The connectivity matrix allowed the identification of different pathways for mussel larvae, showing a northward prevailing dispersion pattern and distinguishing the Arrábida MPA as an important source population. These direct measures of demographic connectivity can be a powerful tool to inform policy-makers on the conservation and management of ecological coherent networks of protected areas.

Introduction

Population connectivity plays a fundamental role in metapopulation composition, genetic diversity and community dynamics, structure and resilience (Botsford *et al.* 2001; Pineda *et al.* 2007). As a result, understanding the patterns of larval dispersal among populations is an essential requirement to set-up and successfully manage networks of MPAs. In this study we investigated larval dispersal patterns of the widely distributed Mediterranean mussel, *Mytilus galloprovincialis*, within two Portuguese MPAs. This species has a planktonic larval duration of medium length with high dispersal potential, representing interesting model systems for comparative studies of population connectivity in open coast and bay habitats. Using a geochemical approach (location-specific chemical signatures imprinted in larval calcified structures) we investigated and compared pathways of connectivity from spawning locations to recruitment sites, allowing for the reconstruction of the larval origin of settled juveniles, based on geographical differences in water chemistry (Thorrold *et al.* 2002).

Materials and Methods

Wild *Mytilus galloprovincialis* adults were induced to spawn by exposure to thermal disturbance and fertilized *ex-situ* (in the laboratory). The mytilid larvae were incubated *in situ* (outplanted inside PVC tubes "larval homes", Becker *et al.* 2007) at 19 moorings along the Portuguese coast at ca 25 km intervals each, offshore of a known source of mytilid population. After 5-7 days of *in situ* exposure to seawater at each site, the "larval homes" were recovered, and the newly formed larval shells were analyzed using inductively coupled plasma mass spectrometry coupled to a laser ablation system (LA-ICPMS). Newly recruited juvenile mussels were obtained from the intertidal zone, inshore from the outplanting sites (one month after the mooring's deployment to match planktonic larval duration of mussels). Individuals smaller than 1 mm length were separated and the shells kept for LA-ICPMS

analysis. Linear Discriminant Function Analysis (LDFA) was applied to examine differences between the chemistry of larval shells raised at the various sites and build an atlas of geochemical fingerprints. Prodissoconchs (larval shells) of the juveniles were then compared with the atlas of local signatures previously build and assigned a site of origin, generating a connectivity matrix with the proportion of larvae that recruit into different settlement locations.

Results and Discussion

Larvae geochemistry raised in different sites showed distinctive signatures at the regional level: Promontório da Estremadura (including Berlengas MPA), Baía de Cascais and Arrábida MPA (PERMANOVA; $p < 0.001$). LDFA classified the differences in the geochemical signatures of incubated larvae amongst regions, with high reclassification success (74%-81% of jackknifed cross-validated cases) based on 8 of the 16 trace-elements analyzed (11B, 31P, 59Co, 63Cu, 66Zn, 140Ce, 208Pb and 238U, Fig 1). Posterior probabilities in LDFA analysis set the site of origin for each recruited individual (recruits reclassified with less than 90% probability were considered of unknown origin) The connectivity matrix showed differences in self-recruitment (Arrábida 60%, B. Cascais 0% and P. Estremadura 17%), showing significant larval export (70%) from Arrábida MPA to Baía de Cascais (Fig. 2).

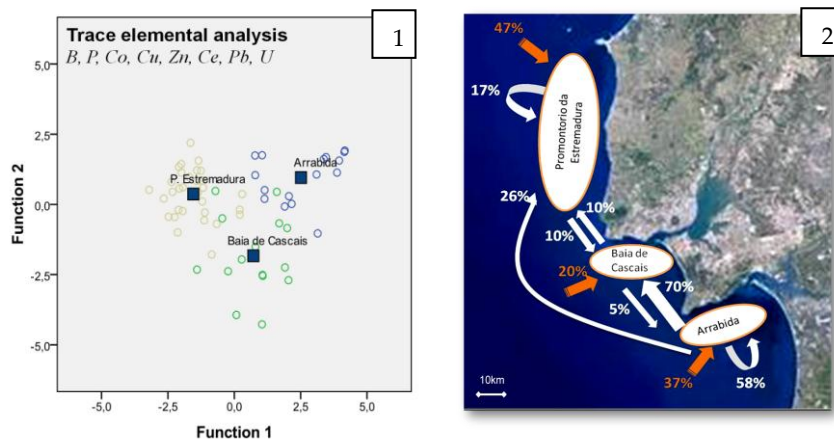


Fig 1- Canonical discriminant plots of larval source population signatures (74%-81% of jackknifed cross-validated cases). Fig 2 - Connectivity matrix showing dispersal patterns of *M. galloprovincialis* larvae among the three regions in central Portuguese West coast (June/July 2013). Orange arrows indicate unknown origin.

The recruit assignment estimation showed larval exchange among regions separated more than 100km apart, with the Arrábida MPA showing greatest contribution as a source population, together with the highest percentages of self-recruitment within its bay. The overall dispersion trend seems to follow a northward pattern, possibly linked with short-term wind circulation, since the Portuguese west coast is characterized by a predominant southward flowing coastal current (Queiroga *et al.* 2007). It is also important to notice the dependence of the mussel population in Baía de Cascais on larvae from the Arrábida MPA (where bivalve harvesting is prohibited). Currently we are also developing new studies to evaluate the temporal stability of the elemental signatures and employing numerical models of circulation to study connectivity patterns. These direct measures of demographic connectivity can be a powerful tool to inform policy-makers on the conservation and management of ecological coherent networks of protected areas.

References

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