

Genetic structure and connectivity assessment with hyper-polymorphic data in a high-dispersal potential mollusk in North Atlantic

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Connectivity is a critical component of marine ecology to address the questions ‘how far do larvae disperse?’ and ‘how much do larvae disperse?’ But measuring connectivity is currently a major challenge because of the difficulty to physically monitor larvae – tiny propagules spreading in an open and wide marine medium (Buston and D’Aloia, 2013). However, genetic connectivity is an alternative and powerful approach using genetic metrics to provide indirect measurement of connectivity by sampling adult specimens without the constraint of directly monitoring larvae (Hellberg *et al.*; 2002). Moreover, it allows integration of connectivity over many generations at evolutionary time-scales. Estimates are therefore more than an average picture of contemporary gene flow, they are a picture of the cumulative effect of gene flow over temporal and spatial scales. Genetic connectivity also provides the lowest possible level of genetic resolution by comparing individuals at the nucleotide level (Kool *et al.*, 2013). To have an understanding of the spatial scales over which populations of marine planktonic-dispersing invertebrates are connected by larval dispersal in North Atlantic, we assess genetic connectivity of the widespread periwinkle *Melarhappe neritoides*. Its long-lived planktonic larval phase lasts 4-8 weeks, this species is then assumed to have a high dispersal potential and to be genetically homogeneous over large areas. Previous genetic studies have shown very little to no broad-scale or fine-scale population genetic differentiation along the European coast (Johannesson, 1992; Cuña *et al.*, 2011; García *et al.*, 2013). Our study aims to reinforce these observations and to validate the absence of genetic differentiation of *M. neritoides* (1) on a complete distance range 1-5000km, (2) by intensifying the sampling effort of specimens and markers, (3) and by properly handling highly polymorphic genetic data to avoid the known potential bias in genetic differentiation estimates (Wright, 1978). We also go further and provide new genetic connectivity data for *M. neritoides* in North Atlantic, inferred from reliable genetic differentiation estimates or using the coalescent. Despite a remarkably high genetic diversity found in *M. neritoides*, results show very weak genetic differentiation at the three mtDNA COI, 16S and Cytb loci. Gene flow is consequently very high between population along the European coastline as well as with the remote Azores archipelago.

References

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