CONNECTIVITY PATTERNS OF THE EUROPEAN GREEN CRAB IN THE ADRIATIC SEA: A COUPLED OCEANOGRAPHIC-GENETIC ANALYSIS

Marcello Schiavina [1]*, Ilaria A. M. Marino [2], Paco Melià [1] and Lorenzo Zane [2]

[1] Dipartimento di Elettronica, Informazione e Bioingengeria, Politecnico di Milano, via Ponzio 34/5, I-20133, Milano, Italy - m.schiavina@gmail.com

[2] Dipartimento di Biologia, Università di Padova, Via U. Bassi 3, I-35131, Padova, Italy

Abstract

Coupling Lagrangian simulation with genetic analyses, we investigated oceanographic and genetic connectivity among six locations of the Adriatic Sea for the European green crab (*Carcinus aestuarii*). Results reveal the role of circulation in determining the observed biogeographic pattern, which reflects a oceanographic subdivision of the Adriatic Sea into three sub-basins.

Keywords: North Adriatic Sea, Central Adriatic Sea, South Adriatic Sea, Biogeography, Circulation models

Introduction Identifying the spatiotemporal scale of connectivity among populations is crucial to understand the factors driving population dynamics, dispersal patterns and gene flow in marine species [1]. Coupled physical-biological models (CPBMs) are increasingly used to investigate mechanisms of larval dispersal and to contrast alternative hypotheses by simulation [2]. Integrating the outputs of CPBMs with population genetic models can provide new insights of verifying model predictions [3]. In this work, we investigated larval dispersal patterns of *Carcinus aestuarii* in the Adriatic Sea by coupling Lagrangian simulations (incorporating early-life-history traits) with a genetic marker analysis and comparing the connectivity matrices resulting from the two approaches. The aim of the work was to study the role of Adriatic Sea currents in determining retention and spillover patterns and their consequences on the genetic structure of the local European green crab populations.

Materials and methods

Genetic analyses were conducted on samples, collected in 2006, 2007 and 2008 from six sites along the Italian Adriatic coast (Marano, Venezia, Goro, Ravenna, Foggia, and Lecce), with an additional sample from the Ionian Sea (Taranto). Total genomic DNA was extracted using a salting-out protocol [4] and individuals (N=381) were genotyped at eleven polymorphic microsatellite loci. Population pairwise F_{ST} were determined with GENETIX, using 10000 permutations for all comparisons. Genetic divergence between populations was analyzed also using the AMOVA approach [5] to define groups of lagoon populations, which are geographically and genetically homogeneous and maximally differentiated from each other. Lagrangian simulations, limited to the Adriatic basin, were performed using daily average circulation fields produced by the Adriatic Forecasting System (AREG model [6]). 1000 larvae were released from each of the 6 sites according to a Gaussian distribution during the spawning season (every autumn, new and full moon [7]) in 2006, 2007 and 2008. Particles were tracked for 35 days (the average pelagic larval duration [7]) and their diel vertical migration was described as in [8]. For each site, connectivity with the others was calculated as the percentage of larvae whose final position fell within a 10-km-radius buffer from the destination site.

Results

Genetic data showed the existence of weak but significant genetic differentiation between samples (overall F_{ST} = 0.002; 95% CI = 0.000–0.004, p<0.01). Pairwise F_{ST} ranged from -0.001 to 0.005 and three values significant at the 5% level were found suggesting some genetic structure among samples (Table 1). Accordingly, AMOVA analysis identified 3 significantly differentiated groups of samples inside the Adriatic (F_{CT} = 0.002, p<0.01), the first including Marano, Venezia, Goro and Ravenna samples, the second including the Foggia sample and the third one represented by the Lecce and Taranto samples.

Table 2 shows the connectivity matrices obtained with the CPBM for the 3 years analyzed. In accordance with the results of the genetic analysis, Lagrangian simulations confirm the existence of a stronger connection among the four northern sites, which, in contrast, are isolated from the other two. The southernmost location (Lecce) is characterized by strong retention and occasional input from Foggia, confirming the observed genetic distance between these two populations.

Conclusion A coupled oceanographic-genetic analysis allowed us to derive potential dispersal patterns of *C. aestuarii* in the Adriatic Sea and, at the same time, to elucidate the genetic consequences of larval dispersal. Genetic analyses revealed the existence of weak but significant differentiation, apparently

reflecting a oceanographic subdivision of the Adriatic Sea in three sub-basins. However, when dealing with such subtle differences the challenge is to discriminate between minor but real population structure and artifacts due to noise related to sampling errors [9].

Tab. 1. *Carcinus aestuarii* pairwise F_{ST}. Estimates of pairwise genetic differentiation (F_{ST} values) among 7 populations. Asterisk: significant values, uncorrected p < 0.05.

	Marano	Venezia	Goro	Ravenna	Foggia	Lecce
Marano	-					
Venezia	0.002	-				
Goro	0.002	0.001	-			
Ravenna	0.002	0.001	-0.001	-		
Foggia	**0.004***	0.000	0.000	0.002	-	
Lecce	**0.003***	0.003	0.002	0.001	**0.003***	-
Taranto	**0.003***	0.003	0.002	0.003	**0.005***	0.000

Tab. 2. Connectivity matrices resulting from Lagrangian simulations

	Marano	Venezia	Goro	Ravenna	Foggia	Lecce
Marano	33.23%	0.38%	0.73%	0.36%	0.00%	0.00%
Venezia	0.09%	1.22%	3.73%	1.03%	0.00%	0.00%
Goro	0.00%	0.02%	49.93%	5.42%	0.00%	0.00%
Ravenna	0.00%	0.00%	1.03%	5.51%	0.00%	0.00%
Foggia	0.00%	0.00%	0.00%	0.00%	0.11%	0.05%
Lecce	0.00%	0.00%	0.00%	0.00%	0.00%	87.86%

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