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Genetic variability of the striped venus *Chamelea gallina* in the northern Adriatic Sea

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ABSTRACT

Chamelea gallina is a valuable commercial species in the Mediterranean Sea. The strong fishing pressure on *C. gallina* in the northern and central Adriatic Sea has paralleled a clear-cut decrease in clam population density and the occurrence of several irregular mortality events. Despite the commercial interest in this species, nothing is known about its genetic sub-structuring at the geographic and/or temporal scale, nor its levels of genetic variability. Analyzing microsatellite genotypes for samples collected in the Adriatic Sea, we detected large geographic genetic homogeneity with gene flow guided by broad scale circulation in the north-south direction. Our results also indicate weak genetic differentiation among size classes at the local and temporal scale. These small genetic differences might be determined by variability of local circulation and reproductive success, partial overlapping generations and high larval mortality rates as suggested by our estimates of the effective number of breeders. In fact, global effective population size estimates over multiple generations are medium-high, but a low number of breeders are responsible for the small clams size class recruitment. Notwithstanding, it was not possible to detect signatures of bottleneck. Future efforts in fishery management should aim to maintain genetic diversity – essential to the long-term sustainability of the resource – and limit effective population size fluctuations while considering the need to improve water quality to avoid mass mortality events.

1. Introduction

Bivalves represent important economic resources for fisheries and aquaculture and play a key role in coastal ecosystems where they typically face multiple stresses due to the variability of environmental conditions. Fishing pressure can decrease genetic variation through bottlenecks and interfere with genetic connectivity among populations (Hutchings and Reynolds, 2004; Munguía-Vega et al., 2015).

In this study, we examine the case of the clam *Chamelea gallina* (Fig. 1a), which is distributed throughout the Mediterranean, the Black Sea (Moschino and Marin, 2006), along the Portuguese coast and in a few sites of the Northern Atlantic (Backeljau and Gofas, 1994; Eggleton et al., 2007). This endobenthic clam lives in wild banks on sandy or sandy/muddy seabeds 1000–4000 m off the coastline (Casali, 1984). *C. gallina* is gonochoric and reaches sexual maturity between the first and second year of life, when the shell length attains 12 mm (Casali, 1984; Froglia, 1989). Its spawning period is long, occurring in two intervals between April and October (Morello et al., 2005b), and is largely influenced by environmental conditions, which may anticipate or delay gamete emission (Froglia, 1975; Romanelli et al., 2009). Larvae are pelagic for 15–30 days before settling into the seabed (Froglia, 1975; Romanelli et al., 2009).

The strong fishing pressure on *C. gallina* in the sandy coastal bottoms (3–12 m depth) of the northern and central Adriatic Sea has existed for over 30 years, escalating progressively since the 1970s and reaching an apex when the species became of extreme economic importance in the early 1980s (Froglia, 1989; Morello et al., 2005a,b). After the first high fishing yields, the landings soon started declining to one sixth of the output recorded 25–30 years prior, despite various measures adopted to limit the fishing effort (cuts in landings allowed,

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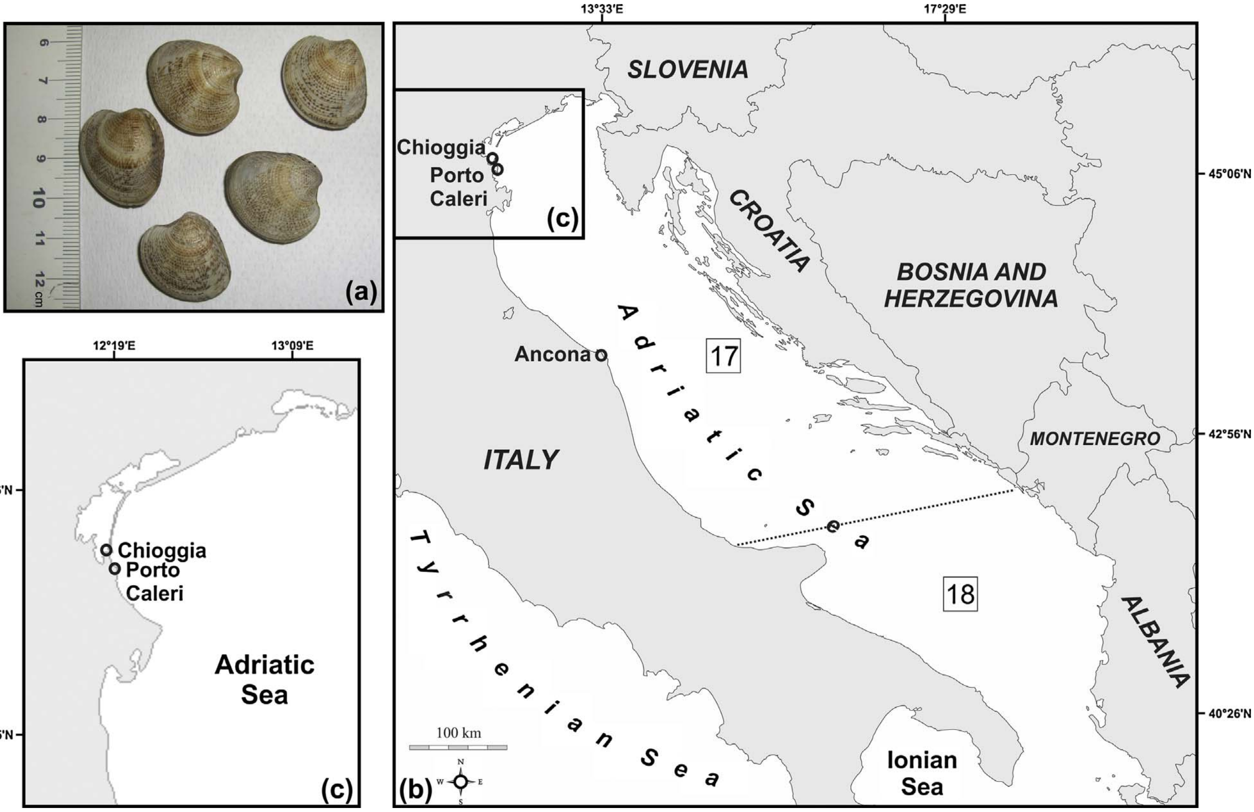

Fig. 1. *Chamelea gallina* sampling area. In a) specimens of *C. gallina* collected in Chioggia in 2009 (photograph taken by the authors), b) three sampling localities in the central-northern Adriatic Sea and in detail c) the two sampling localities off the Venice lagoon (Chioggia and Porto Caleri). All collection sites belong to the Geographical Subarea 17 (GSA 17 for the northern–central Adriatic; General Fisheries Commission for the Mediterranean, www.gfcm.org). Straight-line geographic distance between Porto Caleri and Chioggia is less than 10 km. Mean distance between Chioggia/Porto Caleri and Ancona is less than 200 km.

fleet reduction, creation of local fishermen consortia). Lately, the decline in *C. gallina* biomass has also been aggravated by the occurrence of several irregular mortality events in the Adriatic Sea (Gizzi et al., 2016; Milan et al., 2016).

One of the main goals of fishery management of *C. gallina* should be to ensure sufficient reproductive potential in a stock to allow for sustainable exploitation. This would help to preserve not only standing genetic diversity, but also the evolutionary potential of the species over long-time scales. So far, despite the commercial interest in this species, nothing is known about *C. gallina* genetic sub-structuring at the geographic and/or temporal scale, nor its levels of genetic variability.

In light of these premises, our study was designed with a specific focus on the northern-central Adriatic Sea, to improve our knowledge about *C. gallina* for future efficient management plans. The main aim of this study was to determine the genetic sub-structuring of *C. gallina* in three intensively exploited sites (Porto Caleri, Chioggia and Ancona) of the northern-central Adriatic Sea and the connectivity among sites in terms of relative gene flow. Notably, besides the geographic scale, we have also considered whether temporal differences occur among size classes within each location by comparing small clams (likely immature and resulting from the most recent reproductive season) and big clams (presumably representing the pool of parental cohorts).

We also searched for potential effects of long-term fishing pressure and mortality events in *C. gallina* by determining the contemporary effective population size N_e, indicative of the species potential to maintain genetic variability (Frankham, 1995) and by assessing whether populations experience signatures of recent bottleneck.

2. Materials and methods

2.1. Biological sample collection and handling

Chamelea gallina (Fig. 1a) samples were collected between October 2009 and December 2010 from Chioggia, Porto Caleri and Ancona (between 0.3 and 3 miles off the coast, Table 1, Fig. 1b and c) by commercial fishermen. Sampling location coordinates and samples related data are shown in Table 1.

Specimens were immediately placed in ice after fishing and sorting. Clams were cold-transported within three hours from collection to the laboratory where they were stored at -80 °C to preserve genomic DNA until subsequent analysis.

2.2. Size class definition

To check for temporal variability of genetic structure and assess whether the parental pools have a different genetic composition from offspring in the same geographic location, we separated individuals that likely resulted from the most recent reproductive season (the small size class) from potential parental cohorts (the big size class). For each sampling event, we collected two random samples of individuals with the length of the left shell (maximum distance on the anterior-posterior axis) smaller and larger than 12 mm. Owing to lack of information about the age vs. size and growth rates of *C. gallina* in the northern Adriatic Sea, the threshold between the two groups was set at 12 mm according to literature (Casali, 1984; Froglia, 1989, MG Marin personal communication). Sampling occurred by hydraulic dredge and this method does not give access to very small clams (below 5 mm, MG Marin personal communication, see Section 4.1 Caveats in the Discussion). The length of the left shell was measured for all genotyped clams