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Larval connectivity of the invasive blue crabs *Callinectes sapidus* and *Portunus segnis* in the Mediterranean Sea: A step toward improved cross border management

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Highlights

- Two invasive <u>blue crabs</u>, *Callinectes sapidus* and *Portunus segnis* have spread rapidly
- We simulated the dispersal of blue crab larvae using a Lagrangian model on 3-year period
- Callinectes sapidus showed a large dispersal and connectivity
- *Portunus segnis* is confined to the Tunisia gulf but showed a large self-recruitment
- We recommend to implement overfishing measures at local scales to cut the connection between each population

Abstract

The two invasive <u>blue crabs</u>, *Callinectes sapidus* and <u>Portunus segnis</u> have spread rapidly in the Mediterranean and no data exists on the connectivity of populations. Determining the source and recruitment areas is crucial to prioritize where population control measures should be put into immediate action. We simulated the dispersal of blue crab larvae using a Lagrangian model coupled at high resolution to estimate the potential connectivity of blue crab populations over a 3-year period. Our results reveal that the main areas at risk are the Spanish, French, Italian Tyrrhenian and Sardinian coasts for *Callinectes sapidus* with high populations connectivity. Tunisia and Egypt represent high auto recruitment zones for *Portunus segnis* restricted to the central and western basins. This study provides an overview of the connectivity between populations and will help define priority areas that require the urgent implementation of management measures.

Introduction

Understanding connectivity and the processes it involves can help us to make predictions on the likelihood Non-Indigenous Species (NIS) is an important point to explore to define international management plan of these species at diverse spatial scales: global, regional and local level (Cowen et al., 2000, Cowen et al., 2006). In the case of NIS, studying larval planktonic exchange and the consequent movement between populations is crucial to determine the connections and the risk associated with larval dispersal of NIS. Yet the underlying mechanisms of larval exchange and movement between populations remain 9/4/24, 5:27 PM

poorly understood for most species. Understanding these underlying mechanisms is a key focus of modern ecology (Cowen and Sponaugle, 2009). Dispersal, usually termed 'connectivity', is one of the most important ecological processes of larval exchange between distinct populations, and when assessing its ecological role in shaping local biodiversity (Cowen and Sponaugle, 2009; Wood et al., 2014). High connectivity can enhance a species resilience to exploitation (Jones et al., 2015; Marchessaux et al., 2020; Strathmann et al., 2002); climate change (Peterson, 2002); and genetic diversity (Garant et al., 2007; Reynes et al., 2021; Thibaut et al., 2016). However, studying larval dispersal in the field can be a major challenge (Kinlan and Gaines, 2003). This is because small planktonic larvae (often <1 mm) incur high rates of natural mortality and sampling methods to identify their migrations have some limitations. Direct estimates of larval connectivity rely on mark-recapture of artificially marked larvae or by analyzing geochemical signatures in calcified structures (Thorrold et al., 2002). However, the results yielded are not generalizable due to the reduced sampling effort. For some taxa these methods are difficult or impossible to apply, for example crustacean larvae, do not contain calcified parts and frequently molt (Anger, 2001). In these cases indirect estimates of connectivity using genetic markers often remain too expensive (Hedgecock et al., 2007). There is therefore a clear need to adopt affordable, feasible, and effective solutions to understand larval dispersal.

The increased power of computer-based systems and the availability of high-resolution hydrodynamic datasets that allow the implementation of Lagrangian particle tracking models, means that, when applied at the correct biogeographic scale, effective estimates of the potential connectivity among distant populations. Lagrangian particle tracking models allow us to simulate the movement of individual particles, that in this context represent "larvae", through hydrodynamic current fields. These models are being used in numerous studies with varied applications including: stock management of commercially valuable species (Criales et al., 2019), creation of marine protected areas (Hinrichsen et al., 2009), conservation of protected species (Reynes et al., 2021), and to research invasive species (Marchessaux et al., 2020). These models could provide credible and salient knowledge, that proves fruitful when assessing the invasive potential of an alien species. Larval dispersal models therefore provide an optimal tool for determining connections between populations and areas of larval stage retention in Early Detection and Rapid Response (EDRR) programs (Reaser et al., 2020). The early detection of invasive species is one of the first measures to prevent an invasion (Reaser et al., 2020). Surprisingly, these connectivity models are not being extensively applied to biological invasions, even though, in marine ecosystems, species do not have borders and understanding the connections among populations in the same biogeographical area could be crucial to the design and implementation of effective

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management measures for these species. Identification of source and recruitment areas could be useful to disrupt the connectivity dynamics.

For species such as the two invasive blue crabs in the Mediterranean, *Callinectes sapidus* (Rathbun, 1896) and *Portunus segnis* (Forskål, 1775), collecting such information is critical for its management. Native to the American coast and Indo-Pacific Ocean, respectively, these blue crab species have both recently shown a large expansion in the Mediterranean Sea (Mancinelli et al., 2021; Marchessaux et al., 2022; Shaiek et al., 2021). Their biological traits, such as: early maturity, rapid growth rates, opportunist diet, high reproductive rates, generalist habitat use, long-range larval dispersal, and effective physical and aggressive behavior (Castriota et al., 2022; Mancinelli et al., 2017), facilitate their invasiveness and boost their successful spread across regions (Mancinelli et al., 2021; Shaiek et al., 2021). Despite local observations of competitive interactions with native species (Gennaio et al., 2006; Mancinelli et al., 2013) and impacts on the artisanal fishery (Fuentes et al., 2019; Kampouris et al., 2019; Marchessaux et al., 2023), the ecological and economic consequences of these two blue crabs remains theoretical (Mancinelli et al., 2017; Suaria et al., 2017).

The implementation of effective cross-border management measures to limit the impacts of blue crabs in the Mediterranean basin is urgently needed. Several authors have proposed the development of specific blue crab fisheries to be the only possible effective management measure to control populations (Ennouri et al., 2021). However, these strategies remain localized at the regional level (Ayas and Ozogul, 2011; Ennouri et al., 2021; Kevrekidis et al., 2013). Therefore, identifying the source and recruitment areas for these two species would allow for prioritization of the areas where population control measures would be most effective. Creating population control in source areas (capture of vulnerable life stages such as ovigerous females for example) would limit the arrival of new individuals in recruitment areas (Barbour et al., 2011; Hussner et al., 2017; Ramula et al., 2008). Thus, this type of measure could be an effective strategy for the cross-border management of these invasive blue crabs. We therefore simulated the dispersal of blue crab larvae using a Lagrangian particle tracking model coupled with a high-resolution hydrodynamic model to estimate the potential connectivity of blue crab species C. sapidus and P. segnis at the Mediterranean scale. Our results provide an overview of the connectivity between populations and can be used to help define priority areas where management measures should focus and be rapidly implemented.

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Materials and methods

The Mediterranean Sea, a semi-enclosed basin with its own physical circulation and ecological functioning, is under significant human pressure (de Madron et al., 2011). It represents a natural laboratory for connectivity studies as it is subject to various pressures from invasive species such as the blue crabs *C. sapidus* and *P. segnis* (Mancinelli et al., 2021; Shaiek et al., 2021). We partitioned the Mediterranean sea surface into hydrodynamic provinces, i.e., a set of oceanic sub-regions in...

Results

Particle dispersal dynamics for *Callinectes sapidus* showed little variability regardless of the simulation time (Fig. 2A, Supplementary Figs. 1–2). For the remainder of the study, we will present the results of the 40-day scenario, the intermediate larval growth time. The Moroccan populations were connected with Southern Spain (Table 1A). The southern Spanish populations exported larvae to the northern Spanish coasts. Northern Spanish populations exported larvae to France where a...

Discussion

The high-resolution, multi-scale biophysical model, based on spatial population distribution data and habitat colonization at the Mediterranean scale, developed in this study provides much needed insight to support successful cross-border management of Non-Indigenous Species (NIS). This was the first study on the connectivity of invasive blue crab species in the Mediterranean Sea. Having applied our models to the invasive blue crabs, *Callinectes sapidus* and *Portunus segnis*, we have improved the ...

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CRediT authorship contribution statement

G.M and C.C. contributed to the conception and design of the study, performed the simulations and the statistical analyses. G.M. wrote the first version of the manuscript. M.C.M. and G.S. conceived the project. M.C.M., C.C. and G.S. contributed to the data analyses and revised the manuscript. All authors contributed to manuscript revision, read, and approved the submitted version....

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper....

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