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ORIGINAL PAPER

# Multiscale modelling of dispersal pathways for the invasive blue crab larvae (*Callinectes sapidus*) in the Mediterranean Sea

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**Abstract** The blue crab (*Callinectes sapidus*) is an invasive species present in the Mediterranean Sea since the mid-twentieth century, which has undergone a significant population increase in the last decade. This demographic explosion raises urgent concerns, necessitating detailed information on its dispersal dynamics at multiple scales. To investigate the dispersal pathways and connectivity patterns of *C. sapidus*, we conducted a biophysical modelling study over an eleven-year period (2010–2020), combining a Lagrangian particle-tracking tool with two hydrodynamic models of contrasting resolutions: a basin-scale model (MedMFC, ~ 4 km) and a high-resolution regional model (MARS3D, 1.2 km). By analyzing the path-use density of millions of simulated larvae, we identified major links connecting distant sub-basins, while highlighting the critical role of high-resolution modelling in resolving coastal retention features. An ensemble analysis of larval fate revealed strong spatial heterogeneity: while distant settlement drives recruitment in sink areas such as the Ligurian Sea and Eastern Corsica, local retention is the dominant mechanism in semi-enclosed environments such as the Gulf of Lion, the Gulf of Gabès and the Adriatic Sea, particularly during the summer spawning season. Connectivity matrices identified robust regional clusters, notably linking Tunisia, Sicily, Sardinia, and the Tyrrhenian coast, suggesting that islands act as critical stepping stones in the colonization process. These findings provide a quantitative baseline of larval exchange networks, highlighting key areas for future investigation to support the development of operational tools for management strategies.

**Keywords** Larval dispersal · Marine connectivity · Lagrangian model · Invasive species · *Callinectes sapidus*

## Introduction

Biological invasions, along with various forms of pollution, habitat destruction, and overexploitation of resources, exacerbated by global changes, are significant drivers of global biodiversity decline (Coll et al. 2010; Simberloff et al. 2013; Katsanevakis et al. 2014; Verma et al. 2020). The introduction of non-native

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species can have profound ecological and economic consequences, making it one of the primary threats to biodiversity conservation (Occhipinti-Ambrogi 2007; Diagne et al. 2020). This phenomenon has a particularly strong impact and may be considered irreversible within human generations or even on geological timescales, especially in marine environments (Boudouresque, 2005). The Mediterranean Sea, along with its wetlands and lagoons, is significantly affected by biological invasions (Zenetos et al. 2012). Since 1870, nearly 91 exotic crustacean species have been documented in the Mediterranean Sea, with 85 suspected to have originated from human activities and 18 classified as invasive, including the blue crab *Callinectes sapidus* (Rathbun, 1896), which is indigenous to the western part of the Atlantic Ocean, spanning from Nova Scotia to Argentina. The first scientific reports of its presence in the Mediterranean Sea refer to observations made around Turkey between 1935 and 1945 (Enzenrob et al. 1997). Since then, the blue crab has steadily expanded its range and is now found in all the Mediterranean Sea sub-basins. Over the last decade, its populations have experienced a marked demographic explosion (Mancinelli et al. 2021).

Since the early 2010s, its presence has been reported on the Tunisian coast (Bdioui, 2016), where it is now heavily commercially exploited (Rifi et al 2023). The species is also experiencing a significant expansion in the Northwestern Mediterranean Sea basin, with population explosions in certain lagoons (Labrune et al. 2019). In Spain, particularly in the Ebro Delta, the blue crab has shown strong expansion since 2012, threatening the local ecosystem and fisheries (Fuentes et al. 2019). The blue crab is also present in Corsica (Veyssiere et al. 2022), Sardinia (Piras et al. 2019), and Sicily, where it is the subject of intensive studies to adapt management and exploitation measures (Marchesseaux et al., 2023). In the central and eastern regions of the Mediterranean Sea, it is also recorded in the Adriatic (Zupan et al., 2016; Manfrin et al. 2016), Greece (Katsanevakis et al. 2020), Italy (Tyrrhenian and Ionian Seas, Azzurro et al. 2019), Turkey (Yaglioglu et al., 2014), Lebanon (Katsanevakis et al. 2020), Egypt (Ragheb & Rizkalla 2019), and Libya (Corsini-Foka et al. 2021). With such an extensive distribution in the Mediterranean Sea, the blue crab has become a crustacean with a strong ecological impact (Clavero et al. 2022). Its voracious nature has already had consequences for certain fisheries, such as the collapse of green crab (*Carcinus aestuarii*) populations and associated fisheries, observed in both the Ebro Delta (Prado et al. 2022) and Greece (Kampouris et al., 2019).

The blue crab has a complex life cycle with pelagic early life stages and benthic adult stages. As for all benthopelagic marine organisms, larval dispersal plays a vital role in the life cycle of biphasic cycle species (Okubo 1994). This phenomenon encompasses the physical and biological mechanisms that facilitate the transport of larvae from specific spawning sites to settlement sites . Larval dispersal is influenced by physical factors in the ocean, such as currents and turbulence (Power 1984). The behavior of larvae, including vertical migration and swimming, also impacts their pathways (Hovel & Fonseca 2005). Spawning, larval behavior, survival, dispersal duration, recruitment, and trophic interactions involving the consumption of zooplanktonic larvae by predators all contribute to larval connectivity within marine populations (Pineda et al. 2009). Improving our understanding of species invasion dynamics and their impacts on ecosystems and other populations is essential for ecologists and evolutionary biologists. This requires a better grasp of their biological cycles, particularly their larval stages (Cowen et al. 2006).

Various methodologies are available for studying larval dispersal and connectivity in marine benthopelagic species. In situ direct methods, although rare and costly, have been successfully applied to ascidian larvae, with *Ecteinascidia turbinata* being a classic example due to its large larval size (approximately 2 mm). This species has facilitated both early studies (Bingham & Young 1991; Olson 1985) and more recent research on larval activity (Carballo 2000; Stach & Kirbach 2009; Casso et al. 2018). Indirect biogeochemical methods, such as fluorescent dye marking and radiotagging for short-term tracking, or sclerochronology and otolithometry for species with appropriate calcified structures for long-term tracking, enable the assessment of larval dispersal and connectivity (DiBacco & Levin 2000; Lugo-Fernández et al. 2001; Marko & Moran 2009; Sandin et al. 2005; Thorrold et al. 2002). However, these methods also have limitations, particularly for species with highly variable dispersal or when applying calcified structure-based methods to groups like crustaceans. Genetic analyses of individuals overcome these limitations by quantifying gene flow between populations, complementing hypothesis validation and numerical models, albeit at different time scales and a relatively higher cost. Numerical modelling approaches have significantly advanced in recent decades, facilitated by increasing computational power, enabling the study of larval dispersal at different temporal and spatial scales (Swearer et al. 2019). The potential of numerical approaches to investigate marine biological invasions has been demonstrated, with recent studies emphasizing the utility of current models in assessing the diverse impacts of invasive species populations and the need to enhance their predictive capabilities for future impacts (Corrales et al., 2020). Across the globe, several studies have employed Lagrangian transport tools as a methodology to elucidate and forecast the dispersal of invasive species. For instance, to identify larval retention processes for *Carcinus maenas* along the northeastern Pacific Ocean (Banas et al. 2009), or to evaluate the role of changing advective pathways between the Pacific and Atlantic Oceans in the potential invasion of species in the North Atlantic (Kelly et al. 2020).

For the blue crab in the Mediterranean Sea, an initial modelling study of larval dispersal covering three years (2017 to 2019) revealed the species' capability to disperse across basins, aided by its extended larval lifespan. In contrast, the same study showed that another invasive crab, *Portunus segnis*, exhibits higher local retention and strong self-recruitment, primarily in Tunisia (Marchessaux et al. 2023). Furthermore, this preliminary study did not consider larval connectivity patterns over a more extended time period and at different spatial scales, which may limit its relevance for developing large-scale management measures. Additionally, Swearer et al. (2019) reviewed and conducted meta-analyses of Lagrangian dispersal models, highlighting the scarcity of studies conducted at different scales to explore dispersion-related questions, which often focus on more localized phenomena. They also emphasized the lack of research over extended periods, which can impede a comprehensive spatial and temporal understanding of the observed processes.

In this study, the spatiotemporal variability of larval dispersal for the invasive species *Callinectes sapidus* is investigated over an eleven-year period (2010–2020). Two hydrodynamic circulation products, one covering the entire Mediterranean Sea at 4–5 km horizontal resolution and one focusing on the Northwestern Mediterranean Sea at 1.2 km resolution, are employed to analyse larval transport patterns at both basin-wide and regional scales. Seasonal differences are further examined by comparing simulations performed for two contrasted spawning periods, enabling an assessment of how release timing influences dispersal distances and connectivity structure. Throughout the manuscript, the term dispersal pathways is used to describe recurrent larval movement corridors predicted by the model, derived from the cumulative spatial occurrence of simulated particle trajectories across grid cells over multiple years, reflecting preferential spatial use of the seascape. This concept is distinct from connectivity links, which refer to discrete source-to-destination relationships between geographic areas, habitats, or populations, inferred from connectivity estimates and associated with origin–destination transition probabilities.

## Material and methods

### The blue crab in the Mediterranean Sea

The model species chosen for this study is the blue crab, which is invasive in the Mediterranean Sea. Studies from its native range indicate that females are found closer to the sea in coastal lagoons and bays where the water has a higher salinity. Epifanio (2019) provided a detailed description of the life cycle of the blue crab. The blue crab is known for its exceptional adaptability to different habitats, facilitated by its well-developed osmoregulatory abilities. In addition, adults and older juveniles exhibit a wide range of thermal tolerance (Towle & Burnett 2007). In contrast, the larval and early juvenile stages require relatively high salinities and temperatures characteristic of warm season coastal waters (Costlow 1967). Reproduction occurs in low salinity waters, with female crabs migrating to polyhaline zones to lay and incubate their eggs, while adult males remain in low salinity waters (Aguilar et al. 2005). Once the eggs mature, females migrate to the sea to release the planktonic larvae (Epifanio 2019). During the larval stage, the blue crab undergoes several developmental stages, the duration of which varies according to environmental conditions (Costlow 1967). This period includes seven zoeal stages during which the larvae remain high in the water column by active swimming (Epifanio 1995). Shortly before the transition to juveniles, zoea larvae develop into a megalopal stage capable of vertical migration. Zoeal development takes three to four weeks under favourable conditions, while the duration of the megalopal stage is more variable and depends on several chemical and physical factors (Epifanio 2019). Regardless of the stage, the swimming speed of *Callinectes sapidus* larvae is slower than the speed of surface currents in the Mediterranean Sea ($<10$ cm/s, Luckenbach et al., 1992; Epifanio 2019), suggesting that horizontal active swimming does not play a significant role in their dispersal. However, vertical migration facilitates the return of larvae to the estuary entrance, where they find habitats such as seagrass beds, patches of macroalgae and oyster reefs, which provide food and protection from predators for larvae and juveniles (Hovel & Fonseca 2005; Litvin et al. 2018). To date, research on the reproduction of the blue crab in the Mediterranean Sea is still limited. Observations suggest a reproductive period that can extend from April to September, with regional variability (Cilenti et al. 2015; Gaber et al. 2021; Safaie et al. 2013; Marchessaux et al. 2023). Two spawning seasons have been identified in their native range, which could correspond to a spring and summer season in the Mediterranean Sea, based on the thermal tolerances of the crab (Criales et al. 2019).

## Surface circulation

The large-scale water circulation in the Northwestern Mediterranean Sea is subject to thermohaline circulation, which is characterised by cyclonic currents generated by the continental slopes (Millot & Taupier-Letage 2005). A recent overview of the general circulation pattern in the Mediterranean Sea, both at the overall scale and at the sub-basin level, is provided by Pinardi et al. (2015). The Mediterranean Sea is subdivided into two principal basins, separated by the Sicily-Tunisia Strait. The western basin is connected to the Atlantic Ocean via the Strait of Gibraltar, and comprises the Alboran Sea, the Liguro-Provençal Sea, the Algerian Basin and the Tyrrhenian Sea, extending from west to east. The eastern basin includes the Adriatic Sea, the Ionian Sea, the Libyan Sea, the Aegean Sea and the Levantine Sea. The complex surface circulation of the Mediterranean Sea is a consequence of its division into subseas and its rugged seafloor topography (Millot & Taupier-Letage 2005). In general, the surface circulation is anticyclonic. Fresher Atlantic water (AW) enters the Mediterranean Sea through the Strait of Gibraltar, becomes denser as it moves towards the western basin due to strong evaporation, and exits the Mediterranean Sea through the Strait of Gibraltar after about 50 to 100 years (Millot & Taupier-Letage 2005). Surface currents give rise to eddies up to one kilometre in diameter. These eddies are formed by the destabilisation of the flow along the continental slope. In contrast, gyres formed by wind and seafloor topography remain stable and stationary, although some parts may become unstable over time. These characteristics are influenced by a range of atmospheric and physicochemical factors, as discussed in the comprehensive study by Pinardi et al. (2015) (Fig. 1A). In terms of surface currents (0–15 m), the Liguro-Provençal-Catalan current (LPCC) flows from east to west between the Ligurian Sea, the Gulf of Lion and the northern areas of the Balearic Islands. The Gulf of Lion Gyre (GLG) circulates in the opposite direction to the prevailing Gulf of Lion current. The Eastern Corsican Current (ECC) flows east of the Corsican coast, and the Northern Tyrrhenian Gyre (NTG) circulates southeast of Corsica. The South-Western Tyrrhenian Gyre circulates to the south of the Tyrrhenian Sea and passes close to the eastern coasts of Sardinia. In addition, the Southern Sardinia Current (SSC), which flows from west to east, circulates north of the Balearic Islands before flowing south of Sardinia, and the Middle Tyrrhenian Current (MTC), which is a continuation of the Southern Sardinia Current (SSC), flows northward in the Tyrrhenian Sea (Fig. 1B). The Corsica Channel connects the Tyrrhenian Sea to the east of Corsica with the Northwestern Mediterranean Sea. To the east of the Strait of Bonifacio—between Sardinia and Corsica—the westerly winds are channeled and intensified, resulting in a cyclonic circulation to the north. Finally, to the north of the island, the East Corsican Current joins the West Corsican Current, accompanied by the presence of eddies, to form the Liguro-Provençal-Catalan Current.

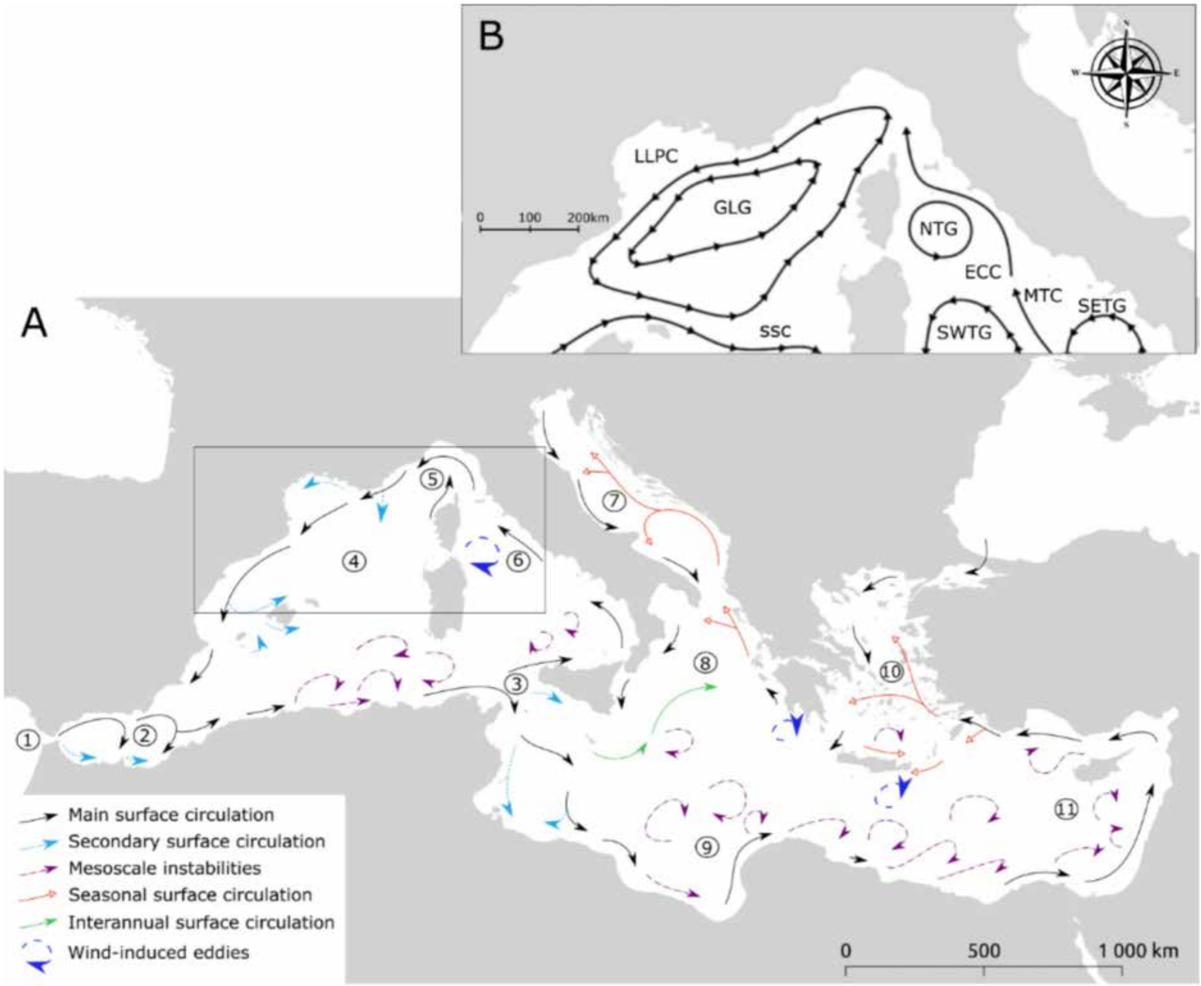


**Fig. 1** Map of the general circulation currents in the Mediterranean Sea **A**, covering all basins (adapted from Millot & Taupier-Letage 2005). 1: Strait of Gibraltar, 2: Alboran Sea, 3: Sicilia-Tunisia Strait, 4: Algero-Provençal Basin, 5: Ligurian Sea, 6: Tyrrhenian Sea, 7: Adriatic Sea, 8: Ionian Sea, 9: Libyan Sea, 10: Aegean Sea, 11: Levantine Sea. Focus on the Northwestern Mediterranean Sea **B** adapted from the study by Pinardi et al. (2015). LPCC: Liguro-Provençal-Catalan Current, GLG: Gulf of Lion Gyre, NTG: Northern Tyrrhenian Gyre, ECC: Eastern Corsica Current, SSC: Southern Sardinia Current, MTC: Middle Tyrrhenian Current, and SETG: South-Eastern Tyrrhenian Gyre

## Hydrodynamic models

The simulations conducted for this study rely on two hydrodynamic models, with data sourced from the Mediterranean Sea Physics Reanalysis (MedMFC) model and the MARS3DMed model for the Northwestern Mediterranean Sea (Fig. 2). MedMFC is based on the NEMO code from the MERCATOR consortium and encompasses the entire Mediterranean Sea at a horizontal resolution of 1/24° (approximately 4–5 km) with 141 unevenly spaced vertical levels (Escudier et al., 2021). MARS3DMed, derived from the MARS3D (Model for Application at Regional Scales 3D) code developed by Ifremer, has a horizontal resolution of about 1.2 km and 60 vertical levels using a generalized sigma coordinate system on an Arakawa-C grid, extending from the seafloor to the surface and suited for fine-scale graphics (Arakawa & Lamb 1977; Lazure & Dumas 2008). These two models solve the primitive equations, coupling barotropic and baroclinic modes with temperature and salinity data for eleven consecutive years from 2010 to 2020. The MedMFC model features a daily temporal resolution, meaning that data are aggregated on a daily

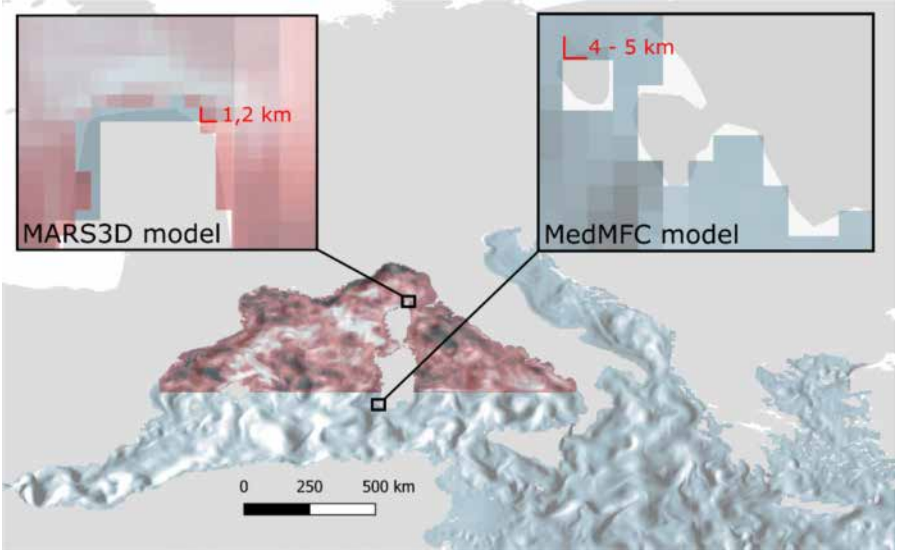


**Fig. 2** The schematic maps illustrate the two geographical areas used in the larval dispersion study: MARS3D, situated in the North-Western Mediterranean Sea, with a spatial resolution of 1.2 km, and MedMFC, which encompasses the entire Mediterranean Sea, with a resolution of 4–5 km

basis. Thus, each variable recorded in the file (e.g., salinity, temperature, current velocity) is averaged or aggregated over a complete day. On the other hand, the MARS3DMed model has a 3-hourly temporal resolution.

### Larval dispersal model and parameterization of simulations

The offline Lagrangian software Ichthyop v.3.3.12 (Lett et al. 2008) was used to study the larval dispersal of C. sapidus. Current direction and velocities from the MedMFC and MARS3DMed models were used as inputs in Ichthyop. Particles trajectories were calculated using a fourth-order Runge–Kutta method with a constant time step (Van Sebille et al. 2018). Horizontal dispersion was set according to Ichthyop's standard parameterization based on Peliz et al. (2007), with a dissipation rate of 10–9 $m^2$ $s^{-3}$. Horizontal and vertical advection was applied at a time step set according to the Ichthyop configuration for having an acceptable estimate of the Courant-Friedrichs-Lewis (CFL) condition: 720 s for simulations with the MARS3DMed model and 2880 s for simulations with the MedMFC model. Model outputs were saved at regular time intervals, capturing the particle positions every 12 h.

A proportional release strategy was applied to ensure that the number of particles released was proportional to the total surface area of the spatially defined spawning zones. This approach respects the hypothesis that larger suitable habitats potentially contribute a greater propagule pressure. Specifically, 450,000 particles were released per simulation year within the Northwestern Mediterranean Sea window (MARS3DMed). To maintain a comparable proportionality ratio across the larger domain, 2,250,000 particles were released per simulation year from the spawning zones covering the entire Mediterranean Sea basin (MedMFC).

The maximum larval dispersal duration (PLD) was set to 40 days (Costlow 1967; Marchessaux et al. 2023). Two consecutive spawning periods were investigated: a Spring scenario (April to June) and a Summer scenario (July to September), based on existing literature (Safaie et al. 2013; Gaber et al. 2021; Marchessaux et al. 2023) and local testimonies provided by the Office de l'Environnement de la Corse. To capture temporal variability in circulation, particles were released on the 5th, 15th, and 25th of each month during these periods.

In the model, larvae were considered horizontally passive but underwent daily vertical migration (DVM) at sunrise and sunset. Depths were defined by the photic zone, averaging about 30 m deep during the day and about 1 m deep at night (Anger et al. 2015; Ospina-Alvarez et al., 2018). Horizontal active swimming was not included, as the swimming capabilities of early stages are negligible compared to surface currents. The buoyancy of the particles was governed by a density of 0.9 g cm$^{-3}$ (Epifanio & Garvine 2001). Lastly, a rebounding behavior upon contact with physical barriers was assigned to the particles. All model parameters are summarized in Table 1.

## Spawning and settlement sites

The release and settlement zones corresponding to potential spawning and recruitment areas (Fig. 3) were defined based on a thorough bibliographic review. This review incorporated the blue crab presence database compiled by Mancinelli et al. (2021) and was supplemented with additional surveys from Morocco (Chaouti et al. 2022), Algeria (Benabdi et al. 2019), Tunisia (Taybi et al., 2020), and Libya (Corsini-Foka et al. 2021). These spatially defined areas represent potential spawning and recruitment habitats, allowing us to assess potential connectivity between blue crab habitats across the different Mediterranean Sea basins. All areas were delineated using QGIS v3.24.0. To ensure overlap with the hydrodynamic model grid while encompassing the species' full depth range, zones were defined within bathymetric limits ranging from 0 m to the 100-m isobath (Safai et al., 2013).

## Analysis of simulation outputs

Post-processing and analysis of simulation outputs were performed using Python (v3.11). Key libraries included NetCDF4 for data extraction, Shapely and Rasterio for spatial vector-to-raster operations, Pandas for matrix computations, and Cartopy/Matplotlib for mapping and visualization.

First, to identify and visualize the main dispersal features, we computed a path-use density metric. Unlike simple presence/absence maps, this metric quantifies the intensity of use of the seascape by larvae that successfully reached a recruitment zone. This rasterization approach is consistent with established methodologies in marine ecology, where path-use densities are computed to identify high-use areas and critical habitats for top predators (Fossette et al., 2014). Furthermore, this metric is applied across diverse disciplines to quantify flow intensity and residence times, ranging from the identification of

**Table 1** Ecological parameters used to conFig. larval dispersal simulation scenarios for *Callinectes sapidus* in the Mediterranean Sea and in the Northwestern Mediterranean Sea's sub-basin with the simulations run with the hydrodynamic models MARS3DMed and MedMFC

| Parameter | MARS3DMed | MedMFC | References |
|---|---|---|---|
| Number of larvae released | 50 000 each release date (450,000 for each scenario, every year) | 250 000 each release date (2,250,000 for each scenario, every year) | |
| Pelagic larval duration | 40 days | | Costlow (1967) and Marchessaux et al. (2023) |
| Time period | 2010 to 2020 | | |
| Spring spawning scenario | April to June | | adapted from Costlow (1967) and Criales et al. (2019) |
| Summer spawning scenario | July to September | | adapted from Costlow (1967) and Criales et al. (2019) |
| Release days | 5th, 15th, and 25th day of each month | | |
| Release depth | 35 m | | Aguilar et al. (2005) |
| Coastline behavior | bouncing (particles bounce on the coastline as a billiard ball) | | |
| Numerical scheme | Runge Kutta 4 | | |
| Swimming behaviour | no | | Forward (1986) |
| Horizontal dispersion | dissipation rate ($10^{-}$ m$^2$ s$^{-3}$) | | Peliz et al. (2007) |
| Buoyancy | 0.9 g cm$^{-3}$ | | Epifanio & Garvine (2001) |
| Vertical migration depth | day 30 m–night 1 m | | Ospina-Alvarez et al. (2018) |

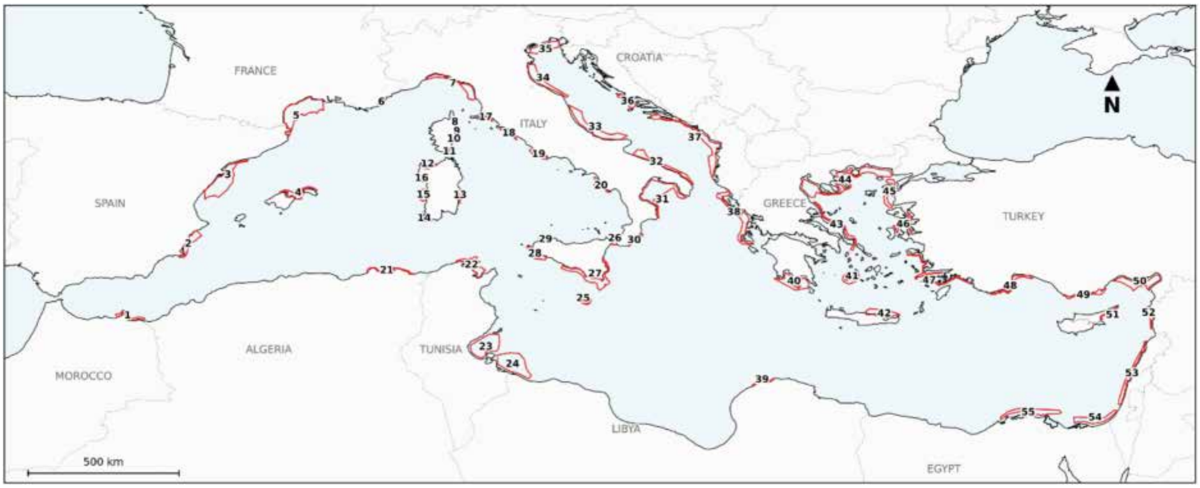


**Fig. 3** Map showing the 55 zones used as both spawning and settlement areas for the blue crab in the Mediterranean Sea and the geographical coverage of the two hydrodynamic models employed. Key to areas: 1: MOR—Morocco (Nador Province); 2: SPA1—Spain (Alicante); 3: SPA2—Spain (Ebre Delta); 4: BAL—Spain (Balearic Islands); 5: GOL—France (Gulf of Lion); 6: LIG—France (Ligurian Sea Coast); 7: IT1—Italy (Ligurian Sea Coast); 8: BIG—France (Biguglia, Corsica); 9: DIA—France (Diana, Corsica); 10: URB—France (Urbino, Corsica); 11: SGI—France (Santa Giulia, Corsica); 12: NWS—Italy (Northwestern Sardinia); 13: TOR—Italy (Tortoli, Sardinia); 14: SWS—Italy (Southwestern Sardinia); 15: ORI—Italy (Oristano, Sardinia); 16: ALG—Italy (Alghero, Sardinia); 17: IT2—Italy (Tyrrhenian Coast); 18: IT3—Italy (Tyrrhenian Coast); 19: IT4—Italy (Tyrrhenian Coast); 20: IT5—Italy (Tyrrhenian Coast); 21: ALGe—Algeria; 22: TUN1—Tunisia (Bizerte); 23: TUN2—Tunisia (Gabes); 24: TUN3—Tunisia (Bibane); 25: MAL—Malta; 26: SIC1—Italy (Messina, Sicily); 27: SIC2—Italy (South Sicily); 28: SIC3—Italy (Sicily Canal); 29: SIC4—Italy (North Sicily); 30: IT6—Italy (Ionian Sea Coast); 31: IT7—Italy (Ionian Sea Coast); 32: ADR1—Italy (Adriatic Sea Coast); 33: ADR2—Italy (Adriatic Sea Coast); 34: ADR3—Italy (Adriatic Sea Coast); 35: ADR4—Italy (Adriatic Sea Coast); 36: ADR5—Italy (Adriatic Sea Coast); 37: ADR6—Croatia (Adriatic Sea Coast); 38: GRE1—Greece (Ionian Sea Coast); 39: LYB—Libya; 40: GRE2—Greece (Peloponnese); 41: GRE3—Greece (Aegean Sea); 42: GRE4—Greece (Sea of Crete); 43: GRE5—Greece (Aegean Sea); 44: GRE6—Greece (Aegean Sea); 45: TUR1—Turkey (Aegean Sea); 46: TUR2—Turkey (Aegean Sea); 47: TUR3—Turkey (Levantine Basin); 48: TUR4—Turkey (Levantine Basin); 49: TUR5—Turkey (Levantine Basin); 50: TUR6—Turkey (Levantine Basin); 51: CHY—Cyprus; 52: LEB—Lebanon (Levantine Basin); 53: ISR—Israel (Levantine Basin); 54: EGY1—Egypt (Levantine Basin); 55: EGY2—Egypt (Levantine Basin)

atmospheric pollutant source regions (White et al., 2021) to the visualization of traffic bottlenecks in air traffic management (Standfuss et al., 2023). For each simulation year (2010–2020) and season (Spring and Summer), the analysis followed a four-step procedure: 1) the Lagrangian trajectories of all particles that successfully settled (i.e., recruited zone > 0 at the final time step) were extracted; 2) the discrete time-stepped positions (latitude/longitude) of each particle were reconstructed into continuous spatial geometries; 3) these geometries were rasterized onto a high-resolution reference grid, where the value of each grid cell represents the cumulative count of trajectory segments crossing that location; and 4) annual rasters were aggregated to compute a multi-year mean path-use density for each season. This approach was applied to both the basin-scale model (MedMFC) and the high-resolution regional model (MARS3D). To highlight the core arteries of dispersal, we generated "high-intensity pathway masks" by isolating grid cells falling within the top 50% of the non-zero density distribution. Maps were visualized using a logarithmic scale to account for the high variability in particle flux. To quantify larval fate, the outcome of every released particle was classified into one of three mutually exclusive categories: 1) Local Retention (LR), defined as particles settling within their original release zone at the end of the PLD; 2) Distant Settlement (DS), defined as particles settling in any parameterized zone other than their release site; and 3) Non-Retained Particles (NRP), defined as particles that failed to settle in any of the defined recruitment zones by the end of the simulation (i.e., “lost at sea”), likely resulting in mortality.

Then, connectivity between populations was quantified using directional transition matrices. For each release event, the number of particles originating from a specific release zone (i) and settling in a recruitment zone (j) was counted. Matrices were computed annually and then averaged over the eleven-year period to produce robust mean connectivity matrices for the Spring and Summer scenarios. To improve interpretability, zones in the matrices were reordered geographically (West to East) to visually cluster regional retention patterns. To explicitly assess seasonal variability, a difference matrix was computed by subtracting the mean Spring matrix from the mean Summer matrix. Positive values indicate increased recruitment in Summer, while negative values indicate stronger connectivity in Spring. Based on these exchange patterns, source–sink dynamics were characterized: a 'source' was defined as a zone acting as a net exporter (supplying larvae to other areas), while a 'sink' was defined as a zone acting as a net importer, where recruitment is largely driven by the arrival of larvae from external origins.

Analysis of larval travel distances and orientation was performed to characterize the spatial scale of dispersal potential. For every recruited particle, the total distance traveled was calculated by summing the great-circle distances between consecutive timesteps along its trajectory. Distance distributions were visualized using ridgeline plots, allowing for a comparative analysis of dispersal kernels across different release zones and between seasons. These distributions help distinguish between local retention (short travel distances, bell-shaped curves near the origin) and long-distance transport. Finally, wind rose diagrams were generated to illustrate the dominant directional bearing of larvae relative to their release site, providing insights into how surface currents drive the orientation of invasive spread.

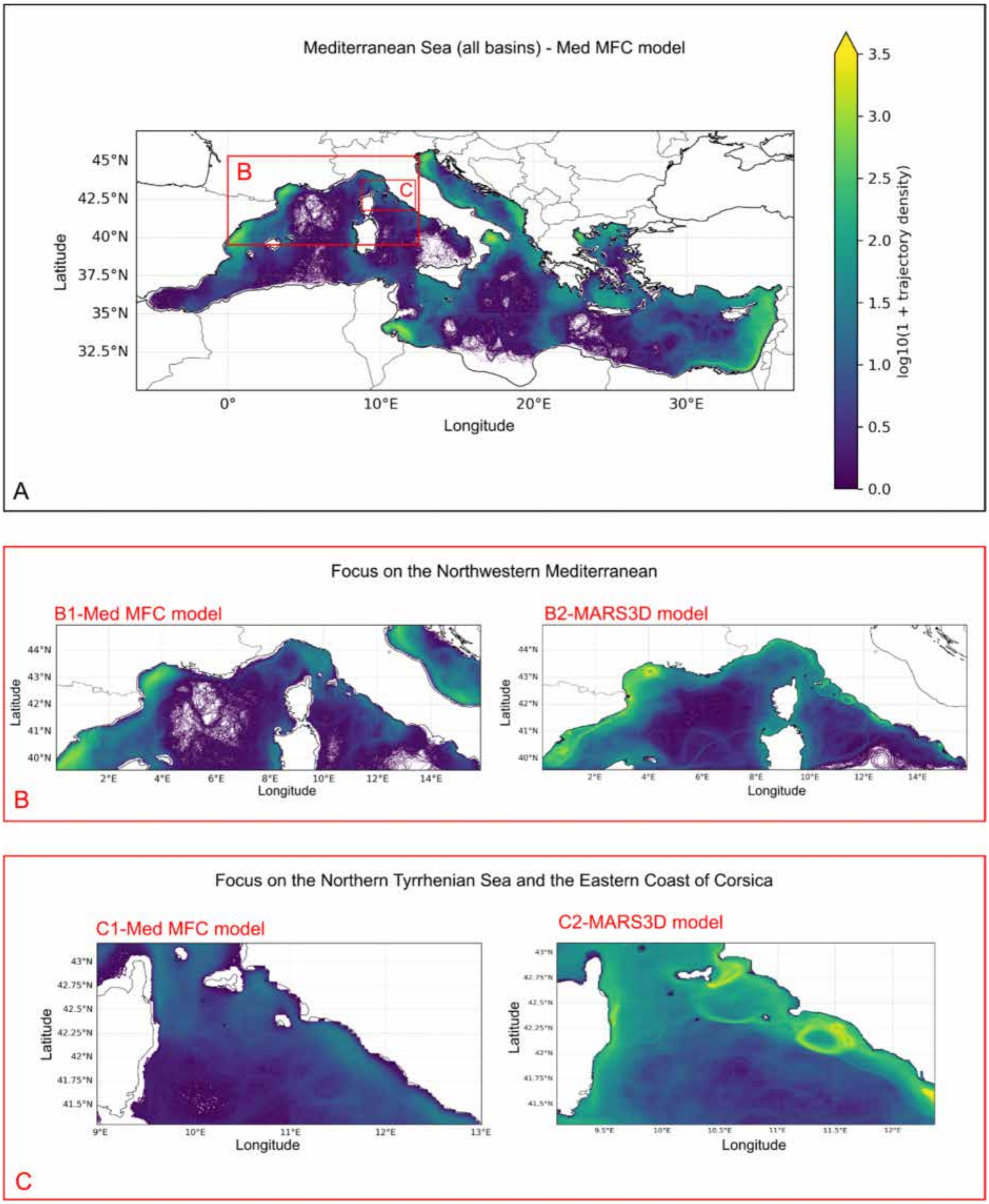
## Results

### Simulated dispersal routes at two different spatial resolutions

The multi-year mean path-use density maps (Fig. 4) illustrate the main dispersal routes used by blue crab larvae during the spring spawning period (averaged over 2010–2020). These maps aggregate the trajectories of all successfully recruited larvae, with color intensity reflecting the cumulative frequency of particle passage through each grid cell on a logarithmic scale. "Hotter" colors (yellow to light green) indicate high-density pathways, major arteries of larval transport, while darker blue areas represent zones of lower, more sporadic transit.

At the basin scale (Fig. 4A, MedMFC model), a complex network of high-density links connects the various sub-basins. Several major connections are clearly identifiable, particularly the routes linking the Spanish coast to the Balearic Islands, the strong connection between the Tunisian and Sicilian coastlines, and the recurrent exchanges within the Tyrrhenian Sea. High-density accumulation zones are also visible in retention-prone areas such as the Gulf of Lion, the Gulf of Gabès, and the northern Adriatic Sea. In the eastern basin, significant connections emerge along the Greek and Turkish coasts and throughout the Levantine basin, highlighting the potential for long-distance connectivity facilitated by the general circulation.

The regional focus on the Northwestern Mediterranean Sea (Fig. 4B) allows for a direct comparison between the basin-scale MedMFC model (Fig. 4B1, ~4 km resolution) and the regional MARS3D model (Fig. 4B2, 1.2 km resolution). While both models capture the broad cyclonic circulation of the basin, the higher-resolution MARS3D model reveals much finer dispersal structures. Specifically, the Liguro-Provençal-Catalan current (flowing westward along the French coast) appears as a more well-defined region of high particle transit in the MARS3D simulation, whereas the MedMFC model depicts a more diffuse transport pattern. This difference in resolution is even more pronounced in the focus on the Northern Tyrrhenian Sea and Eastern Corsica (Fig. 4C). The MARS3D model (Fig. 4C2) resolves complex mesoscale features, such as the Cap Corse dipole and coastal eddies, which create distinct, high-intensity retention structures and transport filaments that are smoothed out in the coarser MedMFC output (Fig. 4C1). The MARS3D simulation highlights a strong, coherent pathway wrapping around the northern tip of Corsica (Cap Corse), facilitating intense local connectivity that links the eastern and western coasts of the island. These comparisons demonstrate that while the basin-scale model effectively identifies long-distance connections, the



high-resolution regional model is essential for resolving the coastal retention mechanisms and fine-scale corridors that drive local recruitment dynamics.

### Larval fate and seasonal connectivity matrices

The ensemble analysis of particle fate over the

◂**Fig. 4** Multi-year mean path-use density maps for *Callinectes sapidus* larvae during the spring spawning period (2010–2020). The maps display the cumulative density of trajectories for successfully recruited larvae on a logarithmic scale (log10(1 + density)). Brighter colors (yellow/green) indicate high-intensity dispersal routes, while darker colors (purple/blue) indicate lower passage frequency. **A** Basin-scale view of the entire Mediterranean Sea simulated with the MedMFC model (approx. 4 km resolution). Red boxes indicate the spatial extent of the regional zooms. **B** Focus on the Northwestern Mediterranean Sea comparing outputs from the MedMFC model (**B1**) and the high-resolution MARS3D model (**B2**, approx. 1.2 km resolution). **C** Focus on the Northern Tyrrhenian Sea and the Eastern Coast of Corsica, comparing MedMFC (**C1**) and MARS3D (**C2**) outputs. The shared color scale applies to all panels, allowing for direct comparison of dispersal intensity across models and regions

2010–2020 period (Fig. 5) quantifies the larval fate patterns for each of the 55 release zones. By aggregating over 11 years and using relative proportions, these metrics allow for a relative comparison of the fate of particles released from different zones, independent of the substantial differences in propagule pressure associated with habitat size. In both Spring and Summer scenarios (Fig. 5A-B), recruitment in the Eastern basin is largely driven by long-distance transport. For instance, the Egyptian coast (EGY1) exhibits a high rate of distant settlement (~ 24%), indicating it acts as a major source of larvae exporting to other areas. Conversely, local retention is the primary driver of recruitment in semi-enclosed, retentive environments. The Gulf of Gabès (TUN2) and the Northern Adriatic (ADR4) stand out as retention hotspots in both seasons. While slight variations exist, for instance, retention in TUN2 reaches ~ 20% in summer compared to ~ 15% in spring, whereas ADR4 shows slightly higher retention in spring (~ 14%) than in summer (~ 10%), these differences do not alter the functional role of these zones.

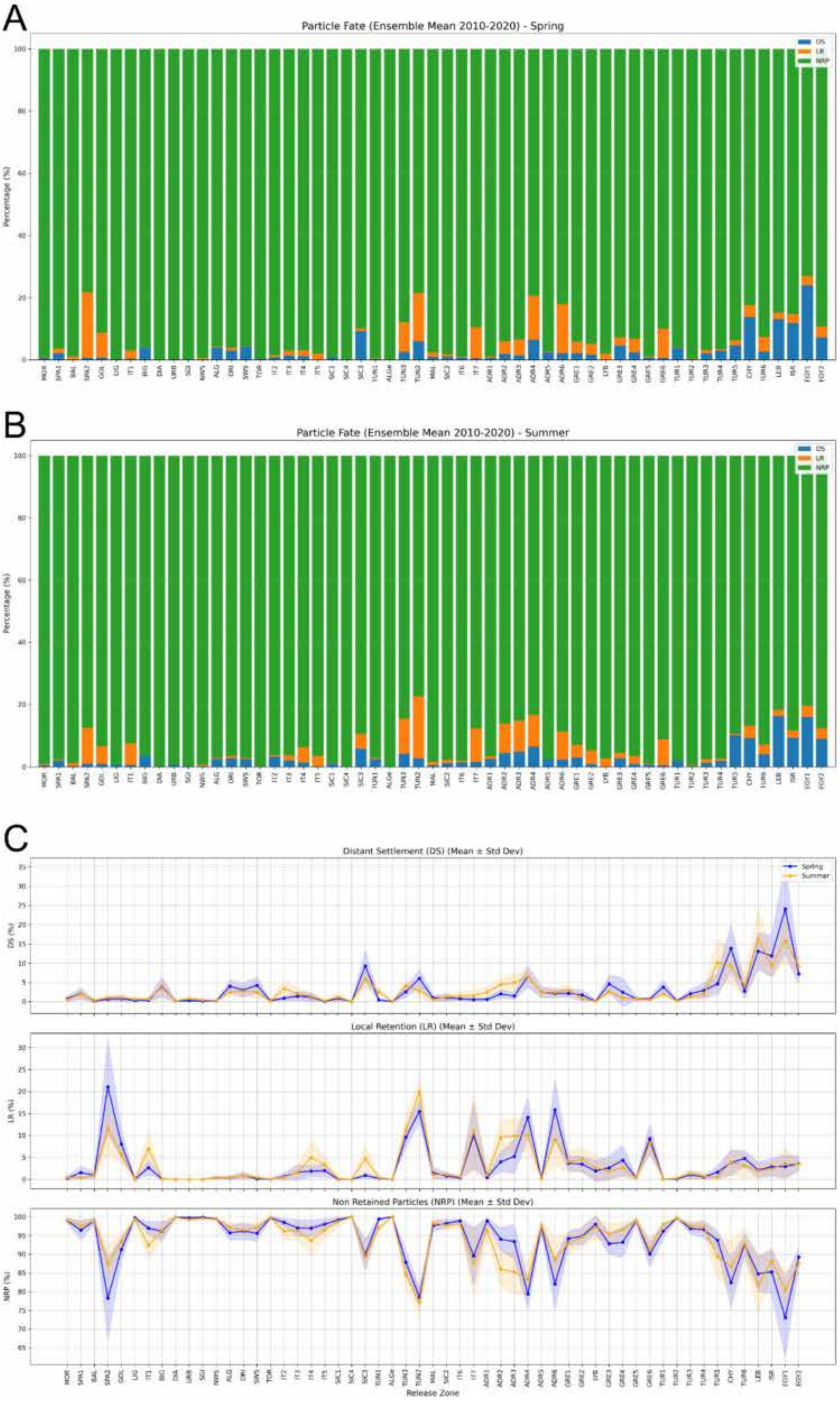
The comparative analysis (Fig. 5C) confirms this stability. The shaded error bands, representing the standard deviation across the 11 years, indicate that while the absolute magnitude of recruitment can fluctuate inter-annually due to meteorological variability, the dispersal patterns remain climatologically stable.

The structure of larval exchange networks is detailed in the connectivity matrices (Fig. 6), where release and recruitment zones are ordered geographically from West to East. This arrangement reveals a strong diagonal structure, confirming that self-recruitment and short-distance dispersal are the dominant mechanisms for population persistence, particularly in the Adriatic Sea (ADR) and the Gulf of Gabès (TUN). Beyond local retention, distinct connectivity clusters emerge off the diagonal, identifying functional sub-regions where mutual larval exchange is high (> 1%). In the Western and Central Mediterranean Sea, a cohesive “Tyrrhenian cluster” is evident, linking the coastlines of Sardinia, Corsica, and Western Italy. Specifically, the matrices highlight recurrent transport from the Tyrrhenian coast (IT2-IT5) towards the islands, as well as strong connectivity between the Tunisian coast (TUN1-2) and Sicily (SIC1-3), facilitating cross-basin exchanges. In the Eastern basin, the Levantine region forms a highly interconnected block, with significant larval flows connecting the Turkish southern coast to the Israeli and Egyptian coastlines. The seasonal comparison (Fig. 6C) further elucidates the dynamics of these exchanges. The difference matrix indicates that summer conditions generally reinforce the diagonal intensity, meaning retention is higher in summer. Conversely, spring conditions tend to facilitate broader connectivity. Notably, the connection between the Western and Eastern basins appears more permeable in spring, whereas summer circulation patterns tend to isolate regional clusters, thereby increasing the local residency of larvae.

## Dispersal distances

The analysis of dispersal distances simulated with the high-resolution MARS3D model (Fig. 7) reveals distinct regional patterns in the transport potential of *C. sapidus* larvae. The distributions of cumulative path lengths (ridgeline plots) are based on emitting zones and represent the predicted distances traveled by larvae that successfully reached a recruitment zone, regardless of their final destination.

Three main dispersal patterns emerge across the release zones. First, several zones exhibit unimodal distributions with narrow peaks, indicating constrained dispersal trajectories dominated by local retention or short-range connectivity. This pattern is characteristic of the Spanish coast near the Ebro Delta (SPA2) and the Southern Tyrrhenian coast (IT5), where the probability density functions show sharp peaks (modes) around 120 km, with median distances of approximately 135 km and 160 km, respectively.


A
Particle Fate (Ensemble Mean 2010-2020) - Spring
DS
LR
NRP
Percentage (%)
0
20
40
60
80
100
B
Particle Fate (Ensemble Mean 2010-2020) - Summer
Percentage (%)
C
Distant Settlement (DS) (Mean ± Std Dev)
Spring
Summer
DS (%)
Local Retention (LR) (Mean ± Std Dev)
LR (%)
Non Retained Particles (NRP) (Mean ± Std Dev)
NRP (%)
Release Zone
MOR
SPA1
BAL
SPA2
GOL
LIG
IT1
BIG
DIA
URB
SGI
NWS
ALG
DRI
SWS
TOR
IT2
IT3
IT4
IT5
SIC1
SIC4
SIC3
TUN1
ALG4
TUN3
TUN2
MAL
SIC2
IT6
IT7
ADR1
ADR2
ADR3
ADR4
ADR5
ADR6
GRE1
GRE2
LYB
GRE3
GRE4
GRE5
GRE6
TUR1
TUR2
TUR3
TUR4
TUR5
CHY
TUR6
LEB
ISR
EGY1
EGY2

◂**Fig. 5** Ensemble analysis of blue crab larval fate in the Mediterranean Sea (2010–2020). The bar plots display the proportion of particles for each release zone classified into three outcomes: Distant Settlement (DS), Local Retention (LR), and Non-Retained Particles (NRP). Zones are ordered geographically from West (left) to East (right). **A** Ensemble mean distribution for the Spring spawning scenario. **B** Ensemble mean distribution for the Summer spawning scenario. **C** Comparative analysis of seasonal trends for each metric (DS, LR, NRP). Solid lines represent the multi-year mean percentage, while the shaded areas indicate the standard deviation (± SD), highlighting the inter-annual variability of dispersal patterns over the 11 year simulation period. Values are normalized relative to the total number of particles released per zone, allowing for a relative comparison of larval fate across zones, independent of the substantial differences in propagule pressure associated with habitat size

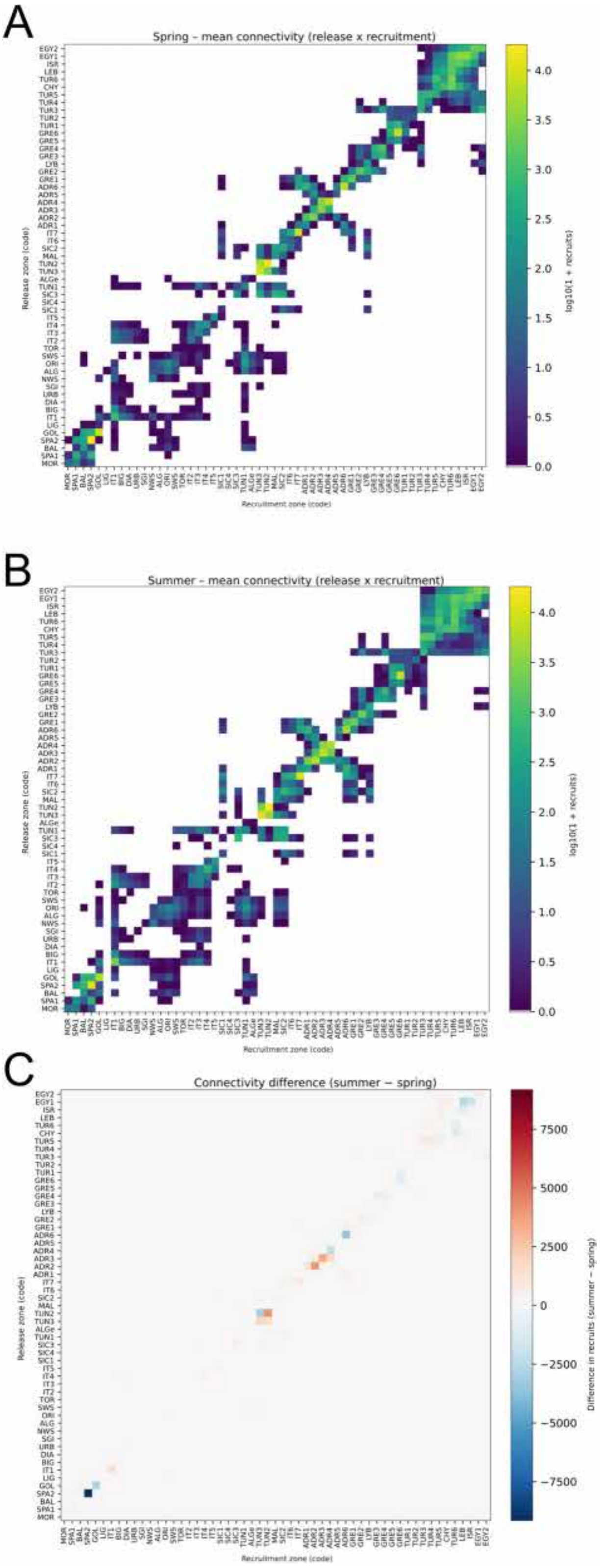
The Balearic Islands (BAL) and the Gulf of Lion (GOL) also fall into this category. For the Gulf of Lion, the primary mode is centered around 140 km with a median of ~ 170–200 km, consistent with the scale of the regional cyclonic gyre. Second, a group of zones displays curves that are more extended, often exhibiting bimodal or multimodal profiles. This pattern is observed for the Eastern Corsican lagoons such as Biguglia (BIG), Diana (DIA), and Urbino (URB). While Biguglia presents a short primary mode (~ 97 km), the distributions for these sites are skewed, with median path lengths generally ranging between 300 and 450 km, suggesting that successful recruitment often involves larvae that have drifted over intermediate distances.

Finally, the third pattern is characterized by highly extended and often multimodal curves, reflecting energetic transport histories where larvae travel much greater distances. These distributions are typical of zones such as Santa Giulia in Southern Corsica (SGI), the Sardinian coasts near Oristano (ORI) and Tortoli (TOR), the Ligurian Sea coasts (IT1), and the Northern Tyrrhenian coast (IT2). In these cases, the distributions are flat with tails frequently exceeding 800 km. For instance, larvae recruiting from Tortoli (TOR) travel a median distance of ~ 300–330 km, with extreme values surpassing 1000 km, indicating a high potential for long-distance connectivity. Regarding seasonal variability, the comparison between Spring (purple) and Summer (yellow) scenarios reveals contrasted dynamics. For zones like the Spanish coast (SPA2), the Ligurian Sea (LIG), or the Southern Tyrrhenian (IT5), the distribution of path lengths remains relatively stable across seasons. Conversely, other zones show marked divergence. In Santa Giulia (SGI), the median path length increases in Summer (+ 134 km compared to Spring), and a similar trend of longer summer trajectories is observed for IT1 and GOL. In terms of orientation, distinct shifts are observed. While zones like SPA2 or GOL maintain consistent headings (strong South-Westward flow for GOL), others such as the Balearic Islands (BAL), Oristano (ORI), and SGI display very different directional transport between seasons (changes > 60°). In SGI, the directional spread is particularly variable with a high circular variance (~ 0.9) in both seasons.

## Discussion

The results of our study confirm, over a more extended time scale, the strong trends of local retention of blue crab larvae, primarily in the western and central basins observed by Marchessaux et al. (2023). However, they also provide further insights into these observations in the eastern basins and shed light on their regularity over time, from 2010 to 2020. For instance, although the current study and those by Marchessaux et al. (2023) do not share the same experimental setup (different dates and release periods), the results from both studies appear to show comparable trends, particularly with more precise hydrodynamic models and local zooms. Therefore, an interesting perspective to add to our study would be to consider longer spawning periods and use models with finer resolutions. Recent studies, both general in scope on larval dispersal models and specific to other taxonomic groups, have emphasized the critical importance of spawning timing and the precise parameterization of this factor (Barbut et al. 2024; Di Stefano et al. 2024). In parallel, it has been observed that *Callinectes sapidus* exhibits unique ecological traits in the Mediterranean Sea compared to its native range, as well as a degree of heterogeneity within the Mediterranean Sea basins themselves (Castriota et al. 2024). This highlights the importance of refining this parameter through additional methodological approaches before reintegrating it into future larval dispersal models, thereby enhancing predictive accuracy. Lacking homogeneous abundance data across the Mediterranean, larval production was assumed proportional to the surface area of the defined release zones (0–100 m). While this simplification overlooks

**Fig. 6** Connectivity matrices between release (y-axis) and recruitment (x-axis) zones derived from MedMFC model simulations across the Mediterranean Sea. Zones are ordered by their geographic ID (1–55), generally following a West-to-East progression along the northern and southern coastlines. White squares indicate zero larval exchange. As the matrices are square, local retention events appear along the diagonal. Values represent the percentage of particles reaching each recruitment zone relative to the total released from the corresponding source zone. Panel **A** Mean Spring connectivity (2010–2020); Panel **B** Mean Summer connectivity; Panel **C** Difference matrix (Summer minus Spring), highlighting seasonal shifts. Positive values indicate increased recruitment in Summer, negative values in Spring. Distinct off-diagonal clusters (e.g., connecting zones 12–20) highlight functional sub-regions such as the Tyrrhenian network



local density variations, such as higher abundances in shallow lagoons, it establishes a necessary baseline. Future fine-scale modelling will require high-resolution field data to refine larval supply and recruitment predictions.

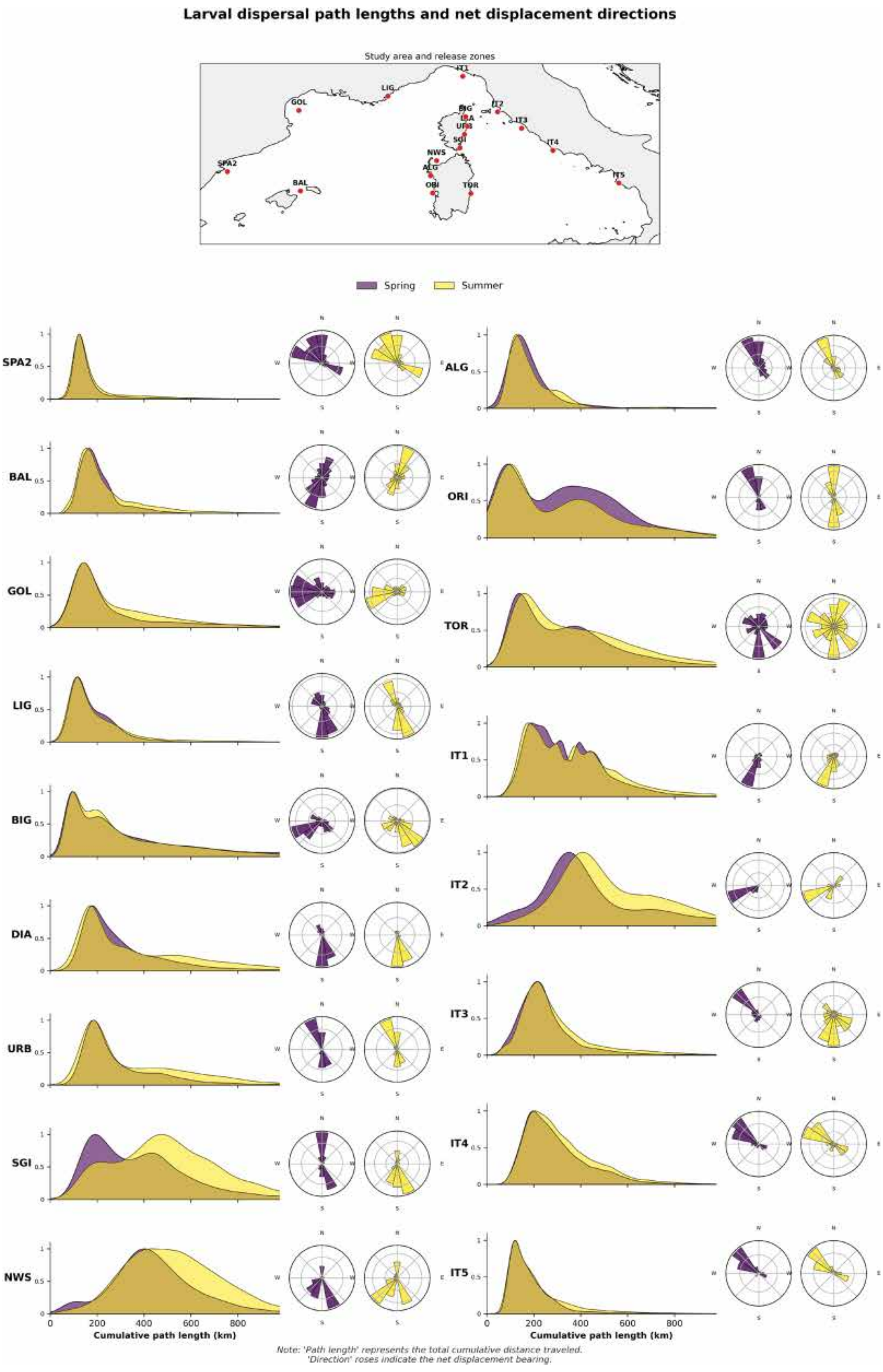
Our study shows that within 40 days of pelagic larval duration, larvae travel a minimum of 250 km, even in areas with strong retention due to ocean currents, and can travel distances approaching 1,000 km, but typically range between 200 and 500 km. These long dispersal distances facilitate connectivity between various coastlines and areas favorable to the development of blue crab populations. Over the eleven years studied, this recurring larval movement leads to the establishment of robust connectivity clusters, defined here as geographic networks maintaining regular larval exchange. For example, the connectivity matrices (Fig. 6) reveal stable exchanges between the larval spawning zones along the Corsican, Sardinian, and Tunisian coastlines, with consistent recruitment in these same areas over time. Consequently, these recurrent exchanges help establish stable population linkages, potentially contributing to the persistence of blue crab populations that spawn in the same areas year after year. These functional units are clearly identifiable in regions such as Tunisia, Sicily, Sardinia, Corsica, and the coastal areas of the Ligurian Sea and Tyrrhenian Sea.

The present study highlights the need of using two models with different resolutions, covering different extents and multiple basins, to investigate larval dispersal routes and connectivity, aligning with the recommendations of Swearer et al. (2019). While the large scale MedMFC model can be used for assessing larval travel distances, it lacks precision in coastal phenomena and requires coupling with a finer model like MARS3DMed, as demonstrated in the focus on the Northwestern Mediterranean Sea.

To assess the temporal consistency of these patterns without relying on single summary metrics that can obscure variability, we employed an ensemble analysis approach over the eleven-year period. Rather than masking interannual fluctuations, the use of standard deviation bands (as shown in the analysis of particle fate) and multi-year mean path-use density maps allows for a robust identification of persistent features versus sporadic events. As highlighted by Mitarai et al. (2009) and Huret et al. (2007), interannual variability in dispersal and connectivity can be substantial and driven by complex oceanographic processes. For example, Mitarai et al. (2009) demonstrated, through multi-year Lagrangian particle tracking, that connectivity matrices can vary markedly between years, particularly under contrasting oceanographic regimes. Similarly, Huret et al. (2007) showed that the timing of particle releases and short-term circulation variability significantly influence transport success. These studies collectively underscore that ensemble modelling and multiple temporal replicates enable a more robust quantification of dispersal uncertainty. Future research would benefit from integrating such advanced approaches—including ensemble hydrodynamic simulations, Lagrangian PDFs (Probability Density Functions), and sensitivity analyses on both biological and physical parameters—to better characterize and predict year-to-year variability in larval dispersal and connectivity, which is particularly critical in the context of ongoing climate change.

The results of this study highlight, over a recent eleven-year period, trends in the dispersal routes of blue crab larvae, as well as the connectivity between the habitats where this species has been observed, which serve as favorable spawning and settlement habitats. Consequently, certain dispersal routes exhibit remarkable persistence over time, particularly in areas of local retention, leading to strong self-recruitment. These observations align with genetic studies on marine species with planktonic larvae, which have revealed limited oceanographic connectivity in Australia's coasts, even without major dispersal barriers, and found high levels of self-recruitment in a marine gastropod due to low-velocity nearshore currents retaining planktonic larvae near their birth sites (Teske et al. 2016). Thus, over a period of eleven years or more, coastal areas and the presence of islands, as is the case in various sub-basins of the Mediterranean Sea, could play a significant role in the larval dispersal dynamics of this invasive crab, and the results appear to align with on-ground findings. For instance, in the Northwestern Mediterranean Sea, the Ebro Delta and the Gulf of Lion (Fuentes et al. 2019; Labrune et al. 2019) have witnessed and continue to experience a surge in blue crab abundances.

More recent studies, such as the one conducted by Schubart et al. (2023), aimed at comparing the phylogeography of the blue crab in both its native range and the Mediterranean Sea. This study highlighted


Larval dispersal path lengths and net displacement directions
Study area and release zones
IT1
LIG
GOL
BIG
IT2
LIA
URB
IT3
SGI
IT4
NWS
SPA2
ALG
BAL
ORI
TOR
IT5
Spring
Summer
SPA2
BAL
GOL
LIG
BIG
DIA
URB
SGI
NWS
ALG
ORI
TOR
IT1
IT2
IT3
IT4
IT5
N
E
S
W
0
0.5
1
0
200
400
600
800
Cumulative path length (km)
Note: 'Path length' represents the total cumulative distance traveled.
'Direction' roses indicate the net displacement bearing.

◂**Fig. 7** Larval dispersal path lengths and net displacement directions for Callinectes sapidus larvae in the Northwestern Mediterranean Sea (MARS3D model, 2010–2020). The panel displays dispersal characteristics for the 17 release zones included in the high-resolution domain, ordered geographically from West (SPA2) to East (IT5). Left/Main plots: Probability density functions (PDF) of the cumulative path length (total trajectory distance) traveled by successfully recruited larvae. The peaks of the curves represent the modal (most frequent) distances. Purple curves represent the Spring spawning scenario, and yellow curves represent the Summer scenario (dark yellow indicates overlap). The *Y*-axis represents the normalized density (0–1), and the *X*-axis indicates the cumulative path length (km). Right/Polar plots: Wind roses illustrating the net displacement bearing (direction from release to settlement) of recruited larvae for Spring (purple) and Summer (yellow). Bars indicate the frequency of transport toward each cardinal direction. Top center: Context map showing the location and 3-letter code of each release zone

that the genetic composition of Mediterranean populations reflects a strong founder effect, suggesting that only a few individuals were responsible for the initial establishment and subsequent spread. Consequently, invasive populations in the Mediterranean are characterized by remarkably low genetic diversity compared to the native range. While this homogeneity results primarily from the initial invasion history (Schubart et al. 2023), our modelling results suggest that the existing connectivity could favor the persistence of this genetic homogeneity over time. Although our study identifies zones of local retention, sufficient gene flow between distant sub-basins likely occurs through oceanographic circulation to prevent isolation. A similar lack of spatial genetic structure across the Mediterranean has already been documented for native species with comparable Pelagic Larval Duration (PLD), such as the common dentex *Dentex dentex* (Viret et al. 2018) or other littoral fishes (Pascual et al. 2017), where larval dispersal maintains panmixia despite potential oceanographic barriers. Conversely, in the blue crab's more open native range, high genetic diversity coexists with regional differentiation, suggesting that gene flow dynamics differ across scales (McMillen-Jackson & Bert 2004). Thus, further analyses coupling larval dispersal models with fine-scale genetic studies remain necessary to fully resolve the mechanisms driving the species' expansion and to guide management. The methods and outputs from our study can inform the development of adaptive management tools, particularly in the context of rapidly advancing non-native species spread, as exemplified in this study over a decade. Thus, the predictions from these models could help to better direct management measures (Mangano et al. 2020). For example, the production of productivity indicators for spawning zones and receptivity indicators for nursery zones, and their stability over time, could guide managers towards a more spatially focused approach to fisheries management. It is evident that larval dispersion routes and connectivity are key processes to study for the implementation of more effective management measures and protected areas (Hidalgo et al. 2017).

Regarding the case of *Callinectes sapidus*, this study supports the hypothesis of the essential role of islands in the dispersal and colonization dynamics of this invasive species, over a more extended timeframe and considering two spatial extents. This aligns with ecological island theories (MacArthur, 1963), which describe islands as functioning both as intermediate recruitment zones in colonization dynamics and as sites for genetic exchange due to their proximity to suitable spawning habitats for blue crabs. Our study supports this by highlighting the formation of persistent connectivity clusters between geographically proximate zones, where larvae consistently travel between spawning and recruitment areas over the eleven-year period. These recurring routes contribute to the persistence of populations, as observed in areas such as Tunisia, Sicily, Sardinia, and Corsica. This regular exchange of larvae likely explains the increasing biomass of blue crab populations in certain areas (Culurgioni et al. 2020; Mancinelli et al. 2021), particularly in zones with high local retention due to ocean currents, such as the Gulf of Lion and the Gulf of Gabès. Our results support the idea that these areas are zones of high larval productivity, where the frequent retention of larvae leads to strong self-recruitment, a conclusion supported by recent literature (Marchessaux et al. 2023). Furthermore, the connections observed between adjacent and distant areas, such as between Sicily and Tunisia or between Sardinia and Tunisia, indicate that these larval productivity pools can supply sub-basins, enabling effective species circulation and potentially leading to rapid colonization and widespread distribution over an extended time frame.

The trends observed in this study would benefit from further interpretation through comprehensive research on the biology and population dynamics of the blue crab, including growth, survival, reproduction, thermal tolerance conditions, and mortality (Reynes et al. 2021). Seawater temperature significantly impacts the life cycles, reproductive periods, and overall metabolism of planktonic organisms, especially those inhabiting surface waters. Even slight increases in water temperature can potentially lead to significant changes in individuals and populations (Edmunds et al. 2005), particularly affecting larval development and dispersal (O'Connor et al. 2007). In recent decades, increased global warming has been documented in the Mediterranean region, particularly affecting surface waters (Pastor et al. 2020) across various Mediterranean basins and sub-basins (Margirier et al. 2020). Simultaneously, research has shown that this warming can facilitate biological invasions on a global scale (Stachowicz et al. 2002), with more localized effects observed in the Mediterranean Sea (Albano et al. 2021). The geographic expansion of tropical and subtropical species into cooler waters, such as the Aegean, Adriatic, and western Mediterranean Seas, is indicative of how rising water temperatures in the Mediterranean Sea, driven by climate change, are likely to promote the spread of non-indigenous species (Zenetos & Galanidi 2020). Additionally, climate change-related shifts, including variations in the frequency and intensity of storms, can potentially alter the oceanographic characteristics of fronts that traditionally act as barriers to larval dispersal (Yamada et al. 2017). These changes, predicted by hydrodynamic models, highlight the need for ongoing study and adaptive management to anticipate potential shifts in dispersal routes and connectivity clusters, particularly for invasive species such as *Callinectes sapidus*. For instance, during storms, a change in wind direction can redirect post-larvae of blue crabs towards bays, thereby promoting their recruitment (Etherington & Eggleston, 2003). Additionally, strong cyclones usually expand nursery habitats for juveniles, leading to increased recruitment of this species (Eggleston et al. 2010). Consequently, a potential intensification of cyclones (Kang & Elsner 2015) could enhance the abundance of species reliant on these extreme events for specific critical recruitment years. Hence, investigating blue crab larval dispersal and population connectivity in the context of climate change and integrating these studies with temporal assessments of surface temperatures and other climate-related environmental parameters appears to be a promising avenue for enhancing these models.

## Conclusions

This study aimed to characterize the spatiotemporal variability of *Callinectes sapidus* larval dispersal over a decadal scale (2010–2020), addressing the need for a multiscale understanding of post-establishment spread. By integrating a basin-wide approach with a high-resolution focus on the Northwestern Mediterranean Sea, we demonstrated the specific added value of using two spatial resolutions. While the basin-scale model (MedMFC) successfully captured broad-scale dispersal pathways across the Mediterranean basin, including connections between the Eastern and Western basins, the high-resolution regional model (MARS3D) proved essential for resolving fine-scale coastal features, such as the Liguro-Provençal-Catalan current dynamics and the Cap Corse eddy, that drive local retention in the Gulf of Lion and around Corsica. The results highlight three major findings: (1) the formation of persistent connectivity clusters, particularly linking the Tunisian and Sicilian coastlines as well as the Tyrrhenian archipelago, supporting the hypothesis that islands function as "stepping stones" for expansion; (2) a significant seasonal shift, where summer hydrodynamic conditions reinforce local retention and self-recruitment compared to spring; and (3) a clear dichotomy between retentive habitats (e.g., Gulf of Gabès, Adriatic) and dispersive corridors (e.g., Ligurian Sea). From a perspective of future research, these stable routes provide a basis for targeted monitoring. Efforts should now focus on refining these predictions by incorporating spatially explicit biological data on blue crab physiology and investigating how climate-driven warming may alter these established connectivity patterns.

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## Declarations

**Conflict of interest** The authors have not disclosed any competing interests.

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