Estimating spawning locations of the deep-sea red and blue shrimp *Aristeus antennatus* (Crustacea: Decapoda) in the northwestern Mediterranean Sea with a backward trajectory model

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Context

❖ *Aristeus antennatus* is a deep-sea and commercially valuable shrimp species for Spanish fishing harbors in the northwestern Mediterranean Sea.

❖ *A. antennatus* larvae are found in surface waters and eggs-carrying females are found between 500 and 1200 m

❖ Since 2012, fishermen from Palamós harbor (Fig.1) have controlled their fishing activities using a management plan to ensure sustainable harvests.

❖ Little is known about the dispersal of larvae; specifically, it is not known how far larvae can be transported from spawning areas and if there could be mixing of larvae from different fishing grounds.

Objectives

Objectives of this study were to:

1) **Estimate** the spawning sites of larvae that were collected on the CONECTA field campaign in 2016,

2) **Evaluate** uncertainty related to hydrodynamics and biology,

3) **Determine** if collected larvae could have come from the restricted fishing areas.

Main tools

An Individual-Based models (IBM) was applied based on:
❖ 3D hydrodynamic model ROMS (Shchepetkin and McWilliams, 2005).
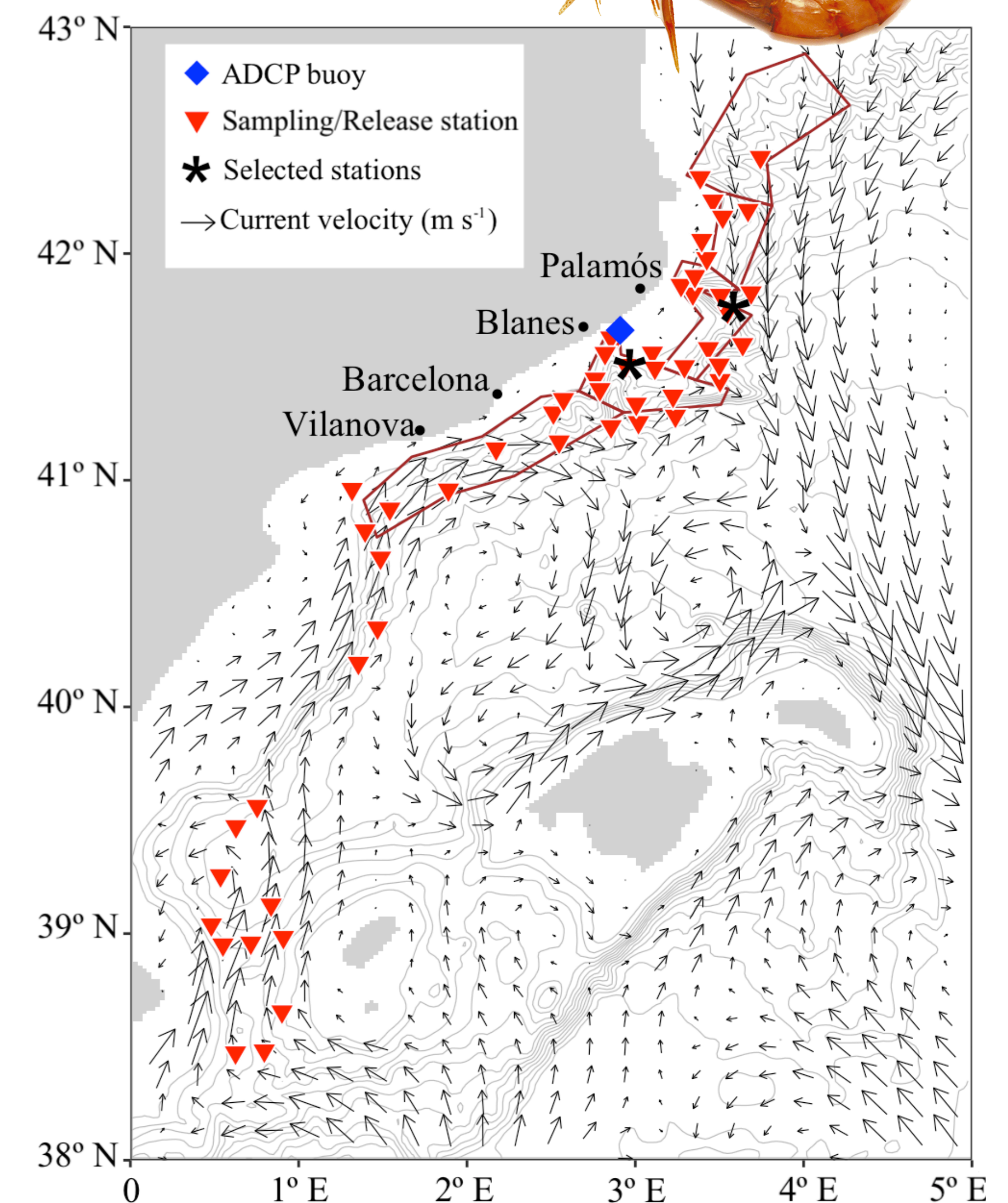❖ Lagrangian transport model Opendrift with backtracking abilities (Dagestad and Röhrs, 2018).

Methods

General approach

❖ Backtracking from sampling stations began at the time samples were collected.

❖ Backtracking ended when eggs duration was complete.

❖ Particle buoyancy occurred when larval stage retrograded into *eggs*.

Table 1. Model runs, parameter settings and objectives
U: advection, H: horizontal turbulence, V: vertical turbulence.

Parameter	Estimating spawning sites[a]	Assessing uncertainty due to advection[b]	Assessing uncertainty due to diffusion[c]	Assessing uncertainty due to drift duration[a]
Release location	▼	◆	*	▼
Release depth	0.75 m	7, 14, 21 m	0.75 m	0.75 m
Diffusion	U + HV	None (U)	None (U), U + H, U + V, U + HV	None (U), U + H, U + V, U + HV
Buoyancy	Yes	No	No	Yes
Drift duration	Temperature-dependent	21 d	14 d	Temperature-dependent
Objectives	1) and 3)	2)	2)	2)

[a] Drift duration was set to be minimum (Min; 2 larval stages) or maximum (Max; 3 larval stages).
[b] We compared trajectories estimated from current velocities measured by an ADCP & predicted by ROMS.
[c] We compared the spreading of particles with Okubo's (1971) ocean diffusion diagram.

Fig. 1. Hydrodynamics of the NW Mediterranean Sea and location of particles releases for backward transport simulations. Release locations were the sites of collections of *A. antennatus* larvae during the CONECTA field campaign.

Results

General

❖ Backtracking lasted 4–10 days which placed spawning sites in different locations (Fig. 2).

❖ Spawning sites were located 10.9–37.6 km away from sampling/release stations.

❖ A combination of U+HV-Min and U+HV-Max model runs were determined to have the most reliable results that had the best chance of bracketing the actual spawning sites.
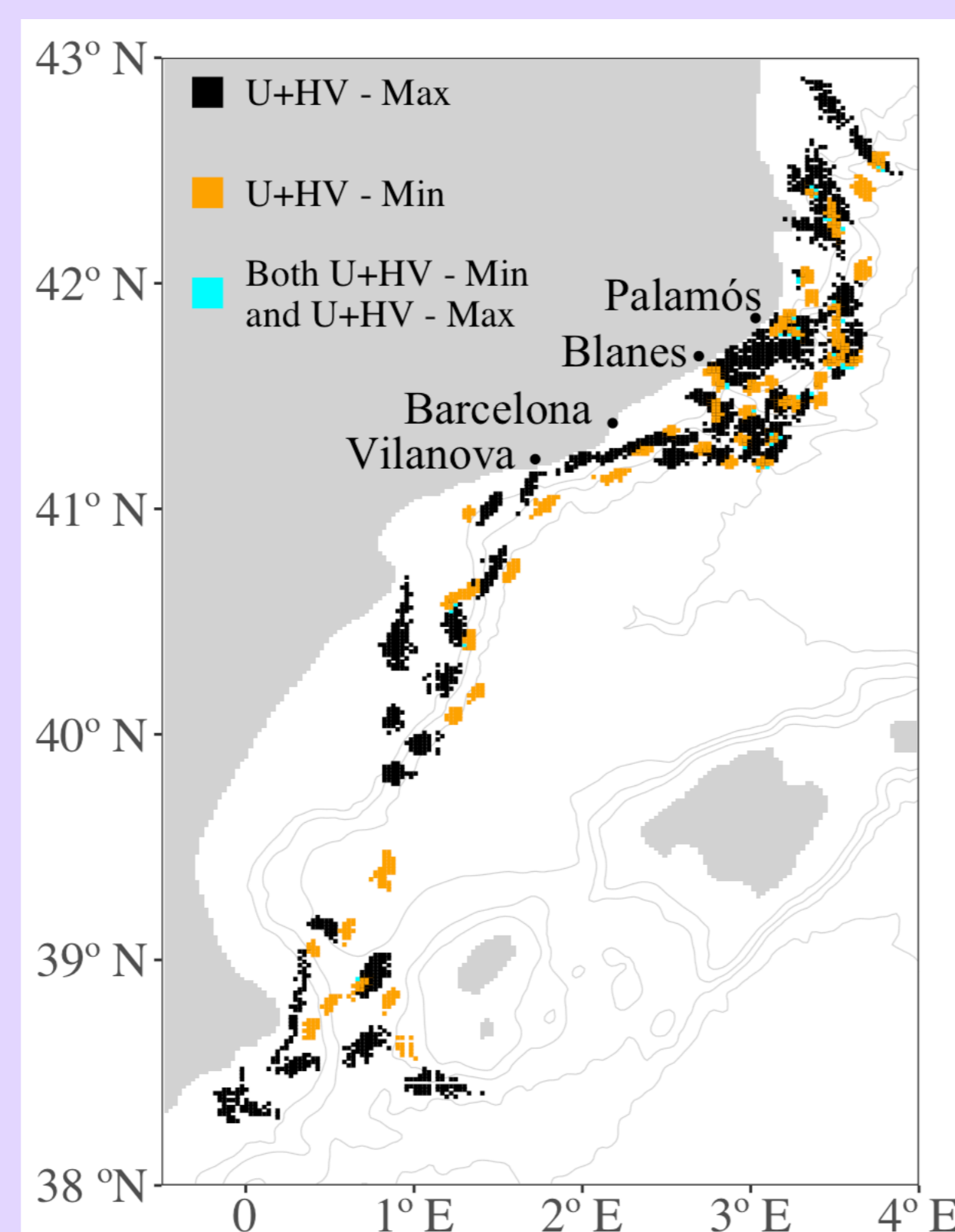

Fig 2. Location of the spawning areas according to model runs with minimum (U+HV-Min) and maximum (U+HV-Max) pelagic larval durations.

Advection

❖ Trajectories estimated from ROMS and measured velocity currents had similar directions and magnitude near surface but were slightly shorter at depths from 14 to 21 m.

Diffusion

❖ Relation between time and diffusion is $0.0108*t^{2.34}$ in Okubo (1971). Model runs with U+HV best approximated this relationship, with $0.0138*t^{2.27}$.

Biology (Drift duration)

❖ Estimated spawning ground areas were 4.4 to 6.5 times smaller for model runs with minimum drift duration (Fig. 3).
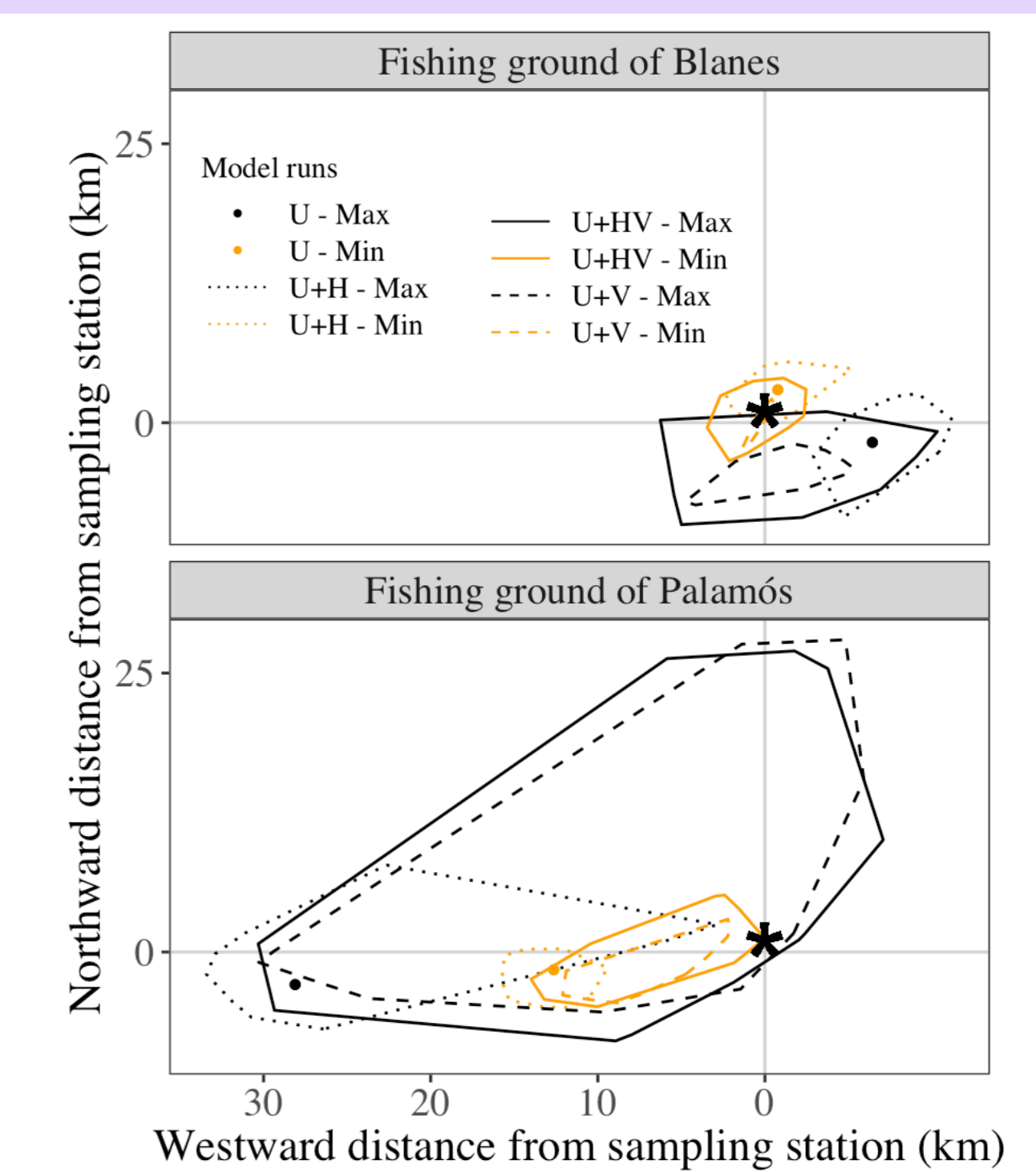

Fig. 3. Ending locations of simulated larvae with different drift durations and turbulent parameters from two selected stations (see Fig. 1 for station location). The * indicates the position of the sampling/release station. The shapes outline the area where particles were backtracked.
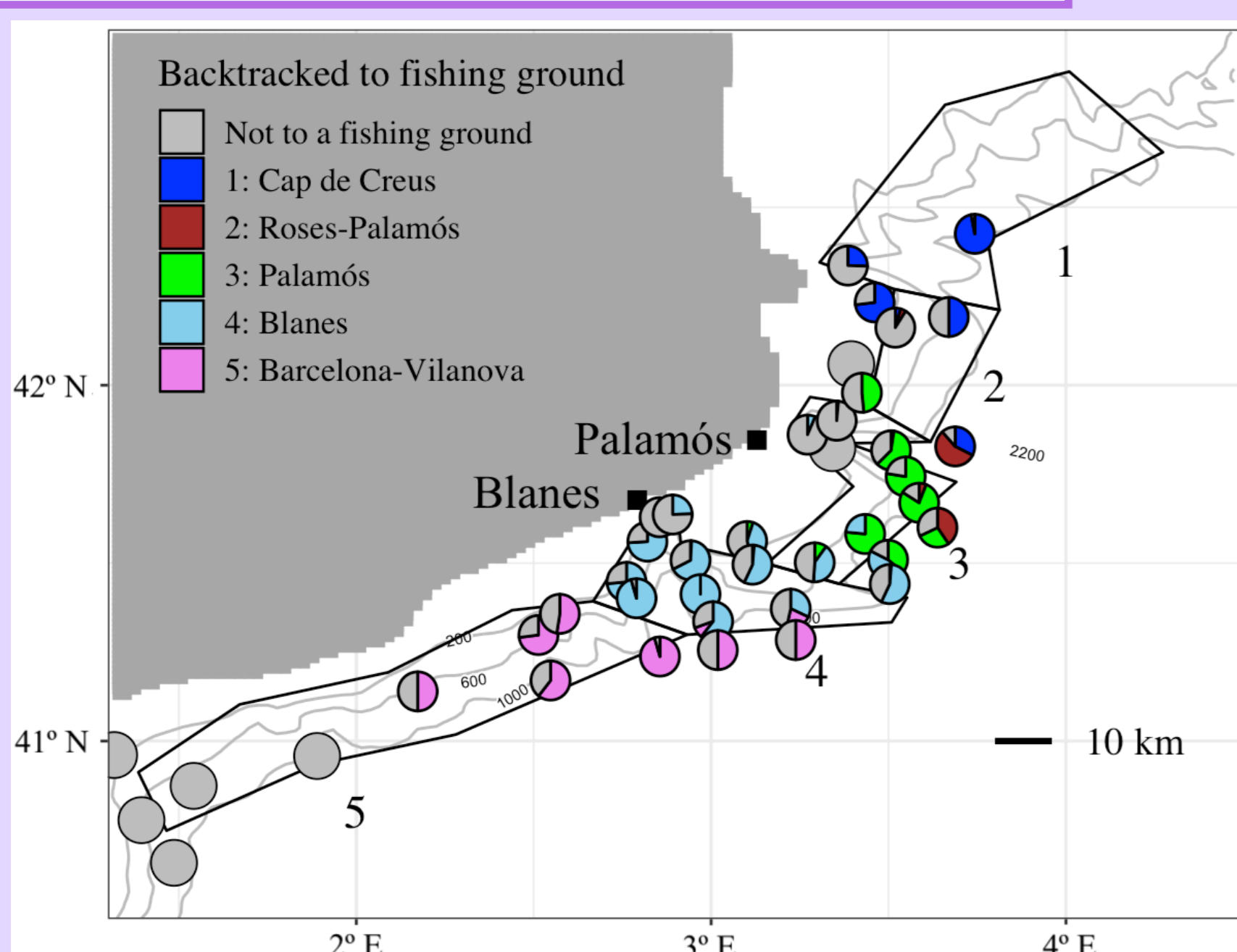
Further results for decision makers

Fig. 4. Fishing ground of origin of simulated *A. antennatus* larvae collected at 35 CONECTA sampling stations

Backtracking model runs around intense fishery grounds revealed:

❖ All 35 sampling stations had at least one larva backtracked to a fishing ground (Fig. 4).

❖ 13 of the 35 sampling stations had simulated larvae that were backtracked to more than one fishing ground (Fig. 4)

❖ Large proportions of larvae (48.9–69.6%) came from the fishing ground over which they were released.

❖ Some larvae collected at stations over the protected fishing ground of Palamós (Fig. 4) could have came from a northern fishing ground (2.5% and 6.5%: Roses-Palamós) and a southern fishing ground (23.5% and 46.5%: Blanes).

Bring it home:

❖ Backtracking is a method that can be used to explore the connectivity between populations and estimate the origin of collected larvae.

❖ Vertical and horizontal turbulence should be included in backtracking simulations.

❖ Source of uncertainties in the spawning sites can be identified and acknowledged.

❖ Improved understanding of larval behavior would enhance model predictions.

❖ Bibliography
Dagestad K-F, Röhrs J. OpenDrift v1.0: a generic framework for trajectory modelling. *Geosci Model Dev.* 2018;11:1405-20.
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Shchepetkin AF, McWilliams JC. The regional oceanic modeling system (ROMS): a split-explicit, free-surface, topography-following-coordinate oceanic model. *Ocean Modelling.* 2005; 9(4): 347–404.