

Population connectivity and speciation of vent mussels from the Mid-Atlantic Ridge

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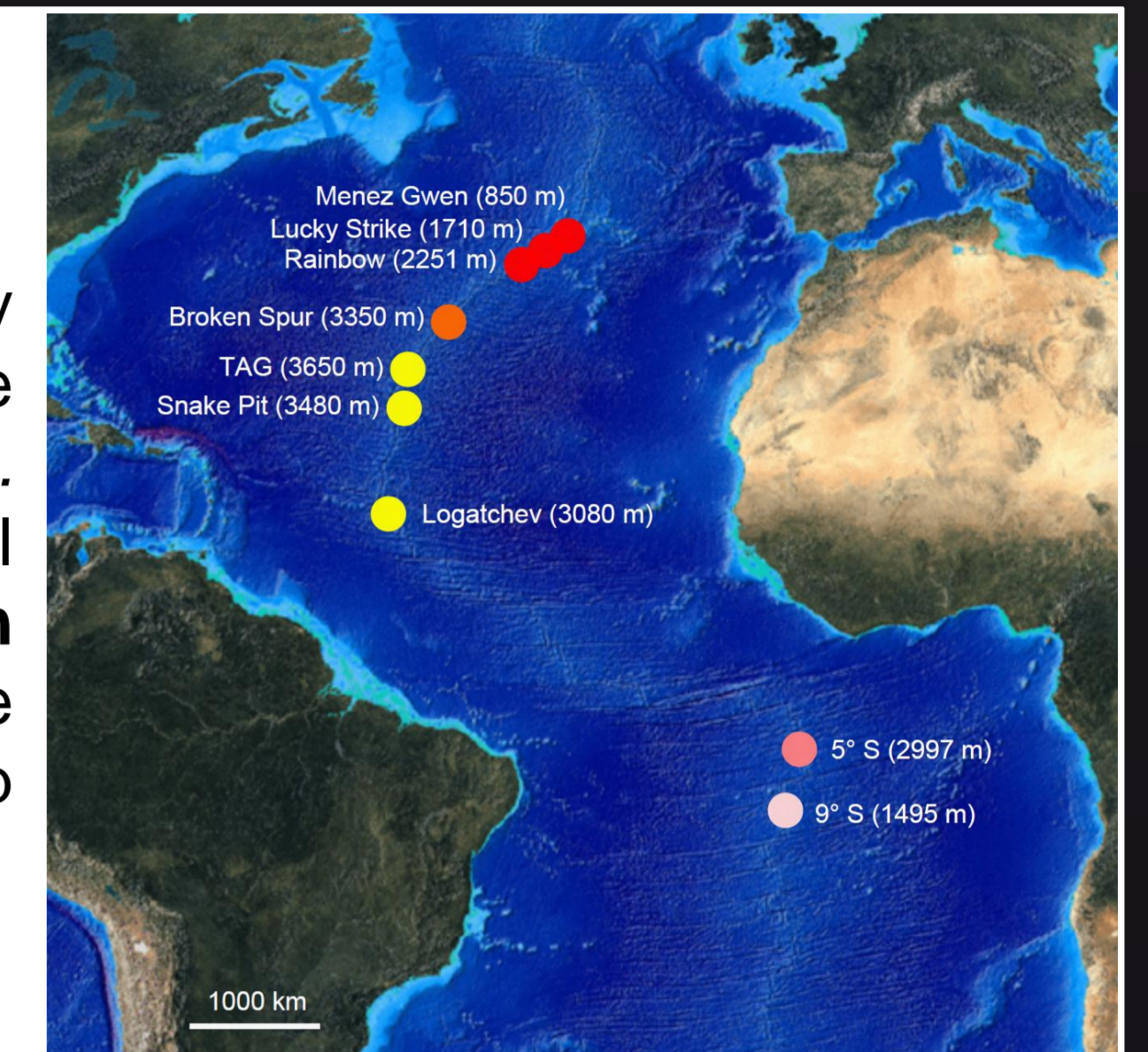
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Background & Aims

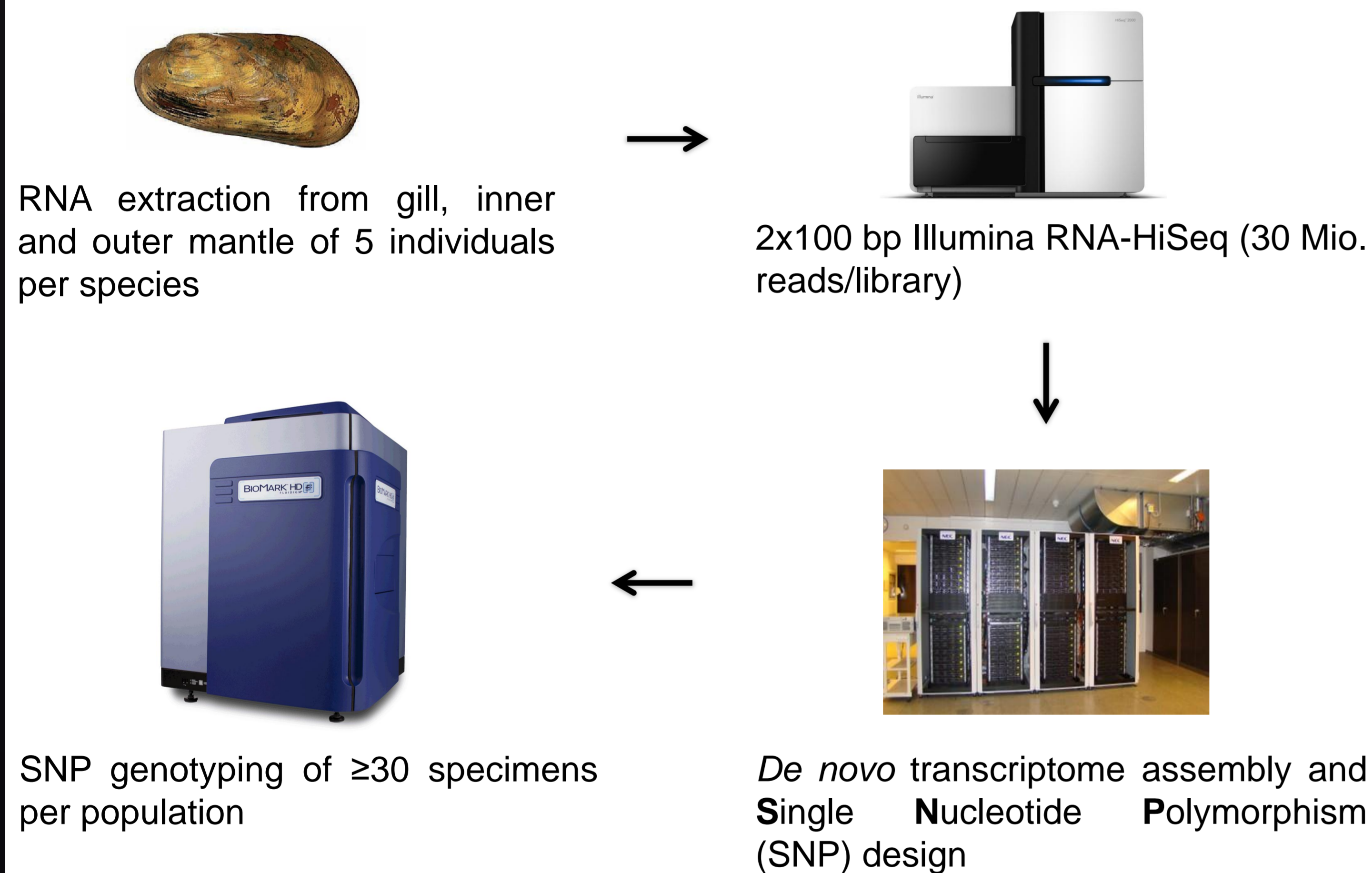
Knowledge about the genetic connectivity of populations and the mechanisms underlying speciation is an important requirement for biodiversity conservation. However, despite the fact that such information is generally sparse for deep sea biota, hydrothermal vent communities become increasingly endangered by demands for mining of seafloor massive sulphides. Using mussel species of the genus *Bathymodiolus* (*B. azoricus*, *B. puteoserpentis*, *Bathymodiolus* spp.) as a study system and integrating results from eco-physiology, genetics and numerical modelling, we want to investigate how (1) physical, (2) reproductive and (3) ecological barriers influence gene flow between hydrothermal vent populations of the Mid-Atlantic Ridge (Figure 1). By comparing the outcomes of different experimental approaches, we expect that this work will make fundamental contributions to a better understanding of population connectivity and diversification in the deep sea as well as help to manage anthropogenic threats to hydrothermal vent ecosystems.

Figure 1. The study area. Red = *B. azoricus*; yellow = *B. puteoserpentis*; orange = hybrid zone; dark & light pink = *Bathymodiolus* spp.

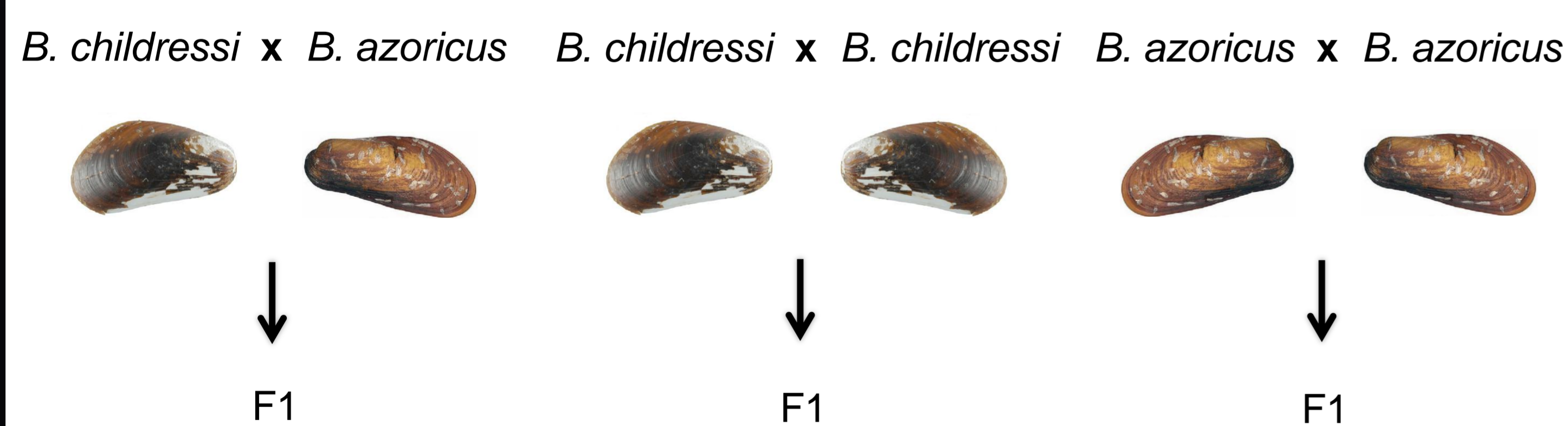


Are species reproductively and/or ecologically isolated?

a) Population genetics



b) Cross experiments under atmospheric pressure



For each cross, we will determine:

- Fertilization success (pre-zygotic isolation)
- F1 mortality (post-zygotic isolation)
- Larval temperature and salinity tolerances
- Larval horizontal and vertical swimming speeds

Integration

Are there physical barriers to larval dispersal?

Methods

- Lagrangian simulations using a 1/4° global ocean circulation model (ORCA025) and particle tracking routines (ARIANE)
- Releases of ~120000 virtual passively drifting particles from each of eight vents (Figure 1, TAG site excluded)
- Releases in different years (1988/89, 1992/93, 1997/98) and depths (0-109 and 109-336 metres above bottom (mab) depending on the vent site)

Preliminary results

- Larval trajectories vary among dates (Figure 2) and depths (data not shown)
- Current variability decreases with depth (data not shown)
- Most larvae remain near release site and do not reach other vents during the pelagic stage (Figure 2)

Future approaches

- Incorporation of:
 - Vertical & horizontal migration
 - Temperature & salinity tolerances
 - Chemotaxis
- Attenuating release of larvae (0-300 mab) with distance from seafloor
- Higher vertical resolution (250 m to 20 m steps near bottom)
- Repeated releases of particles from new 'settlement sites'

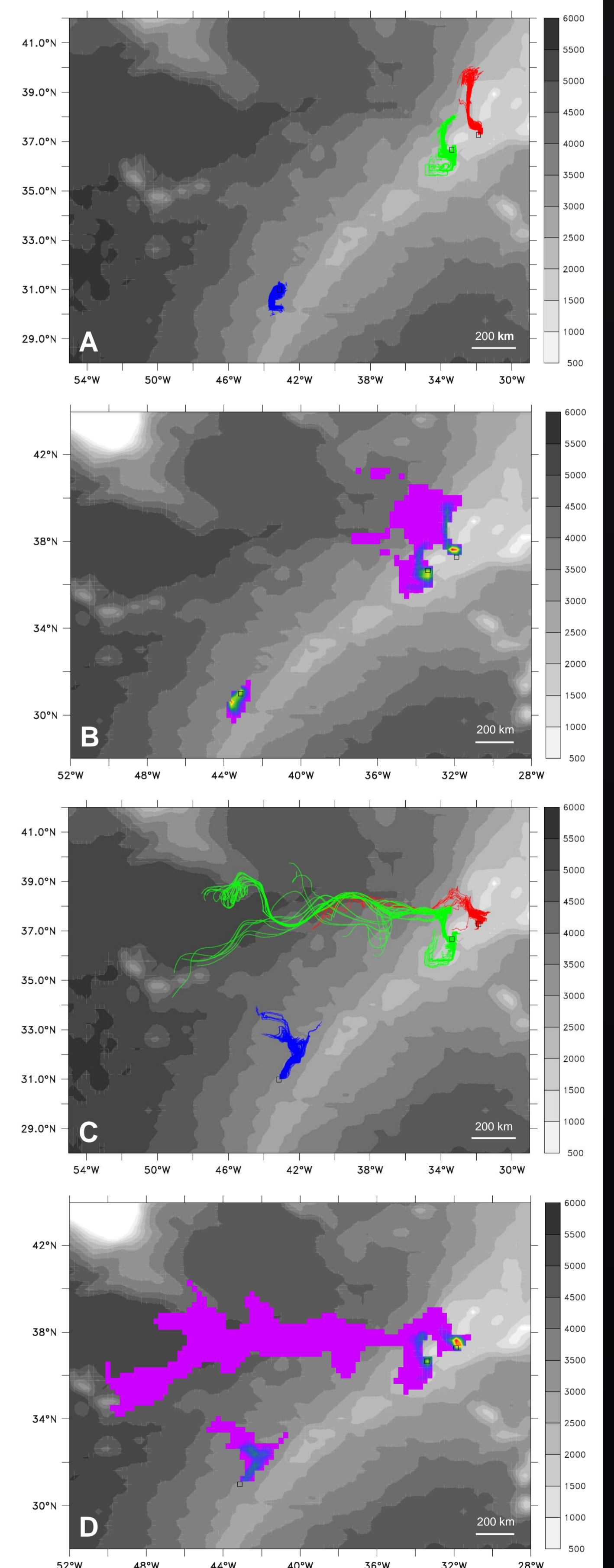


Figure 2. Sample passive larval trajectories and corresponding probability plots for Lucky Strike (0-33 metres above bottom (mab)), Rainbow (0-62 mab) and Broken Spur (0-56 mab) in 1988/89 (A, B) and 1992/1993 (C, D) based on ORCA025-K353. Black boxes indicate areas of virtual release. The abundance of larvae increases with colour temperature (violet to red).

Acknowledgements

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