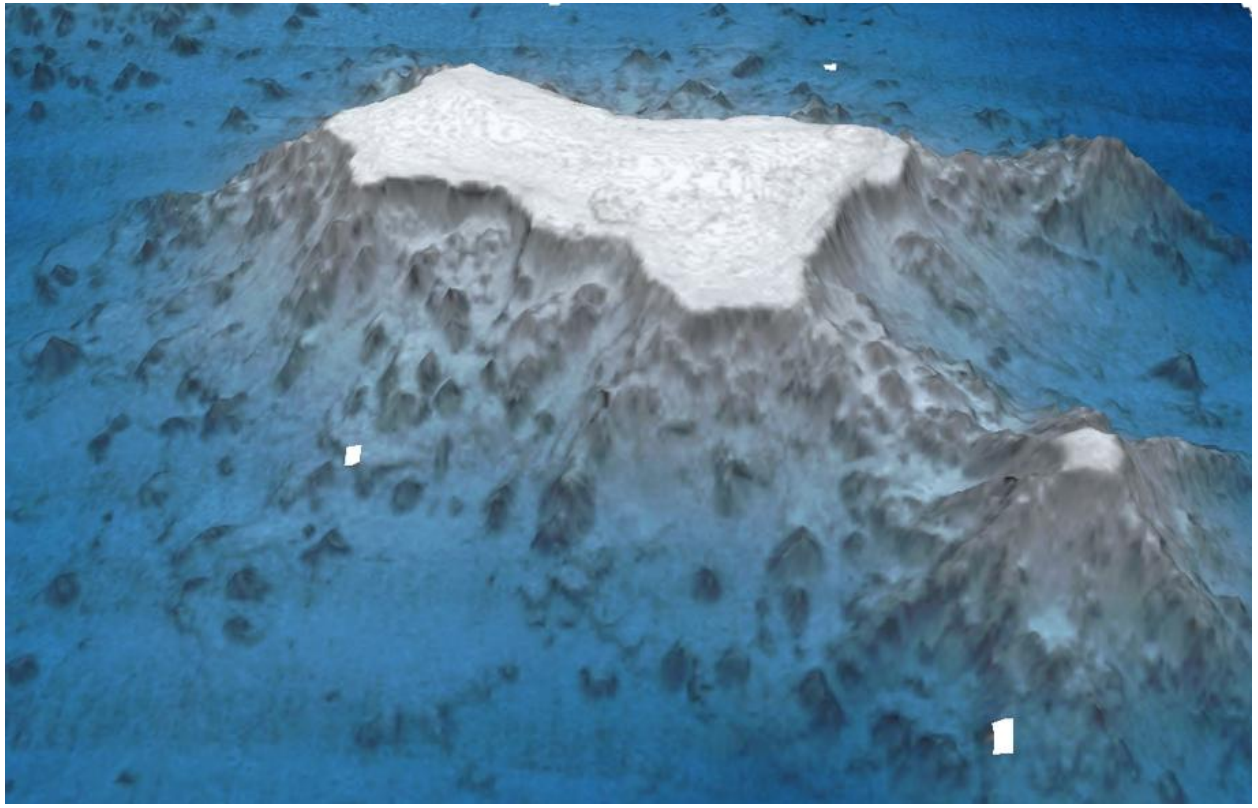
Modelling larval dispersal networks among seamounts for connectivity conservation under deep-sea mining



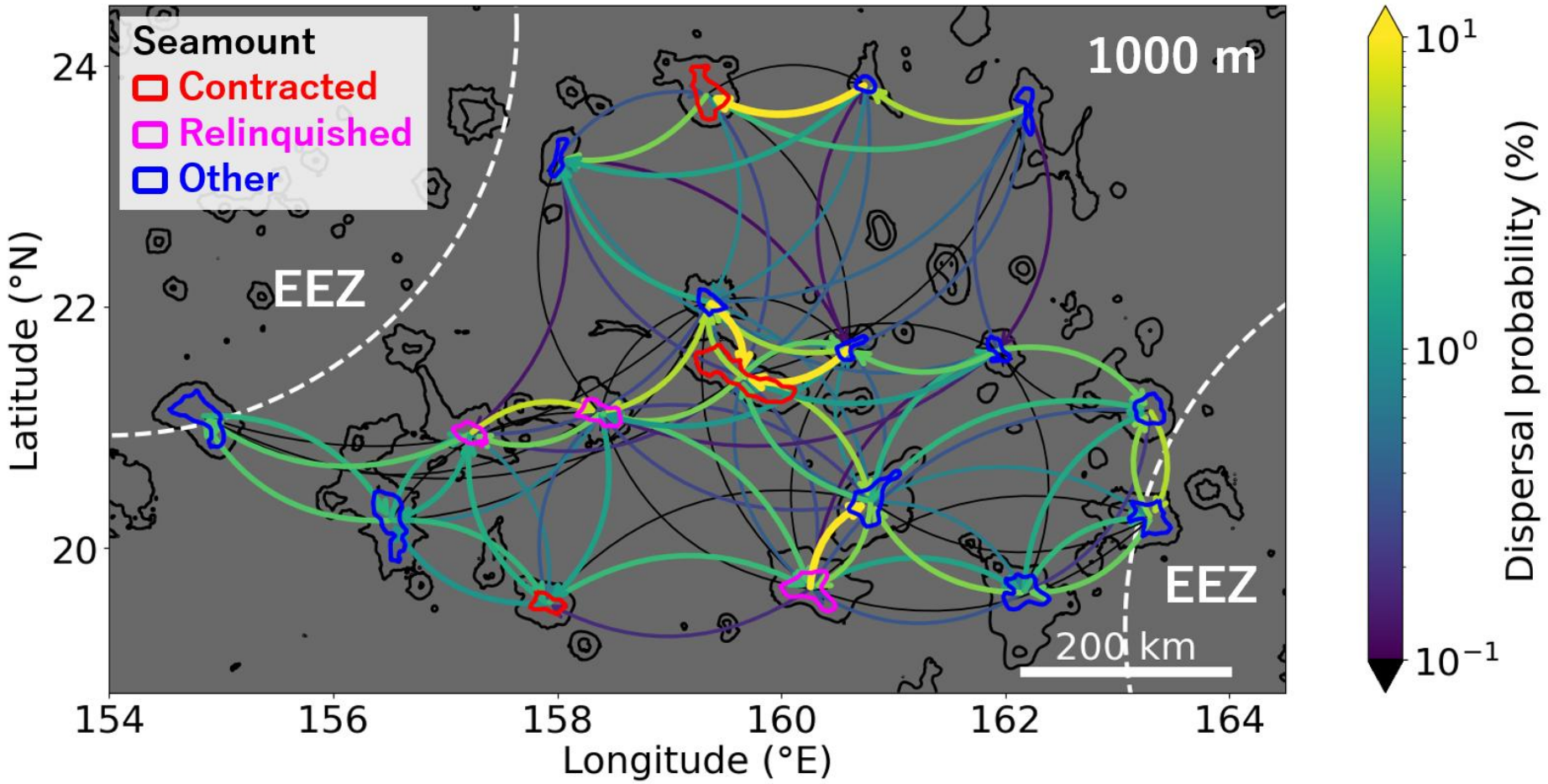
Naoki Saito[1], Hiroki Kise[1],
Travis Washburn[1,2], Eri Ikeuchi[1],
Akira Iguchi[1], Hiroko Kamoshida[3],
Atsushi Suzuki[1]

[1] AIST
[2] Texas A&M University-Corpus Christi
[3] JOGMEC

[Acknowledgments]
This project was commissioned by Japan's Ministry of Economy, Trade and Industry.

Summary

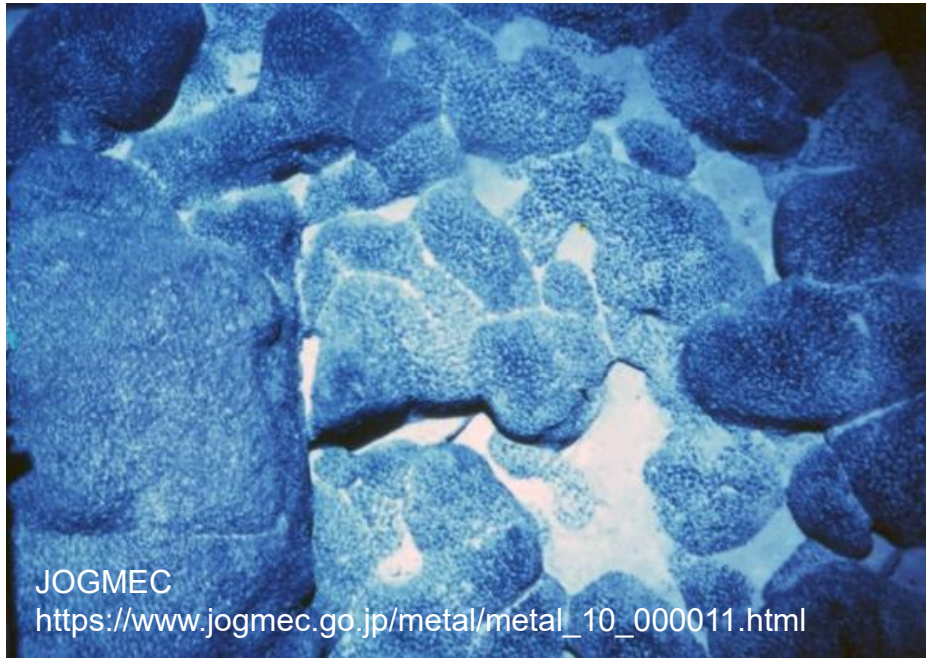
In this study, we modelled connectivity among seamounts to support environmental conservation efforts associated with deep-sea mining.



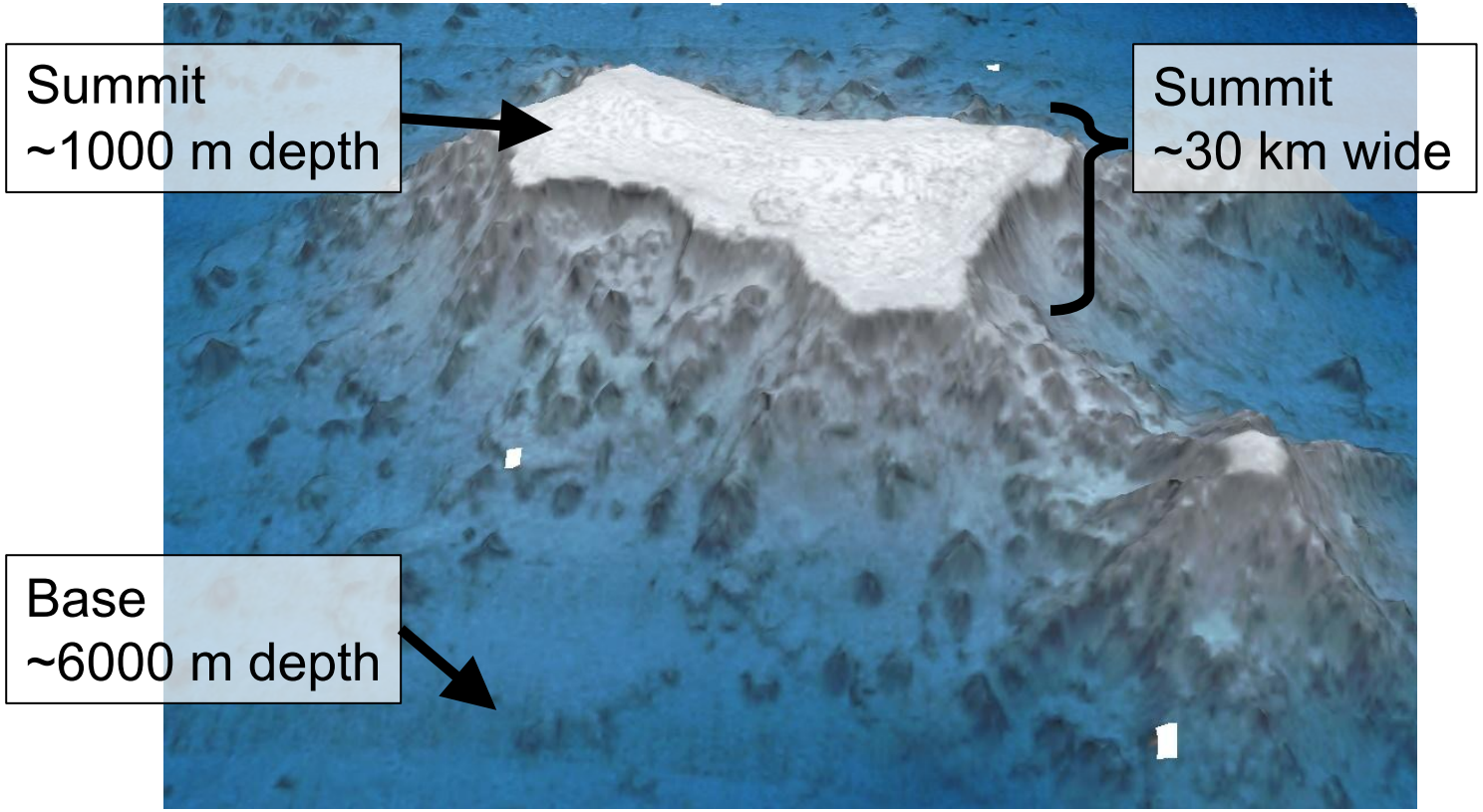
Modelled larval dispersal network among seamounts.

Introduction

Cobalt-rich crusts, potential targets for deep-sea mining,
occur on the summits and slopes of seamounts in the Northwest Pacific.



Cobalt-rich crust.

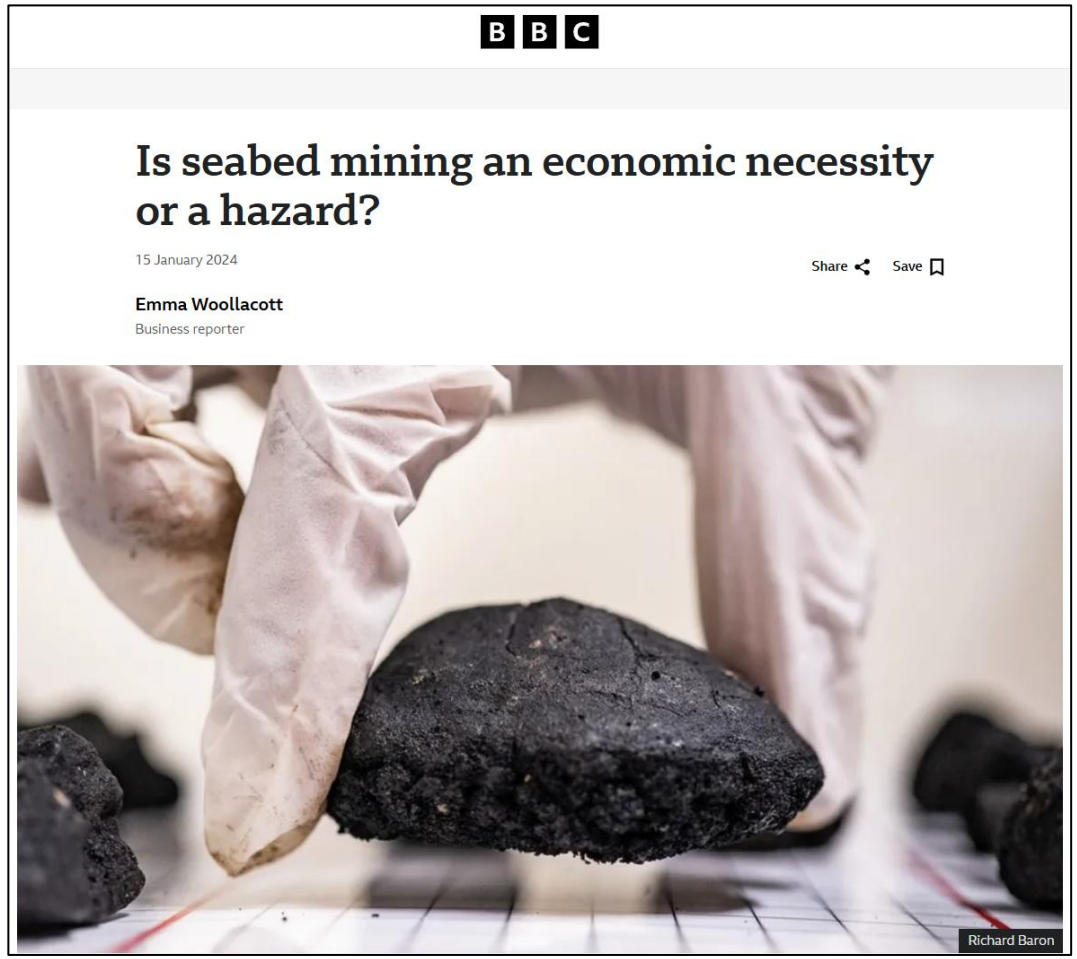


Example of seamount topography.

Introduction

There are concerns about the environmental impacts of cobalt-rich crust mining.

However, **limited knowledge of seamount ecosystems** hinders conservation planning.



BBC (2024)

(https://www.bbc.com/news/business-67935057)

Introduction

One key knowledge gap is **connectivity among seamounts** (Clark et al. 2010 *Annu. Rev. Mar. Sci.*).

➡ Are populations on seamounts tens to hundreds of kilometres apart connected or isolated?

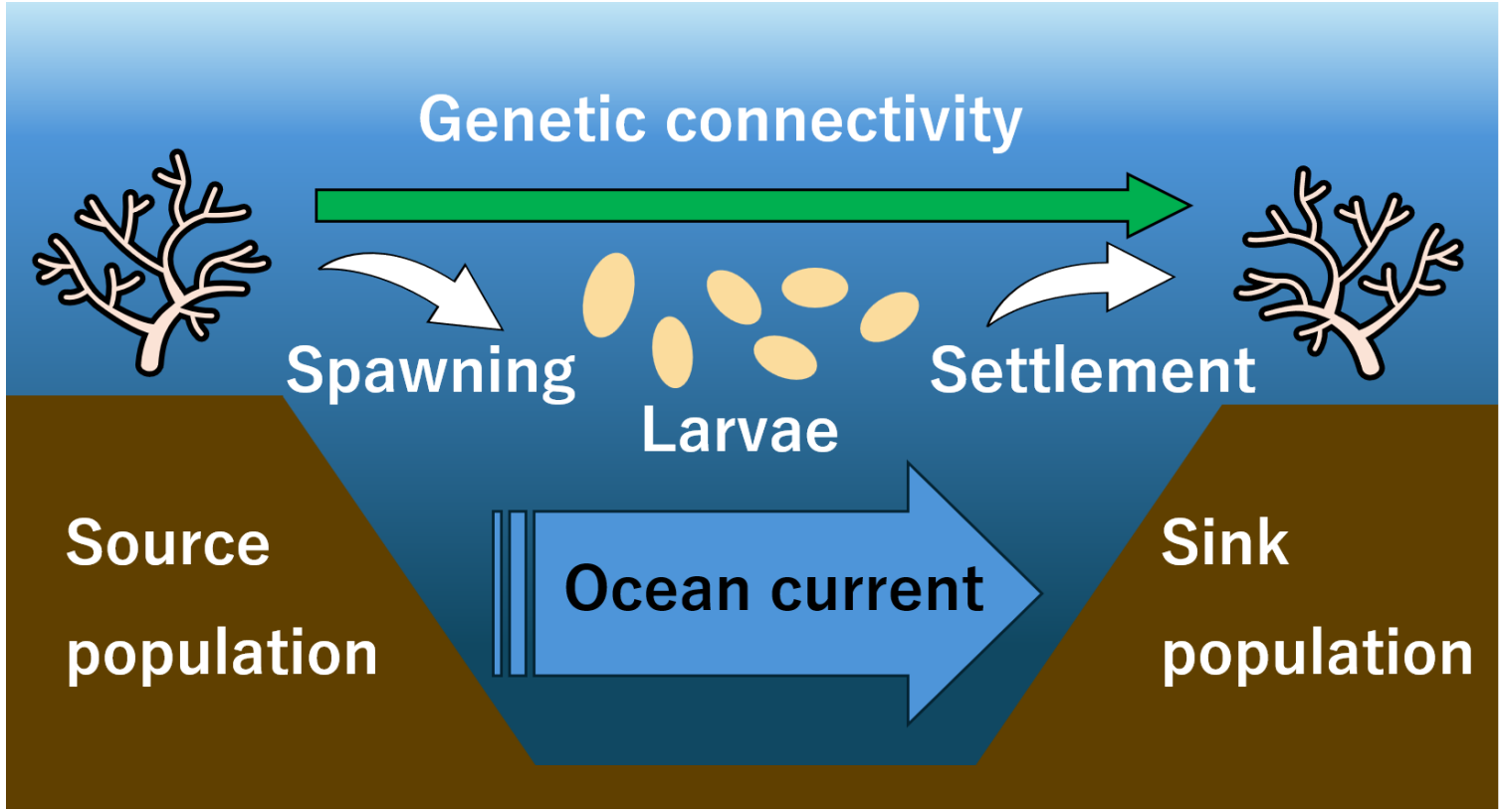


Seamounts provide habitats for benthic organisms.

Introduction

Many benthic species maintain connectivity through **larval dispersal**.

Identifying key source populations that supply larvae is fundamental to effective conservation planning.

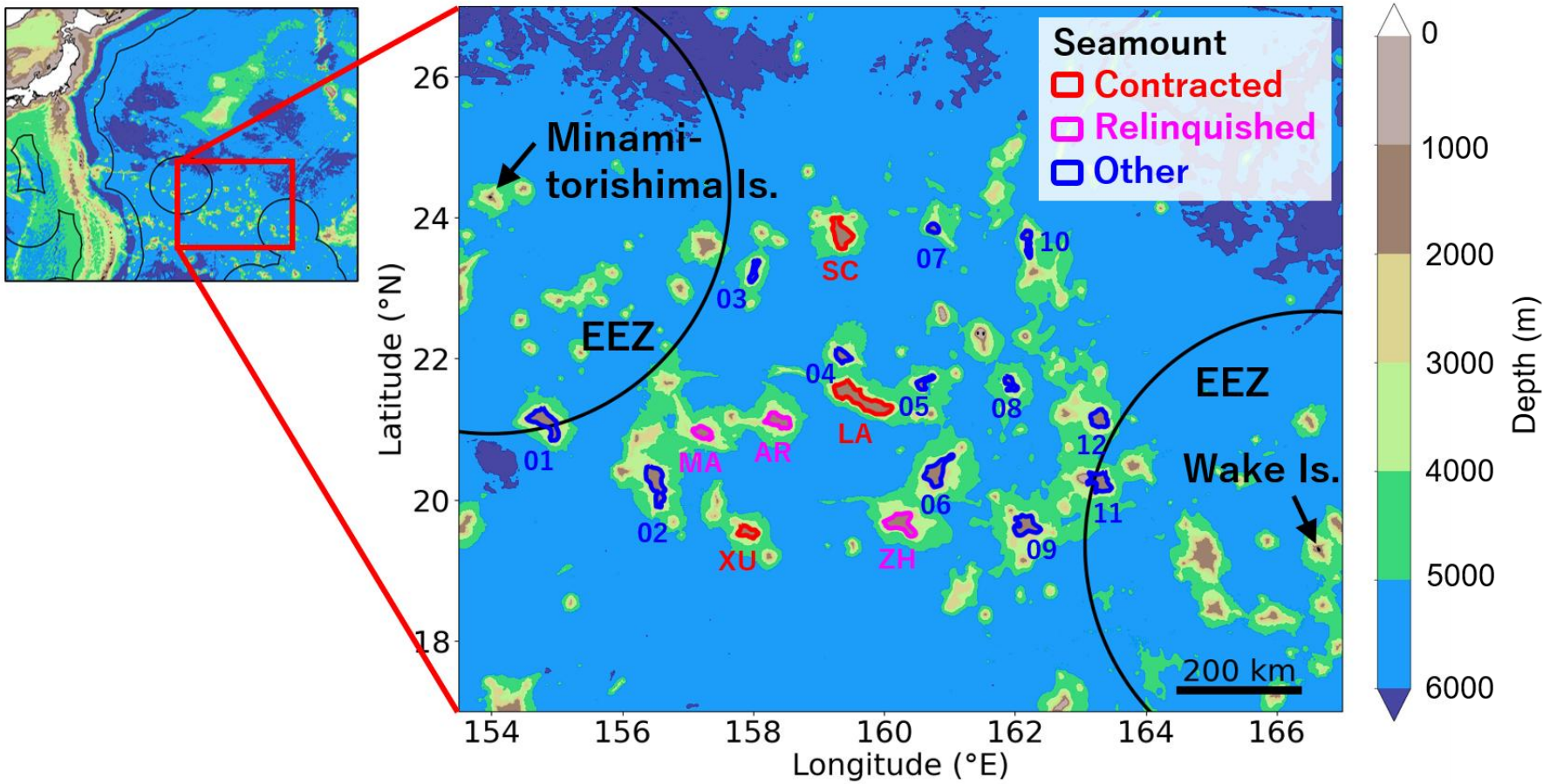


Connectivity through larval dispersal.

Methods

In this study, we modelled larval dispersal among 18 seamounts.

These seamounts included three under resource exploration contracts, three whose exploration contracts were relinquished in 2024, and twelve others.

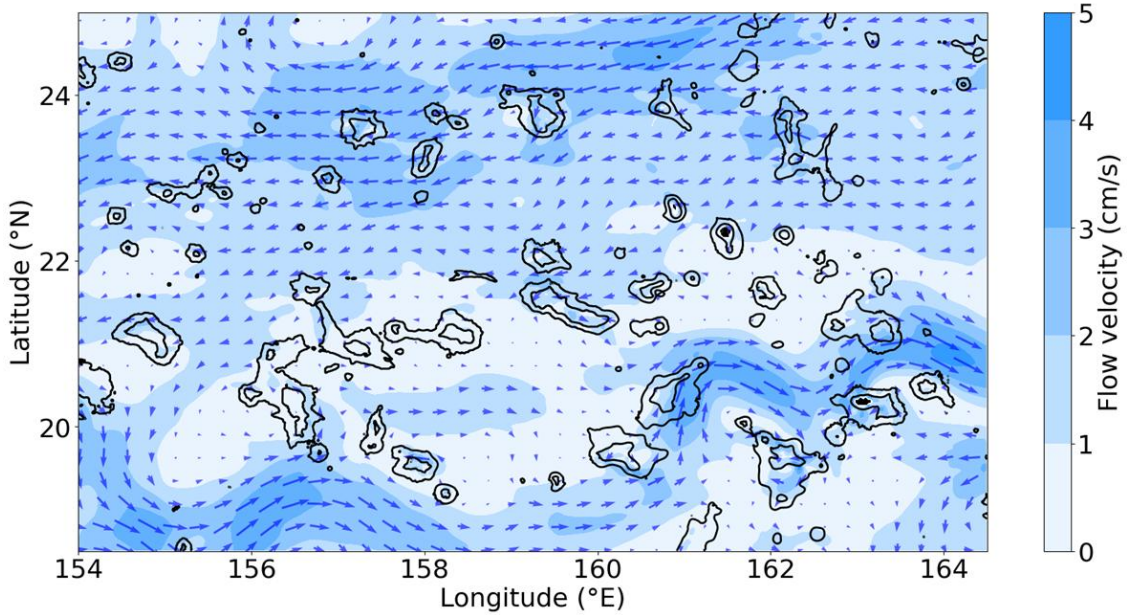


Study area.

Methods

Larval dispersal modelling setup

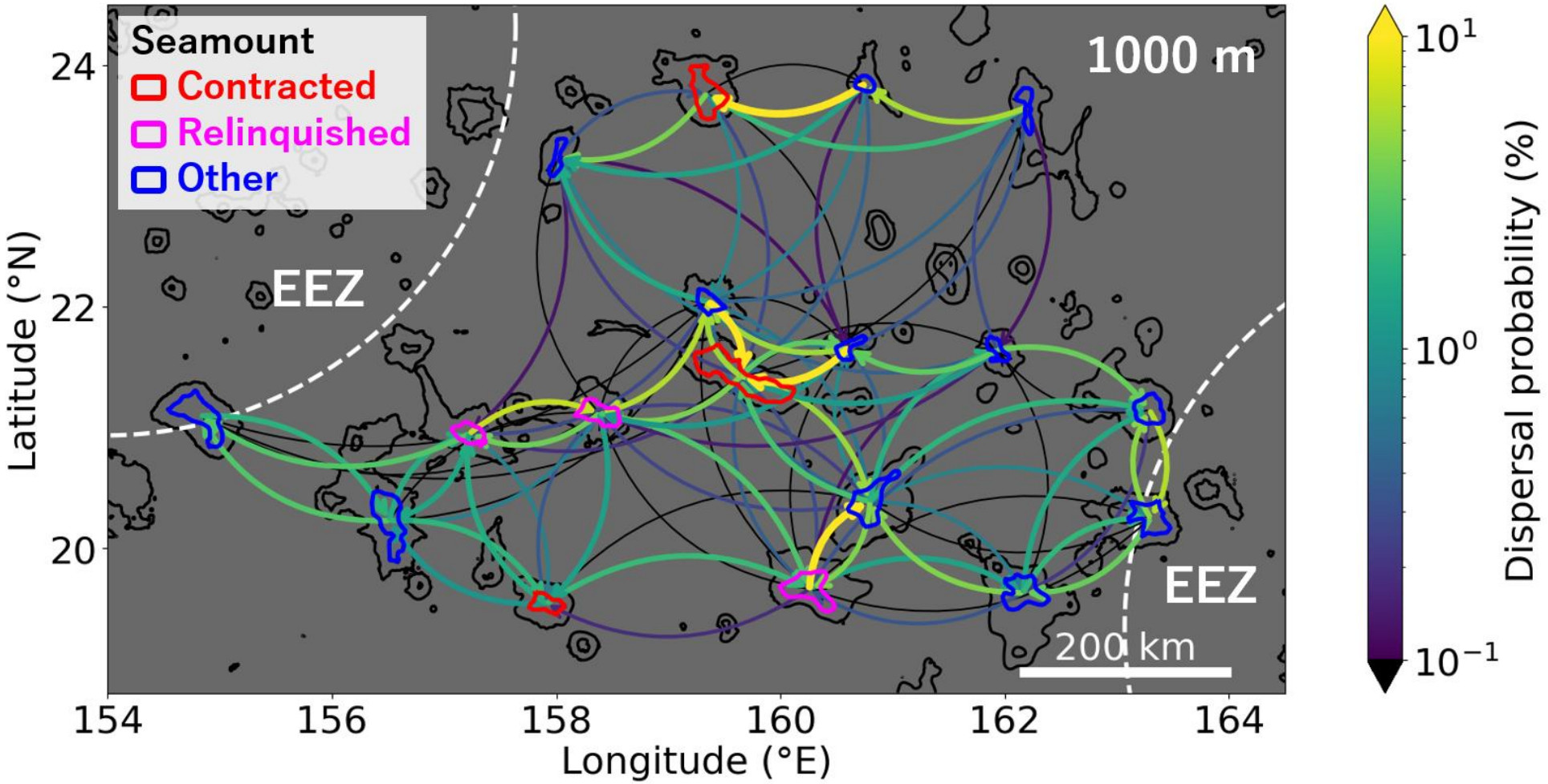
Target period	2020–2022 (3 years)
Target depth	Shown here: 1000 m (simulated: 100–1700 m)
Larval release	Over 20,000 particles were released from each seamount summit
Flow velocity data	Downscaled from the JCOPE2M ocean model ~3 km horizontal resolution



3-year mean flow at 1000 m depth.

Results & Discussion

All 18 seamounts were connected to at least one other via larval dispersal.

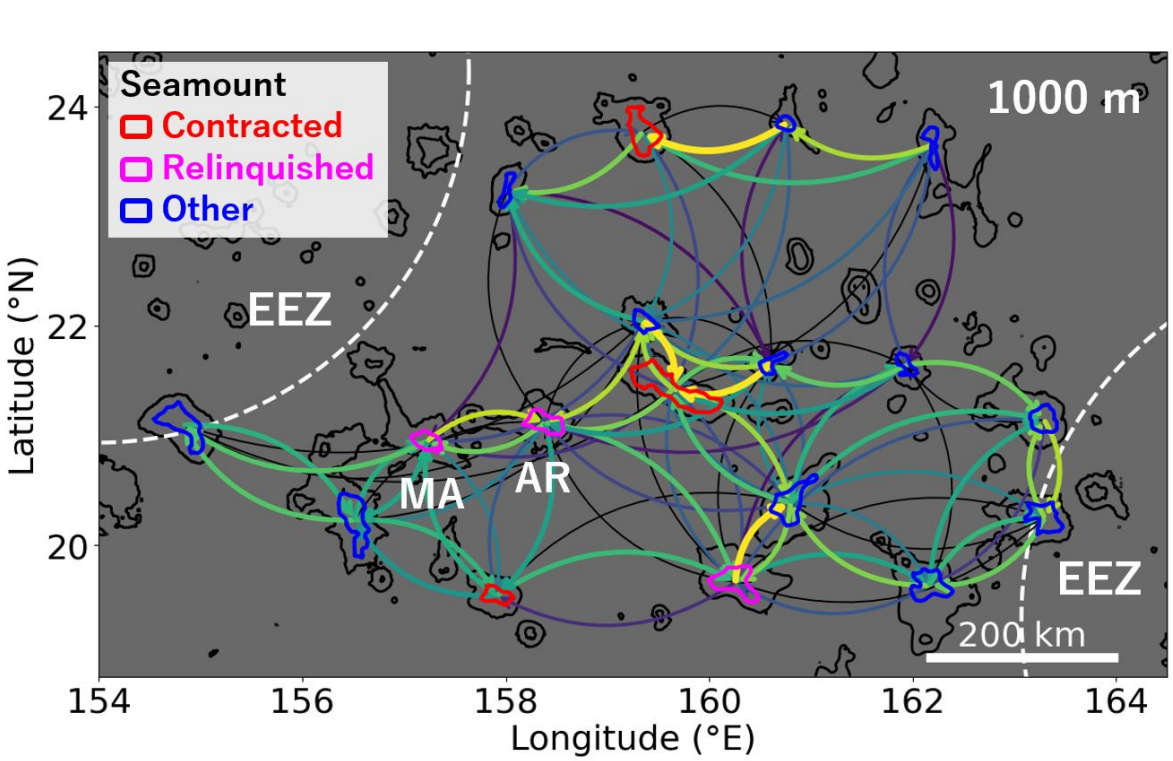


Modelled larval dispersal network among seamounts.

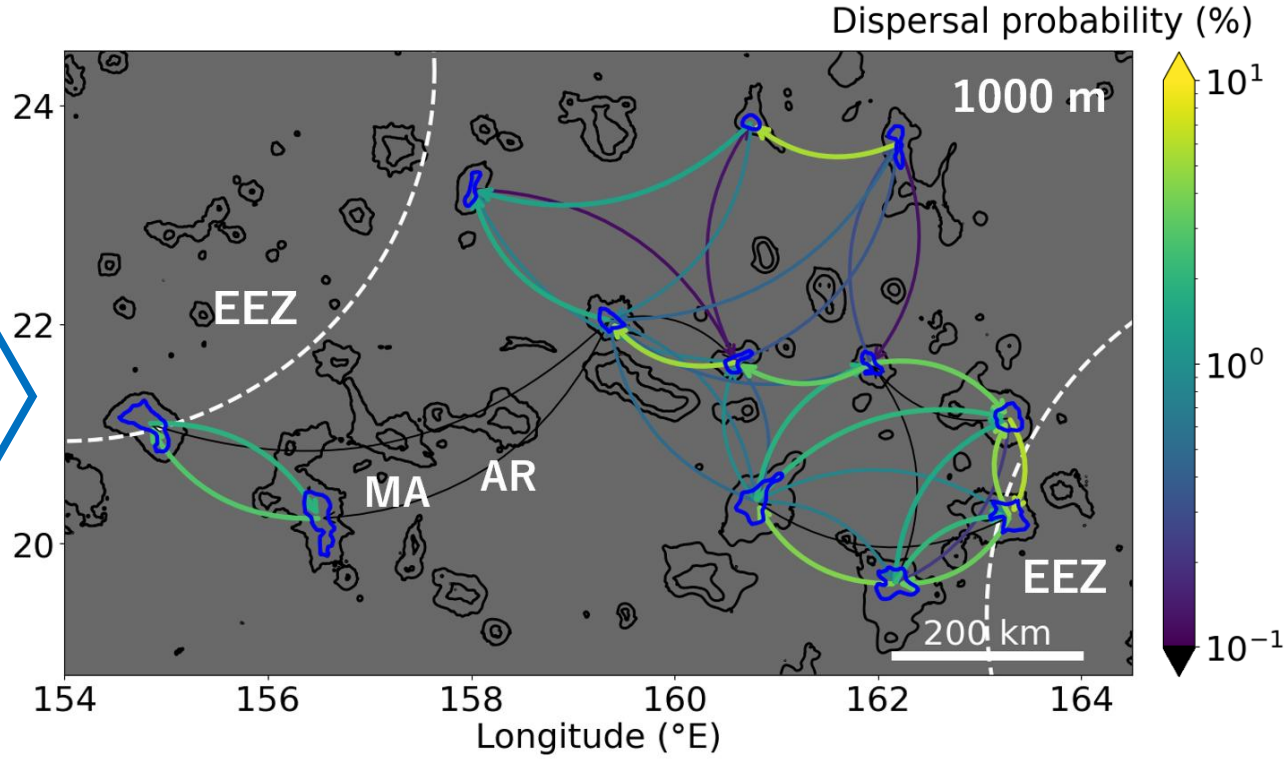
Results & Discussion

Without seamounts MA and AR, east–west regional connectivity is greatly reduced.

To maintain regional connectivity, seamounts MA and AR may deserve particular attention in conservation planning.



When all seamounts are included in the dispersal network.



When seamounts with exploration contracts are excluded from the dispersal network.

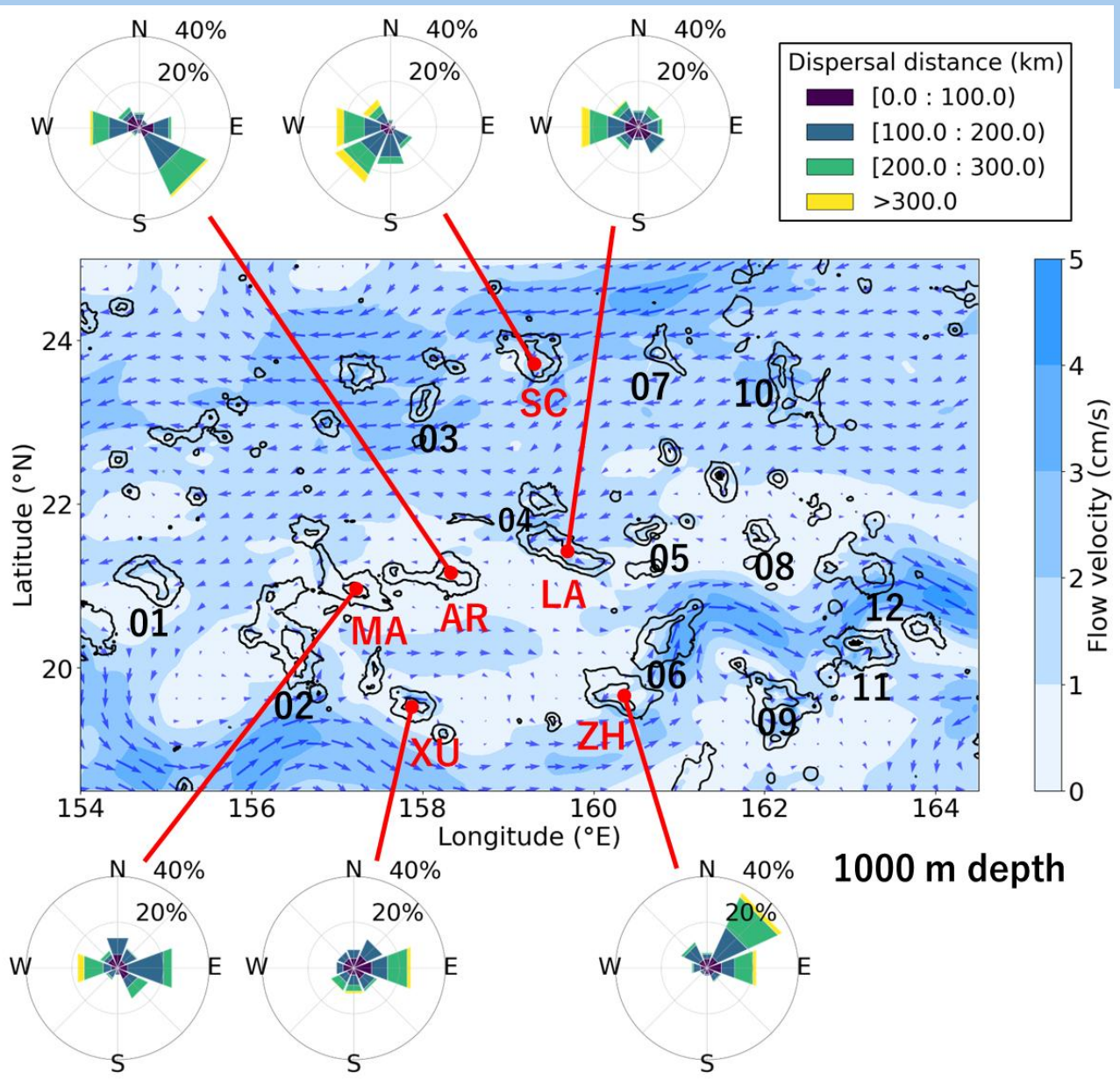
Results & Discussion

Dominant dispersal direction

Westward dispersal dominated at higher latitudes, whereas eastward dispersal dominated at lower latitudes.

➡ Consistent with observations of the **North Equatorial Intermediate Current** (Qiu et al. 2013 *GRL*).

Placing conservation areas upstream within the North Equatorial Intermediate Current may help protect larval source populations.



Directional frequencies of larval dispersal from the seamounts with exploration contracts.

Results & Discussion

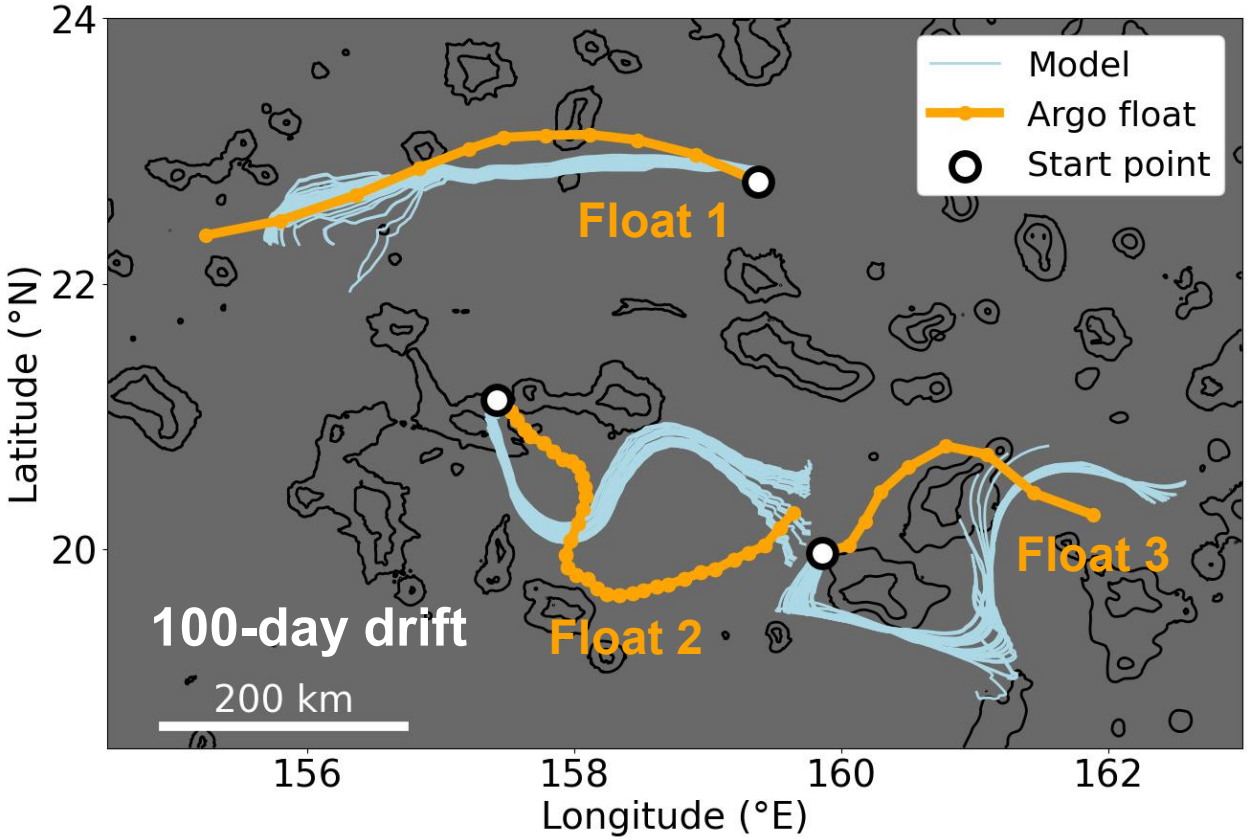
Physical validation

Model currents were validated by simulating **Argo float** trajectories at 1000 m depth.

➡ The model broadly reproduced the directions and distances of three Argo float trajectories.



Argo float: a drifting instrument.



Observed (orange) and modelled (blue) drift trajectories.

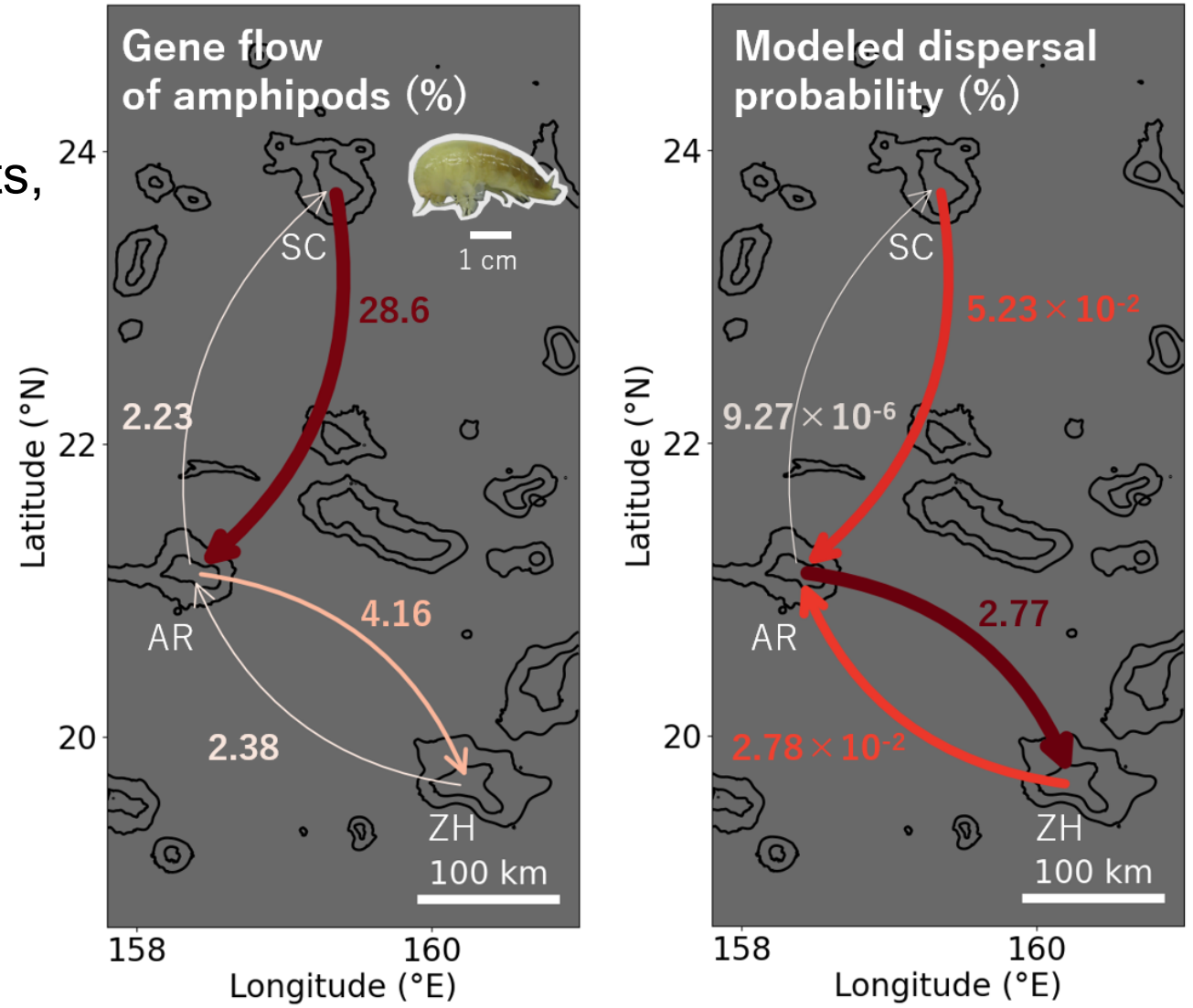
Results & Discussion

Biological validation

Amphipods were sampled at three seamounts, and **gene flow** among them was analysed.

➡ The dominant direction was consistent between gene flow and modelled dispersal.

Modelled dispersal was consistent with both physical and biological field data.



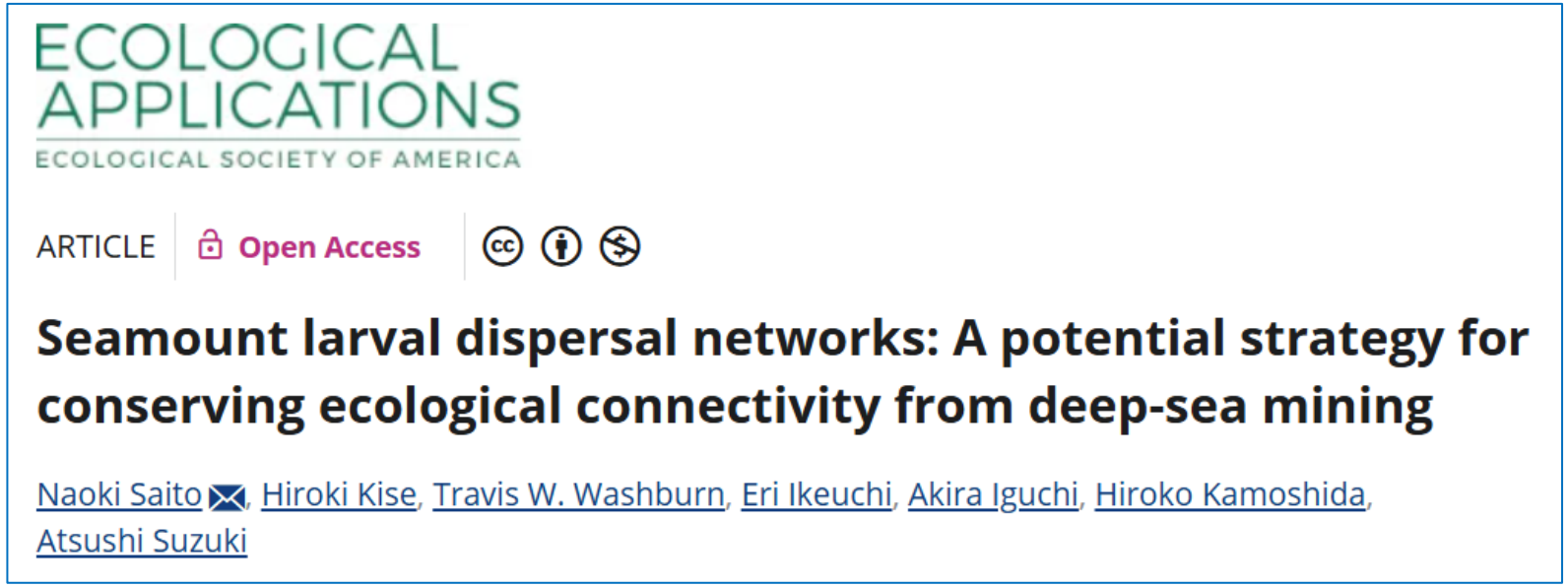
Gene flow (left) and modelled dispersal (right).

Conclusions

1. Two seamounts were key nodes in the larval dispersal network and may warrant priority in conservation planning.

2. Placing conservation areas upstream of the North Equatorial Intermediate Current may help maintain larval sources.

3. Further validation requires multi-species sampling (e.g., corals and sponges) and gene flow analyses.



🔎 **For details:** Saito, N. et al. (2025) *Ecological Applications*, 35(7), e70086.