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TITLE: Biophysical and Population Genetic Models Predict the Presence of 'Phantom' Stepping Stones Connecting Mid-Atlantic Ridge Vent Ecosystems

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ABSTRACT:

Deep-sea hydrothermal vents are patchily distributed ecosystems inhabited by specialized animal populations that are textbook meta-populations. Many vent-associated species have free-swimming, dispersive larvae that can establish connections between remote populations. However, connectivity patterns among hydrothermal vents are still poorly understood because the deep sea is undersampled, the molecular tools used to date are of limited resolution, and larval dispersal is difficult to measure directly. A better knowledge of connectivity is urgently needed to develop sound environmental management plans for deep-sea mining. Here, we investigated larval dispersal and contemporary connectivity of ecologically important vent mussels (*Bathymodiolus* spp.) from the Mid-Atlantic Ridge by using high-resolution ocean modeling and population genetic methods. Even when assuming a long pelagic larval duration, our physical model of larval drift suggested that arrival at localities more than 150 km from the source site is unlikely and that dispersal between populations requires intermediate habitats ("phantom" stepping stones). Dispersal patterns showed strong spatiotemporal variability, making predictions of population connectivity challenging. The assumption that mussel populations are only connected via additional stepping stones was supported by contemporary migration rates based on neutral genetic markers. Analyses of population structure confirmed the presence of two southern and two hybridizing northern mussel lineages that exhibited a substantial, though incomplete, genetic differentiation. Our study provides insights into how vent animals can disperse between widely separated vent habitats and shows that recolonization of perturbed vent sites will be subject to chance events, unless connectivity is explicitly considered in the selection of conservation areas.

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