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# Can biophysical processes explain copepod connectivity and distribution across the Atlantic Ocean basin?

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Although there are few obvious dispersal barriers in the ocean, holoplanktonic copepods exhibit species-specific distribution patterns and significant genetic structure among ocean basins and within gyres. To explain these patterns, we develop and implement a comprehensive biophysical model to examine connectivity of holoplanktonic copepods across the Atlantic Ocean basin. These tools include an individual-based model (IBM) coupled with physical forcing to examine the effects of interactions among biological traits and the environment on connectivity. Our tool allows for the characterization of meaningful variability in biological responses to the environment both among individuals and across species. First, we apply the new modeling tools to disentangle underlying drivers of genetic structure for a globally distributed copepod, *Pleuromamma xiphias*. The life history of *P. xiphias* is modeled with empirical estimates of reproduction, growth, development, mortality, and vertical migration, which are environmentally forced (e.g. chlorophyll-a concentration, advection, temperature). We compare our model results to observations of genetic diversity across the species’ range to assess model performance and gain insight into the functional traits that affect connectivity. Second, we explain distribution and connectivity patterns for other copepod species by linking our modeled variability to influential life history traits varying across species. We discuss our results with respect to species-specific genetic diversity estimates (i.e. adaptation potential), distributions, and resulting community dynamics across the ocean basin, including how these might vary with environmental changes in the future.

Keywords: connectivity, holoplankton, copepod, Pleuromamma xiphias, genetic structure, Atlantic Ocean, individual-based model, biophysical model

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