Estimating dispersal distance in the deep sea: challenges and applications to marine reserves

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Population connectivity refers to the exchange of individuals among populations: it affects gene flow, regulates population size and function, and mitigates recovery from natural or anthropogenic disturbances. Many populations in the deep sea are spatially fragmented, and will become more so with increasing resource exploitation. Understanding population connectivity is critical for spatial management. For most benthic species, connectivity is achieved by the planktonic larval stage, and larval dispersal is, in turn, regulated by complex interactions between biological and oceanographic processes. Coupled biophysical models, incorporating ocean circulation and biological traits, such as planktonic larval duration (PLD), have been used to estimate population connectivity and generate spatial management plans in coastal and shallow waters. In the deep sea, knowledge gaps in both the physical and biological components are delaying the effective use of this approach. Here, we review the current efforts in conservation in the deep sea and evaluate (1) the relevance of using larval dispersal in the design of marine protected areas and (2) the application of biophysical models in the study of population connectivity. Within biophysical models, PLD can be used to estimate dispersal distance. We propose that a PLD that guarantees a minimum dispersal distance for a wide range of species should be used in the planning of marine protected areas in the deep sea. Based on a review of data on species found at depths >200 m, a PLD of 35 and 69 days ensures a minimum distance for 50 and 75%, respectively, of eurybathic and deep-sea species. We note that more data are required to enhance accuracy and address the high variability in PLD between and within taxonomic groups, limiting generalizations that are often appealing to decision-makers. Given the imminent expansion of resource exploitation in the deep sea, data relevant to spatial management are needed urgently.

Keywords: deep sea, connectivity, larval dispersal, biophysical models, marine reserve

INTRODUCTION

The deep sea, although the largest biome on the planet, remained unexplored until the late 19th century (Tyler, 2003) when the cosmopolitan occurrence of deep-sea fauna was established for the first time. Another 100 years of research and technological developments were necessary before the habitat heterogeneity (Ramirez-Llodra et al., 2010), high biodiversity (e.g., Grassle and Maciolek, 1992), and contribution to global ocean processes (Jahnke, 1996) of the deep sea challenged prevailing views and raised new ecological questions (Danovaro et al., 2014). In the last few decades, demand for deep-sea products, such as those from fishing, hydrocarbon extraction, and mining, has been rapidly expanding (Ramirez-Llodra et al., 2011; Thurber et al., 2014), and deep-sea ecologists are

asked to provide solutions for the mitigation of exploitation impacts.

Although the deep seafloor includes some of the largest contiguous features of the planet, such as the abyssal plains and the sedimentary slopes of the continental margins (Ramirez-Llodra et al., 2010), many deep-sea populations are spatially fragmented, and may become more so as a consequence of human disturbance during resource exploitation and extraction. Concurrently, one of the main challenges of deep-sea ecology is the elucidation of the processes that lead to connectivity among spatially isolated populations, which would ultimately regulate their persistence and recovery after disturbance (reviewed in Cowen et al., 2007). Differences in population connectivity contribute greatly to the spatiotemporal patterns in the distribution of organisms and