

ID: W2395049520

TITLE: A synthesis of genetic connectivity in deep-sea fauna and implications for marine reserve design

AUTHOR: ['Amy R. Baco', 'Ron J. Etter', 'Pedro A. Ribeiro', 'Sophie von der Heyden', 'Peter Beerli', 'Brian P. Kinlan']

ABSTRACT:

With anthropogenic impacts rapidly advancing into deeper waters, there is growing interest in establishing deep-sea marine protected areas (MPAs) or reserves. Reserve design depends on estimates of connectivity and scales of dispersal for the taxa of interest. Deep-sea taxa are hypothesized to disperse greater distances than shallow-water taxa, which implies that reserves would need to be larger in size and networks could be more widely spaced; however, this paradigm has not been tested. We compiled population genetic studies of deep-sea fauna and estimated dispersal distances for 51 studies using a method based on isolation-by-distance slopes. Estimates of dispersal distance ranged from 0.24 km to 2028 km with a geometric mean of 33.2 km and differed in relation to taxonomic and life-history factors as well as several study parameters. Dispersal distances were generally greater for fishes than invertebrates with the Mollusca being the least dispersive sampled phylum. Species that are pelagic as adults were more dispersive than those with sessile or sedentary lifestyles. Benthic species from soft-substrate habitats were generally less dispersive than species from hard substrate, demersal or pelagic habitats. As expected, species with pelagic and/or feeding (planktotrophic) larvae were more dispersive than other larval types. Many of these comparisons were confounded by taxonomic or other life-history differences (e.g. fishes being more dispersive than invertebrates) making any simple interpretation difficult. Our results provide the first rough estimate of the range of dispersal distances in the deep sea and allow comparisons to shallow-water assemblages. Overall, dispersal distances were greater for deeper taxa, although the differences were not large (0.3-0.6 orders of magnitude between means), and imbalanced sampling of shallow and deep taxa complicates any simple interpretation. Our analyses suggest the scales of dispersal and connectivity for reserve design in the deep sea might be comparable to or slightly larger than those in shallow water. Deep-sea reserve design will need to consider the enormous variety of taxa, life histories, hydrodynamics, spatial configuration of habitats and patterns of species distributions. The many caveats of our analyses provide a strong impetus for substantial future efforts to assess connectivity of deep-sea species from a variety of habitats, taxonomic groups and depth zones.

SOURCE: Molecular ecology

PDF URL: <https://rss.onlinelibrary.wiley.com/doi/am-pdf/10.1111/mec.13689>

CITED BY COUNT: 109

PUBLICATION YEAR: 2016

TYPE: article

CONCEPTS: ['Biological dispersal', 'Pelagic zone', 'Biology', 'Ecology', 'Invertebrate', 'Fauna', 'Habitat', 'Range (aeronautics)', 'Benthic zone', 'Population', 'Taxon', 'Marine invertebrates', 'Materials science', 'Demography', 'Sociology', 'Composite material']