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Analyzing pelagic food webs leading to top predators in the Pacific Ocean: A graph-theoretic approach

Jeffrey M. Dambacher, Jock W. Young, Robert J. Olson, Valérie Allain, Felipe Galván Magaña, Matthew J. Lansdell, Noemí Bocanegra-Castillo, Vanessa Alatorre-Ramírez, Scott P. Cooper & Leanne M. Duffy

This work examined diet data from studies of top pelagic predators from three large regions of the equatorial and South Pacific Ocean. Food webs of each of these three systems were found to have relatively high species diversity, but in contrast to other marine systems, relatively low connectance. Food webs were examined using graph-theoretic methods, which included aggregating species based on food-web relationships and identification of potentially influential species. Species aggregations were used to construct simplified qualitative models from each region's food web. Models from each region were then analyzed to make predictions of response to climate change for six commercially important species: mahi mahi, skipjack tuna, albacore tuna, yellowfin tuna, bigeye tuna, and swordfish. We found little commonality in the structure of the three food webs, although the two regions in the equatorial Pacific had food webs composed of four predation tiers, as defined by network levels of predation, whereas the south-western region had only three predation tiers. We also found no consistent pattern in the predicted outcomes of the perturbations, which underlines the need for detailed trophic databases to adequately describe regional pelagic ecosystems. This work demonstrates that food-web structure will be central to understanding and predicting how top pelagic predators, and the ecosystems in which they are embedded, will respond to climate change.

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