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MPA Perspective: Genetics, Marine Dispersal Distances, and the Design of Marine Reserve Networks

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[Editor's note: Steve Palumbi, author of the following piece, has studied the genetics, evolution, population biology, and systematics of a diverse array of marine and terrestrial organisms. His current work is on the genetics of marine populations in the context of the design and implementation of MPAs. Palumbi has been co-leader of a three-year effort to examine the effects of marine reserves on fish populations, based at the National Center for Ecological Analysis and Synthesis ([see previous story](#)).]

The seas are increasingly in serious trouble. Coral bleaching, blankets of hypoxic or anoxic water, radical changes in species composition, toxic algal blooms, marine epidemic diseases, mass mortalities, and fisheries collapses are all symptoms of complex but fundamental alterations in the health of marine ecosystems. As both the value and vulnerability of marine ecosystems become broadly recognized, there is an increasing search for effective mechanisms to prevent or reverse widespread declines, and to sustain or restore ocean ecosystems.

Fully protected marine reserves are a powerful tool for marine conservation and management. Defined as areas in which no extractive activities are allowed, "fully protected marine reserves" are a special category of "marine protected areas" (MPAs), which are sites in which some activities are constrained.

These reserves are different than terrestrial parks because marine species are fundamentally different in how they use habitat. Because many larvae or spores of marine species disperse through the water column, populations from one generation to the next live in different places, and may move outside the boundaries of a single reserve. A confluence of recent empirical and theoretical results indicates that these species will benefit most from a network of reserves, and that such protective necklaces can accomplish both conservation and fisheries goals and provide enhanced ecosystem impact.

How should networks be designed to enhance their function, protect species and provide the most value? Although the morphology of a network of marine protected areas can be complex, there are a few key features shared by all networks that play fundamental roles in their functioning. The minimum set of network features that captures the most important functional attributes consists of:

- the span of the network (the length of coast line or area of habitat between the most distant protected units)
- the size of individual reserves
- their number
- their placement

Together these features determine other critical network features like the amount of area dedicated to protection and connectivity among units.

Other researchers (Warner 2001, Botsford 2001) have shown the critical importance of larval dispersal distance on functioning of individual reserves. Network span also requires knowledge of likely dispersal distances of larvae, juveniles, or adults. To preserve most community components, the span of a network must encompass the dispersal range of species with the greatest potential for movement. To reduce edge effects, and keep loss of individuals from the system of reserves below 10%-20%, the span of a reserve network should be 5-10 times greater than the maximum dispersal range for species to be protected by the network.

Because virtually all marine communities have a significant fraction of species with pelagic periods of 30-60 days, most marine reserve networks should be large enough to encompass the dispersal distances associated with this larval duration. As a result, determining the span of a marine reserve network should be informed by an estimate of average larval dispersal ranges for the variety of species within the communities to be protected. There are few concrete data on this topic, but useful inferences can be made from a number of studies that focus on 1) range expansion of invading species, 2) correlations of population size along a coastline, and 3) the scale of genetic differentiation in broadly distributed populations.

For example, we have recently shown (Barber *et al.* 2000) that populations of common Indonesian mantis shrimp species show extremely abrupt genetic boundaries in unexpected places. Despite very strong current flow patterns that should transport larvae long distances, genes from populations as close as 200 km show radically different sequences, indicating nearly complete lack of population exchange. Such data are in complete agreement with recent reports of high larval retention of fish larvae around coral islands (Warner 2001), and suggest strong ocean currents are not always enough to waft planktonic larvae far away.

A summary of available data on dispersal potential shows a striking surprise: average movement of successful larvae may be 10 times lower than expected, on the order of 50-100 km for species with high potential for dispersal. Nonetheless, these figures suggest two important points. First, the waters set aside to effectively sustain these species must span 500-1000 km. Second, few single reserves will be large enough to sustain these species -- they must rely on functioning networks for survival. Thus, network design will often cross political boundaries and require cooperation in areas defined not by map borders but by the ecosystems themselves.

References:

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