California MLPA Master Plan Science Advisory Team

Methods Used to Evaluate Draft MPA Proposals in the North Coast Study Region (DRAFT)

Chapter~~s 6 and~~ 7: ~~Size and~~ MPA Spacing

~~January 18~~February 4, 2010

7. Spacing (Goals 2 and 6)

Status of this chapter: Pending approval by the SAT. This chapter was previously MPA size and MPA spacing combined, but has since been divided; changes from the January 18 version are in underline and strikeout.

Spacing guidelines were developed to provide for the dispersal of important bottom-dwelling fish and invertebrate groups between marine protected areas (MPAs) and to promote connectivity in the network (Goals 2 and 6 of the Marine Life Protection Act (MLPA)).

Connectivity

Connectivity between different places in the north coast study region was evaluated using known life history characteristics of fish and invertebrate larvae in conjunction with models of potential movement. ~~The model used to predict connectivity is~~ Connectivity estimates are based on ~~realistic~~ the University of California, Santa Cruz (UCSC) implementation[1] of the Regional Ocean Modeling System (ROMS) ~~simulations[2]. The model assumes larvae and young behave as Lagrangian particles transported through ocean circulation. The ROMS simulations of ocean circulation are driven by realistic winds and currents at lateral open boundaries (Conil & Hall 2006) (Dong & McWilliams 2007). The lateral-boundary conditions~~ for the California Current System. The region that is modeled extends from the middle of the Baja Peninsula to Vancouver Island and offshore over 1,000 km. The baseline model is driven by the output from the Coupled Ocean Atmosphere Mesoscale Prediction System (COAMPS) and lateral boundaries are derived from ~~Simple Ocean Data Assimilation (SODA) (Carlton & Cao 2000) (Carlton et al 2000), while the wind field is~~ the global ocean state estimate provided by ECCO (Estimating the Circulation and Climate of the Ocean). Connectivity matrices are calculated from ~~the Fifth-Generation Pennsylvania State University-National Center for Atmospheric Research Mesoscale Model (MM5) (Hughes et al 2008). The circulation model for the north coast study region is based on data gathered during the period of XXXX-XXXX.~~

~~ROMS simulations were validated through a series of comparisons with other types of data (Dong et al. In review), including data from the National Data Buoy Center's Acoustic Doppler Current Profilers (ADCP), high frequency radar, California Cooperative Oceanic Fisheries Investigations (CalCOFI), and Advanced Very High Resolution Radiometer (AVHRR). The mean ocean circulation and variations based on ROMS simulations show high levels~~numerical trajectories of ~~agreement with other~~model floats that follow the 3-dimensional circulation

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[1] Researchers are C. Edwards et al., at the University of California, Santa Cruz.

described in the model. Our calculations represent multi-year averages (January 1999 - July 2007) for various spawning periods and pelagic larval durations.

The model has been evaluated using several types of observations~~. ROMS has limited ability to predict small-scale water movement near shore, which may contribute to local retention of larvae. As a consequence, the model likely underestimates self-replenishment~~, including remotely sensed sea surface temperature (SST), hydrographic data from CalCOFI, and temperature and velocity measurements from nearshore moorings supported by both Monterey Bay Aquarium Research Institute (MBARI) and the Partnership for Interdisciplinary Studies of Coastal Oceans (PISCO). In addition, the UCSC scientists compared modeled estimates of surface eddy kinetic energy and bulk horizontal diffusivities with those estimated from drifters. Modeling studies that describe related implementations of this physical model and float calculations are found in Veneziani et al. (2009), Petersen et al. (2009), and Drake and Edwards (2009).

Modelers used ocean circulation from the ROMS simulation together with known life history characteristics of representative fishes and invertebrates (Table 7-1) to predict expected dispersal patterns throughout northern California. The modelers created “dispersal kernels” or expected dispersal by simulating the release of approximately a million particles from each location throughout northern California. Particles, which simulate larvae, were released in suitable habitats during the appropriate spawning period and for the period of larval duration for all representative species. ~~Modelers explored the full range of potential movement based on release of particles every one kilometer throughout the study region and every six hours for a period of XXXX-XXXX.~~ Particles were passively transported by the simulated currents, and limited behavior (e.g. maintaining depth at a convergent front or edge of an eddy) was incorporated in the model. For each representative species, the model calculated numbers and locations of particles (or model larvae) reaching suitable habitat for settlement and growth at the end of their period of larval duration. ROMS has limited ability to predict small-scale water movement near shore, which may contribute to local retention of larvae. As a consequence, the model likely underestimates self-replenishment.

Table 7-1: Life History Characteristics of Representative Fish and Invertebrates

Species	Common Name	Spawning Season	Larval Duration
Sebastes melanops	Black rockfish	Jan-May	4-6 months
Sebastes auriculatus	Brown rockfish	Dec-Jun in NCSR	1-2 months
Scorpaenichthys marmoratus	Cabezon	Nov-Mar	3-4 months
Metacarcinus magister	~~Burrowing shrimp~~Dungeness crab	Nov-Feb	3-4 months
Haliotis rufescens	~~Dungeness crab~~Red abalone	Apr-Jul	4-7 days
Strongylocentrotus franciscanus	Red ~~abalone~~sea urchin	Dec-Mar	50-120 days

Species	Common Name	Spawning Season	Larval Duration
~~Strongylocentrotus *franciscanus*~~	~~Red sea urchin~~	~~Dec-Feb~~	~~40-60 days~~

Although connections tend to be stronger within bioregions, there is some connectivity between bioregions. In other words, bioregions may be influenced to some extent by movement of animals, nutrients, pollutants, etc., which may be transported from adjacent regions.

Connectivity is different for different species. Dispersal patterns are strongly influenced by seasons and interannual variation. Ocean circulation and resulting movement of particles respond to dominant wind patterns and are not the same from season to season or year to year (although there are underlying patterns). Collectively, the larval dispersal kernels from the ROMS simulations provide a framework for understanding how different parts of the north coast study region are connected.

Spacing of MPAs in the North Coast Study Region

Guidance on spacing of adjacent MPAs, excerpted from the draft *Marine Life Protection Act Master Plan for Marine Protected Areas* (January 2008) (Master Plan), is:

> "For an objective of facilitating dispersal of important bottom-dwelling fish and invertebrate groups among MPAs, based on currently known scales of larval dispersal, MPAs should be placed within 50-100 kilometers (31- 62 miles or 27- 54 nautical miles) of each other."
>
> Note that neighboring MPAs placed closer than 50 km (31 miles) apart also meet the guideline for spacing for the goal of designing a network of MPAs.

This guideline arises from a number of studies that examine the persistence of marine populations with a network of marine reserves[3] and its connection to larval dispersal. The spacing distances arise from a number of recent syntheses of data on larval dispersal in marine fish, invertebrates and seaweeds[4] and advances in modeling of larval transport (Siegel et al 2003, Cowan et al 2006). As with adult movement, scales of larval movement vary enormously among species (meters to hundreds of kilometers). In contrast to adult movement, however, short-distance dispersers pose the biggest challenge for connections between MPAs.

Since the MPA spacing guidelines are intended to help ensure connectivity between marine life populations, and populations only occur in suitable habitat, spacing analyses must consider

[3] Botsford et al 2001, Gaines et al 2003, Gaylord et al 2005

[4] Shanks et al 2003, Kinlan et al 2003, Kinlan et al 2005

the habitats encompassed by each MPA. Thus, the SAT conducts a separate spacing analysis for each key habitat (Chapter 4). Only MPAs that meet the minimum size guidelines (Chapter 6) and contain at least the critical extent of a habitat (Chapter 5) are counted as replicates of that habitat. The spacing analysis is conducted by measuring the distance between “replicate” MPAs or MPA clusters for each key habitat. Additionally, the spacing analysis is conducted for the three highest levels of protection afforded by MPAs: at least "moderate-high" protection; at least "high" protection; and, only MPAs with "very high" levels of protection.

To summarize the evaluation of MPA spacing, the SAT:

- tabulates the maximum gaps between MPAs or MPA clusters in relation to the SAT spacing guidelines of 31-62 statute miles,
- considers spacing for each key habitat separately,
- considers only MPAs or MPA clusters that are of sufficient size to contain adult movement ranges,
- considers only MPAs or MPA clusters that include a sufficient extent of habitat to be counted as meaningful biological replicates, and
- considers only MPAs or MPA clusters that have the three highest levels of protection.

Integrated Evaluation of Alternative MPA Proposals

The SAT will use spatially explicit models to evaluate contributions of proposed MPAs to conservation value (biomass or population persistence) and economic value (fishery catch or profit; Chapter 8 – Bioeconomic Modeling). Evaluations using models consider the actual size and spacing of alternative MPA proposals without imposing minimum thresholds levels for these characteristics. The models integrate spatial data on habitat, fishery effort, and proposed MPA locations and regulations and ultimately predict spatial distributions of fish abundances, fishery yields, and (for one model) fishery profits generated for each proposed network of MPAs.

To summarize the SAT evaluation of proposed MPAs using spatially explicit population models, the models can:

- integrate spatial data on habitat, fishery effort, and proposed MPA locations and regulations;
- consider potential contributions of proposed MPAs, regardless of size or spacing;
- consider potential impacts of allowed uses in proposed MPAs, regardless of the level of protection;
- predict biomass and larval supply (a proxy measure of population sustainability) for about 10 representative species, across space; and
- predict fish yield for the representative species, across space.

Additional detail about the modeling evaluation is provided in Chapter 8.

Chapter 7 References

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