# California Marine Life Protection Act Initiative Methods Used to Evaluate Draft Marine Protected Area Proposals in the MLPA South Coast Study Region (Draft) Section 8.0 – Spacing

Draft revised January 15, 2009

# 8.0 SPACING (GOALS 2 AND 6)

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 in the MLPA South Coast Study Region

Connectivity throughout southern California was evaluated using known life history characteristics of fish and invertebrate larvae in conjunction with models of potential movement<sup>1</sup>. The model used to predict connectivity is based on realistic Regional Ocean Modeling System (ROMS) simulations. 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<sup>2,3</sup>. The lateral-boundary conditions are derived from Simple Ocean Data Assimilation (SODA)<sup>a,b</sup>, while the wind field is calculated from the 5<sup>th</sup> generation Pennsylvania State University-National Center for Atmospheric Research Mesoscale Model (MM5)<sup>c</sup>. The circulation model is based on data gathered during the period of 1996 – 2003, including a strong El Niño and La Niña event.

ROMS simulations were validated through a series of comparisons with other types of data<sup>4</sup>, 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 of agreement with other types of observations. ROMS has limited ability to predict small scale water movement nearshore, which may contribute to local retention of larvae. As a consequence, the model likely underestimates self-replenishment.

Ocean circulation in southern California is dominated by the California Countercurrent, which moves water toward the mainland and north through the Southern California Bight, toward the Channel Islands, while the California Current moves water southward and offshore of the Channel Islands<sup>5</sup>. The northward flow along the mainland tends to be strengthened during the winter and during El Niño events. A counterclockwise gyre tends to form in the Santa Barbara Channel as water moves west along the mainland and eastward along the north side of the Channel Islands. The mean flow is less important in this region.

<sup>&</sup>lt;sup>1</sup> Mitarai, S., D. Siegel, J. Watson, C. Dong & J. McWilliams

<sup>&</sup>lt;sup>2</sup> Conil & Hall 2006

<sup>&</sup>lt;sup>3</sup> Dong, C. & J. McWilliams 2007

<sup>&</sup>lt;sup>4</sup> Dong, C., E. Icida and J. McWilliams. 2008. Circulation and Multiple-Scale Variability in the Southern California Bight.

<sup>&</sup>lt;sup>5</sup> Dever, E. et al. 1991

<sup>&</sup>lt;sup>a</sup> Carlton, J., G. Chepurin & X. Cao (2000)

<sup>&</sup>lt;sup>b</sup> Carlton, J., G. Chepurin, X. Cao & B. Giese (2000)

<sup>&</sup>lt;sup>c</sup> Hughes, M., A. Hall & R. Fovell (2007)

Modelers used ocean circulation from the ROMS simulation together with known life history characteristics of representative fishes and invertebrates (Table 1) to predict expected dispersal patterns throughout southern California. The modelers created "dispersal kernels" or expected dispersal by simulating the release of approximately a million particles from each location throughout southern 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 January 1, 1996 through December 31, 2002, including a strong El Niño and La Niña. 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.

Table 1: Life History Characteristics of Representative Fish and Invertebrates

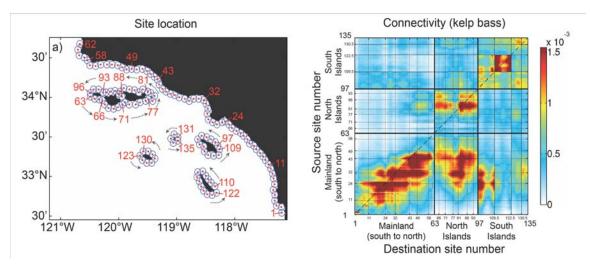
Species	Common Name	Spawning Season	Larval Duration
Paralabrax	Kelp bass	Apr-Nov (peak	25-33 days
clathratus		is May-Sep)	
Paralabrax nebulifer	Barred sand bass	Jul-Aug	24-28 days
Semicossyphus	California	Jul-Oct	34-78 (median
pulcher	sheephead		is 37)
Scorpaena guttata	California scorpionfish	May-Sep	30-60 days
Sebastes	Kelp rockfish	Mar-Apr	50-75 days
atrovirens			
Girella nigricans	Opaleye	Jun-Jul	
Caulolatilus princeps	Ocean whitefish	Jun-Aug	~90 days
Strongylocentrotus	Red sea urchin	Dec-Feb	40-60 days
franciscanus			
Lottia gigantea	Owl limpet	To be updated	To be updated
Kelletia kelletti	Kellet's whelk	To be updated	To be updated
Embiotoca	Black perch	Apr-Jun	livebearer, no
jacksoni			pelagic larvae

Lagrangian particles representing larvae spread out across the entire Southern California Bight within about 30 days. The model results suggest that connectivity in southern California is heterogeneous and asymmetric reflecting the variable flow features in the southern California Bight. 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. General patterns that emerge from modeling are strong poleward transport of particles along the mainland and some retention of particles in the Santa Barbara Channel and near San Clemente Island. For the representative species modeled, there is some connectivity between Santa Catalina and San Clemente islands, while there is more limited connectivity between San Nicolas Island and the other Channel Islands.

Connectivity is different for different species. For species with short larval duration, the mainland and islands tend not to be strongly connected. For species with longer larval duration, there is a stronger connection from mainland to islands, but the connection in the opposite direction tends to be weaker. The model predicts that northwestern and southeastern islands tend not to be strongly connected, except for representative species with longer larval duration, such as cabezon and kelp rockfish. Although San Nicolas Island is more isolated than the other Channel Islands, models predict some exchange of larvae between San Nicolas, Santa Catalina and San Clemente for species characteristic of the warm temperate waters and exchange of larvae between San Nicolas and the northwestern Channel Islands (San Miguel and Santa Rosa) for species characteristic of the cooler California Current. 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).

Figure 1. Connectivity of sites in southern California for kelp bass. Site location (lower left) describes the locations of release points for Lagrangian particles representing larvae. Mainland sites are labeled 0-62; northern Channel Islands sites (including San Miguel, Santa Rosa, Santa Cruz and Anacapa) are labeled 63-96; southern Channel Islands sites (including San Nicolas, Santa Barbara, Santa Catalina and San Clemente) labeled 97-135. [Note that the grouping of these islands for the purpose of modeling connectivity is intended to simplify interpretation of results on graphics and does not reflect differences between bioregions.] The connectivity matrix (below right) represents the number of Lagrangian particles representing kelp bass larvae that are released from a particular source site (y-axis) and arrive at a particular destination site (x-axis). Red points indicate strong connections between sources and destinations, while blue points represent limited or no connections. For kelp bass, mainland sources are strongly connected to other mainland and island destinations, particularly the northern Channel Islands and Santa Catalina Island. However, island sources tend to be more isolated and are not as strongly connected to other island groups or mainland destinations.



Collectively, the larval dispersal kernels from the ROMS simulations provide a framework for understanding how different parts of the Southern California Bight are connected. The model results suggest that the mainland coast of southern California is an important source of larvae for the entire Southern California Bight and movement of larvae along the mainland coast is similar to other regions of California. The model results suggest that movement of larvae is more limited from the Channel Islands to the mainland and between the islands. As a consequence, spacing of MPAs at the Channel Islands must be evaluated differently from other regions of California.

#### **Design of MPAs along the Mainland Coast**

Guidance on spacing of adjacent MPAs along the mainland coast, excerpted from the California Marine Life Protection Act Master Plan for Marine Protected Areas, 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."

This guideline arises from a number of studies that examine the persistence of marine populations with a network of marine reserves<sup>6,7,8</sup> 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<sup>9,10,11</sup> and advances in modeling of larval transport<sup>12,13</sup>. 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 spacing guidelines are intended to help ensure connectivity between marine life populations, and populations only occur in suitable habitat, spacing analyses must consider the habitats encompassed by each MPA. Thus, the MLPA Master Plan Science Advisory

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<sup>&</sup>lt;sup>6</sup> Botsford, L.W., Hastings, A., and Gaines, S.D. 2001. Dependence of sustainability on the configuration of marine reserves and larval dispersal distance. Ecology Letters 4: 144-150.

<sup>&</sup>lt;sup>7</sup> Gaines, S. D., B. Gaylord, and J. Largier. 2003. Avoiding current oversights in marine reserve design. Ecological Applications. 13:S32-46

<sup>&</sup>lt;sup>8</sup> Gaylord, B., S. D. Gaines, D. A. Siegel, M. H. Carr. 2005. Consequences of population structure and life history for fisheries yields using marine reserves. *Ecological Applications*. 15:2180-2191.

<sup>&</sup>lt;sup>9</sup> Shanks, A.L., Grantham, B.A. & Carr, M.H. 2003. Propagule dispersal distance and the size and spacing of marine reserves. Ecological Applications, **13**, S159–S169.

<sup>&</sup>lt;sup>10</sup> Kinlan, B. and S. D. Gaines. 2003. Propagule dispersal in marine and terrestrial environments: a community perspective. Ecology. 84:2007-2020.

<sup>&</sup>lt;sup>11</sup> Kinlan, B., S. D. Gaines, and S. Lester. 2005. Propagule dispersal and the scales of marine community process. Diversity and Distributions. 11:139-148.2005.

<sup>&</sup>lt;sup>12</sup> Siegel, D., B. P. Kinlan, B. Gaylord and S. D. Gaines. 2003. Lagrangian descriptions of marine larval dispersion. Marine Ecology Progress Series. 260:83-96.

<sup>&</sup>lt;sup>13</sup> Cowen, R. K., C. B. Paris, A. Srinivasan. 2006 Scaling of connectivity in marine populations. Science. 311:522-527.

Team (SAT) conducts a separate spacing analysis for each key habitat (Section 5.0). Only MPAs that meet the minimum size guidelines (Section 7.0) and contain at least the critical extent of a habitat (Section 6.0), 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 along the mainland coast, the SAT:

- Tabulates the maximum gaps between MPAs or MPA clusters along the mainland coast in relation to the SAT spacing guidelines of 31-62 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.

# **Design of MPAs at the Channel Islands**

Because of the complex geography and circulation in the Channel Islands region, the SAT recommends that spacing between adjacent MPAs on offshore islands is not an initial criterion for design. SAT guidelines for bioregions (Section 3), representative habitats (Section 5), including retention areas, and replication of habitats (Section 6) should be used as a starting point to design a network of MPAs for the Channel Islands region. Specifically, the SAT recommends establishing MPAs in each bioregion encompassing all representative habitats.

At the Channel Islands, three bioregions were identified based on ecological differences: (1) San Miguel, Santa Rosa, San Nicolas islands and the mainland coast at Point Conception, (2) Santa Cruz, Anacapa and Santa Barbara islands and (3) Santa Catalina and San Clemente islands (Section 3). The SAT tabulates the number and size of MPAs proposed in each bioregion. As noted above, only MPAs that meet minimum size guidelines (Section 7.0) and contain at least the critical extent of a habitat (Section 6.0), are counted as replicates of that habitat. Consistent with the evaluation of MPAs proposed along the mainland coast, the 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 design at the Channel Islands, the SAT:

- Considers the extent and level of protection afforded to each bioregion,
- Considers only MPAs or MPA clusters that are of sufficient size to contain adult movement ranges,

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- Considers extent of key and unique habitats protected within proposed MPAs,
- 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; Section 10 - Modeling). Evaluations using models incorporate 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;
- Predict fish yield for the same 10 representative species, across space.

Additional detail about the modeling evaluation is description in Section 10.