California MLPA Master Plan Science Advisory Team, Bioregions Work Group Draft Analysis of Biogeographical Subregions in the MLPA South Coast Study Region

Revised November 7, 2008

Species abundances, species diversity, and the makeup of ecological communities vary across habitats (e.g., shallow rock reefs, deep rock reefs, sandy bottom), but also vary geographically within a habitat type along with changing environmental conditions. Thus, the biological community within a particular habitat or ecosystem (e.g., kelp forest) can differ markedly from one part of the coast to another. Geographic areas that contain substantially distinct species compositions are known as biogeographic or biogeographical regions. These biogeographical regions reflect collections of species that share similar geographic ranges that are largely limited to each region.

In order to help ensure that marine protected areas (MPAs) established under the Marine Life Protection Act (MLPA) capture adequate representation of the species communities and species diversity representative of California, MPAs must be distributed across biogeographically distinct areas. Both the MLPA and the *California Marine Life Protection Act Master Plan for Marine Protected Areas* identify a single, large-scale "biogeographical region" that is identical to the MLPA South Coast Study Region (Point Conception to the California/Mexico border, including the eight Channel Islands in the Southern California Bight). Compared with previous study regions, the south coast study region is characterized by strong gradients in environmental conditions (e.g., water temperature) and species abundances across the study region. Some parts of the study region (e.g., the western Channel Islands) contain biotic assemblages highly similar to central California while others support quite different species communities that resemble those found in Mexican waters to the south.

As in previous study regions, the MLPA Master Plan Science Advisory Team (SAT) conducted analyses to identify biogeographically relevant subregions (hereafter referred to as subregions) within the large-scale biogeographical region. This is to ensure that distinct species assemblages ***within*** the larger study region are adequately represented in MPAs proposed under the MLPA process. In order to determine these subregions, the SAT analyzed five sources of data across four habitat types and various taxonomic species groups, to develop a synthetic model that best defines existing spatial patterns of community variation. Not all data sets included sites distributed throughout the full extent of the Southern California Bight. These data sets and habitat types were:

- For deep (>30m) rocky reef habitat, Dr. Milton Love described three geographic subregions of distinct fish assemblages in the Southern California Bight[1] (Fig. 1).
- For deep (>30m) soft habitat, bottom trawl surveys conducted by the Southern California Coastal Water Research Project (SCCWRP) were used to describe geographic variation in benthic macroinvertebrate and fish assemblages[2]. These data indicate three subregions of distinct fish assemblages in the south coast study region (Fig. 2).

[1] M. Love et al., unpublished data
[2] Southern California Coastal Water Research Project, Annual Report, 2003

- For shallow (<30m) rocky reef habitat, diver surveys conducted by the Partnership for Interdisciplinary Studies of Coastal Oceans (PISCO) and the Cooperative Research and Assessment of Nearshore Ecosystems (CRANE) were used to describe patterns of geographic variation across the northern Channel Islands and bight-wide, respectively. PISCO surveys defined two subregions of distinct fish assemblages[3] across the northern Channel Islands (Fig. 3) and four similar subregions of distinct invertebrate assemblages (Fig. 4). Crane surveys across the Southern California Bight identified four distinct subregions of fish and invertebrate assemblages[4] (Fig. 5).
- For rocky intertidal habitats, surveys of community structure conducted by the Multi-Agency Rocky Intertidal Network (MARINe), showed five geographic subregions of distinct intertidal communities[5] (Fig. 6).

Geographic distinctions between fish and algal assemblages were detected in three of these five datasets (PISCO and CRANE shallow subtidal and PISCO intertidal) using hierarchical cluster analysis (Primer ver. 6). Bray-Curtis similarity measures are first calculated between all pairs of survey sites by comparing abundances of individual species. Raw species counts were first square-root transformed to ensure sensitivity to both rare and super-abundant species. A group-average linkage technique was then used to find clusters among sites with the highest within group similarity, and produce a hierarchical structure or dendrogram which shows how individual sites and site groups are related to one-another. This method of cluster analysis is the most commonly used and widely accepted approach for this type of data[6]. Statistical significance of these cluster groupings was then tested using SIMPROF tests, a permutation technique which assigns probability values to each site or site group detected in the data. In all cluster analyses, differences between groups were evaluated at the 99% significance level, but in most cases some finer scale site groupings were subsequently combined into larger groupings by taking a slice through the dendrogram at a given level (e.g. 60%) of similarity.

These five datasets indicated very similar, but not identical, biogeographically relevant subregions between Point Conception and the California/Mexico border. To develop a synthesis, a number of models were tested against all these datasets to generate a single subregional scheme that best reconciled the data contained in these five datasets. The best fit model suggested five biogeographically relevant subregions across the south coast study region (Fig. 7).

For some species assemblages and regions for which data were not available in the data sets we analyzed, the literature was reviewed to determine if prior studies had identified patterns of regionally distinct species assemblages. For example, PISCO and CRANE surveys of shallow rocky reef fish assemblages were not conducted along the mainland coast of the Santa

[3] Partnership for Interdisciplinary Studies of Coastal Oceans (PISCO), unpublished data
[4] Cooperative Research and Assessment of Nearshore Ecosystems (CRANE), Draft Final Report, Ca. DFG
[5] Multi-Agency Rocky Intertidal Network (MARINe), unpublished data
[6] Clarke, K. R and R. E. Warwick. 2001. Change in marine communities: An approach to statistical analysis and interpretation, 2nd edition. PRIMER-E Ltd., Plymouth, United Kingdom.

Barbara Channel. However, Ebeling et al. (1980)[7] conducted extensive fish surveys in this region and a similar analysis of assemblage structure and found that the structure of shallow reef fish assemblages differed by 80% between the islands and mainland (Fig. 8). Similarly, Pondella and Allen (2000)[8] compared shallow fish assemblages between Santa Catalina island and sites along the southern California mainland and found distinctive assemblage structure between island and mainland sites. A broader bight-wide comparison of rocky reef fish assemblages on islands and mainland sites defined similar differences between island and mainland sites that were independent of distances between islands[9]. Taken together, these studies reinforce the general conclusion that islands and the Southern California mainland define separate biogeographic subregions.

One other key study that supports both the island-mainland contrasts and, more broadly, the five biogeographic subregions proposed from this analysis, is the biogeographic survey of rocky intertidal macrophyte communities conducted by Murray and Littler (1981)[10] throughout the islands and mainland of the Southern California Bight. Both previous studies cited from the literature and analyses conducted by the SAT indicate a close relationship between the distribution of distinct assemblage structures and large scale oceanographic patterns (i.e. currents and associated water temperatures).

The number and exact location of divisions between the geographic groupings varied across the five datasets; as a result, additional analyses were undertaken to assess how well the data correspond to the structure imposed by proposed subregions in the best fit model. Both rocky intertidal and shallow rock reef community data showed significant differences among groups when sites were assigned a priori to the five proposed subregions (ANOSIM, P=0.01) supporting our synthetic scheme (Fig. 7). Oceanographic and geologic conditions were not directly assessed in the process of determining subregions, but the patterns of diversity and community structure generally reflect known oceanographic and geologic gradients in the Southern California Bight. Thus the SAT concludes that these five subregions reflect real spatial patterns of biodiversity and community structure in the south coast study region.

Implications of Biogeographical Subregions on Habitat Representation and Replication

Because the analyses presented here indicate that each of the five biogeographically relevant subregions in Figure 7 contain different species compositions and/or assemblages, it is recommended that key habitats from within each subregion are represented in MPAs. As noted earlier, this is to ensure that the different community assemblages, and the ecosystem functioning, representative of the MLPA South Coast Study Region are appropriately represented in the MPA network. For purposes of habitat representation this implies that, at a

[7] Ebeling, A.W., R.J. Larson, and W.S. Alevizon. 1980. Habitat groups and island-mainland distributions of kelp-bed fishes off Santa Barbara, California. In D.M. Power ed. Multidisciplinary Symposium California Islands. Santa Barbara Museum of Natural History, pages 403-431.
[8] Pondella, D.J. II, and L.G. Allen. 2000. The nearshore fish assemblage of Santa Catalina Island. Proceedings of the Fifth California Islands Symposium.
[9] Pondella, D.J. II, B.E. Gintert, J.R. Cobb and L.G. Allen. 2005. Biogeography of the nearshore rocky-reef fishes at the southern and Baja California islands. Journal of Biogeography 32:187–201.
[10] Murray, S.N. and M.M. Littler. 1981. Biogeographical analysis of intertidal macrophyte floras of southern California. Journal of Biogeography 8:339-351.

minimum, a single replicate of suitable size for each key habitat should be included in an MPA in each subregion. In practice, however, it is expected that MPA proposals will include more than one MPA in each biogeographically relevant subregion in order to meet SAT spacing guidelines.

Figure 1

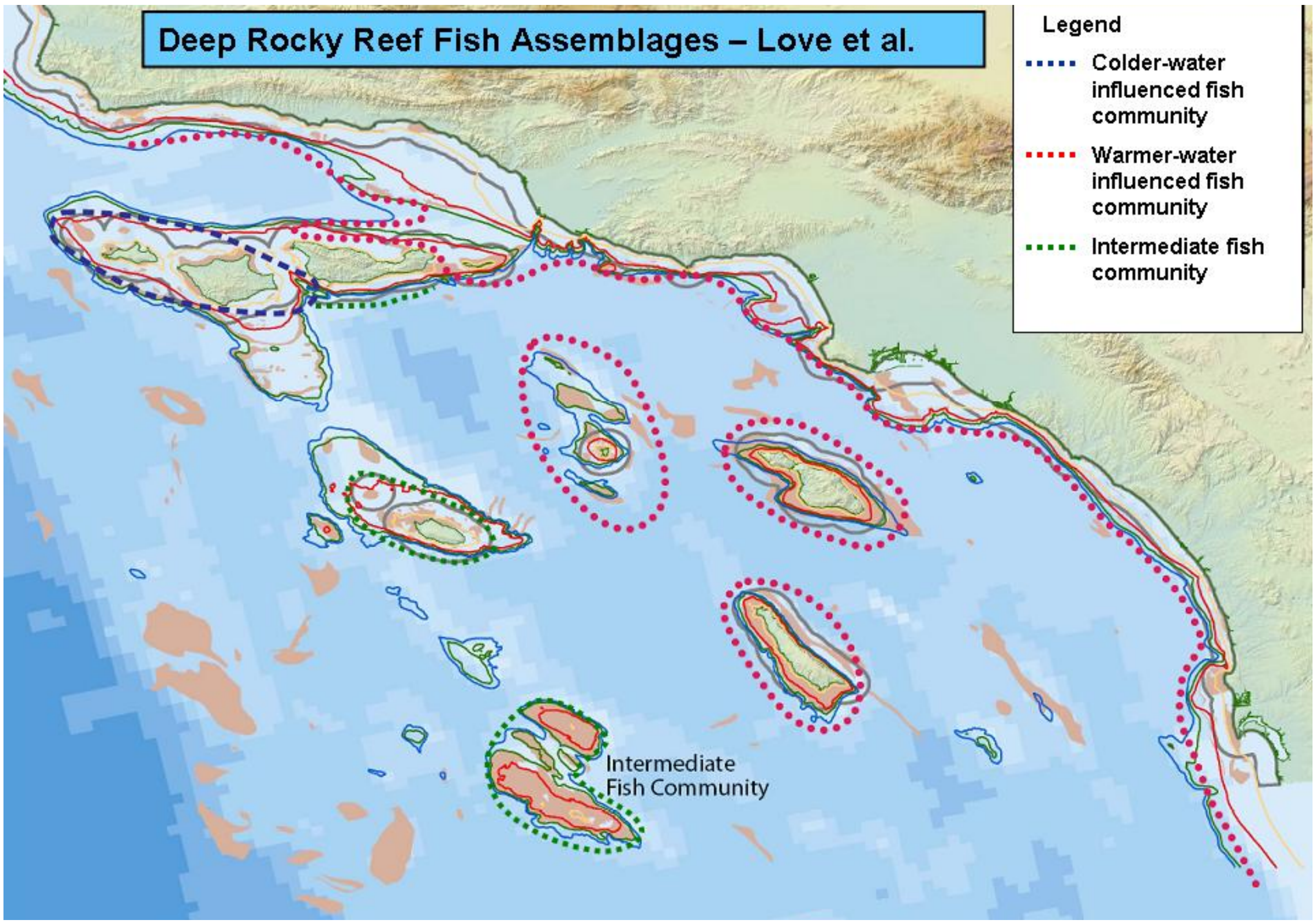
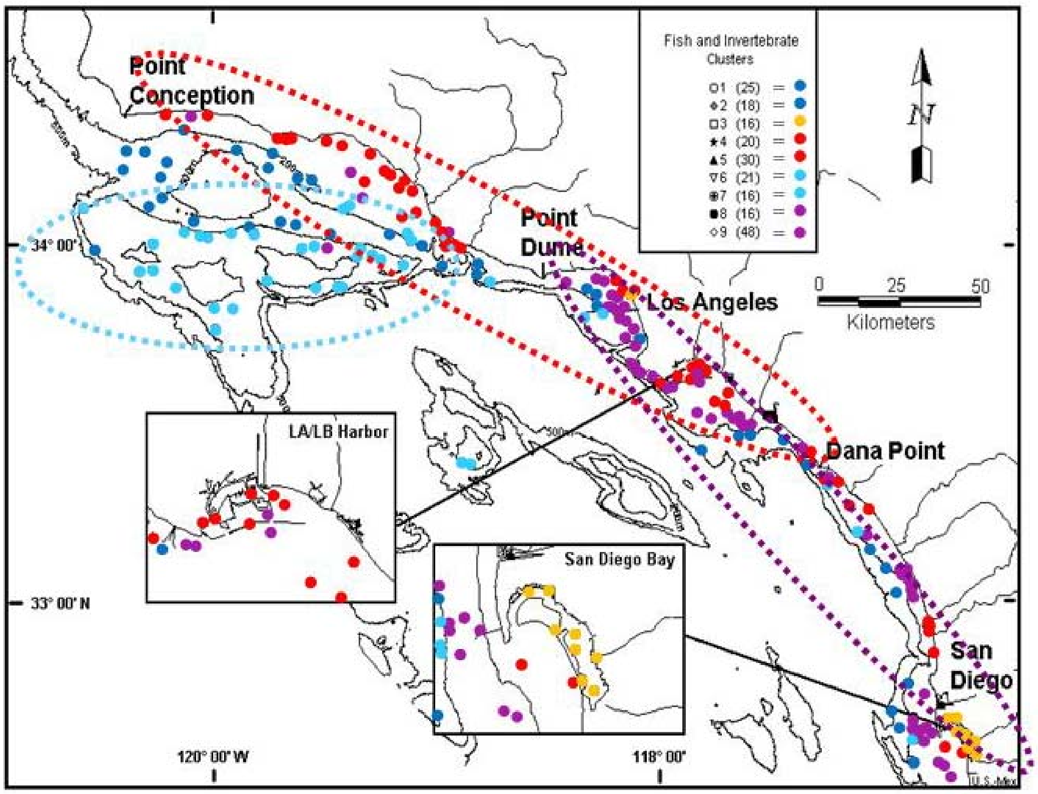


Figure 2

Distribution of demersal fish and megabenthic invertebrate site cluster on the southern California shelf and upper slope at depths of 2-476 m, July-October 2003.



SCCWRP 2003 Annual Report - Figure VI-14.

Figure 3

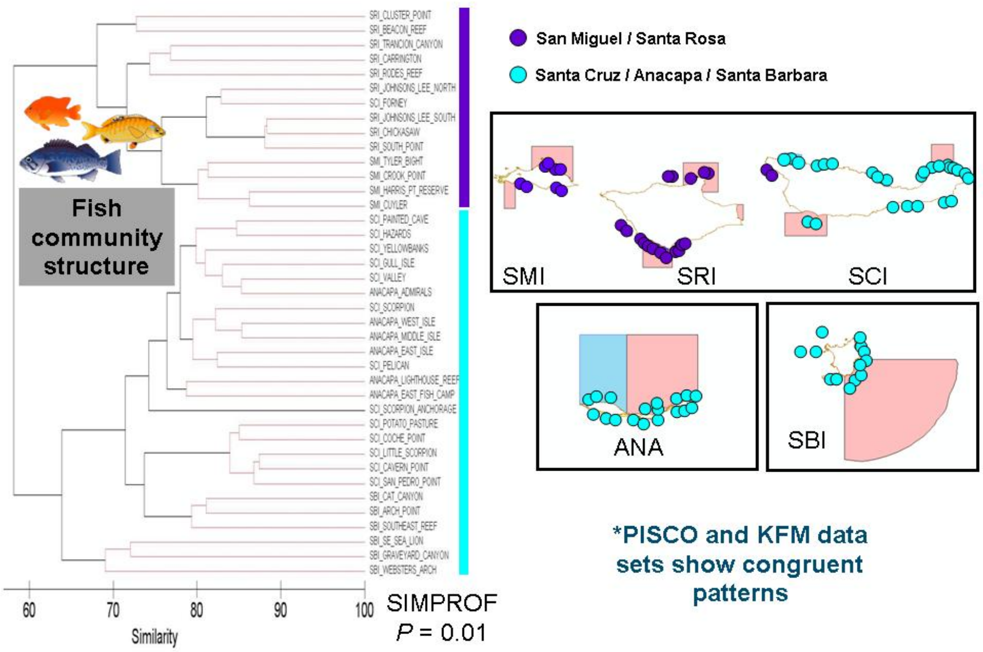


Figure 4

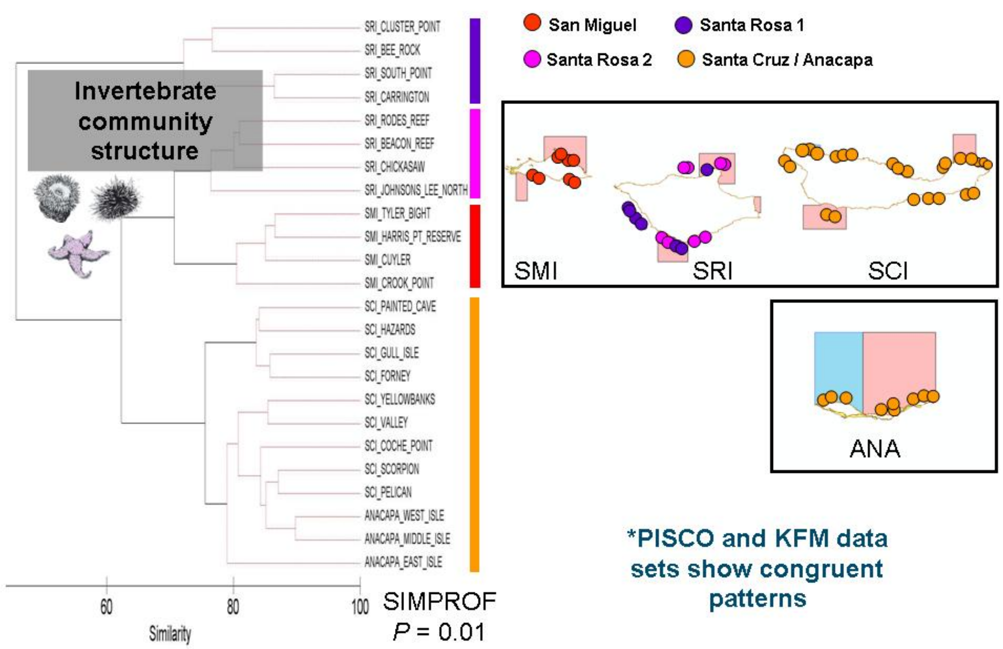


Figure 5

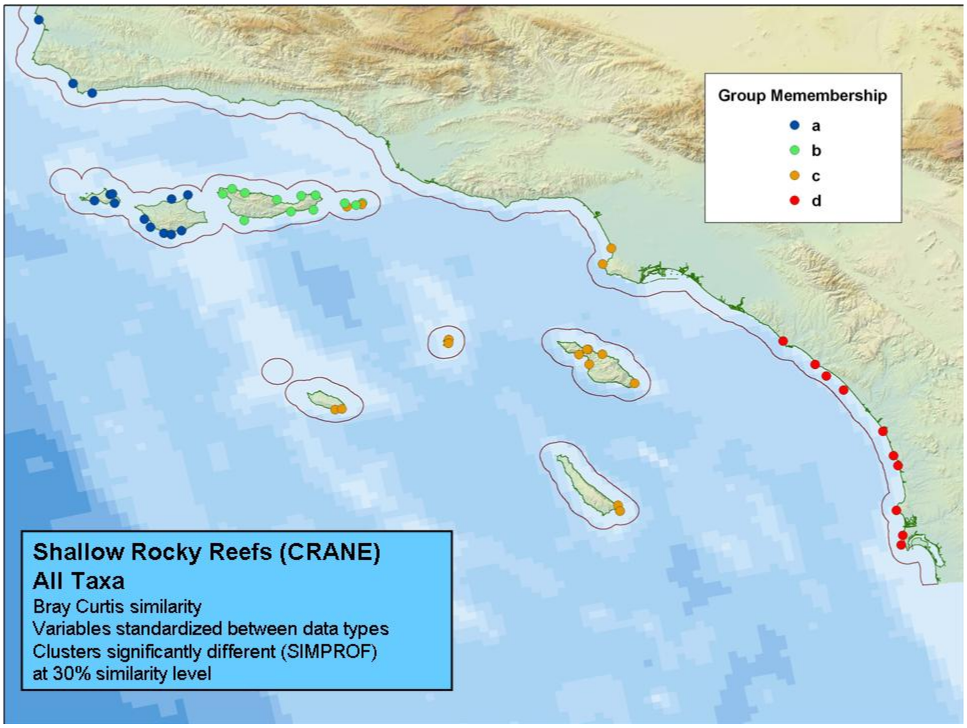


Figure 6

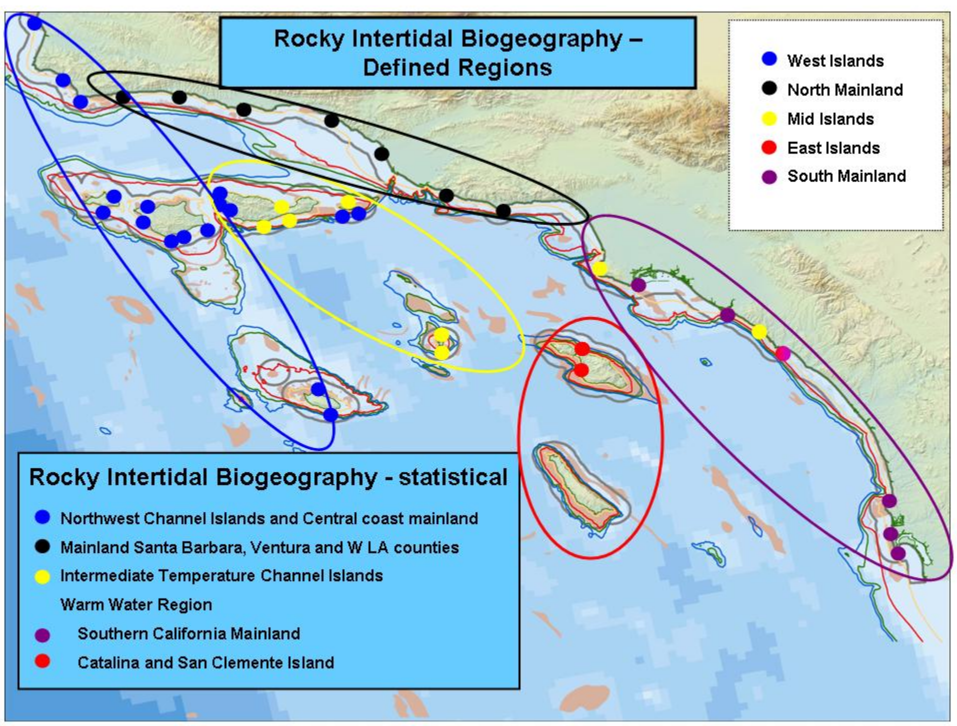


Figure 7

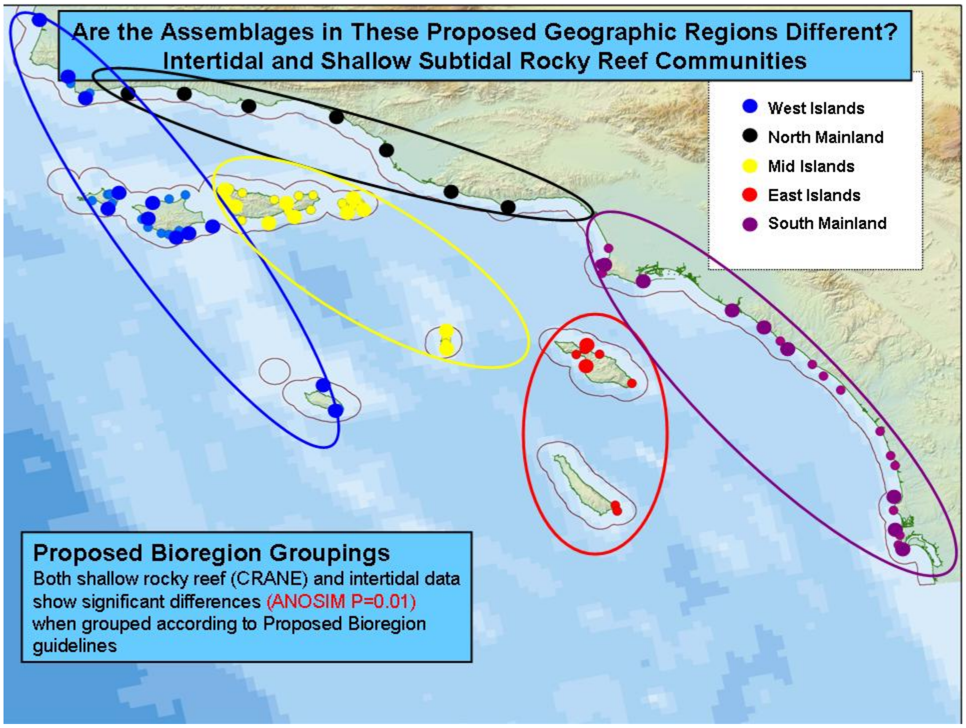

Are the Assemblages in These Proposed Geographic Regions Different?
Intertidal and Shallow Subtidal Rocky Reef Communities
West Islands
North Mainland
Mid Islands
East Islands
South Mainland
Proposed Bioregion Groupings
Both shallow rocky reef (CRANE) and intertidal data show significant differences (ANOSIM P=0.01) when grouped according to Proposed Bioregion guidelines

Figure 8. Island-mainland differences in kelp forest fish assemblages in the Santa Barbara Channel. Dendrogram illustrates the relative similarities (20%) in relative abundance of reef fish species from sites sampled along the mainland on benthic (MB) and canopy (MC) and island benthic (IB) and canopy (IC) transects, respectively. From Ebeling et al. (1980).

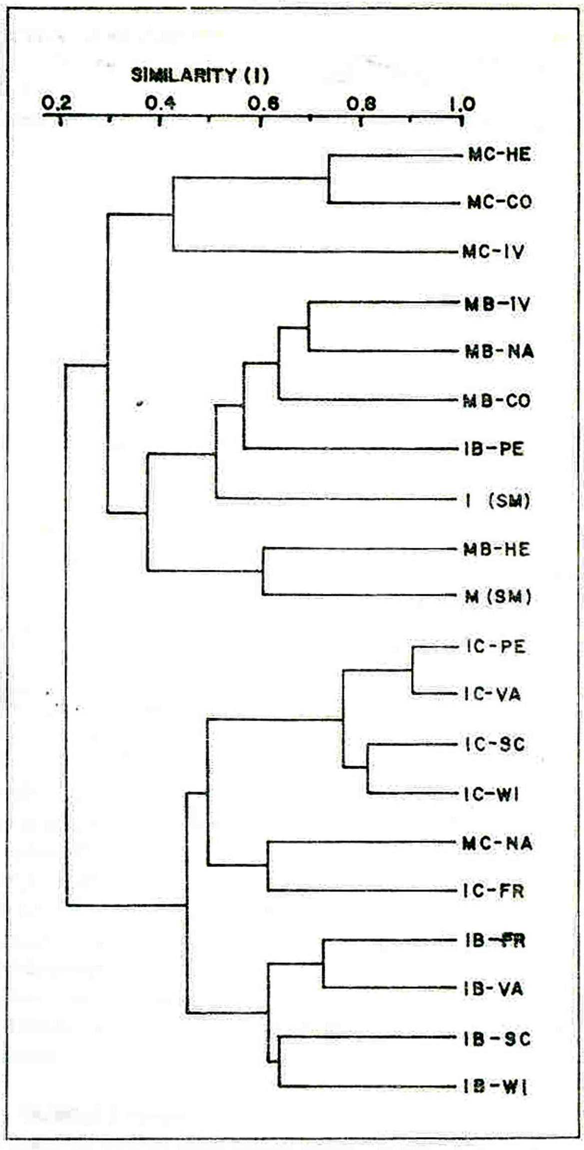


FIGURE 4. *Interlocality cluster analysis of kelp-bed fish assemblages sampled from 175 cinetransects filmed off Santa Barbara. Units are mainland (M) or Santa Cruz Island (I) canopy (C) or bottom (B) samples from the localities (right-hand letter pairs) in Figure 1 and Table 1. The dendrogram was derived from a similarity matrix based on relative species abundances (see text) by means of the unweighted pair-group clustering method using arithmetic averages (Sneath and Sokal 1973).*