

New tools for designing effective marine reserves

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Abstract

Marine reserves represent an emerging management tool, and are a challenge to the application of basic marine ecology to applied problems. Although some aspects of reserve science are extensively researched, new information on reserves is badly needed in at least two major areas 1) the impact that reserves have on the ecosystems in which they are imbedded, and 2) the way we can use complex ecological and environmental information to inform management decisions. We describe application of four new tools in oceanography and marine ecology, developed largely in other contexts, that are being recruited to help design marine reserves. Ocean sensing over short spatial and temporal scales charts the dynamics of ocean environments, allowing us to see physical connections between reserve and non-reserve areas. Indirect monitoring of species dispersal through chemical tags and genetic comparisons can allow us to map movements of populations from place to place and measure the spread of species. Computer-based mapping tools facilitate the flexible use of GIS data bases in management decisions, and allow multiple stakeholders to have access to powerful tools to explore management options. Together these basic tools in ecology help inform management because they describe ecosystem patterns over the spatial and temporal scales that are directly relevant to conservation and ecosystem management.

In a nutshell:

Marine reserves are imbedded in large ecosystems, but we don't know enough about how reserves affect areas outside their borders, requiring new tools to advance our understanding.

Remote sensing provides real time data about the ocean environment at scales as small as 1 km.

The chemical signal of trace metals in growing skeletons provides a tracking device for where larvae and juveniles drift in the sea.

Genetic differences among populations can reveal barriers to dispersal otherwise unseen, and are beginning to be used to measure the scale of dispersal inside and outside reserves.

Layers of ecosystem information, placed in a geographic context by GIS mapping, provide an accessible summary of this complex information that can be used by computer search engines to list alternative management solutions.

Introduction

Protecting marine habitats helps regulate the impact of humans on marine ecosystems, through regulation of fishing, dumping or other forms of coastal use (Peterson and Estes 2001). Although partial protection has been an important management tool, recently attention has shifted to implementing full habitat protection in at least a portion of all major marine ecosystems (Palumbi 2001, 2003, Lubchenco et al. 2003). Areas in which no extractive use is allowed are termed fully protected marine reserves, and a wide range of studies from around the world have shown the efficacy of such protection in augmenting populations of exploited species (reviewed in Halpern 2003, Palumbi 2001, 2003). No regional marine management plan can rely solely on marine reserves, of course, and traditional fisheries management and area-based protection of the physical environment are needed to address the myriad threats to marine ecosystems (Hilborn et al. 1995, Palumbi 2002). In this context, marine reserves provide addresses protection of marine ecosystems in ways that complement and extend other management approaches (Palumbi 2002; Lubchenco et al. 2003).

Over the past decade, a great deal of information has emerged from experimental and monitoring studies of reserve functioning (e.g., east Africa, the Caribbean, South Africa, New Zealand, and the Philippines: McClanahan and KaundaArara. 1996, McClanahan and Arthur 2001, Roberts 1995, Bennett and Attwood 1991, Babcock et al

1999, Alcala 1988). Tabulation of over fifty examples from the peer-reviewed literature shows consistent impact of reserves on marine communities within their boundaries (Halpern 2003; Palumbi 2001, 2003). However, these impacts are concentrated within reserve borders, and so an important question about reserves is whether they will have measurable effects beyond their boundaries.

Spillover of adults from reserves produces local fisheries benefits in a handful of well-studied cases (Roberts et al. 2001), but this benefit varies from species to species depending on growth and movement patterns (Attwood and Bennet 1994; McClanahan and Mangi 2000). In addition, benefits external to reserves may depend on local environment, patterns of exploitation outside the reserves, and reserve size and placement. As a result, a key unresolved ecological and management question is how reserves can be expected to affect the ecosystems in which they are imbedded.

Connection of reserves to the outside ecosystem is mediated by the ocean environment and the life histories of the species involved. For populations with sedentary adults and dispersing larvae, Roberts (1997) proposed that ocean currents are convenient proxies for the connections among different reserves, a suggestion that echoes decades of work on the impact of currents on marine dispersal (Hedgecock 1986; Hellberg et al. 2002; Andrefouet et al. 2002). Net export of eggs and larvae might be expected in some oceanographic circumstances, whereas net import might result in other circumstances. However, recent evidence suggests that patterns of ocean movement are not well

represented by average current speed and direction because ocean currents vary over small temporal and spatial scales. In addition, indirect measurements of marine dispersal do not always correspond to predictions based on simple current models (Barber et al. 2000). As a result, tools that allow rapid and accurate measurement of marine dispersal and ocean currents are needed.

An additional need is for tools to integrate information about connections among habitats with their physical and biological features. These compilations, along with information about the socio-economic impacts of marine resource exploitation, can facilitate policy decisions by diverse public stakeholder groups, as well as provide the basic map for ongoing management of areas after reserves are implemented. Without this type of summary, the welter of basic data from diverse sources is in danger of being lost.

In the past five years, new tools to understand marine populations at a regional scale have been forged, and these tools can play a fundamental role in advancing the science of marine ecology and the designation of marine reserves. These tools focus on better understanding of the oceanic environment, early life histories of fish and invertebrates with mobile egg or larval phases, and more transparent procedures for using geographic data in siting reserves. In this review, we highlight how advances in ocean monitoring, measurement of dispersal distances and patterns, and use of GIS-based computer mapping have accelerated our understanding of basic marine population biology in ways that have a direct role in marine reserve design. These tools have largely

been developed for reasons other than a focus in marine reserves, and have afforded major advances, so their recruitment into this field represents a valuable blending of basic environmental biology and applied ecology.

Monitoring the Pulse of the Oceans

Because dispersal distances set the scale for reserve spillover and for the ability of reserves to be self-seeding (Barber et al. 2000; Palumbi 2002; Gaines *et al.* 2003), measuring dispersal is receiving increased attention. The oceanographic setting greatly affects the directions larvae go and the distances they travel. The last decade has seen enormous improvement in our ability to measure ocean currents on spatial and temporal scales particularly relevant to ecosystem management. One expanding technology is remote sensing via satellites that measure characteristics of the ocean – e.g., its color, temperature, or surface elevation – and the overlying atmosphere – e.g., winds. Some of these observations map the physical forces that drive ocean circulation. For example, by watching how temperature shifts over time, current direction and speed can be inferred, generating a time-lapse view of ocean currents on scales of 100s to 1000s of km (e.g., Strub & James 1995, Strub *et al.* 1995). On a much smaller scale, new land based remote sensing, such as CODAR (Coastal Ocean Dynamics Application Radar), allow fine-scale measurement of surface currents within a few kilometers of shore.

This rich palette of new data document in detail never before possible that currents often change direction and speed dramatically from day to day. For example, the west coast of the USA is washed in the summer by the south-flowing California current; along much of this coastline, alongshore winds force surface water away from the coast (Fig. 1), pulling deeper, colder water toward the surface. This upwelling of nutrient-rich waters from the deep sea powers a bloom of ocean productivity near the coast. If the wind stops for a few days, or reverses direction, upwelling ceases, and water previously pushed offshore can rebound back to the coast. This brings different planktonic organisms, including larvae of many marine species, back to settle in shallow water habitats (Farrell et al. 1991). The emerging details of these circulation processes show that certain shore locations predictably receive more recruiting larvae and other plankton than others (Menge et al. 1997). Other current changes are seasonal. The California current can move offshore in winter, for example, and be replaced nearshore by a countercurrent running in the opposite direction. Longer-term changes are associated with cyclical climate changes, such as the El Niño Southern Oscillation and the Pacific Decadal Oscillation, and can dramatically change the patterns of connection between different coastal locations.

The reason for understanding these patterns is not because we hope to change them. Instead, we need to know what drives ocean circulation, so we can predict its impacts on coastal ecosystems and take these impacts into account when evaluating our

management practices. For example, James et al. (2002) used numerical models of ocean currents around individual reefs in the Great Barrier Reef to predict the retention of marine larvae near shore, and to estimate which reefs were likely to be overall sources of young and which are likely to be sinks. Similarly, recent studies combining moored instruments and remote sensing have led to dramatic advancements in our understanding of ocean circulation in the vicinity of Pt. Conception on the California coast (Winant 1996, Harms and Winant 1998). The emerging revelations about the details of circulation in this complex region played a critical role in evaluating the likely connectivity among sites for proposed networks of marine reserves in the Channel Islands National Marine Sanctuary (Fig 2).

The emerging details about circulation in this complex region played a critical role in evaluating the likely connectivity among sites for proposed networks of marine reserves in the Channel Islands National Marine Sanctuary (Fig. 2). Enhancements in our understanding of the complex flows among the islands of this sanctuary helped show which proposed reserve networks were unlikely to be connected by regular exchange of planktonic larvae.

Measuring dispersal: new hope and unconventional wisdom

Ocean current patterns are one proxy of the connectivity among reserves and between reserves and the regional ecosystems, but physical patterns do not always

perfectly predict biological connectivity (Barber et al 2002). Although it is impractical to require precise dispersal information from thousands of species prior to a management decision, it may be feasible to test predictions from oceanographic models with a suite of species that represent different dispersal traits. Although we know a great deal about the dispersal *potential* of marine species based on their larval biology (e.g. Shanks et al. 2003, Kinlan and Gaines 2003), we actually know very little about where in the oceans larvae go and how far they travel from their parents. Dispersal distances have been estimated for very few marine species.

For large animals, it is possible to directly measure migration across oceans with matchbook-size navigational computers, or even smaller acoustic tags (Block et al. 2001). Smaller scale movement of adults, such as tracking of reef fish within marine reserves, provides direct measures of the fraction of time individuals remain within the protective boundaries of a given reserve (e.g., Lowe *et al.* 1998, Meyer *et al.* 2000). However, smaller animals, especially the microscopic dispersing larvae of many species, cannot be burdened with such tags and other methods must be used.

Microchemistry and larval flight recorders

Luckily, fish and some invertebrates carry their own internal environmental recorders in the form of otoliths or statoliths, used by the animals for balance and orientation.

Growing like a tiny pearl, each of these small structures daily adds a thin layer of calcium

carbonate laced with trace metals pulled from the surrounding sea. Because the composition of trace metals in ocean water changes from place to place, trace-element content of a whole otolith has long been used for stock identification (Campana and Thorrold 2001). New technology allows us to record trace elements continuously within the otolith, suggesting this kind of "flight recorder" be used to retrace an individual's geographic history.

For species in which young fish move from fresh to salt water such as salmon (Zimmerman and Reeves 2000), shad (Gillanders 2002) and weakfish (Thorrold et al. 1998, 2001), analyses are relatively straightforward because the otoliths are large and the environmental differences between different streams or estuaries are great. For species that spend their entire lives in salt water, the challenge has been to show that chemical differences from place to place along the open coast are sufficiently strong to leave a readable signature in the otolith or statoliths. The most recent information indicates the proper equipment, usually laser ablation in conjunction with the mass spectrometer (Thorrold et al. 2002; Zacherl 2002), can indeed read and interpret the subtle chemical signals (Swearer et al. 2002). For a small larva, this can potentially give us a record of its origin, which is the key to establishing the patterns of connections between marine populations (Campana and Thorrold 2001).

The first attempt at using this approach showed that island populations of fishes recruit back to their native island. These results have been startling because they show

fish larvae travel less than we thought, sometimes settling near their parents even after a pelagic larval phase of several weeks (Swearer et al. 1999). Thus there may be more potential for marine reserves to seed themselves than we once thought. This may mean that local marine conservation efforts may yield local benefits - because reefs that are protected may produce offspring that help replenish that particular reef.

On the other hand, the impact of marine reserve production on surrounding areas depends on how far other larvae travel from their parents. Fortunately, many marine animals begin forming their otoliths or statoliths while still in the egg, before they begin their pelagic phase (Jones et al. 1999). Thus the core of the otolith or the statolith contains the natal signature. Can we distinguish a series of natal signatures along a coastline and assign newly-settled recruits to a birthplace? The prospects are encouraging. For example, Zacherl (2002) has shown good geographic separation in the microchemical signatures of pre-release larvae in egg capsules of the gastropod *Kelletia kelletii* taken from north and south of Point Conception, CA. Equally, larvae of the live-bearing rockfish *Sebastes atrovirens* show excellent between-site discrimination for places only a few kilometers apart (Fig. 3).

DNA and population neighborhoods

Even smaller tags exist inside every cell of every animal and plant and microbe-- the DNA they carry in some cases can be turned into a mapping device for discerning

dispersal. Recent advances in molecular genetics and population genetics theory provide a host of new tools to measure dispersal by examining the geography of genetic differences between populations of the same species. The first use of these tools was to examine gene flow over evolutionary time frames, which tended to show that species with high potential for dispersal tended to have very low population structure driven by rare long distance gene flow (Palumbi 1994, Palumbi et al. 1997), or patchy genetic structure possibly related to the fate of larval clouds (Hellberg et al. 2002). But higher resolution data sets allow gene flow to be examined over smaller spatial and temporal scales, and sometimes these higher resolution genetic results are at odds with the conventional wisdom derived from oceanography or larval biology (Awise 1994). For example, populations of mantis shrimp on reefs near reserves in Indonesia show dramatic genetic differences over a few 100 km, despite strong ocean currents and the potential of larvae of these species to drift 500-1000 km in a single generation (Barber et al. 2000, 2001). Similar patterns for Caribbean gobies (Taylor and Hellberg 2003) and coastal species in the SE United States (Awise 1994) show that there sometimes is very little movement of individuals among populations.

The challenge in this approach is that subtle genetic structure often occurs at about with same magnitude as noise from sampling variance (i.e. when the geographic signal is about 1% of the total genetic variation, Waples 1998). A second problem is that, over evolutionary time scales, it only takes a small amount of gene flow to drop genetic

structure to this level. Third, this level of gene flow typically represents movement of only a tiny fraction of a population, 1% or less. This means that a population that has high enough gene flow over evolutionary time to have little genetic structure may have rare immigrants from outside. So the quandary has been that the difference between subtle structure and no structure is slight, and that a population with little structure may be open to gene flow over evolutionary time scales but be effectively closed over ecological time scales (Waples 1998).

New tools try to address this problem by carefully measuring the build-up of genetic differences over space, and comparing these patterns to simulations of genetic differentiation in virtual populations that have explicitly defined dispersal parameters (Palumbi 2003). These Isolation-by-distance methods in principle can help define genetic neighborhoods (Wright 1978), which are the approximate ranges over which offspring disperse from their parents. For example, comparison of mtDNA sequences of populations of the barnacle *Balanus glandula* along the coast of Oregon suggest that larvae may sometimes travel only short distances before settling. Coastal populations of barnacles adjacent to Heceta Bank, which directs south-flowing currents offshore, have genetic compositions different than populations more distant from the Bank. These differences are slight, but they indicate that coastal populations bordering Heceta Bank are demographically separate from populations of the same species further away (Fig. 4, Erik Sotka and S. R. Palumbi, ms in prep.).

Larvae from other sedentary invertebrates and fish that spend a month or so in the water may drift less than 50 kilometers or so before settling (Palumbi 2003, Kinlan and Gaines 2003). Although these species are not necessarily targets of conservation, they serve as proxies that may point to dispersal barriers important to other species. In addition, they highlight the need to test the assumption that ocean currents will move marine larvae large distances.

The first results of this approach are surprising because conventional wisdom in marine biology is that species with high dispersal potential have high amounts of gene flow (e.g. Palumbi 1994). However, those generalizations are only true over the evolutionary time frames that the original analyses were designed to examine. Over short, ecological time frames, the two approaches are completely concordant. Isolation-by-distance methods have drawbacks and pitfalls (Hellberg et al. 2002), and require large data sets to be reliable. However, they offer hope that dispersal profiles of many marine species can be mapped.

GIS-based data archives: a Genbank for ecology

An additional challenge is to collate the kinds of information described above so it can be used for both basic ecological research and effective conservation and management. Geographic information systems (GIS) and similar spatial analysis tools are one approach that enables the synthesis of data on the biogeophysical as well as the

social and economic characteristics of a region for use in ecological research as well as management (Wright 2002). Projection of these data in a common visual framework facilitates both the social and scientific aspects of reserve design, and provides a area-based focus for integration of multiple data sets. In many ways, these advanced information systems have the potential to play the same role in ecology as Genbank does in molecular biology - a repository of information from diverse sources that can be put at the fingertips of many different users.

For example, in the Channel Islands National Marine Sanctuary (California, USA), the Marine Reserves Working Group (MRWG) – made up of managers, conservationists, commercial and recreational fishermen, divers, scientists, and other members of the community – divided the 4300 km² Sanctuary into hundreds of planning units and compiled a list of 119 species of special concern, along with seventeen different habitat and ecosystem types. The number of possible reserve locations was so large, and the complexity of environmental and economic constraints so complex that systematic consideration of all possible configurations was impractical. Instead, the group used a GIS to organize and integrate the relevant information, and then applied a computer-based siting tool called SITES to generate potential options for the reserve network (Airamé et al. 2003).

In practice, the computer started by using the geographic information to create a map of reserves placed randomly, and then improved it slightly, stage by stage, searching

progressively for maps that were closer to criteria input by the MRWG users. Previous applications of the siting tool demonstrated that the reserve configurations generated were almost always superior to those found by simpler algorithms (Possingham et al. 2000). The outputs were used as a starting point for discussions about where to implement individual reserves, and what trade-offs were inherent in the different possible network configurations.

To decide which biological and socioeconomic criteria should be used to select the reserves the MRWG drew on scientific information to suggest goals for the representation of species, habitat-types, and network size, and used SITES to explore the effects of altering these goals on potential network configurations (Airamé et al. 2003). Ultimately these deliberations were subject to political compromise, but that compromise was facilitated by the existence of many different options in reserve design. In November 2002, the California Fish and Game Commission approved the Channel Islands reserve network, which will encompass 25% of Sanctuary waters when it is fully implemented by both the state and federal authorities.

Other examples show the effectiveness of a siting tool plus GIS to facilitate reserve design (Florida Keys, Leslie et al. 2003; The Gulf of Mexico, Beck and Odaya 2001; British Columbia, Ardron et al. 2002). Overall, these approaches show that there more than one way to implement a network of marine reserves in a particular area. In this sense, the science of marine reserves does not demand a particular, narrow answer.

Instead, it can suggest a range of options that can then be evaluated for other criteria such as their economic, social, or political impact.

Using ecology to help manage marine ecosystems

None of these tools provide a precise road map for how to implement marine reserves. Rather, they have been co-opted from other disciplines to guide the complex process of understanding the biology, oceanography and geography of marine ecosystems, and place this information at the disposal of managers, local communities, scientists, and other management stakeholders. At the same time, these tools are not only useful in marine reserve design - they are fundamental to many area-based approaches to marine management. This generality stems from the fact that these tools seek answers to long-standing questions in marine ecology, questions that are important to standard fisheries research as well as to traditional management schemes.

Questions at the heart of marine ecology are in fact at the heart of applied to management of marine ecosystems. Ecology and other scientific disciplines can help through development of tools that allow scientific principles to be applied to marine management. Interest in implementing marine reserve shows how much basic ecological information (environmental data, life history features, dispersal patterns, etc.) can be fundamental to good management choices. However, interest in reserves also highlights how little we know about the way populations of many marine species are regulated at

the regional level, or how protecting small areas of ocean habitats will alter the larger areas between them. Combining emerging tools in marine ecology with the needs of reserve research will greatly help us promote the best use of living marine resources in a sustainable way.

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Figures and legends

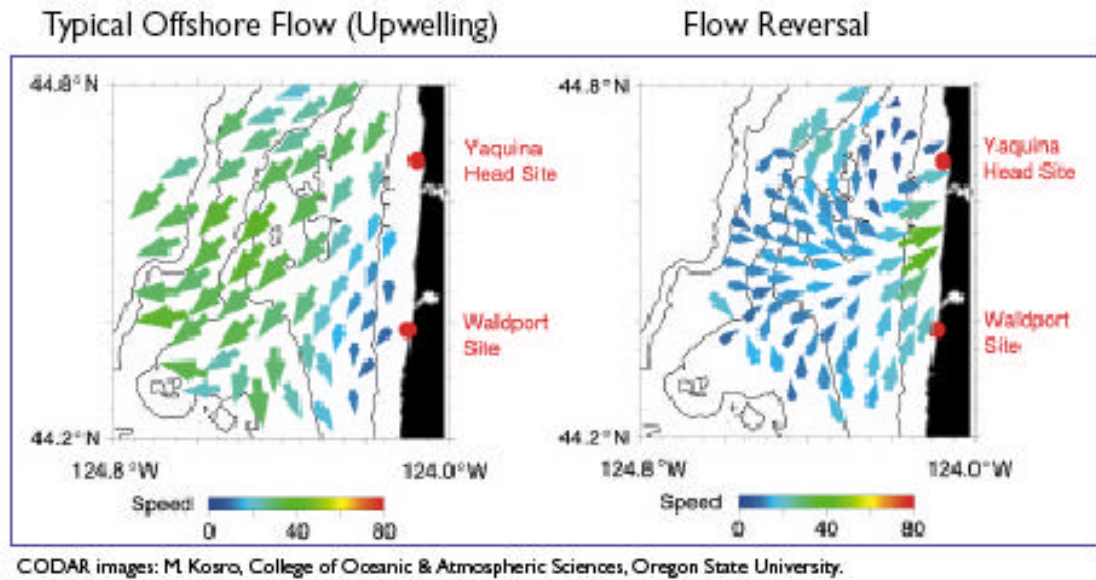


Figure 1 CODAR showing surface current patterns off the coast of Oregon during normal current conditions (upwelling pattern, left side) and during flow reversal conditions (left side). Both direction and speed are seriously affected by local winds, and can dramatically affect the dynamics of local larval settlement.

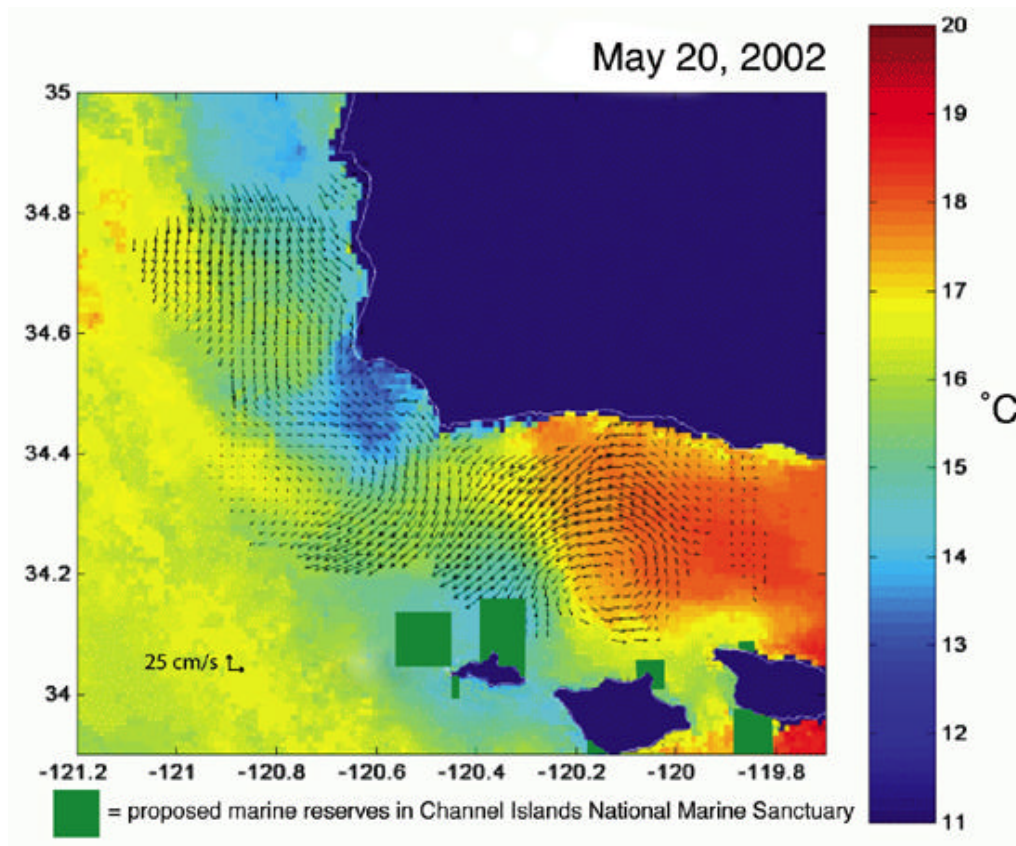


Figure 2 : Combined sea surface temperature and current trajectory map for May 20, 2002 from the Channel Islands National Marine Sanctuary. Currents and temperatures vary greatly throughout the sanctuary, generating a mosaic of environments. Some of the marine reserves are indicated, and are washed by a spectrum of different water masses.

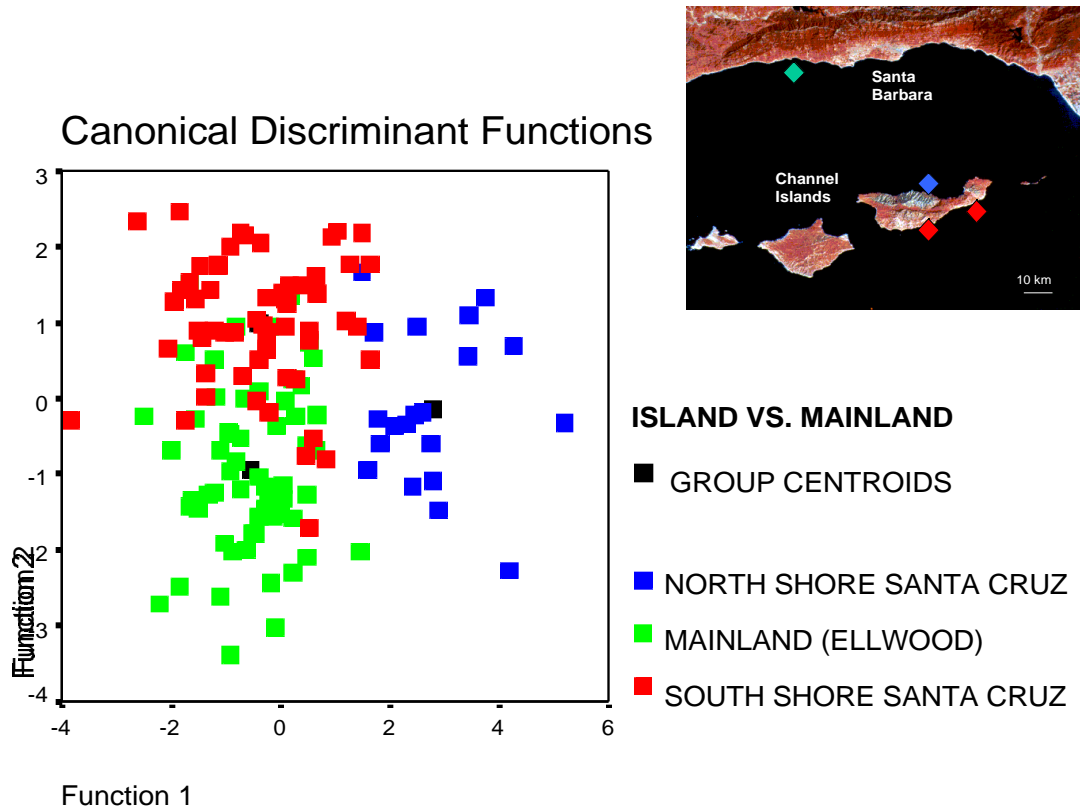


Figure 3. Otoliths taken from embryos of the kelp rockfish (*Sebastes atrovirens*) show different chemical signatures depending on where they originated. Colored dots on the map of the Channel Islands and mainland Southern California show locations where broods were collected from several female fish. Levels of Ba, Pb, Zn, Fe, and Sr relative to Ca are graphed together by discriminant function analysis, which decomposes the complex variation into a dot on a two-dimensional graph. Each dot on the graph represents one embryo from the brood.

Ocean currents near Heceta Bank

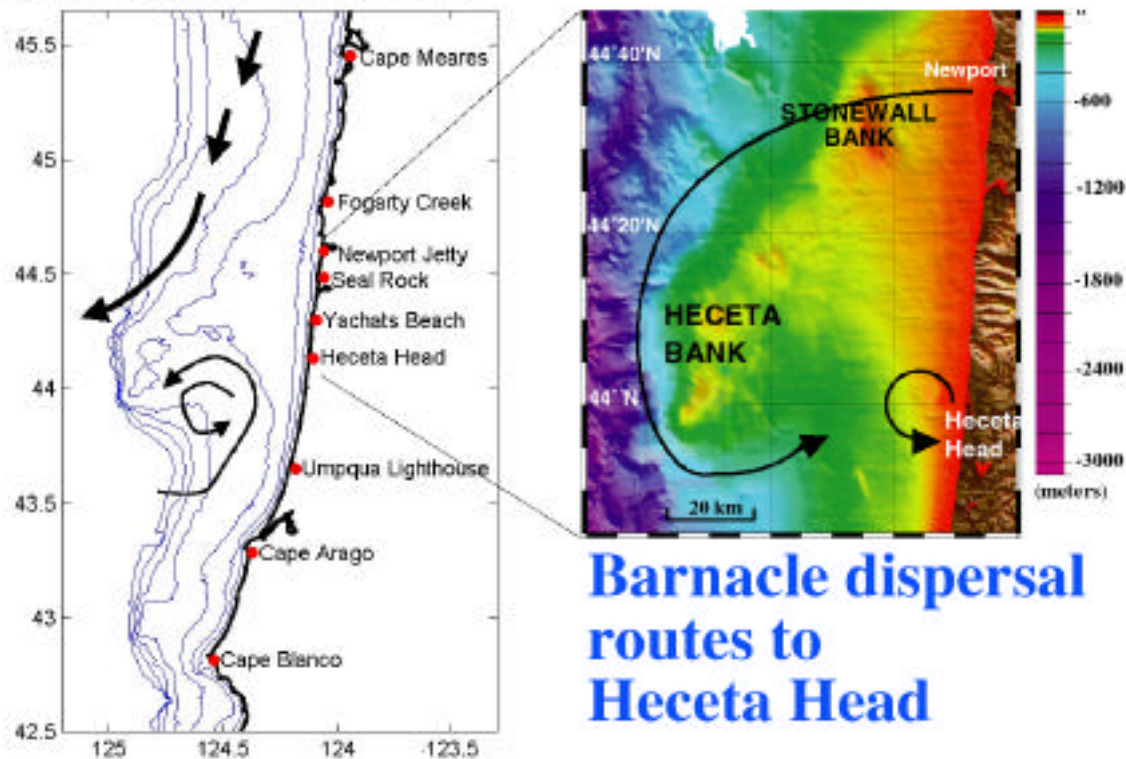


Figure 4 - Genetic indications of local larval retention in barnacle populations along the Oregon coast. Left) Heceta Bank directs longshore currents away from the coast in Central Oregon, and generates an eddy downstream. Right) Intertidal barnacles at Heceta Head show higher genetic similarity to one another than to barnacles from other populations (such as Newport), suggesting the larvae from Heceta Head populations are somewhat retained by the ocean eddy. Larvae from Newport would need to travel around Heceta Bank to reach Heceta Head and may have a lower chance of dispersal. These genetic patterns are subtle, and would be easily missed without high sample sizes and high-resolution genetic tools that assay many polymorphisms.