

New wave: high-tech tools to help marine reserve research

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Marine reserves are an emerging management tool, and can serve as examples of the practical application of basic marine ecology. Although some aspects of reserve science are well known, new information is badly needed in at least two major areas: the impact that reserves have on their surrounding ecosystems, and how we can use complex ecological and environmental data to inform management decisions. We describe the application of four new tools being used in oceanography and marine ecology to help design ocean reserves. Ocean sensing charts the dynamics of ocean environments, allowing us to see physical connections between protected and non-protected areas. The indirect monitoring of species dispersal through chemical tags and genetic comparisons can help us to map population movements and measure the spread of species. Computer-based mapping programs enable us to use GIS databases in management decisions, and give multiple stakeholders access to powerful decision-making tools. Together, these methods describe ecosystem patterns over spatial and temporal scales that are directly relevant to conservation and ecosystem management.

Front Ecol Environ 2003, 1(2), 73–79

Protecting marine habitats, through the regulation of fishing, dumping, and other forms of coastal use, helps regulate human impacts on these ecosystems (Figure 1) (Peterson and Estes 2001). Although partial protection has been an important management strategy, attention has recently shifted to full habitat protection in at least part of all the major oceanic ecosystems (Palumbi 2001, 2003; Lubchenco *et al.* 2003). Fully protected marine reserves, in which all extractive use is prohibited, have proven effective in increasing populations of exploited species according to a range of studies worldwide (Halpern 2003; Palumbi 2001, 2003). However, no regional management plan can rely solely on reserves, so traditional fisheries management and area-based protection of the physical environment are needed to address the many threats that marine organisms face (Hilborn *et al.* 1995; Palumbi 2002). In this context, reserves provide protection that complements and extends 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 in places such as East Africa, the Caribbean, South Africa, New Zealand, and the Philippines (Alcala 1988; Bennett and Attwood 1991; Roberts 1995; McClanahan and Kaunda-Arara 1996; Babcock *et al.* 1999; McClanahan and Arthur 2001). Over 50 examples consistently show a positive impact on the marine communities within their boundaries (Halpern 2003; Palumbi 2001, 2003). However, this leaves unanswered the question of whether these protected areas have measurable effects beyond their boundaries.

Some well-studied cases have shown that the spillover of adult organisms from reserves benefits local fisheries (Roberts *et al.* 2001), but this varies from species to species, depending on growth and movement patterns (Attwood and Bennet 1994; McClanahan and Mangi 2000). Furthermore, these external benefits may depend on the local environment, outside patterns of exploitation, and reserve size and placement. An important ecological and management question, as yet unresolved, is how the protected areas might be expected to affect the ecosystems in which they are embedded.

The connection between a reserve and its surrounding ecosystems is mediated by the ocean environment and the life histories of the species present. For populations with sedentary adults and dispersing larvae, Roberts (1997) proposed that ocean currents act as the agent connecting the different reserves, echoing decades of work on the impact of currents on marine dispersal (Hedgecock 1994; Andrefouet *et al.* 2002; Hellberg *et al.* 2002). Net export of eggs and larvae might be expected in some cases, while net import might occur in others. However, recent evidence suggests that ocean movement patterns are not well represented by average current speed and direction, because ocean currents vary over small temporal and spatial scales. In addition,

In a nutshell:

- Marine reserves are important conservation tools, but new information is needed to determine how they affect the ecosystems beyond their borders
- A number of tools, previously developed for other purposes, can be used to help make better management decisions
- These include remote sensing, chemical and genetic tracking, and computer-based mapping programs

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Figure 1. Hopkins Marine Life Refuge, California.

indirect measurements of dispersal do not always follow the predictions based on simple current models (Barber *et al.* 2000). We need tools that allow the rapid and accurate measurement of marine dispersal and ocean currents.

We also need instruments that will integrate information about the connections between habitats and their physical and biological features. This knowledge, together with information about the socioeconomic impacts of marine resource exploitation, will facilitate policy decisions by diverse stakeholder groups, and provide a basic map for the ongoing management of areas after reserves are created. Without this tool for summarizing data, the flood of information from diverse sources can sometimes seem overwhelming.

In the past 5 years, we have developed new tools to help us understand marine populations at a regional scale, and these can play a fundamental role in advancing the science of marine ecology and ocean reserves. They provide a better understanding of the oceanic environment and the early life histories of fish and invertebrates with mobile egg or larval phases, and lead to more transparent procedures for using geographic data to choose the best areas for reserves. In this review, we highlight how advances in ocean monitoring, the measurement of dispersal distances and patterns, and the use of GIS-based computer mapping have accelerated our understanding of basic marine population biology, and have directly affected reserve design. Although these tools have largely been developed for other purposes, they are proving to be highly valuable in combining basic environmental biology and applied ecology.

■ Monitoring the oceans

The ocean greatly affects where and how far larvae travel. Because dispersal distances set the scale for spillover and the ability of reserves to be self-seeding (Barber *et al.* 2000; Palumbi 2002; Gaines *et al.* 2003), measuring dispersal has received increased attention lately. There

has been an enormous improvement in our ability to measure ocean currents on spatial and temporal scales over the past 10 years, an improvement that is particularly relevant to ecosystem management. One expanding technology is remote sensing using satellites to measure characteristics of the ocean (including color, temperature, and surface elevation) and the overlying atmosphere (wind and other phenomena). These observations allow us to map the physical forces that drive ocean circulation. By watching how temperature shifts over time, for example, we can infer current direction and speed, and generate a time-lapse view of ocean currents on scales of hundreds to thousands of kilometers (Strub and James 1995; Strub *et al.*

1995). On a much smaller scale, new land-based remote sensing techniques, such as Coastal Ocean Dynamics Application Radar, allow the precise measurement of surface currents within a few kilometers of shore.

This rich array of new data shows, in detail never before possible, how currents often change direction and speed dramatically from day to day. For instance, in the summer, the west coast of the US is washed by the south-flowing California current. Along much of this coastline, along-shore winds force surface water away from the coast (Figure 2), pulling deeper, colder water towards the surface. This upwelling of deep, nutrient-rich water powers a productivity bloom near the coast. If the wind stops or reverses direction, even for a few days, upwelling ceases, and water pushed offshore returns to the coast. This brings different planktonic organisms, including larvae of many species, back to 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 plankton than others (Menge *et al.* 1997).

Some current changes are seasonal. The California current, for example, can move offshore in winter and be replaced by a countercurrent running near shore in the

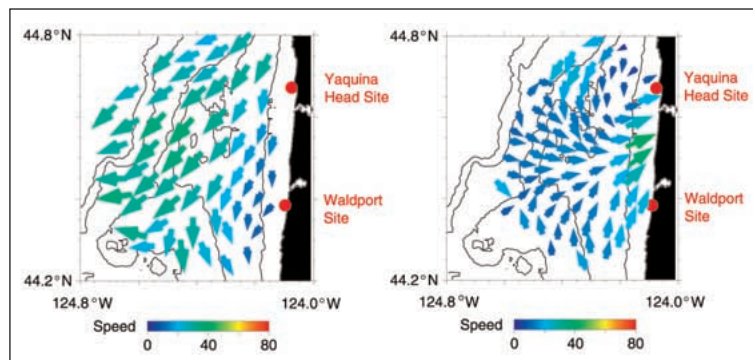


Figure 2. Coastal Ocean Dynamics Application Radar showing surface current patterns off the coast of Oregon during (a) normal current conditions and (b) flow reversal. Both direction and speed are greatly influenced by local winds, and can dramatically affect the dynamics of local larval settlement.

opposite direction. Longer-term alterations are associated with cyclical climate changes, such as the El Niño Southern Oscillation and the Pacific Decadal Oscillation, and these can dramatically change the patterns of connection between different coastal locations.

We need to know what drives ocean circulation, so we can predict its impacts on coastal ecosystems and take these effects into account when making management decisions. For example, James *et al.* (2002) used numerical models of ocean currents around individual reefs in the Great Barrier Reef to predict how many marine larvae stayed near shore, and to estimate which reefs were likely to be overall sources of young and which were 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 Point Conception on the California coast (Winant 1996; Harms and Winant 1998). Emerging details on ocean circulation in this complex region played a critical role in the evaluation of connectivity between sites being considered for a network of proposed marine reserves in the Channel Islands National Marine Sanctuary (Figure 3). A better understanding of the complex flows between the sanctuary islands helped show which networks were unlikely to be connected by the regular exchange of planktonic larvae.

■ Measuring dispersal

Physical patterns such as currents do not always perfectly predict biological connectivity (Barber *et al.* 2002). Although it is impractical to gather precise dispersal information for thousands of species for every 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 (Shanks *et al.* 2003), we actually know very little about where larvae go in the oceans 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 measure migration across oceans with matchbook-sized navigational computers, or even smaller acoustic tags (Block *et al.* 2001). Smaller-scale movement of adults, such as the tracking of reef fish within marine reserves, provides direct measurements of the amount of time individuals stay within the boundaries of a given reserve (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, calcareous inner-ear particles used for balance and orientation. Growing like tiny pearls, thin layers of calcium carbonate laced with trace metals pulled from the surrounding sea are added daily to these small structures. Because the composition of ocean water changes from place to place, the trace element content of a whole otolith has long been used to identify fish stocks (Campana and Thorrold 2001). New technology allows us to record trace elements continuously within the otolith, so this “flight recorder” could be used to retrace a fish’s path through the sea.

For species where 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), this analysis is relatively straightforward, because their otoliths are large and the environmental variations between different streams or estuaries are substantial. For species that spend their entire lives in salt water, however, the challenge is to show that chemical differences from place to place along the open coast are large enough to leave a readable signature in the inner ear. The most recent information indicates that the proper equipment – usually laser ablation in conjunction with a mass spectrometer (Thorrold *et al.* 2002; Zacherl 2002) – can read and interpret the subtle chemical signals (Swearer *et al.* 2002). This may give us a record of the origins of small larvae, which will be vital for establishing the patterns of connections

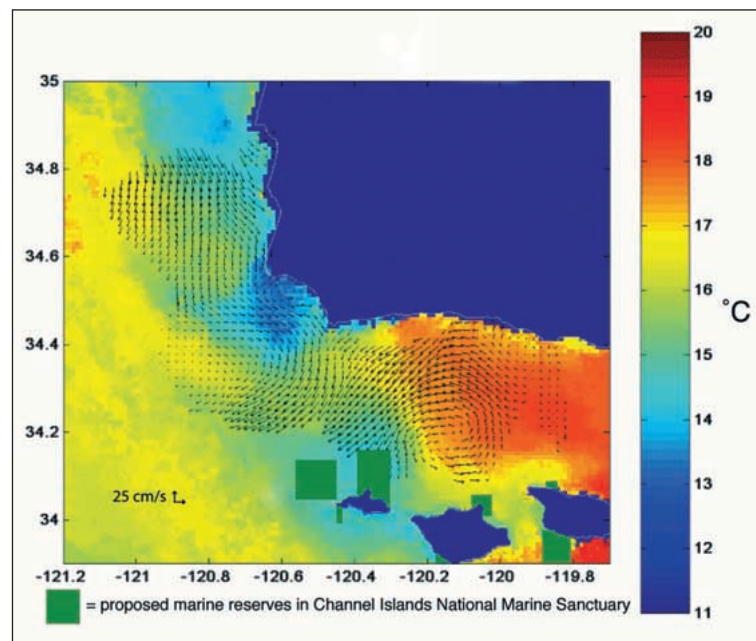


Figure 3. Map of sea surface temperature and current trajectory on May 20, 2002 in the Channel Islands National Marine Sanctuary, California. Currents and temperatures vary greatly throughout the sanctuary, resulting in a mosaic of environments. Some of the marine reserves are indicated, and are washed by many different water masses.

between marine populations (Campana and Thorrold 2001).

The first attempt at using this approach showed that the larvae of some reef fish stay close to their native island instead of drifting far away. These fish larvae do not travel as far as we thought, and sometimes settle near their parents, even after a pelagic larval phase of several weeks (Swearer *et al.* 1999). These results are surprising, because they indicate that there may be more potential for marine reserves to seed themselves than we suspected. Local conservation efforts may therefore yield local benefits, as a

protected reef can produce offspring to replenish its own resident populations.

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 while still in the egg, before they begin their pelagic phase (Jones *et al.* 1999), thereby leaving a natal signature at the core of these structures. Can we distinguish a series of such signatures along a coastline and determine the birthplace of newly settled recruits? 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 near Point Conception, California. Results from larvae of the live-bearing rockfish *Sebastes atrovirens* also show excellent between-site discrimination for areas only a few kilometers apart (Figure 4).

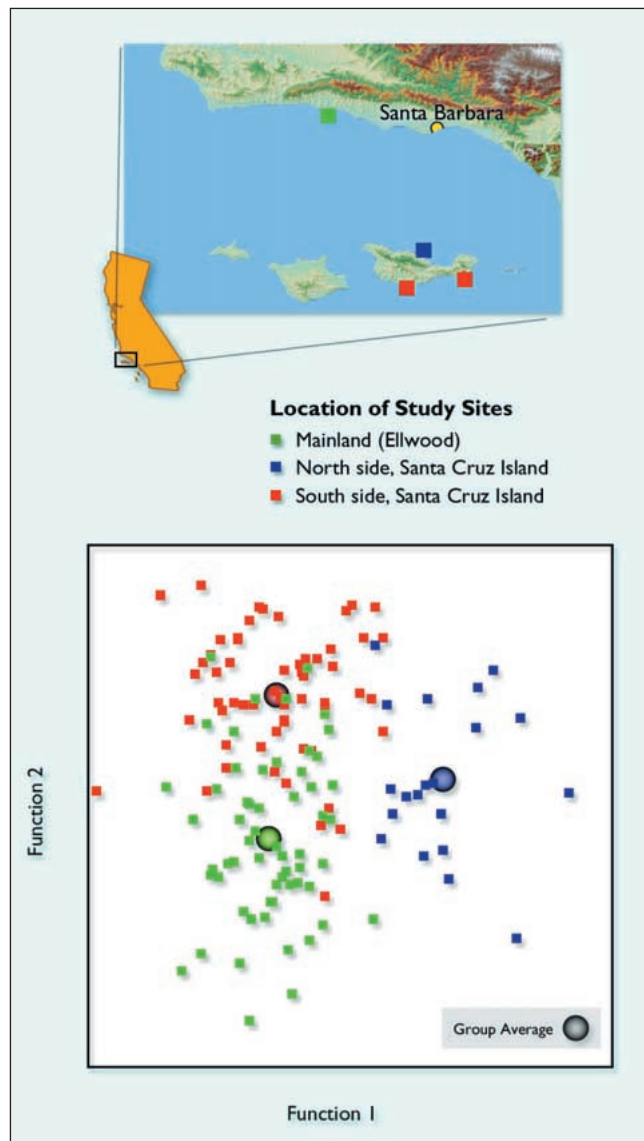


Figure 4. Otoliths taken from embryos of the kelp rockfish (*Sebastes atrovirens*) show different chemical signatures depending on where they originated. Colored dots on the map of the Channel Islands and mainland Southern California show locations where broods were collected from several female fish. Levels of Ba, Pb, Zn, Fe, and Sr relative to Ca are graphed together by discriminant function analysis, which decomposes the complex variations into a dot on a two-dimensional graph (each dot represents one embryo).

DNA and population neighborhoods

Even smaller tags exist inside the DNA of all living cells, which in some cases can be turned into a mapping device for determining dispersal. Recent advances in molecular genetics and population genetics theory provide a host of new tools to measure dispersal by examining the genetic differences between geographically separated populations of the same species. The first uses of these tools examined gene flow over evolutionary time frames, and showed that, in general, species with a high potential for dispersal tended to have only slight genetic variation from place to place (Hellberg *et al.* 2002).

However, higher resolution data sets allow us to examine gene flow over smaller spatial and temporal scales, and these higher resolution genetic results sometimes contradict 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 hundred kilometers, 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, 2002). Similarly strong genetic patterns for Caribbean gobies (Taylor and Hellberg 2003) and coastal species in the southeast US (Awise 1994) show that marine populations, even ones close together, are not always linked by high levels of migration.

The problem with this approach is that subtle differences in genetic structure often occur at about the same magnitude as noise from sampling variance, with the geographic signal being about 1% of the total genetic variation (Waples 1998). A second difficulty is that, over evolutionary time scales, it only takes a small amount of gene flow to decrease the amount of genetic structural variation to this level. Third, this amount of gene flow can be occurring even if most of a population does not migrate. Movement of less than 1% of a population – if it occurs

consistently for many generations – can reduce genetic structure to nearly undetectable levels. The quandry then is that a population in which 99% of the individuals do not migrate may have extremely low amounts of genetic structure. Such population is open to gene flow over evolutionary time, but effectively closed over the ecological time scales relevant to managers (Waples 1998).

New tools help address this problem by allowing us to carefully measure the buildup of genetic differences over distance, and compare these patterns to simulations of genetic differentiation in virtual populations that have explicitly defined dispersal parameters (Palumbi 2003). In principle, these isolation-by-distance methods can help define genetic neighborhoods (Wright 1978), which represent the approximate ranges over which offspring disperse from their parents. For example, comparisons of mtDNA sequences of populations of the barnacle *Balanus glandula* along the coast of Oregon suggest that the larvae may sometimes travel only short distances before settling. Coastal populations of barnacles adjacent to Heceta Bank, which directs south-flowing currents offshore, are genetically different from populations farther from the Bank. These differences are slight, but they indicate that the populations along Heceta Bank are demographically separate from populations further away (Sotka and Palumbi unpublished; Figure 5).

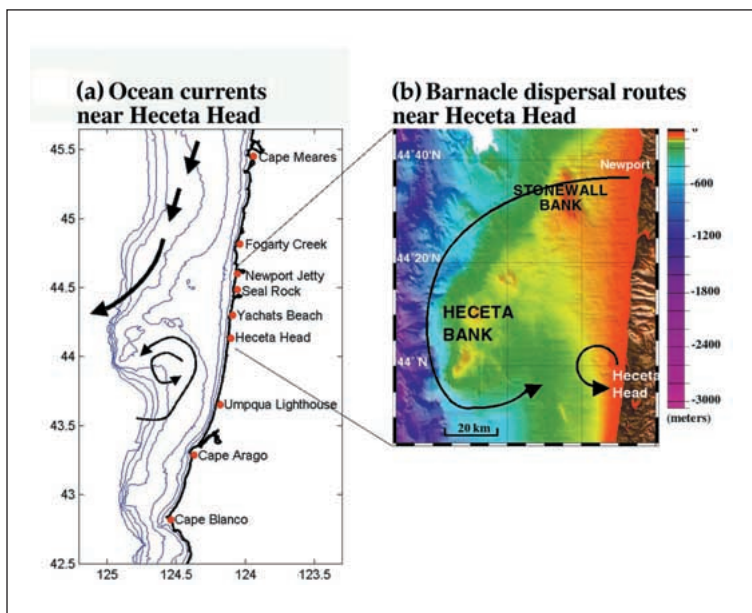


Figure 5. Genetic indications of local larval retention in barnacle populations along the Oregon coast. (a) Heceta Bank directs longshore currents away from the coast in Central Oregon, and generates an eddy downstream. (b) Intertidal barnacles at Heceta Head show greater genetic similarity to one another than to barnacles from other populations (such as Newport), suggesting that larvae from Heceta Head populations are 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.

Larvae from other sedentary invertebrates and fish, which spend about a month in the water, may drift less than 50 km before settling (Palumbi 2003). Although these species are not necessarily the targets of conservation efforts, they can serve as proxies, pointing to dispersal barriers that are important to other species. They also highlight the need to test the assumption that ocean currents move marine larvae over large distances.

The first results of this approach are surprising, because marine biologists generally believed that species with high dispersal potential underwent large amounts of gene flow (Palumbi 1994). However, it turns out that such 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 agree completely. Isolation-by-distance methods have drawbacks and pitfalls (Hellberg *et al.* 2002) and require large data sets to be reliable. They do, however, suggest that we will be able to map the dispersal profiles of many marine species.

■ GIS-based data archives

An additional challenge is to collate the kinds of information described above for use in both basic ecological research and effective conservation and management.

Geographic information systems (GIS) and similar spatial analysis tools are one approach to collecting data on the biogeophysical and socioeconomic characteristics of a region (Wright 2002). Projection of these data as part of a multilayered map facilitates reserve design, because it makes multiple data sets easily accessible to a broad array of stakeholders, and provides a focus for the discussion of alternative reserve configurations. In many ways, these advanced information systems could play the same role in ecology that Genbank does in molecular biology – that of a repository of information from diverse sources that can be put at the fingertips of many different users.

In the Channel Islands National Marine Sanctuary, for example, the Marine Reserves Working Group (MRWG), which is made up of managers, conservationists, commercial and recreational fishermen, divers, scientists, and other community members, divided the 4300-km² sanctuary into hundreds of planning units. They also compiled a list of 119 species of special concern, along with 17 different habitat and ecosystem types. The number of possible reserve locations was so large, and the complexity of environmental and economic constraints so great, that it was impractical to consider all the possible configurations systematically. Instead, the group used GIS data 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 (Airame *et al.* 2003).

The computer used the geographic information to create a network of randomly placed reserves and then improved it slightly, stage by stage, searching progressively for layouts that were closer to the criteria specified by the MRWG. Previous applications of the siting tool showed that the reserve configurations were almost always preferable 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 would be necessary in different potential network configurations.

To decide which biological and socioeconomic criteria should be used to choose 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 examine the effects of changing these goals on potential network configurations (Airame *et al.* 2003). These deliberations were ultimately subject to political compromises, but were facilitated by the existence of many different options in designing the reserves. In November 2002, the California Fish and Game Commission approved the Channel Islands reserve network, which will encompass a quarter of the sanctuary waters when it is fully implemented by state and federal authorities.

Other examples show the effectiveness of combining siting tools and GIS data in designing marine reserves, including those in the Florida Keys (Leslie *et al.* 2003), the Gulf of Mexico (Beck and Odaya 2001), and along the coast of British Columbia (Ardron *et al.* 2002). These approaches make it clear that there is more than one way to implement marine reserve networks in a particular area. The process does not demand a particular, narrow answer; instead, it suggests a range of options which can then be evaluated for their economic, social, and political impact.

■ Using ecology to manage marine ecosystems

None of these new tools provide a precise road map. They have been co-opted from other disciplines to guide the complex process of understanding the biology, oceanography, and geography of marine ecosystems, and to make this information available to managers, local communities, scientists, and other management stakeholders. They are not only useful in designing marine reserves, but are fundamental to many area-based management approaches. They seek answers to long-standing questions in marine ecology, questions that are important to standard fisheries research as well as to traditional management schemes.

Ecology and other scientific disciplines can develop methodologies that allow scientific principles to be applied to marine management. Interest in implementing

marine reserves shows how much basic ecological information (environmental data, life history features, dispersal patterns, etc) can be fundamental to good management choices. However, it also highlights how little we know about the way many oceanic species are regulated at the regional level, or how protecting small areas of ocean habitats will affect the regions between them. Combining emerging ecological tools with the needs of reserve research will help us promote the best, most sustainable use of living marine resources.

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