

### In this review:

- A. Recent articles – no abstract available
- B. Recent articles with abstracts

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## A. Recent articles – no abstract available

Moore, B.S. **Biosynthesis of marine natural products: macroorganisms (Part B).** *Natural Product Reports* 23(4): 615-629, 2006.

Gaston, K.J. and Fuller, R.A. **Biodiversity and extinction: losing the common and the widespread.** *Progress in Physical Geography* 31(2): 213-225, 2007.

Bohannon, J. **Ocean study yields a tidal wave of microbial DNA.** *Science* 315(5818): 1486-1487, 2007.

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## B. Recent articles with abstracts

Zapata, F.A. and Robertson, D.R. **How many species of shore fishes are there in the Tropical Eastern Pacific?** *Journal of Biogeography* 34(1): 38-51, 2007.

**Notes:** *Aim* To assess whether the total richness of the shore-fish fauna of a discrete biogeographical region can be predicted, and to estimate how long it is likely to take to enumerate that fauna. *Location* The Tropical Eastern Pacific (TEP), an isolated biogeographical region with a high level of endemism (72%) among its modestly rich, known fauna of shore fishes (1222 named + 58 known undescribed shallow-water species). *Methods* We used patterns in the long-term dynamics and accumulation curves of descriptions of new species, which began in 1758, correlates of these patterns, and the body size-frequency distributions of various ecological groups of the fauna to (1) try to predict the total richness of that fauna, (2) estimate how many species might be missing and what biological characteristics they might have, and (3) estimate how long their discovery and description will take to complete. *Results* Accumulation curves for the entire fauna, for all TEP endemics or for reef and soft-bottom species (77.5% of the fauna) are not approaching asymptotes, and their description rates have remained fairly stable over the past century. However, curves for pelagic and multi-habitat species (22.5% of the fauna) may be nearing asymptotes, perhaps because these species are relatively accessible to collection. These curves clearly indicate that the total TEP fauna is substantially richer than the presently known fauna, but do not allow reliable prediction of its richness. Extrapolations from frequency distributions of the body size of different ecological groups of TEP fishes indicate that the entire fauna is at least 12-15% larger than the currently known fauna. *Main conclusions* From recent description trends, undiscovered species will tend to be small, have limited geographic and depth ranges, and live in deeper water. Poorly known, priority areas for taxonomic investigation in the TEP include deeper reef habitats, two isolated island groups, and several continental areas with unusual environments. At current levels of traditional taxonomic activity, the description of known unnamed species will take c.15 years, and assessment of the richness of unknown species, which probably number in the hundreds, will take decades.

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Willi, Y., Van Buskirk, J., and Hoffmann, A.A. **Limits to the adaptive potential of small populations.** *Annual Review of Ecology, Evolution, and Systematics* 37: 433-458, 2006.

**Notes:** Small populations are predicted to have reduced capacity to adapt to environmental change for two reasons. First, population genetic models indicate that genetic variation and potential response to selection should be positively correlated with population size. The empirical support for this prediction is mixed: DNA markers usually reveal low heterozygosity in small populations, whereas quantitative traits show reduced heritability only in the smallest and most inbred populations. Quantitative variation can even increase in bottlenecked populations although this effect seems unlikely to increase the adaptive potential of populations. Second, individuals in small populations have lower fitness owing to environmental stress and genetic problems such as inbreeding, which can substantially increase the extinction probability of populations in changing environments. This second reason has not been included in assessments of critical population size assuring evolvability and makes it likely that many small threatened populations have a decreased potential for adaptation.

Seitzinger, S., Harrison, J.A., Bohlke, J.K., Bouwman, A.F., Lowrance, R., Peterson, B., Tobias, C., and Van Drecht, G. **Denitrification across landscapes and waterscapes: A synthesis.** *Ecological Applications* 16(6): 2064-2090, 2006.

**Notes:** Denitrification is a critical process regulating the removal of bioavailable nitrogen (N) from natural and human-altered systems. While it has been extensively studied in terrestrial, freshwater, and marine systems, there has been limited communication among denitrification scientists working in these individual systems. Here, we compare rates of denitrification and controlling factors across a range of ecosystem types. We suggest that terrestrial, freshwater, and marine systems in which denitrification occurs can be organized along a continuum ranging from (1) those in which nitrification and denitrification are tightly coupled in space and time to (2) those in which nitrate production and denitrification are relatively decoupled. In aquatic ecosystems, N inputs influence denitrification rates whereas hydrology and geomorphology influence the proportion of N inputs that are denitrified. Relationships between denitrification and water residence time and N load are remarkably similar across lakes, river reaches, estuaries, and continental shelves. Spatially distributed global models of denitrification suggest that continental shelf sediments account for the largest portion (44%) of total global denitrification, followed by terrestrial soils (22%) and oceanic oxygen minimum zones (OMZs; 14%). Freshwater systems (groundwater, lakes, rivers) account for about 20% and estuaries 1% of total global denitrification. Denitrification of land-based N sources is distributed somewhat differently. Within watersheds, the amount of land-based N denitrified is generally highest in terrestrial soils, with progressively smaller amounts denitrified in groundwater, rivers, lakes and reservoirs, and estuaries. A number of regional exceptions to this general trend of decreasing denitrification in a downstream direction exist, including significant denitrification in continental shelves of N from terrestrial sources. Though terrestrial soils and groundwater are responsible for much denitrification at the watershed scale, per-area denitrification rates in soils and groundwater (kg N.km<sup>-2</sup>.yr<sup>-1</sup>) are, on average, approximately one-tenth the per-area rates of denitrification in lakes, rivers, estuaries, continental shelves, or OMZs. A number of potential approaches to increase denitrification on the landscape, and thus decrease N export to sensitive coastal systems exist. However, these have not generally been widely tested for their effectiveness at scales required to significantly reduce N export at the whole watershed scale.

Nussey, D.H., Wilson, A.J., and Brommer, J.E. **The evolutionary ecology of individual phenotypic plasticity in wild populations.** *Journal of Evolutionary Biology* 20(3): 831-844, 2007.

**Notes:** The ability of individual organisms to alter morphological and life-history traits in response to the conditions they experience is an example of phenotypic plasticity which is fundamental to any population's ability to deal with short-term environmental change. We currently know little about the prevalence, and evolutionary and ecological causes and consequences of variation in life history plasticity in the wild. Here we outline an analytical framework, utilizing the reaction norm concept and random regression statistical models, to assess the between-individual variation in life history plasticity that may underlie population level responses to the environment at both phenotypic and genetic levels. We discuss applications of this framework to date in wild vertebrate populations, and illustrate how natural selection and ecological constraint may alter a population's response to the environment through their effects at the individual level. Finally, we present future directions and challenges for research into individual plasticity.

Rusch, D.B. et al. **The Sorcerer II Global Ocean Sampling expedition: Northwest Atlantic through Eastern Tropical Pacific.** *PLoS Biology* 5(3): 398-431, 2007.

**Notes:** The world's oceans contain a complex mixture of micro-organisms that are for the most part, uncharacterized both genetically and biochemically. We report here a metagenomic study of the marine planktonic microbiota in which surface (mostly marine) water samples were analyzed as part of the Sorcerer II Global Ocean Sampling expedition. These samples, collected across a several-thousand km transect from the North Atlantic through the Panama Canal and ending in the South Pacific yielded an extensive dataset consisting of 7.7 million sequencing reads (6.3 billion bp). Though a few major microbial clades dominate the planktonic marine niche, the dataset contains great diversity with 85% of the assembled sequence and 57% of the unassembled data being unique at a 98% sequence identity cutoff. Using the metadata associated with each sample and sequencing library, we developed new comparative genomic and assembly methods. One comparative genomic method, termed "fragment recruitment," addressed questions of genome structure, evolution, and taxonomic or phylogenetic diversity, as well as the biochemical diversity of genes and gene families. A second method, termed "extreme assembly," made possible the assembly and reconstruction of large segments of abundant but clearly nonclonal organisms. Within all abundant populations analyzed, we found extensive intra-ribotype diversity in several forms: (1) extensive sequence variation within orthologous regions throughout a given genome; despite coverage of individual ribotypes approaching 500-fold, most individual sequencing reads are unique; (2) numerous changes in gene content some with direct adaptive implications; and (3) hypervariable genomic islands that are too variable to assemble. The intra-ribotype diversity is organized into genetically isolated populations that have overlapping but independent distributions, implying distinct environmental preference. We present novel methods for measuring the genomic similarity between metagenomic samples and show how they may be grouped into several community types. Specific functional adaptations can be identified both within individual ribotypes and across the entire community, including proteorhodopsin spectral tuning and the presence or absence of the phosphate-binding gene PstS.

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Gontang, E.A., Fenical, W., and Jensen, P.R. **Phylogenetic diversity of gram-positive bacteria cultured from marine sediments.** *Applied and Environmental Microbiology* 73(10): 3272-3282, 2007.

**Notes:** Major advances in our understanding of marine bacterial diversity have been gained through studies of bacterioplankton, the vast majority of which appear to be gram negative. Less effort has been devoted to studies of bacteria inhabiting marine sediments, yet there is evidence to suggest that gram-positive bacteria comprise a relatively large proportion of these communities. To further expand our understanding of the aerobic gram-positive bacteria present in tropical marine sediments, a culture-dependent approach was applied to sediments collected in the Republic of Palau from the intertidal zone to depths of 500 m. This investigation resulted in the isolation of 1,624 diverse gram-positive bacteria spanning 22 families, including many that appear to represent new taxa. Phylogenetic analysis of 189 representative isolates, based on 16S rRNA gene sequence data, indicated that 124 (65.6%) belonged to the class Actinobacteria while the remaining 65 (34.4%) were members of the class Bacilli. Using a sequence identity value of  $\pm$  98%, the 189 isolates grouped into 78 operational taxonomic units, of which 29 (37.2%) are likely to represent new taxa. The high degree of phylogenetic novelty observed during this study highlights the fact that a great deal remains to be learned about the diversity of gram-positive bacteria in marine sediments.

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Duffy, J.E., Cardinale, B.J., France, K.E., McIntyre, P.B., Thébault, E., and Loreau, M. **The functional role of biodiversity in ecosystems: incorporating trophic complexity.** *Ecology Letters* 10(6): 522-538, 2007.

**Notes:** Understanding how biodiversity affects functioning of ecosystems requires integrating diversity within trophic levels (horizontal diversity) and across trophic levels (vertical diversity, including food chain length and omnivory). We review theoretical and experimental progress toward this goal. Generally, experiments show that biomass and resource use increase similarly with horizontal diversity of either producers or consumers. Among prey, higher diversity often increases resistance to predation, due to increased probability of including inedible species and reduced efficiency of specialist predators confronted with diverse prey. Among predators, changing diversity can cascade to affect plant biomass, but the strength and sign of this effect depend on the degree of omnivory and prey behaviour. Horizontal and vertical diversity also interact: adding a trophic level can qualitatively change diversity effects at adjacent levels. Multitrophic interactions produce a richer variety of diversity-functioning relationships than the monotonic changes predicted for single trophic levels. This complexity depends on the degree of consumer dietary generalism, trade-offs between competitive ability and resistance to predation,

intraguild predation and openness to migration. Although complementarity and selection effects occur in both animals and plants, few studies have conclusively documented the mechanisms mediating diversity effects. Understanding how biodiversity affects functioning of complex ecosystems will benefit from integrating theory and experiments with simulations and network-based approaches.

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Ives, A.R. and Carpenter, S.R. **Stability and diversity of ecosystems.** *Science* 317(5834): 58-62, 2007.

**Notes:** Understanding the relationship between diversity and stability requires a knowledge of how species interact with each other and how each is affected by the environment. The relationship is also complex, because the concept of stability is multifaceted; different types of stability describing different properties of ecosystems lead to multiple diversity-stability relationships. A growing number of empirical studies demonstrate positive diversity-stability relationships. These studies, however, have emphasized only a few types of stability, and they rarely uncover the mechanisms responsible for stability. Because anthropogenic changes often affect stability and diversity simultaneously, diversity-stability relationships cannot be understood outside the context of the environmental drivers affecting both. This shifts attention away from diversity-stability relationships toward the multiple factors, including diversity, that dictate the stability of ecosystems.

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Deutsch, C., Sarmiento, J.L., Sigman, D.M., Gruber, N., and Dunne, J.P. **Spatial coupling of nitrogen inputs and losses in the ocean.** *Nature* 445(7124): 163-167, 2007.

**Notes:** Nitrogen fixation is crucial for maintaining biological productivity in the oceans, because it replaces the biologically available nitrogen that is lost through denitrification. But, owing to its temporal and spatial variability, the global distribution of marine nitrogen fixation is difficult to determine from direct shipboard measurements. This uncertainty limits our understanding of the factors that influence nitrogen fixation, which may include iron, nitrogen-to-phosphorus ratios, and physical conditions such as temperature. Here we determine nitrogen fixation rates in the world's oceans through their impact on nitrate and phosphate concentrations in surface waters, using an ocean circulation model. Our results indicate that nitrogen fixation rates are highest in the Pacific Ocean, where water column denitrification rates are high but the rate of atmospheric iron deposition is low. We conclude that oceanic nitrogen fixation is closely tied to the generation of nitrogen-deficient waters in denitrification zones, supporting the view that nitrogen fixation stabilizes the oceanic inventory of fixed nitrogen over time.

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Brandt, A., Gooday, A.J., Brandao, S.N., Brix, S., Brokeland, W., Cedhagen, T., Choudhury, M., Cornelius, N., Danis, B., De Mesel, I., Diaz, R.J., Gillan, D.C., Ebbe, B., Howe, J.A., Janussen, D., Kaiser, S., Linse, K., Malyutina, M., Pawlowski, J., Raupach, M., and Vanreusel, A. **First insights into the biodiversity and biogeography of the Southern Ocean deep sea.** *Nature* 447(7142): 307-311, 2007.

**Notes:** Shallow marine benthic communities around Antarctica show high levels of endemism, gigantism, slow growth, longevity and late maturity, as well as adaptive radiations that have generated considerable biodiversity in some taxa. The deeper parts of the Southern Ocean exhibit some unique environmental features, including a very deep continental shelf and a weakly stratified water column, and are the source for much of the deep water in the world ocean. These features suggest that deep-sea faunas around the Antarctic may be related both to adjacent shelf communities and to those in other oceans. Unlike shallow-water Antarctic benthic communities, however, little is known about life in this vast deep-sea region. Here, we report new data from recent sampling expeditions in the deep Weddell Sea and adjacent areas (748 - 6,348 m water depth) that reveal high levels of new biodiversity; for example, 674 isopods species, of which 585 were new to science. Bathymetric and biogeographic trends varied between taxa. In groups such as the isopods and polychaetes, slope assemblages included species that have invaded from the shelf. In other taxa, the shelf and slope assemblages were more distinct. Abyssal faunas tended to have stronger links to other oceans, particularly the Atlantic, but mainly in taxa with good dispersal capabilities, such as the Foraminifera. The isopods, ostracods and nematodes, which are poor dispersers, include many species currently known only from the Southern Ocean. Our findings challenge suggestions that deep-sea diversity is depressed in the Southern Ocean and provide a basis for exploring the evolutionary significance of the varied biogeographic patterns observed in this remote environment.

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Edmands, S. **Between a rock and a hard place: evaluating the relative risks of inbreeding and outbreeding for conservation and management.** *Molecular Ecology* 16(3): 463-475, 2007.

**Notes:** As populations become increasingly fragmented, managers are often faced with the dilemma that intentional hybridization might save a population from inbreeding depression but it might also induce outbreeding depression. While empirical evidence for inbreeding depression is vastly greater than that for outbreeding depression, the available data suggest that risks of outbreeding, particularly in the second generation, are on par with the risks of inbreeding. Predicting the relative risks in any particular situation is complicated by variation among taxa, characters being measured, level of divergence between hybridizing populations, mating history, environmental conditions and the potential for inbreeding and outbreeding effects to be occurring simultaneously. Further work on consequences of interpopulation hybridization is sorely needed with particular emphasis on the taxonomic scope, the duration of fitness problems and the joint effects of inbreeding and outbreeding. Meanwhile, managers can minimize the risks of both inbreeding and outbreeding by using intentional hybridization only for populations clearly suffering from inbreeding depression, maximizing the genetic and adaptive similarity between populations, and testing the effects of hybridization for at least two generations whenever possible.

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Pommier, T., Canback, B., Riemann, L., Bostrom, K.H., Simu, K., Lundberg, P., Tunlid, A., and Hagstrom, A. **Global patterns of diversity and community structure in marine bacterioplankton.** *Molecular Ecology* 16(4): 867-880, 2007.

**Notes:** Because of their small size, great abundance and easy dispersal, it is often assumed that marine planktonic microorganisms have a ubiquitous distribution that prevents any structured assembly into local communities. To challenge this view, marine bacterioplankton communities from coastal waters at nine locations distributed world-wide were examined through the use of comprehensive clone libraries of 16S ribosomal RNA genes, used as operational taxonomic units (OTU). Our survey and analyses show that there were marked differences in the composition and richness of OTUs between locations. Remarkably, the global marine bacterioplankton community showed a high degree of endemism, and conversely included few cosmopolitan OTUs. Our data were consistent with a latitudinal gradient of OTU richness. We observed a positive relationship between the relative OTU abundances and their range of occupation, i.e. cosmopolitans had the largest population sizes. Although OTU richness differed among locations, the distributions of the major taxonomic groups represented in the communities were analogous, and all local communities were similarly structured and dominated by a few OTUs showing variable taxonomic affiliations. The observed patterns of OTU richness indicate that similar evolutionary and ecological processes structured the communities. We conclude that marine bacterioplankton share many of the biogeographical and macroecological features of macroscopic organisms. The general processes behind those patterns are likely to be comparable across taxa and major global biomes.

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Selkoe, K.A., Gaines, S.D., Caselle, J.E., and Warner, R.R. **Current shifts and kin aggregation explain genetic patchiness in fish recruits.** *Ecology* 87(12): 3082-3094, 2006.

**Notes:** The scales of population structure in marine species depend on the degree to which larvae from different populations are mixed in the plankton. There is an intriguing trend in marine population genetic studies of significant genetic structure for larvae, recruits, or populations at fine scales that is unpatterned across space and changes through time. This "chaotic genetic patchiness" suggests that larval pools are not well mixed in the plankton. However, few studies have been able to distinguish among potential causes of spatial and temporal genetic heterogeneity: changes in larval migration patterns, changes in environmental selection, or stochasticity caused by "sweepstakes" reproductive success of spawners creating detectable family structure. Here we use microsatellite markers to show that significant allele frequency shifts occurred sporadically in space and time for cohorts of recruits of *Paralabrax clathratus* (kelp bass) collected once every two weeks over two years from five sites in the Santa Barbara Channel, California, USA. We found that the pattern of genetic differentiation among cohorts was explained by a combination of (1) family structure in some cohorts, evidenced by half and full siblings, and (2) an indication of changes in larval delivery. It is unlikely but possible that environmental selection also plays a role. Although sampling of potential source populations was incomplete, cohorts arriving during western current flows show most genetic similarity with a population sample collected in the west, and cohorts arriving during current flows from the southeast show similarity with population samples collected in the south and east. Despite the family structure apparent in some cohorts, these "sweepstakes" events occur on too fine a scale to create lasting year class genetic structure. The results

corroborate oceanographic models of larval dispersal, which suggest that larval mixing in the plankton is less extensive than previously believed.

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Burkepile, D.E. and Hay, M.E. **Herbivore vs. nutrient control of marine primary producers: Context-dependent effects.** *Ecology* 87(12): 3128-3139, 2006.

**Notes:** Pervasive overharvesting of consumers and anthropogenic nutrient loading are changing the strengths of top-down and bottom-up forces in ecosystems worldwide. Thus, identifying the relative and synergistic roles of these forces and how they differ across habitats, ecosystems, or primary-producer types is increasingly important for understanding how communities are structured. We used factorial meta-analysis of 54 field experiments that orthogonally manipulated herbivore pressure and nutrient loading to quantify consumer and nutrient effects on primary producers in benthic marine habitats. Across all experiments and producer types, herbivory and nutrient enrichment both significantly affected primary-producer abundance. They also interacted to create greater nutrient enrichment effects in the absence of herbivores, suggesting that loss of herbivores produces more dramatic effects of nutrient loading. Herbivores consistently had stronger effects than did nutrient enrichment for both tropical macroalgae and seagrasses. The strong effects of herbivory but limited effects of nutrient enrichment on tropical macroalgae suggest that suppression of herbivore populations has played a larger role than eutrophication in driving the phase shift from coral-to macroalgal-dominated reefs in many areas, especially the Caribbean. For temperate macroalgae and benthic microalgae, the effects of top-down and bottom-up forces varied as a function of the inherent productivity of the ecosystem. For these algal groups, nutrient enrichment appeared to have stronger effects in high-vs. low-productivity systems, while herbivores exerted a stronger top-down effect in low-productivity systems. Effects of herbivores vs. nutrients also varied among algal functional groups (crustose algae, upright macroalgae, and filamentous algae), within a functional group between temperate and tropical systems, and according to the metric used to measure producer abundance. These analyses suggest that human alteration of food webs and nutrient availability have significant effects on primary producers but that the effects vary among latitudes and primary producers, and with the inherent productivity of ecosystems.

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Pohnert, G., Steinke, M., and Tollrian, R. **Chemical cues, defence metabolites and the shaping of pelagic interspecific interactions.** *Trends in Ecology and Evolution* 22(4): 198-204, 2007.

**Notes:** Several observations and model calculations suggest that chemically mediated interactions can structure planktonic food webs. However, only recently have improvements in chemical methods, coupled with ecological assays, led to the characterization of chemical cues that affect the behaviour and/or physiology of planktonic organisms. We are currently beginning to elucidate if or how chemical signals can directly affect the interactions between species and even shape complex community structures in aquatic systems. Here, we highlight recent research on the nature and action of chemical signals in the pelagic marine and freshwater environments, with an emphasis on kairomones and defence metabolites.

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Berec, L., Angulo, E., and Courchamp, F. **Multiple Allee effects and population management.** *Trends in Ecology and Evolution* 22(4): 185-191, 2007.

**Notes:** Allee effects, strongly related to the extinction vulnerability of populations and gradually becoming acknowledged by both theoretically oriented and applied ecologists, have already been shown to have important roles in the dynamics of many populations. Although not yet widely recognized, two or more Allee effects can occur simultaneously in the same population. Here, we review the evidence for multiple Allee effects and show that their interactions can take several forms, many of which are far from inconsequential. We suggest that more research is needed to assess the prevalence and interactions of multiple Allee effects, as failing to take them into account could have adverse consequences for the management of threatened or exploited populations.

Frank, K.T., Petrie, B., and Shackell, N.L. **The ups and downs of trophic control in continental shelf ecosystems.** *Trends in Ecology and Evolution* 22(5): 236-242, 2007.

**Notes:** Traditionally, marine ecosystem structure was thought to be determined by phytoplankton dynamics. However, an integrated view on the relative roles of top-down (consumer-driven) and bottom-up (resource-driven) forcing in large-scale, exploited marine ecosystems is emerging. Long time series of scientific survey data, underpinning the management of commercially exploited species such as cod, are being used to diagnose mechanisms that could affect the composition and relative abundance of species in marine food webs. By assembling published data from studies in exploited North Atlantic ecosystems, we found pronounced geographical variation in top-down and bottom-up trophic forcing. The data suggest that ecosystem susceptibility to top-down control and their resiliency to exploitation are related to species richness and oceanic temperature conditions. Such knowledge could be used to produce ecosystem guidelines to regulate and manage fisheries in a sustainable fashion.

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Burgin, A.J. and Hamilton, S.K. **Have we overemphasized the role of denitrification in aquatic ecosystems? A review of nitrate removal pathways.** *Frontiers in Ecology and Environment* 5(2): 89-96, 2007.

**Notes:** The removal of nitrogen (N) in aquatic ecosystems is of great interest because excessive nitrate in groundwater and surface water is a growing problem. High nitrate loading degrades water quality and is linked to eutrophication and harmful algal blooms, especially in coastal marine waters. Past research on nitrate removal processes has emphasized plant or microbial uptake (assimilation) or respiratory denitrification by bacteria. The increasing application of stable isotopes and other tracer techniques to the study of nitrate removal has yielded a growing body of evidence for alternative, microbially mediated processes of nitrate transformation. These include dissimilatory (the reduction of nitrogen into other inorganic compounds, coupled to energy producing processes) reduction of nitrate to ammonium (DNRA), chemoautotrophic denitrification via sulfur or iron oxidation, and anaerobic ammonium oxidation (anammox), as well as abiotic nitrate removal processes. Here, we review evidence for the importance of alternative nitrate removal pathways in aquatic ecosystems and discuss how the possible prevalence of these pathways may alter views of N cycling and its controls. These alternative pathways are of particular importance for the management of excess N in the environment, especially in cases where nitrate is transformed to ammonium, a biologically available and less mobile N form, rather than to dinitrogen gas.

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Agrawal, A.A., Ackerly, D.D., Adler, F., Arnold, A.E., Caceres, C., Doak, D.F., Post, E., Hudson, P.J., Maron, J., Mooney, K.A., Power, M., Schemske, D., Stachowicz, J., Strauss, S., Turner, M. G., and Werner, E. **Filling key gaps in population and community ecology.** *Frontiers in Ecology and Environment* 5(3): 145-152, 2007.

**Notes:** We propose research to fill key gaps in the areas of population and community ecology, based on a National Science Foundation workshop identifying funding priorities for the next 5-10 years. Our vision for the near future of ecology focuses on three core areas: predicting the strength and context-dependence of species interactions across multiple scales; identifying the importance of feedbacks from individual interactions to ecosystem dynamics; and linking pattern with process to understand species coexistence. We outline a combination of theory development and explicit, realistic tests of hypotheses needed to advance population and community ecology.

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Peters, D.P.C., Sala, O.E., Allen, C.D., Covich, A., and Brunson, M. **Cascading events in linked ecological and socioeconomic systems.** *Frontiers in Ecology and Environment* 5(4): 221-224, 2007.

**Notes:** Cascading events that start at small spatial scales and propagate non-linearly through time to influence larger areas often have major impacts on ecosystem goods and services. Events such as wildfires and hurricanes are increasing in frequency and magnitude as systems become more connected through globalization processes. We need to improve our understanding of these events in order to predict their occurrence, minimize potential impacts, and allow for strategic recovery. Here, we synthesize information about cascading events in systems located throughout the Americas. We discuss a variety of examples of cascading events that share a common feature: they are often driven by linked ecological and human processes across scales. In this era of globalization, we recommend studies that explicitly examine connections across scales and examine the role of connectivity among non-contiguous as well as contiguous areas.

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Becker, B. J., Levin, L. A., Fodrie, F. J., and McMillan, P. A. **Complex larval connectivity patterns among marine invertebrate populations.** *Proceedings of the National Academy of Sciences [USA]* 104(9): 3267-3272, 2007.

**Notes:** Based on the belief that marine larvae, which can spend days to months in the planktonic stage, could be transported considerable distances by ocean currents, it has long been assumed that populations of coastal species with a planktonic larval stage are demographically open and highly "connected." Such assumptions about the connectivity of coastal populations govern approaches to managing marine resources and shape our fundamental understanding of population dynamics and evolution, yet are rarely tested directly due to the small size and high mortality of marine larvae in a physically complex environment. Here, we document a successful application of elemental fingerprinting as a tracking tool to determine sources of settled invertebrates and show that coastal mussel larvae, previously thought to be highly dispersed, can be retained within 20-30 km of their natal origin. We compare two closely related and co-occurring species, *Mytilus californianus* and *Mytilus galloprovincialis*, and determine that, despite expected similarities, they exhibit substantially different connectivity patterns. Our use of an *in situ* larval culturing technique overcomes the previous challenge of applying microchemical tracking methods to species with completely planktonic development. The exchange of larvae and resulting connectivities among marine populations have fundamental consequences for the evolution and ecology of species and for the management of coastal resources.

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Wood, C.L., Byers, J.E., Cottingham, K.L., Altman, I., Donahue, M.J., and Blakeslee, A.M.H. **Parasites alter community structure.** *Proceedings of the National Academy of Sciences [USA]* 104(22): 9335-9339, 2007.

**Notes:** Parasites often play an important role in modifying the physiology and behavior of their hosts and may, consequently, mediate the influence hosts have on other components of an ecological community. Along the northern Atlantic coast of North America, the dominant herbivorous snail *Littorina littorea* structures rocky intertidal communities through strong grazing pressure and is frequently parasitized by the digenean trematode *Cryptocotyle lingua*. We hypothesized that the effects of parasitism on host physiology would induce behavioral changes in *L. littorea*, which in turn would modulate *L. littorea*'s influence on intertidal community composition. Specifically, we hypothesized that *C. lingua* infection would alter the grazing rate of *L. littorea* and, consequently, macroalgal communities would develop differently in the presence of infected versus uninfected snails. Our results show that uninfected snails consumed 40% more ephemeral macroalgal biomass than infected snails in the laboratory, probably because the digestive system of infected snails is compromised by *C. lingua* infection. In the field, this weaker grazing by infected snails resulted in significantly greater expansion of ephemeral macroalgal cover relative to grazing by uninfected snails. By decreasing the per-capita grazing rate of the dominant herbivore, *C. lingua* indirectly affects the composition of the macroalgal community and may in turn affect other species that depend on macroalgae for resources or habitat structure. In light of the abundance of parasites across systems, we suggest that, through trait-mediated indirect effects, parasites may be a common determinant of structure in ecological communities.

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Payne, J.L. and Finnegan, S. **The effect of geographic range on extinction risk during background and mass extinction.** *Proceedings of the National Academy of Sciences [USA]* 104(25): 10506-10511, 2007.

**Notes:** Wide geographic range is generally thought to buffer taxa against extinction, but the strength of this effect has not been investigated for the great majority of the fossil record. Although the majority of genus extinctions have occurred between major mass extinctions, little is known about extinction selectivity regimes during these "background" intervals. Consequently, the question of whether selectivity regimes differ between background and mass extinctions is largely unresolved. Using logistic regression, we evaluated the selectivity of genus survivorship with respect to geographic range by using a global database of fossil benthic marine invertebrates spanning the Cambrian through the Neogene periods, an interval of ~ 500 My. Our results show that wide geographic range has been significantly and positively associated with survivorship for the great majority of Phanerozoic time. Moreover, the significant association between geographic range and survivorship remains after controlling for differences in species richness and abundance among genera. However, mass extinctions and several second-order extinction events exhibit less geographic range selectivity than predicted by range alone. Widespread environmental disturbance can explain the reduced association between geographic range and extinction risk by

simultaneously affecting genera with similar ecological and physiological characteristics on global scales. Although factors other than geographic range have certainly affected extinction risk during many intervals, geographic range is likely the most consistently significant predictor of extinction risk in the marine fossil record.

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Lozupone, C.A. and Knight, R. **Global patterns in bacterial diversity.** *Proceedings of the National Academy of Sciences [USA]* 104(27): 11436-11440, 2007.

**Notes:** Microbes are difficult to culture. Consequently, the primary source of information about a fundamental evolutionary topic, life's diversity, is the environmental distribution of gene sequences. We report the most comprehensive analysis of the environmental distribution of bacteria to date, based on 21,752 16S rRNA sequences compiled from 111 studies of diverse physical environments. We clustered the samples based on similarities in the phylogenetic lineages that they contain and found that, surprisingly, the major environmental determinant of microbial community composition is salinity rather than extremes of temperature, pH, or other physical and chemical factors represented in our samples. We find that sediments are more phylogenetically diverse than any other environment type. Surprisingly, soil, which has high species-level diversity, has below-average phylogenetic diversity. This work provides a framework for understanding the impact of environmental factors on bacterial evolution and for the direction of future sequencing efforts to discover new lineages.

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Emslie, S.D. and Patterson, W.P. **Abrupt recent shift in  $\delta^{13}\text{C}$  and  $\delta^{15}\text{N}$  values in Adélie penguin eggshell in Antarctica.** *Proceedings of the National Academy of Sciences [USA]* 104(28): 11666-11669, 2007.

**Notes:** Stable isotope values of carbon ( $\delta^{13}\text{C}$ ) and nitrogen ( $\delta^{15}\text{N}$ ) in blood, feathers, eggshell, and bone have been used in seabird studies since the 1980s, providing a valuable source of information on diet, foraging patterns, and migratory behavior in these birds. These techniques can also be applied to fossil material when preservation of bone and other tissues is sufficient. Excavations of abandoned Adélie penguin (*Pygoscelis adeliae*) colonies in Antarctica often provide well preserved remains of bone, feathers, and eggshell dating from hundreds to thousands of years B.P. Herein we present an ~38,000-year time series of  $\delta^{13}\text{C}$  and  $\delta^{15}\text{N}$  values of Adélie penguin eggshell from abandoned colonies located in three major regions of Antarctica. Results indicate an abrupt shift to lower-trophic prey in penguin diets within the past ~200 years. We posit that penguins only recently began to rely on krill as a major portion of their diet, in conjunction with the removal of baleen whales and krill-eating seals during the historic whaling era. Our results support the "krill surplus" hypothesis that predicts excess krill availability in the Southern Ocean after this period of exploitation.