

1. [Plant diversity controls arthropod biomass and temporal stability](#)

ผู้แต่ง: Borer, E. T., Seabloom, E. W., Tilman, D.

วารสาร: Ecology Letters, Volume 15, Issue 12, December 2012, pages 1457–1464

**สาระสังเขป:** Understanding the linkages among species diversity, biomass production and stability underlies effective predictions for conservation, agriculture and fisheries. Although these relationships have been well studied for plants and, to a lesser extent, consumers, relationships among plant and consumer diversity, productivity, and temporal stability remain relatively unexplored. We used structural equation models to examine these relationships in a long-term experiment manipulating plant diversity and enumerating the arthropod community response. We found remarkably similar strength and direction of interrelationships among diversity, productivity and temporal stability of consumers and plants. Further, our results suggest that the frequently observed relationships between plant and consumer diversity occur primarily via changes in plant production leading to changed consumer production rather than via plant diversity directly controlling consumer diversity. Our results demonstrate that extinction or invasion of plant species can resonate via biomass and energy flux to control diversity, production and stability of both plant and consumer communities.

2. [Biodiversity effects on ecosystem functioning change along environmental stress gradients](#)

ผู้แต่ง: Bastian Steudel, Andy Hector, Thomas Friedl, Christian Löffke, Maike Lorenz, Moritz Wesche, Michael Kessler

วารสาร: Ecology Letters, Volume 15, Issue 12, December 2012, pages 1397-1405

**สาระสังเขป:** Positive relationship between biodiversity and ecosystem functioning has been observed in many studies, but how this relationship is affected by environmental stress is largely unknown. To explore this influence, we measured the biomass of microalgae grown in microcosms along two stress gradients, heat and salinity, and compared our results with 13 published case studies that measured biodiversity–ecosystem functioning relationships under varying environmental conditions. We found that positive effects of biodiversity on ecosystem functioning decreased with increasing stress intensity in absolute terms. However, in relative terms, increasing stress had a stronger negative effect on low-diversity communities. This shows that more diverse biotic communities are functionally less susceptible to environmental stress, emphasises the need to maintain high levels of biodiversity as an insurance against impacts of changing environmental conditions and sets the stage for exploring the mechanisms underlying biodiversity effects in stressed ecosystems.

3. [Species dynamics alter community diversity–biomass stability relationships](#)

ผู้แต่ง: Mike S. Fowler, Jouni Laakso, Veijo Kaitala, Lasse Ruokolainen, Esa Ranta

วารสาร: Ecology Letters, Volume 15, Issue 12, December 2012, pages 1387-1396

**สาระสังเขป:** The relationship between community diversity and biomass variability remains a crucial ecological topic, with positive, negative and neutral diversity–stability relationships reported from empirical studies. Theory highlights the relative

importance of Species–Species or Species–Environment interactions in driving diversity–stability patterns. Much previous work is based on an assumption of identical (stable) species-level dynamics. We studied ecosystem models incorporating stable, cyclic and more complex species-level dynamics, with either linear or non-linear density dependence, within a locally stable community framework. Species composition varies with increasing diversity, interacting with the correlation of species' environmental responses to drive either positive or negative diversity–stability patterns, which theory based on communities with only stable species-level dynamics fails to predict. Including different dynamics points to new mechanisms that drive the full range of diversity–biomass stability relationships in empirical systems where a wider range of dynamical behaviours are important.

#### 4. [Food webs: reconciling the structure and function of biodiversity](#)

**ผู้แต่ง:** Ross M. Thompson, Ulrich Brose, Jennifer A. Dunne, Robert O. Hall, Sally Hladyz, Roger L. Kitching, Neo D. Martinez, Heidi Rantala, Tamara N. Romanuk, Daniel B. Stouffer, Jason M. Tylianakis

**วารสาร:** Trends in Ecology & Evolution, Volume 27, Issue 12, December 2012, Pages 689–697

The global biodiversity crisis concerns not only unprecedented loss of species within communities, but also related consequences for ecosystem function. Community ecology focuses on patterns of species richness and community composition, whereas ecosystem ecology focuses on fluxes of energy and materials. Food webs provide a quantitative framework to combine these approaches and unify the study of biodiversity and ecosystem function. We summarise the progression of food-web ecology and the challenges in using the food-web approach. We identify five areas of research where these advances can continue, and be applied to global challenges. Finally, we describe what data are needed in the next generation of food-web studies to reconcile the structure and function of biodiversity.

#### 5. [Nutrient reduction and climate change cause a potential shift from pelagic to benthic pathways in a eutrophic marine ecosystem](#)

**ผู้แต่ง:** Lindegren, M., Blenckner, T. and Stenseth, N. C.

**วารสาร:** Global Change Biology, Volume 18, Issue 12, December 2012, pages 3491–3503

**สาระสังเขป:** The degree to which marine ecosystems may support the pelagic or benthic food chain has been shown to vary across natural and anthropogenic gradients for e.g., in temperature and nutrient availability. Moreover, such external forcing may not only affect the flux of organic matter but could trigger large and abrupt changes, i.e., trophic cascades and ecological regime shifts, which once having occurred may prove potentially irreversible. In this study, we investigate the state and regulatory pathways of the Kattegat; a eutrophied and heavily exploited marine ecosystem, specifically testing for the occurrence of regime shifts and the relative importance of multiple drivers, e.g., climate change, eutrophication and commercial fishing on ecosystem dynamics and trophic pathways. Using multivariate statistics and nonlinear regression on a comprehensive data set, covering abiotic factors and biotic variables across all trophic levels, we here propose a potential regime shift from pelagic to benthic regulatory pathways; a possible first sign of recovery from eutrophication likely triggered by

drastic nutrient reductions (involving both nitrogen and phosphorus), in combination with climate-driven changes in local environmental conditions (e.g., temperature and oxygen concentrations).

## [6. Impacts of a half century of sea-level rise and development on an endangered mammal](#)

**ผู้แต่ง:** Schmidt, J. A., McCleery, R., Seavey, J. R., Cameron Devitt, S. E. and Schmidt, P. M.

**วารสาร:** Global Change Biology, Volume 18, Issue 12, December 2012, pages 3536–3542

**สาระสังเขป:** The extraordinary growth of human populations and development in coastal areas over the last half century has eliminated and degraded coastal habitats and threatened the persistence of associated wildlife. Moreover, human-induced sea-level rise (SLR) is projected to further eliminate and alter the same coastal ecosystems, especially low-lying regions. Whereas habitat loss and wildlife population declines from development are well documented, contemporary SLR has not yet been implicated in declines of coastal faunal populations. In addition, the projection of severe synergistic impacts from the combination of development and SLR is well described, yet the scientific literature offers little empirical evidence of the influence of these forces on coastal wildlife. Analysis of aerial photographs from 1959 to 2006 provided evidence of a 64% net loss of the endangered Lower Keys marsh rabbit's (*Sylvilagus palustris hefneri*; LKMR) habitat, the majority due to SLR (>48%). Furthermore, there was a strong negative relationship between the proportion of development per island and the amount of new habitat formed. Islands with modest development (less than 8% of land area) saw formation of new areas of marsh vegetation suitable for rabbits, whereas islands with 8% or more of their lands developed between 1959 and 2006 saw little to no addition of LKMR habitat. Only 8% of habitat loss was directly due to conversion to impervious surfaces, indicating that the greatest threats from development were indirect, including blocking of the inland migration of habitat triggered by SLR. Our results were consistent with an ongoing squeeze of coastal ecosystems between rising seas and development as a threat to LKMR habitat, which raises concern for a wide variety of coastal species. Our results provide evidence that SLR has become a contemporary conservation concern, one that is exacerbated by development, and expected to increase in magnitude as ocean waters continue to rise.

## [7. Temperature-driven shifts in a host-parasite interaction drive nonlinear changes in disease risk](#)

**ผู้แต่ง:** Paull, S. H., LaFonte, B. E. and Johnson, P. T. J.

**วารสาร:** Global Change Biology, Volume 18, Issue 12, December 2012, pages 3558–3567

**สาระสังเขป:** Climate change may shift the timing and consequences of interspecific interactions, including those important to disease spread. Because hosts and pathogens may respond differentially to climate shifts, however, predicting the net effects on disease patterns remains challenging. Here, we used field data to guide a series of laboratory experiments that systematically evaluated the effects of temperature on the full infection process, including survival, penetration, establishment, persistence, and virulence of a highly pathogenic trematode (*Ribeiroia ondatrae*), and the development and survival of its amphibian host. Our results revealed nonlinearities in pathology as a function of temperature, which likely resulted from changes in both host and parasite processes. Both hosts and parasites responded strongly to temperature; hosts accelerated

development while parasites showed enhanced host penetration but reduced establishment (encystment) and survival outside the host. While there were no differences in host survival among treatments, we observed a mid-temperature peak in parasite-induced deformities (63% at 20 °C), with the lowest frequency of deformities (12%) occurring at the highest temperature (26 °C). This nonlinear effect could result from temperature-driven changes in parasite burden owing to shifts in host penetration and/or clearance, reductions in host vulnerability owing to faster development, or both. Furthermore, despite strong temperature-driven changes in parasite penetration, survival, and establishment, the opposing nature of these effects lead to no difference in tadpole parasite burdens shortly after infection. These findings suggest that temperature-driven changes to the disease process may not be easily observable from comparison of parasite burdens alone, but multi-tiered experiments quantifying the responses of hosts, parasites and their interactions can enhance our ability to predict temperature-driven changes to disease risk. Climate-driven changes to disease patterns will therefore depend on underlying shifts in host and parasite development rates and the timing of their interactions.

#### 8. [On the spatial scale of dispersal in coral reef fishes](#)

ผู้แต่ง: Puebla, O., Bermingham, E. and McMillan, W. O.

วารสาร: Molecular Ecology, Volume 21, Issue 23, December 2012, pages 5675–5688

**สาระสังเขป:** Marine biologists have gone through a paradigm shift, from the assumption that marine populations are largely 'open' owing to extensive larval dispersal to the realization that marine dispersal is 'more restricted than previously thought'. Yet, population genetic studies often reveal low levels of genetic structure across large geographic areas. On the other side, more direct approaches such as mark-recapture provide evidence of localized dispersal. To what extent can direct and indirect studies of marine dispersal be reconciled? One approach consists in applying genetic methods that have been validated with direct estimates of dispersal. Here, we use such an approach—genetic isolation by distance between individuals in continuous populations—to estimate the spatial scale of dispersal in five species of coral reef fish presenting low levels of genetic structure across the Caribbean. Individuals were sampled continuously along a 220-km transect following the Mesoamerican Barrier Reef, population densities were estimated from surveys covering 17 200 m<sup>2</sup> of reef, and samples were genotyped at a total of 58 microsatellite loci. A small but positive isolation-by-distance slope was observed in the five species, providing mean parent-offspring dispersal estimates ranging between 7 and 42 km (CI 1–113 km) and suggesting that there might be a correlation between minimum/maximum pelagic larval duration and dispersal in coral reef fishes. Coalescent-based simulations indicate that these results are robust to a variety of dispersal distributions and sampling designs. We conclude that low levels of genetic structure across large geographic areas are not necessarily indicative of extensive dispersal at ecological timescales.

#### 9. [Mosaic structure of native ant supercolonies](#)

ผู้แต่ง: Seppä, P., Johansson, H., Gyllenstrand, N., Pálsson, S. and Pamilo, P.

วารสาร: Molecular Ecology, Volume 21, Issue 23, December 2012, pages 5880–5891

**สาระสังเขป:** According to the inclusive fitness theory, some degree of positive relatedness is required for the evolution and maintenance of altruism. However, ant colonies are sometimes large interconnected networks of nests, which are genetically homogenous entities, causing a putative problem for the theory. We studied spatial structure and genetic relatedness in two supercolonies of the ant *Formica exsecta*, using nuclear and mitochondrial markers. We show that there may be multiple pathways to supercolonial social organization leading to different spatial genetic structures. One supercolony formed a genetically homogenous population dominated by a single mtDNA haplotype, as expected if founded by a small number of colonizers, followed by nest propagation by budding and domination of the habitat patch. The other supercolony had several haplotypes, and the spatial genetic structure was a mosaic of nuclear and mitochondrial clusters. Genetic diversity probably originated from long-range dispersal, and the mosaic population structure is likely a result of stochastic short-range dispersal of individuals. Such a mosaic spatial structure is apparently discordant with the current knowledge about the integrity of ant colonies. Relatedness was low in both populations when estimated among nestmates, but increased significantly when estimated among individuals sharing the same genetic cluster or haplogroup. The latter association indicates the important historical role of queen dispersal in the determination of the spatial genetic structure.

#### 10. [TEMPO AND MODE IN PLANT BREEDING SYSTEM EVOLUTION](#)

**ผู้แต่ง:** Goldberg, E. E. and Igić, B.

**วารสาร:** Evolution, Volume 66, Issue 12, December 2012, pages 3701–3709

**สาระสังเขป:** Classic questions about trait evolution—including the directionality of character change and its interactions with lineage diversification—intersect in the study of plant breeding systems. Transitions from self-incompatibility to self-compatibility are frequent, and they may proceed within a species (“anagenetic” mode of breeding system change) or in conjunction with speciation events (“cladogenetic” mode of change). We apply a recently developed phylogenetic model to the nightshade family Solanaceae, quantifying the relative contributions of these two modes of evolution along with the tempo of breeding system change, speciation, and extinction. We find that self-incompatibility, a genetic mechanism that prevents self-fertilization, is lost largely by the cladogenetic mode. Self-compatible species are thus more likely to arise from the isolation of a newly self-compatible population than from species-wide fixation of self-compatible mutants. Shared polymorphism at the locus that governs self-incompatibility shows it to be ancestral and not regained within this family. We demonstrate that failing to account for cladogenetic character change misleads phylogenetic tests of evolutionary irreversibility, both for breeding system in Solanaceae and on simulated trees.