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There are countless axons in the nervous system that are unmyelinated and they do not “short out.” Myelin organizes the very structure of network connectivity, facilitates modes of nervous system function beyond the neuron doctrine, and regulates the timing of information flow through individual circuits. It is certainly time to set aside the frayed metaphor of myelin as insulation and appreciate the more fascinating reality.

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ECOLOGY

Novelty Trumps Loss in Global Biodiversity

John M. Pandolfi and Catherine E. Lovelock

The ongoing decline of ecosystems around the world is often described in terms of biodiversity loss. But exactly how much of this decline is the result of species loss in local communities (α diversity), and how much is due to shifts in species composition of these communities? On page 296 of this issue, Dornelas *et al.* (1) address this issue with a comprehensive analysis of changes in plant, mammal, bird, fish, and invertebrate diversity in a wide range of biomes. Contrary to expectation, loss of α diversity, though widespread, is not a systematic trend in ecological communities. Rather, communities appear to be undergoing massive turnover in the species that constitute them (β diversity), resulting in the global emergence of communities with novel species configurations.

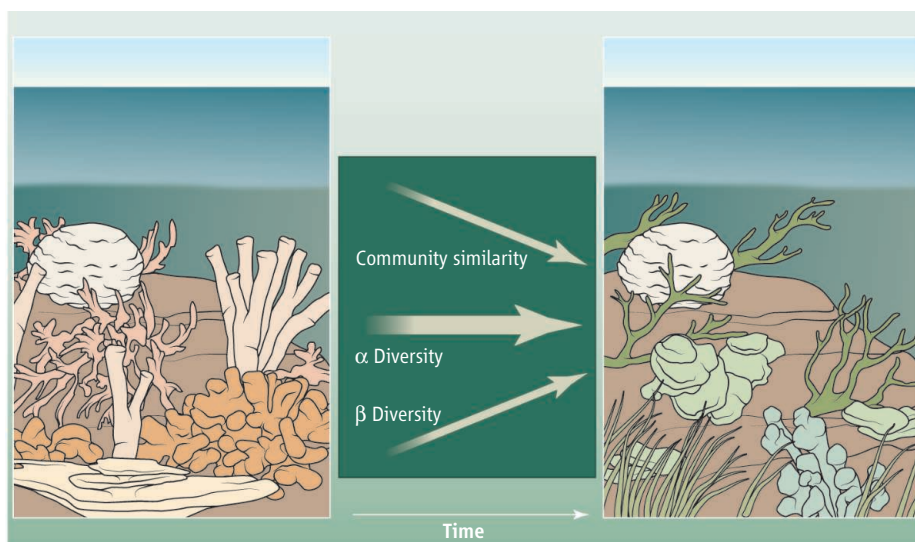
The authors analyzed a massive data set covering more than 35,000 mammal, bird, fish, invertebrate, and plant species from marine, freshwater, and terrestrial biomes ranging from the poles to the tropics. The data comprised 100 individual time series of species composition. Multiple time-series data sets exist for individual biomes and taxa. To standardize sampling in each time series, the authors calculated α and β diversities from the original data. Loss in α diversity, although prevalent in some time series, was not systematic, mostly because species invasions tended to exceed native losses. For example, poleward expansion of species ranges in response to climate change (2) can cause α diversity to remain constant

or potentially increase even if local species go extinct.

However, the authors report significant trends in α diversity in some data series. α diversity is increasing through time in both terrestrial plant communities and temperate communities, but is decreasing in global-scale time series (mostly seabirds and marine invertebrates). It is also declining in tropical biomes, but not significantly so. Even though gains and losses in α diversity are variable among regions and taxa, negative trends in α diversity through time in 41 of the 100 data series leave no room for complacency.

Given the known species losses over the past few centuries (3) and the potential for

species invasions to cancel out local species extinctions and thus maintain consistent levels of α diversity, the species composition in any one place should be subject to large-scale change through time. This is exactly what Dornelas *et al.* find when they compare species composition within a community at any one place between the start of the time series and the ensuing years. Their analysis shows systematic turnover in the species composition of communities through time across climatic regions, realms, and taxonomic groups, with $\sim 10\%$ of species change in communities every decade. The results were robust to tests of temporal autocorrelation (where values at one time in a data



Ecosystem change in the Anthropocene. Dornelas *et al.*'s analysis of long-term studies from many of Earth's biomes shows that species diversity within local communities (α diversity) is equally likely to rise or fall over time, yet the species composition in those communities shows increasing turnover (β diversity) through time. For example, less degraded locally diverse reef communities can be transformed to highly degraded but still locally diverse novel communities.

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series are correlated with values at another time) and were substantially different from predictions derived from a neutral theory of biodiversity that attributes trends in community dynamics to stochastic demographic processes.

The relationship between α diversity and β diversity needs further exploration, especially in the context of the formation and management of novel communities (see the figure) (4). As the species composition of an ecosystem changes in response to loss of species, it is important to understand not only what was lost, but also how that loss affects the emerging novel community. For example, reduction of fast-growing branching corals in the Caribbean (5) causes substantial loss in a major source of carbonate production and might lead to the inability of these reefs to continue accreting, even as sea level continues to rise. Species invasion, such as the introduction of avian malaria into Hawaii or zebra mussels to North American streams and lakes, can similarly impart a legacy of substantial community transformation.

Comprehensive as Dornelas *et al.*'s study is, ecosystem coverage is still patchy, with few data sets from the tropics. Those that do exist from the tropics are focused on terrestrial plants, reef fish, and birds. Inclusion of

data sets for communities with large mammals and amphibians could lead to much worse α diversity trends for the tropics (6, 7). The importance of long-term investment in monitoring in the tropics (such as the Smithsonian's Center for Tropical Forest Science) cannot be overemphasized.

In the new age of human impacts that is increasingly referred to as the Anthropocene (8), how can we reconcile warnings of the next mass extinction (3) with the observation that α diversity largely remains constant? Elucidation of the implications of the mass extinction caused by human impacts will have to be revised to consider the way in which whole communities will respond. Extinction is just one component of the way in which ecological communities will be transformed in the future. Managing the species loss involves building an understanding of species turnover in local communities.

The rapid rate of species turnover in ecological communities that Dornelas *et al.* document means that we can expect widespread emergence of novel communities. Identifying the causes of the biodiversity changes is challenging, but there is some evidence that large-scale drivers may influence regions differentially. For example, the composition of temperate communities can

be strongly influenced by climate change (9, 10), whereas tropical communities suffer disproportionately from other human activities (11). These changes in community composition may affect their resilience or ecosystem function. Ecosystem management approaches must anticipate the widespread emergence of novel ecological communities (12) and their consequences for dependent biota, including humans.

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PLANT SCIENCE

Paired Plant Immune Receptors

Marc T. Nishimura and Jeffery L. Dangl

Plants are constantly interpreting microbial signals from potential pathogens and potential commensals or mutualists. Because plants have no circulating cells dedicated to this task, every plant cell must, in principle, recognize any microbe as friend, foe, or irrelevant bystander. That tall order is mediated by an array of innate immune system receptors: pattern-recognition receptors outside the plant cell and nucleotide-binding oligomerization domain (NOD)-like receptors (NLRs) inside the cell. Despite their importance for plant health, how NLRs function mechanistically has remained obscure. On page 299 of this issue, Williams *et al.* (1) reveal a role for heterodimerization between NLRs and show how the rather limited NLR repertoire of

any plant genome might be enhanced by combinatorial diversity.

When first isolated 20 years ago, it was surprising to find that structurally similar NLRs could individually confer resistance to strains of plant pathogens from all kingdoms—insects, fungi, oomycetes, bacteria, and viruses (2, 3). Plant NLRs are deployed to various intracellular addresses to monitor for pathogen virulence proteins (“effectors”) that target host defense pathways. NLRs in plants and animals function as molecular switches, cycling between a closed “off” conformation bound to adenosine diphosphate (ADP) and an open “active” conformation bound to adenosine triphosphate (ATP). This switch is thought to be controlled by interactions between a C-terminal leucine-rich repeat (LRR) domain folded back across a central nucleotide-binding (NB) domain and an N-terminal dimerization output domain, which in plants is typically either a coiled-

The ability of plant cell immune sensors to combine in different pairs could expand the host's defense against pathogens.

coil (CC) motif or a domain with homology to the Toll–interleukin-1 receptor (TIR) cytoplasmic domains (4). How the conformation of NLRs changes after effector recognition and during the activation cycle, and the consequences of these changes, are major unanswered questions in plant pathology. One hypothesis posits that the N-terminal TIR or CC domains can dimerize upon effector-mediated activation to transduce signals to the nucleus and reprogram the cell for disease resistance responses.

Williams *et al.* demonstrate that in addition to forming a signaling-competent homodimer, one TIR domain can heterodimerize with another (in the resting state) to suppress host defense signaling. The authors studied the TIR domains of an NLR pair (RPS4 and RRS1) that are encoded by genes linked head-to-head in the plant *Arabidopsis*. Both proteins are required for disease resistance to multiple pathogens (5, 6). By

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