EDITED BY GILBERT CHIN AND JAKE YESTON

ECOLOGY/EVOLUTION

## The More the Merrier

The relationship between the number of species in an ecological community and the functional aspects of the ecosystem is usually studied experimentally by observing the effects of random changes in diversity. However, a study of rocky intertidal pools reveals that the nonrandom variation in species diversity that is characteristic of natural habitats yields better predictions of functional effects than experiments in which the species composition is altered randomly. Bracken *et al*. quantified the effects of both kinds of variation in seaweed diversity on nutrient dynamics (nitrogen uptake) in a set of tide pools in which the number of species increased as disturbance (caused by heavy surf) decreased. The effects of natural realistic variation were compared with the effects of artificial diversity gradients established by random groupings of species. Increased diversity in the "real-world" pools was associated with higher rates of nutrient acquisition by the plants, whereas the artificial communities showed no relationship. These results present new challenges for experimental ecologists studying the consequences of biodiversity loss in ecosystems. — AMS

*Proc. Natl. Acad. Sci. U.S.A.* **105**, 924 (2008).

MOLECULAR BIOLOGY

## Wobble and Superwobble

In most cases, more than one triplet codon can specify an amino acid—at one extreme, leucine can be encoded by any of six nucleotide triplets. Degenerate codons tend to vary at the third position, which was the basis for Francis Crick's wobble hypothesis: Each codon must be recognized by its cognate transfer RNA (tRNA) through an anticodon that is strictly complementary at the first two positions, but can use nonstandard base-pairing in the third, or wobble, position. Applying these complementarity rules indicates that a minimum of 32 tRNAs would be needed to read all 64 possible triplet codons. Yet in human mitochondria and plant plastids, there are fewer than 32 distinct tRNAs, leading to the suggestion that tRNAs with U in their wobble position might be able to make up for the deficit by pairing with any of the four bases at the third position of the codon—via a so-called superwobble.

Plastids in tobacco plants have two tRNA genes that code for the amino acid glycine (Gly): $tRNA^{Gly}$(GCC), which can decode GGC and GGU Gly codons, and $tRNA^{Gly}$(UCC), which, according to the superwobble hypothesis, should be able to decode both its regular Gly codons, GGA and GGG, and also GGC and GGU. Rogalski *et al*. support this idea by individually knocking out both $tRNA^{Gly}$ genes and showing that only the superwobble tRNA is essential for cell survival. Although $tRNA^{Gly}$(UCC) suffices for accurate reading of the code through superwobble, translation efficiency nonetheless seems to be reduced, explaining why superwobble is rarely selected for in genetic systems. — GR

*Nat. Struct. Molec. Biol.* **15**, 10.1038/nsmb1370 (2008).

BIOMATERIALS

## Seeping into Cartilage

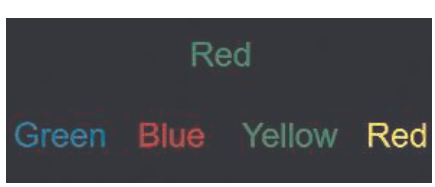
Polymer nanoparticles have been explored for more accurate delivery of drugs to improve efficacy and reduce toxicity within the body. For tissues lacking vasculature, such as articular cartilage, the challenge is to get the drug through the dense extracellular matrix (ECM) via a localized injection without removal in the synovial fluid. Rothenfluh *et al*. synthesized poly(propylene sulfide) (PPS) particles, ranging in size from 20 to 200 nm, that could potentially be used to deliver hydrophobic drugs such as aggrecanase inhibitors used to treat osteoarthritis. The PPS particles were decorated with a peptide sequence obtained from a five-generation phage panning process, where cloning enhances the population of sequences that best bind to a target tissue. For the best sequence obtained, binding tests with the target peptide and a related scrambled sequence showed that binding was sequence-specific to collagen II $\alpha$1. Not only were the smallest particles able to enter the ECM, but the targeting peptide then caused them to bind to the collagen matrix, thus turning a barrier into a reservoir that persisted for more than 96 hours. — MSL

*Nat. Mater.* **7**, 10.1038/nmat2116 (2008).

PHYSIOLOGY

## A Neural Vulnerability to Hypertension

Rising blood pressure is a typical stress response—usually a healthy and adaptive reaction to dangerous situations that increases one's chances of survival. However, individuals with excessive stressor-evoked blood pressure increases are at risk for developing cardiovascular disease later in life.




**Green is the correct choice.**

In an fMRI study of undergraduates charged with choosing the word that names the color of a target word (a Stroop color-word interference

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Published by AAAS

task), Gianaros *et al*. connect stressor processing with the brainstem cardiovascular control mechanisms regulating blood pressure. People with higher stressor-evoked blood pressure reactivity displayed more activation of the amygdala, especially in the dorsal part that contains the central nucleus. Individuals showing greater blood pressure reactivity also had a lower amygdala gray matter volume, which itself predicted greater amygdala activation. In addition, greater stressor-evoked blood pressure reactivity was correlated with stronger functional connectivity between the amygdala and an area in the brainstem, called the pons, which is critical for blood pressure control, as well the perigenual anterior cingulate cortex (pACC). As in the amygdala, greater activation of the pACC was associated with lower pACC gray matter volume. These results indicate a role for the amygdala and some of its projection areas in mediating individual differences in autonomic stress responses and hence vulnerability to psychological stressors. — PRS

*J. Neurosci.* **28**, 990 (2008).

CHEMISTRY

## Tracking Surface Shakes

Two-dimensional infrared (2D-IR) spectroscopy has recently proven useful for tracking chemical dynamics through shifts in detected molecular vibrations. The "2D" refers not to a spatial framework but rather to the initial and final sets of mode populations that are simultaneously monitored at different vibrational frequencies. Bredenbeck *et al*. extend this technique to achieve surface specificity by combining it with sum frequency generation (SFG). This latter, well-established class of spectroscopy affords a background-free signal arising from the additive mixing of two different frequencies of light at an interface—a process that fails to build intensity in a bulk 3D environment where the polarizations of stacked molecular layers cancel one another out. The authors applied their SFG 2D-IR hybrid to the characterization of vibrational energy flow in the hydrophobic alkyl tails protruding from a water-dodecanol interface. — JSY

*J. Am. Chem. Soc.* **130**, 10.1021/ja710099c (2008).

BIOCHEMISTRY

## What's It All Good For?

Enzyme kinetics is a subject dreaded by all but hard-core biochemists. Purifying proteins and measuring product generated or substrate consumed at varying concentrations of enzyme and substrate—not to mention the characterization of competitive and noncompetitive inhibitors—and then integrating these data within a mechanistic scheme that spits out rate constants… well, this is not the stuff that dreams are made of, and neither is reading someone else's enzyme kinetics papers.

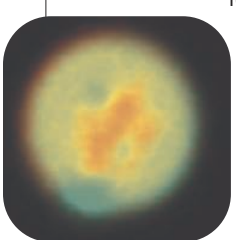
Umejiego *et al.* have applied this kind of information (a random order of substrate binding and a rate-limiting hydrolysis of the covalent enzyme intermediate) in designing a small-molecule screen for inhibitors of the enzyme inosine-5′-monophosphate dehydrogenase (IMPDH). Why should we care? Because IMPDH salvages purines in order to supply guanine in the human pathogen *Cryptosporidium parvum*, and because the *C. parvum* enzyme differs enough from human IMPDH to serve as a drug target. By screening under kinetically defined conditions where the conserved IMP site was occupied, whereas the less conserved NAD site was empty, they managed to fish out 10 candidates from a starting pool of 44,000 compounds. Four of these were more potent inhibitors of *C. parvum* growth than the standard drug paromomycin in a cell culture assay. — GJC

*Chem. Biol*. **15**, 70 (2008).

CHEMISTRY

## DNA's Self-Regard

Recognition of double-stranded (ds) DNA sequences is usually thought to require some unwinding of the double helix to expose the bases for interactions with single-stranded nucleic acid sequences or with proteins. Thus, it would be reasonable to assume that recognition between dsDNA sequences in solution would require processes involving single-stranded DNA, such as triple-helix formation. Baldwin *et al*. examined a binary mixture of two different dsDNA sequences of identical length (294 base pairs) and GC base proportion (50%) in electrolytic solution under minor osmotic stress. Under conditions of low fluorescent labeling to avoid quenching, liquid-crystalline spherulites form, and the two DNAs within these structures prefer to self-associate rather than mix. The authors suggest, based on their recent theoretical work, that association between identical DNAs is favored as this arrangement maintains registry of the phosphate backbone and surrounding counterions; different sequences result in small changes in pitch that can disrupt these interactions and extract an energetic penalty. Other mechanisms may also operate, but dsDNA recognition occurs in the presence of intervening solution. — PDS



**DNA segregation in spherulite.**

*J. Phys. Chem.* B **112**, 1060 (2008).

CREDITS (TOP TO BOTTOM): BALDWIN *ET AL*., *J. PHYS. CHEM. B* **112**, 1060 (2008)



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