



ECOLOGY

Changes at the Core

Airborne pollen grains deposited in sediments—particularly in undisturbed lake beds—are a crucial element in understanding how vegetation and its constituent species respond to changing climates. Research on the high-altitude lake sediments from the Bogotá basin in the Colombian Andes has produced a rich record of climate and vegetation over the Quaternary period. In particular, two deep sediment cores obtained in the late 1980s have provided detailed information on climatic fluctuations and vegetation change. However, interpretation of the record has been hampered by uncertainties. Torres *et al.* now present a new analysis of these cores, in which many of the technical challenges concerning the chronology have been addressed. The development of the Andean forest and high-altitude páramo vegetation—the uniquely Andean biome that occurs above the treeline and has evolved *de novo* with the uplift of the Andes—was shown to be a dynamic process, with ephemeral associations of plant species continually fluctuating over the past 2 million years as temperatures rose and fell with glacial cycles. This unbroken record provides further evidence that plant communities at any given point in time often have no analog, in terms of species composition, with past or future associations of species. — AMS

Quat. Sci. Rev. **63**, 59 (2013).

BIOCHEMISTRY

Signaling by Unfolding

In response to DNA damage, nuclear p53, a tumor suppressor, induces expression of the p53 up-regulated modulator of apoptosis (PUMA). PUMA in turn regulates the activity of cytosolic p53. In the cytosol, p53 is sequestered by the anti-apoptotic protein BCL-xL, a member of the BCL-2 family of anti-apoptotic proteins. PUMA disrupts this interaction and frees p53 to initiate apoptosis. BCL-2 proteins are composed of BCL-2 homology (BH) domains, and PUMA is a single-BH domain protein. Follis *et al.* used NMR spectroscopy and biophysical methods to

show that PUMA is intrinsically unstructured, but that its BH3 domain folds upon binding to a hydrophobic groove in BCL-xL. NMR spectroscopy and x-ray crystallography showed that PUMA binding caused partial unfolding of two helices in BCL-xL. Although PUMA forms complexes with other anti-apoptotic complexes, it did not induce similar structural perturbations in these proteins. Structural data suggested that a π -stacking interaction between Trp-71 of PUMA and His-113 of BCL-xL was key to the destabilization of regions of the BCL-xL structure. Thus, the p53 apoptotic pathway is activated by regulated unfolding of an anti-apoptotic protein. — VV

Nat. Chem. Biol. **10**.1038/NCHEMBO.1166 (2013).

ECOLOGY

Downstream Discharge

Wastewater has the potential to serve as a renewable source of energy, nutrients, and clean water. However, most wastewater is treated minimally to remove pathogens and organic matter and released into the environment. In highly urbanized, developed areas, a single river may receive discharged effluent from several wastewater treatment plants, so that a sizable fraction of the downstream water is recycled wastewater. By studying two rivers in and around Chicago, Drury *et al.* showed that although wastewater effluent released into rivers may meet water quality standards, it can have an impact on downstream ecosystems. Discharged effluent resulted in increased nutrients such as nitrate and phosphate in the water column and, perhaps surprisingly, decreased sediment organic

matter. The downstream sediments showed decreased bacterial abundance and diversity, shifting from communities that included sulfate-reducing bacteria to communities dominated by nitrate-oxidizing bacteria. Although the two rivers have very different biological and chemical properties upstream of the wastewater treatment plants, they were homogenized to the point where they were nearly indistinguishable downstream. — NW

Appl. Environ. Microbiol.
10.1128/AEM.03527-12 (2013).

MOLECULAR BIOLOGY

RNA Methylation and Metabolism

The methylation—and demethylation—of DNA play an important role in the dynamic regulation of gene expression and in genome stability. RNA in eukaryotes is also methylated on the A base (m^6A), the most abundant posttranscriptional modification of mammalian mRNA. The modification is known to have biological function in meiosis and sporulation in yeast and potentially in RNA processing in mammalian cells.

Zheng *et al.* identify a mammalian RNA demethylase, ALKBH5, that is capable of removing the m^6A mark from RNA both *in vitro* and *in vivo*. The ALKBH5 protein localized to nuclear speckles and associated with specific mRNA processing factors there, and also affected mRNA export, with both functions requiring the ALKBH5 demethylation activity. A knockout of the ALKBH5 gene in mice resulted in reduced male fertility and revealed

that the demethylase influences the expression of many genes, including key genes involved in spermatogenesis, resulting in defects in spermatogenesis and aberrant apoptosis in the testes of the mutant male mice. Thus, the dynamic methylation and demethylation of RNA, like DNA, may play an important role in gene regulation. — GR

Mol. Cell **49**, 18 (2013).

MICROBIOLOGY

Probing the Microbial Mix

In the past decade, it has become apparent that we are colonized by microbes that probably shape many of our most important physiological processes. Much of the work has taken a metagenomics approach—characterizing what microbes are there and what genes they express. Maurice *et al.* now go one step further and begin to investigate how our microbial inhabitants respond to pharmacological perturbations. A combination of single-cell analysis by flow cytometry, DNA sequencing, and metatranscriptomics revealed that the bacteria within the human gut vary with respect to membrane integrity, polarization, and metabolic activity. Metabolic activity was enriched in Firmicutes, whereas Bacteroidetes were less metabolically active. Exposure to both antibiotics and host-targeted

drugs resulted in alterations in the physiology, structure, and gene expression profile of the bacteria. An increase in genes associated with resistance, stress responses, and metabolism was observed after antibiotic treatment. These results represent an important step toward understanding on a broad scale how specific perturbations affect our microbial communities. — KLM

Cell **152**, 39 (2013).

CHEMISTRY

Keeping Pigments in Sync

It has been clear for decades that photosynthesis involves an intricate chain of energy transfer steps, channeling the energy in light absorbed by dedicated pigments to a central complex that chemically splits water. Over the past 7 or 8 years, the advent of two-dimensional electronic spectroscopy has offered an increasingly detailed understanding of how the transfer process works. In particular, the data suggest a persistence of quantum-mechanical coherence—essentially a

steady phase relationship in electronic excitation across the donors and acceptors that facilitates efficient transfer—for a much longer time than the complex molecular structure of the system would seem to allow. The underlying mechanism for sustaining coherence has remained somewhat mysterious and subject to debate. Tiwari *et al.* have modeled the transfer process in a framework that allows mixing of vibrational and electronic excitation, and they find that anticorrelated vibrations across the associated proteins (i.e., contraction on one side concurrent with extension on the other) could mediate electronic dynamics that give rise to the spectral signatures observed in the experiments. They further note that certain pigment vibrational frequencies match the associated electronic energy gaps, lending further plausibility to this mechanism. — JSY

Proc. Natl. Acad. Sci. U.S.A. **110**, 1203 (2013).

OCEAN SCIENCE

Runoff in the Arctic

The Arctic is a bellwether region for climate change, with temperatures there increasing at approximately twice the global average rate. That rapid temperature rise has caused widespread melting of sea ice, land ice, and permafrost which,

along with greater amounts of precipitation, have increased the flux of fresh water into northern high-latitude seas. This enhanced freshwater input has many important effects on the Arctic Ocean—namely, on surface salinity, temperature structure, biological productivity, and carbon sequestration.

To determine the distribution of continental runoff in the Arctic Ocean over the past decade, Fichot *et al.* developed an optical proxy for terrigenous dissolved organic matter, which they implemented using remote sensing of ocean color from space. By measuring the amounts of dissolved organic matter in the ocean's surface, they illustrate how runoff has changed over the past decade across the entire pan-Arctic region. This approach should be an important tool for monitoring the effects of climate change on this high-latitude region. — HJS

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