

Human evolution in rapidly changing local ecosystems

Past climate provides a context for understanding the course of early human evolution. But terrestrial proxy records are typically too degraded or incomplete to reveal local ecosystem characteristics and rapid environmental changes. In a pair of papers, Clayton Magill et al. (pp. 1167–1174 and pp. 1175–1180) report a lipid biomarker and isotopic signatures for organic matter preserved in lake sediments at Olduvai Gorge, Africa, dating to a key interval around 2 million years ago when *Homo erectus* (*sensu lato*) emerged and began to disperse across Africa. Us-



Olduvai Gorge, Africa.

Using published data for modern plants and soils, the authors constructed a framework to interpret the stable carbon isotope composition of ancient plants, and found recurring patterns in which open C₄ grasslands abruptly transitioned to closed C₃ forests in just several hundred to a few thousand years. According to the authors, Olduvai Gorge ecosystems shifted at speeds and scales that contradict long-held views linking gradual aridification and grassland expansion to human evolution. The authors also present a continuous record of stable hydrogen-isotope compositions from lipid biomarkers in Olduvai Gorge as a proxy for water availability and the accompanying consequences for local ecosystems. Using modern isotopic ratios to interpret the record, the authors found dramatic fluctuations in aridity, with drier times corresponding to ecosystems dominated by C₄ grasslands and wetter conditions characterized by the expansion of woody cover across the continent. The authors conclude that the high variability in available fresh water influenced ancient eastern African ecosystems and early human proliferation and cognitive development. Taken together, the studies demonstrate that biomarkers preserved in lake sediments can help reconstruct the course of local ecological change and determine how past climates guided human evolution, according to the authors. — T.J.

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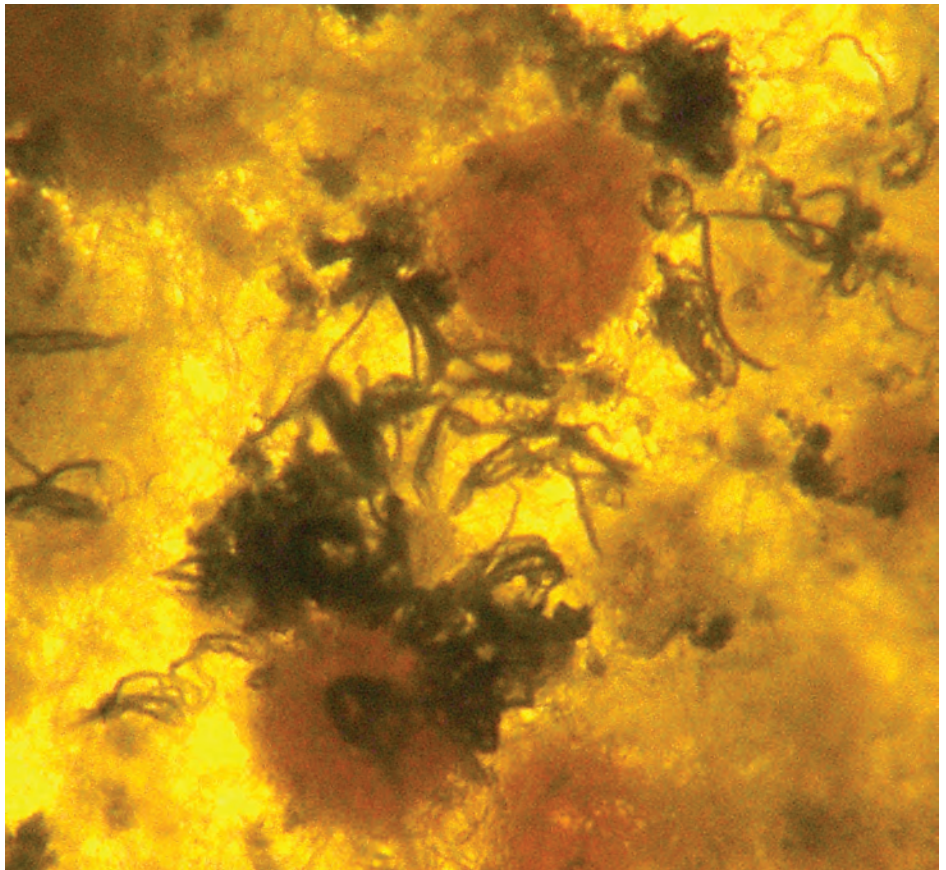
Pigment vibrations drive photosynthetic energy transfer

During photosynthesis, antenna proteins position light-absorbing pigment molecules so that they direct the transfer of electronic energy toward a reaction center. Despite advances in technology and quantum physics, the mechanisms underlying the efficient process of energy transfer remain elusive. Vivek Tiwari et al. (pp. 1203–1208) examined whether small amplitude vibrations inside the pigments, known as nonadiabatic dynamics, contribute to photosynthetic energy transfer. Using a model that mathematically describes coupled vibrational and electronic motion, the authors demonstrate that when the so-called

electronic energy gap of the antenna protein matches an internal pigment vibration, two coupled pigments vibrate out of phase, thus mixing their excited states and driving energy transfer. Such mixing, the authors report, can give rise to delocalized vibrational wavepackets with signatures of quantum coherence and energy transfer. Furthermore, the coherence frequencies match known pigment vibrations found in a number of other photosynthetic antennas. The findings suggest that resonant nonadiabatic coupling represents an important component of photosynthetic energy transfer, according to the authors. — T.J.

Inducing sexual reproduction in a penicillin-producing fungus

Filamentous fungi are used to produce a variety of pharmaceutical products, including statins and antibiotics, and many species have long been considered to lack a sexual cycle. Julia Böhm et al. (pp. 1476–1481) induced sexual reproduction in the filamentous, penicillin-producing fungus *Penicillium chrysogenum*, which has been considered asexual for more than a century. Performing crosses between different wild type and industrial *P. chrysogenum* strains on oatmeal agar medium supplemented with the compound biotin gave rise to sexual reproductive structures with viable progeny. When the authors examined the progeny they found evidence of sexual recombination at the phenotypic and molecular levels. The authors used sexual crosses to combine previously separate traits of interest and created a *P. chrysogenum* strain with a high penicillin titer that lacked a contaminant called chrysogenin. The authors also found that the *MAT1-1-1*



Yellow fruiting bodies of *Penicillium chrysogenum*.

mating-type gene, known primarily for its role in governing sexual identity, controlled the expression of a wide range of genes relevant to biotechnology, including those that regulate penicillin production. According to the authors, sexual recombination could be a valuable tool for creating *P. chrysogenum* strains with increased penicillin yields, and may help improve other economically important fungi that are believed to be exclusively asexual. — S.R.

Protective genes might help some corals survive climate change

The worldwide decline of reef-building corals is expected to exacerbate as climate change intensifies. Certain corals withstand environmental stresses better than others, but the molecular mechanisms behind the enhanced physiological resilience remain unclear. Through recent advances in DNA sequencing technology, Daniel Barshis et al. (pp. 1387–1392) examined gene expression patterns in conspecific thermally sensitive and thermally resilient corals to identify molecular pathways that contribute to coral resilience. The authors determined that the expression patterns of hundreds of genes vary in both resilient and sensitive corals under simulated bleaching stress, but resilient corals express 60 of these



Acropora hyacinthus coral colony in the Ofu, American Samoa back reef.

genes more highly under control conditions than under the experimental conditions. The genetic subset, the authors report, includes thermal tolerance genes such as heat shock proteins and antioxidant enzymes, as well as many others that regulate apoptosis, tumor suppression, innate immune response, and cell adhesion. The authors propose that this expression pattern may act as a mechanism that enables individual corals to survive frequent environmental stresses, similar to established mechanisms in model organisms such as yeast. The findings demonstrate how DNA sequencing can help uncover cellular processes that might allow some organisms to survive future changes in global climate, according to the authors. — T.J.