

## In this issue . . .

### Twin-chain hydrogels for cleaning artworks

Removing soil from painted surfaces is a major challenge in the preservation of art, partly due to the presence in paint of solvent-sensitive pigments, dyes, and additives that can leach and destroy the art. Moreover, works by painters like Van Gogh and Picasso as well as modern artworks dating to the 1940s and later often contain rough, textured, or clotted surfaces that are difficult to clean using conventional methods. Rosangela Mastrangelo et al. (pp. 7011–7020) formulated twin-chain hydrogels made of poly(vinyl alcohol) (PVA) by interpenetrating high-molecular-weight PVA with low-molecular-weight PVA, resulting in a pliant gel with a disordered network of large, interconnected pores, akin to a sponge. The twin-chain hydrogels showed greater cleaning efficacy and improved adherence to rough painted surfaces than pure PVA networks. Compared with conventional cleaning aids such as gellan gels and swabs, the hydrogels showed improved cleaning efficacy without pigment loss when tested on soiled glass slides and mock-ups of contemporary paintings. The authors used the hydrogels to clean a pair of Jackson Pollock paintings—*Two* (1943–1945) and *Eyes in the Heat* (1946–1947)—from the Guggenheim collection in Venice, Italy that had been soiled by dirt accumulated over decades. Unlike swabs, which can dislodge pigments, the hydrogels safely removed soil and restored original hues in the paintings, which represent Pollock's dripping technique and contain highly textured, solvent-sensitive 3D surfaces. According to the authors, the twin-chain hydrogels represent a superior tool for safely cleaning artwork. — P.N.



Pollock's *Eyes in the Heat* before (Left) and after (Right) cleaning using the twin-chain hydrogel. *Eyes in the Heat* by Jackson Pollock, © Pollock-Krasner Foundation/Artists Rights Society (ARS), New York.

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### Phage–bacteria interactions in the bee gut

Phages, which are viruses that infect bacteria, exert selective pressure on their hosts that can enhance the diversity and fitness of bacterial communities. Although honey bee gut bacteria are both central to bee health and studied as a model system for microbiota–host interactions, phages associated with the bee gut remain largely unexplored. Germán Bonilla-Rosso et al. (pp. 7355–7362) report that the honey bee gut houses a large and diverse community of temperate and lytic phages, many of which represent new viral genera with unknown gene functions. Furthermore, the phage communities are seemingly

globally widespread, found in bees from both Switzerland and Japan. To demonstrate that bee gut phages are closely linked and adapted to core bee gut bacterial constituents, the authors identified eight phages that infect the bacterium *Bifidobacterium asteroides* and demonstrated that the phages exhibit widely differing host ranges, which are determined at the strain rather than the species level. This specificity suggests that the honey bee gut contains a complex network of interconnected, coexisting phages and bacterial strains. The findings indicate the foundational contribution of phages to bee gut bacterial diversity and health and suggest that this microbiome represents a promising model system for bacteria–phage dynamics, according to the authors. — T.J.

## Environmental reservoirs and disease impacts

Pathogens persisting in the environment can amplify infectious disease outbreaks, but the influence of environmental reservoir dynamics remains largely unexplored. Joseph Hoyt et al. (pp. 7255–7262) quantified changes in the environmental reservoir of *Pseudogymnoascus destructans*, a fungal pathogen that causes white-nose syndrome in bats, at 101 subterranean sites where bats hibernate and combined the data with population surveys and trans-



A cluster of greater horseshoe bats (*Rhinolophus ferrumequinum*) roosting in a cave in Jilin Province, China.

mission data from 39 species across the globe. An extensive and persistent environmental reservoir led to earlier and more severe infections and high mortality in North America. In contrast, low levels of *P. destructans* in the environment resulted in delayed, less severe infections and stable populations across Eurasia. The authors found that bats in North America became immediately infected upon returning to a heavily contaminated environmental reservoir in early winter, which increased infection levels and mortality rate. In contrast, most bats in Eurasia became infected later in winter and survived until spring, when they could emerge from hibernation and clear infection. The findings suggest that hosts found in areas with high levels of pathogen in the environment suffer from increased disease-related mortality, according to the authors. — M.S.

## Road expansion in the Amazon

Thousands of kilometers of roads are expected to be constructed or improved in the Amazon over the

next 5 years, but the projects' broad impacts on the region are unclear. Over an evaluation period of 20 years, Thais Vilela, Alfonso Malky Harb, et al. (pp. 7095–7102) examined economic, environmental, and social impacts of 75 proposed road projects that include more than 12,000 km of planned roads in the Amazon regions of Brazil, Bolivia, Colombia, Ecuador, and Peru. The authors estimated that implementing all projects will lead to deforestation of at least 2.4 million ha—approximately the size of Belize. Further, at least 17% of the projects would result in legal violations related to environmental statuses or indigenous rights. Almost 50% of the projects are expected to result in economic losses, although canceling these projects would avoid a loss of \$7.6 billion as well as 1.1 million ha of deforestation. The authors also identified 18 projects with the lowest social and environmental impacts and found that focusing on them while cutting the other projects would generate \$4 billion in net gain and result in less than 10% of projected deforestation. The findings suggest that constructing a few carefully chosen projects would be economically sound and mitigate negative impacts in the Amazon, according to the authors. — M.S.

## Evolution of sedentary behaviors

Prolonged sitting has been tied to increased risk of cardiovascular disease and death, likely due to reduced levels of muscle contractions and metabolism. However, evolutionary pressures favor strategies that minimize energy use. To better understand the evolution of inactivity, David Raichlen et al. (pp. 7115–7121) examined sedentary behaviors of the



Hadza participants in resting postures.

Hadza, a hunter-gatherer population in Tanzania, which exemplifies activity patterns in a context typical of humans' evolutionary history. Unlike adults in more industrialized populations, Hadza adults are generally free of cardiovascular disease. For 8 days, 28 Hadza adults wore accelerometers affixed to the thigh that the authors used to measure time spent

in resting postures during waking hours. The authors compared the Hadza data with previous studies that measured inactivity in industrialized populations. While awake, Hadza adults spent an average of almost 10 hours each day in nonambulatory postures, similar to the time adults in industrialized populations spend sitting. The average duration of inactive bouts was also comparable among Hadza adults and adults in industrialized populations. However, Hadza adults spent a significant portion of sedentary time in squatting and kneeling postures, which produce more muscle activity than chair sitting. The findings suggest the importance of daily muscle activity, from both physical movement and resting postures, to human health, according to the authors. — M.S.

### Nutrient dilution and insect decline

Insect populations are declining worldwide. One hypothesis for the drivers behind such declines holds that increasing plant productivity, due to favorable climate oscillations or carbon dioxide fertilization, can dilute the amounts of essential nutrients in plant biomass. Such nutrient dilution can, in turn, stress populations of insect herbivores. Ellen Welti et al. (pp. 7271–7275) tested the hypothesis using data series from a prairie in Kansas covering 16 and 22 years. The data included plant biomass, plant elemental composition, grasshopper abundances, and climate data. Grasshopper abundances exhibited 5-year population cycles as well as declines between 2.1 and 2.7% per year. Natural climate cycles, such as the El Niño Southern Oscillation, North Atlantic Oscillation, and Pacific Decadal Oscillation, accounted for 40–54% of the grasshopper population variation through effects on local climate and plant productivity. However, grass biomass doubled over the study period, with a corresponding decrease in the amounts of nitrogen, phosphorus, potassium, and sodium in leaves. The dilution accounted for 25% of the grasshopper

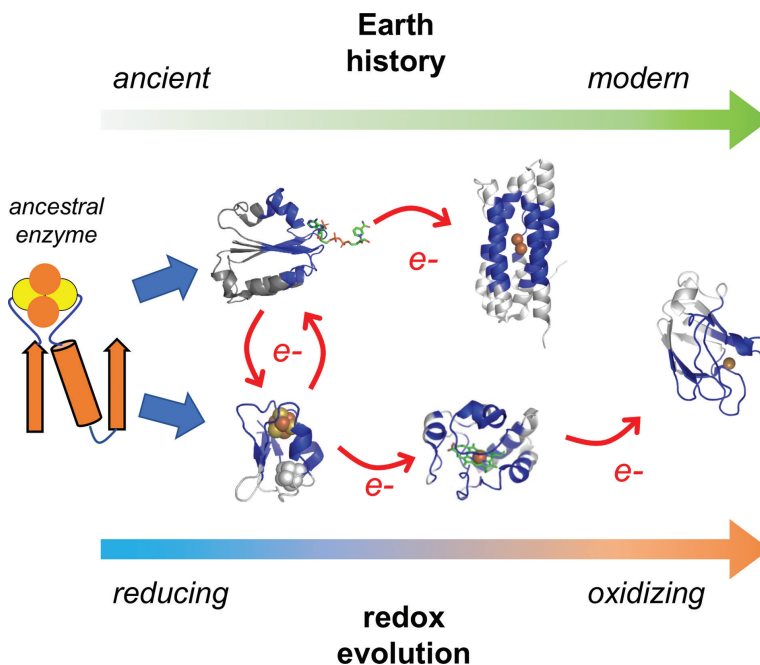


Plains lubber grasshopper (*Brachystola magna*) at Konza Prairie in Kansas.

decline. According to the authors, climate change may cause widespread nutrient dilution, even in relatively undisturbed natural areas. — P.G.

### Putative common ancestor of oxidoreductase enzymes

Enzymes known as oxidoreductases catalyze the fundamental redox reactions that allow organisms to store and release energy. Although the structural



Coevolution of protein topology and electron transfer pathways.

and chemical complexity of modern oxidoreductases likely evolved from a small set of ancient protein folds, retracing this history across billions of years and countless configurations has proven challenging. Expanding previous work showing that protein topologies change more slowly than sequences, Hagai Raanan et al. (pp. 7193–7199) used structural and sequence alignments to identify evolutionary relationships across geological timescales from a database of nearly 75,000 cofactor-binding microenvironments in structurally determined proteins. The authors report that the histories of the microenvironments—many of which are catalytic centers and metal coordination sites—trace back to two recurring folds: ferredoxin and Rossmann-like folds. Furthermore, the analysis suggests that these ancient forms, both commonly studied as key to the origin of modern metabolism, likely share a common ancestor that evolved to aid electron transfer and catalysis via gene duplication, diversification, and recruitment. The authors note that reconstructing histories through deep time requires assumptions and inferences, and the findings can inform experimental models designed to test whether modern metabolism evolved from a handful of ancient oxidoreductase progenitors. — T.J.

## Impact of COVID-19 containment efforts

To contain the spread of the 2019 novel coronavirus (COVID-19), China enacted lockdowns of Wuhan, the city where the outbreak originated, as well as other cities in Hubei province, in late January 2020. Other countries have instituted airport screening measures and restrictions on travel to and from China. Chad Wells et al. (pp. 7504–7509) estimated the effects of these and other prevention measures on the global COVID-19 spread. The authors estimated that in the absence of travel restrictions, 779 cases of COVID-19 would have been exported by February 15, 2020. The Chinese lockdowns reduced

this number by more than 70% and reduced the estimated daily exportation rate by more than 80%. Nearly two-thirds of exported cases were estimated to be presymptomatic upon arrival at their destination, which limited the effectiveness of airport screening measures. Thus, the authors suggest, while travel restrictions and border controls likely delayed the spread of COVID-19, they are unlikely to contain the outbreak on their own. Additional containment measures, such as sufficiently rapid contact tracing within the epicenter of the outbreak and travelers' self-reporting of virus exposure and self-isolation, could be important for limiting global disease spread, according to the authors. — B.D.