In this issue . . .

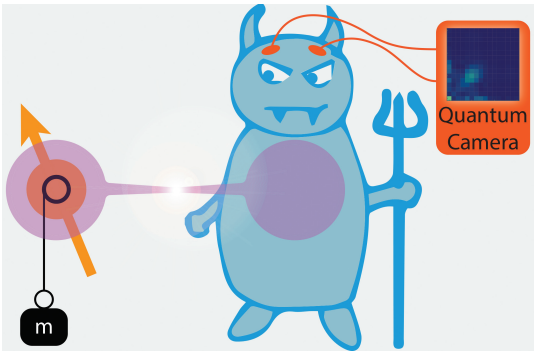
Barley gene might hold a key to improving beer quality

Malting, which involves the enzymatic breakdown of proteins and starch found in barley grains during beer production, is known to be under genetic control, but few of the underlying genes have been pinpointed. Unlike feed varieties of barley, malt varieties contain low levels of beta-glucan, a polysaccharide that increases wort viscosity and creates unsightly haze in beer. Surinder Singh et al. (pp. 7725–7730) used genetic methods to parse a DNA segment at the tail-end of barley chromosome 4H that was previously implicated in malting and accounts for nearly 29% of the variation in barley's beta-glucan content. From a set of 22 candidate genes, the authors identified *thaumatin-like protein 8* (*TLP8*), an enzyme that breaks down beta-glucan and is expressed at up to threefold higher levels in malt varieties, compared with feed varieties. Expression levels of *TLP8* correlated with those of beta-glucan as seed germination progressed. Further, 2 days after germination, malt varieties exhibited a 60% drop in beta-glucan levels, compared with a 20% drop in feed varieties. The presence of strong reducing agents during malting decreased the binding of beta-glucan to the TLP8 protein, whereas some oxidizing agents boosted binding, suggesting that oxidation might ease the removal of beta-glucan during wort preparation. According to the authors, adjusting redox conditions during the beer-making process could help alter the TLP8–beta-glucan interaction and potentially improve beer quality. — P.N.

Altering redox conditions might improve beer quality. Image courtesy of iStockphoto/Givaga.

Quantum Maxwell demon

Conceived as an imaginary creature in a physics thought experiment, a Maxwell demon is a device capable of converting thermal energy into work with apparently greater efficiency than that permitted by the laws of thermodynamics by using information about the microstate of a system. Maxwell demons have been realized experimentally for classical systems but not for quantum systems. Nathanaël Cottet et al. (pp. 7561–7564) experimentally realized a quantum Maxwell demon using a superconducting circuit with resonant frequency f_S as the system, embedded inside a microwave cavity functioning as the demon. The system and the demon were coupled such that the demon would only be in an excited state if the system were in the ground state and vice versa, and the resonant frequency of the system shifted whenever the demon was excited. Thus, the demon would allow photons of frequency f_S to stimulate emission from the system in the excited state, but prevented the photons from being absorbed by the ground state system. The result was a greater amount of work extracted in the form of photons in the presence of the demon. Quantum tomography of the demon



Imaging a Maxwell demon's information about a working quantum bit to which it is entangled.

verified that the demon's informational entropy was always greater than the decrease in system entropy. According to the authors, the results suggest the usefulness of superconducting circuits for quantum thermodynamics experiments. — B.D.

Global priorities for mammal conservation

Conservation plans designed to protect biodiversity are often based on taxonomic variables, including species distribution, endemism, and vulnerability. However, relying solely on taxonomic variables may result in underrepresentation of species with unique functional roles or evolutionary histories. Fernanda Brum et al. (pp. 7641–7646) created global maps that identify priority regions for mammal conservation based on three biodiversity measures: taxonomy, phylogenies, and functional roles. The authors identified the 17% of terrestrial surfaces that are most important for mammal conservation according to each of the three dimensions of biodiversity, and found that of the three sets of conservation priorities, only 4.6% of global land area overlapped. The authors also found that of the lands identified as high conservation priorities by all three biodiversity measures, only 1% is currently protected. The authors suggest that the currently protected areas are not advantageously placed for conserving mammal species, phylogenetic diversity, trait diversity, and threatened species. According to the authors, conservation planning using multiple dimensions of biodiversity could help maximize species preservation, evolutionary potential, and ecosystem function. — L.C.

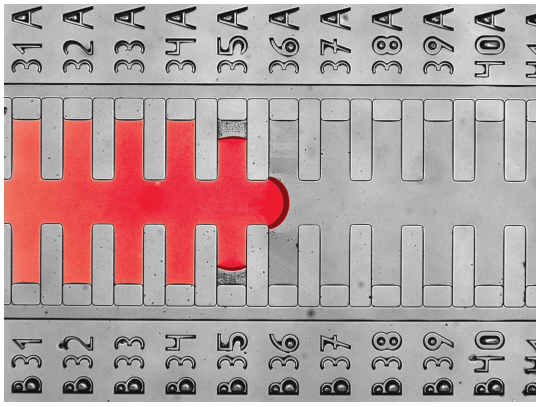
Endangered red panda. Image courtesy of Flickr/Mathias Appel.

Gerbil genome sequence suggests how mutation shapes adaptation

Sand rats, which inhabit North African and Middle Eastern deserts, are gerbils that have long been used as models of diet-induced diabetes, partly because the species tends to develop type 2 diabetes and obesity upon consuming carbohydrate-rich diets. Because previous studies in gerbils failed to detect the *Pdx1* gene, which encodes an insulin-activating gene switch thought to be conserved across mammals, researchers hypothesized that sand rats' propensity for diabetes might be due to the lack of the gene. Adam Hargreaves et al. (pp. 7677–7682) examined a paradox embodied in the hypothesis: Pdx1 is essential for normal pancreatic development. Standard shotgun sequencing and assembly of the sand rat genome failed to turn up *Pdx1*. However, sequencing and reassembly with longer-read sequence data unearthed what had eluded standard sequencing: a mutation-ridden genomic region enriched in GC nucleotides and replete with essential genes, including a modified *Pdx1*, which was found to be expressed in the pancreatic islets and duodenum. The sand rat's *Pdx1* mutations compromised the encoded protein's ability to regulate insulin production but seemingly conserved the portion of the protein crucial for pancreatic development, solving the paradox. The authors suggest that the mutations in the highly variant *Pdx1* gene may have enabled sand rats to adapt to arid habitats and low calorie intake. The findings suggest how mutation hotspots might shape natural selection, according to the authors. — P.N.

Antimicrobial susceptibility testing with droplet arrays

Antimicrobial susceptibility testing (AST) is a method used to probe pathogens for resistance or susceptibility to specific antibiotics. Although AST can help mitigate antibiotic resistance, current tests are time-consuming, taking up to 1 week or more. Jonathan Avesar et al. (pp. E5787–E5795) describe a rapid method for antimicrobial susceptibility testing



Loading a stationary nanoliter droplet array.

that is both practicable in a clinical setting and can deliver results on the same day. The system uses a stationary nanoliter droplet array (SNDA) to chemically isolate and culture cells, as well as the minimally toxic blue dye resazurin, which fluoresces in proportion to the number of bacteria in the assay. Fluorescence is measured every 30 minutes, and a custom algorithm analyzes the kinetic growth curves in each well to yield rapid results. Furthermore, the SNDA can interface with commonly available laboratory equipment, such as a microscope glass slide, and can be loaded by hand with a conventional pipette, enabling its use in resource-limited settings, according to the authors. — T.J.

Frog evolution following Cretaceous–Paleogene extinction

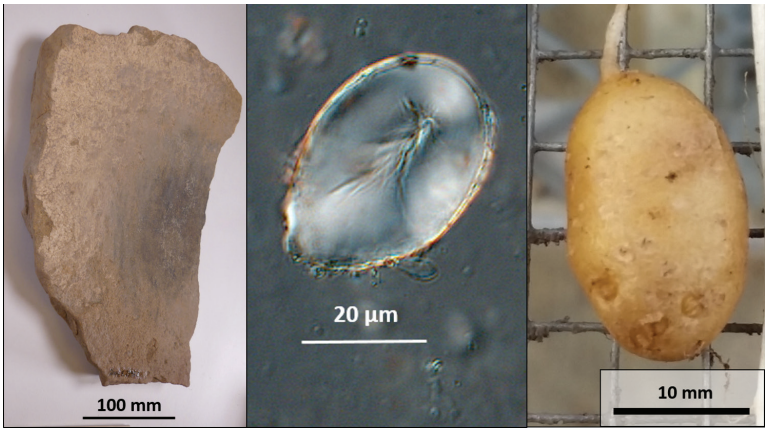
Frogs make up around 90% of living amphibian species and are among the most diverse vertebrate groups. The global distribution and biological characteristics of frogs make them a prime candidate for studies on evolutionary and conservation biology. However, the evolutionary history and timing of frog diversification remain unclear. Yan-Jie Feng et al. (pp. E5864–E5870) used phylogenetic and biogeographic analyses to study frog evolution. Using genetic data from more than 300 frog species, the authors report that the majority of living frog species originated

The Bornean ranid frog *Chalcorana raniceps*. Image courtesy of Yu Zeng (University of California, Merced, CA).

from three frog lineages—Hyloidea, Microhylidae, and Natatanura—that underwent rapid diversification at the end of the Mesozoic, around 66 million years ago, following the Cretaceous–Paleogene (K–Pg) extinction event. The three radiations, the authors suggest, might account for approximately 88% of living frog species. Additionally, results from biogeographical analyses indicate that Africa is likely the region of origin of modern frogs, and that the current distribution of frogs is likely associated with the breakup of Pangaea and later fragmentations of Gondwana. According to the authors, the K–Pg mass extinction event reshaped frog evolution, thereby influencing modern frog diversity and geographic distribution. — C.S.

Potato use in North America

Despite the diversity of wild potato species found in the New World, only a few archaeological records attest to the importance of wild potatoes as an energy



(*Left to Right*) Metate grinding stone (~8,500 years old) from North Creek Shelter, starch granule with eccentric hilum and other characteristics diagnostic of *S. jamesii,* and tuber and stolon from *S. jamesii*.

source during prehistoric times. Lisbeth Louderback and Bruce Pavlik (pp. 7606–7610) identified wild potato starch granules from ground stone artifacts at North Creek Shelter near Escalante, Utah. The authors extracted granules adhering to artifacts from archaeological deposits dating between 10,900 and 10,100 years ago, making this the earliest documented use of wild potatoes in North America. The authors identified 323 starch granules and used five diagnostic characteristics to identify nine of the granules as *Solanum jamesii*, a tuber-bearing species native to the American Southwest. An additional 61 starch granules were identified as likely *S. jamesii* because they possessed at least three diagnostic characteristics. Tools found in younger deposits, which were approximately 6,900 years old, also contained *S. jamesii* granules, indicating that Native Americans consumed *S. jamesii* intermittently for at least 4,000 years. According to the authors, botanical evidence can provide insights into the study of human diets and foraging behaviors. — L.C.