

Engineering cultured human cells to survive desiccation

Water is considered essential for active life, but some organisms can survive severe desiccation for extended periods by expressing various protective proteins such as late embryogenesis abundant (LEA) proteins. Shumin Li et al. (pp. 20859–20864) engineered a human liver cancer cell line to express LEA2 or LEA3, both of which are naturally found in brine shrimp embryos, and investigated whether either protein protected the cells against desiccation. Because many desiccation-tolerant organisms also accumulate low molecular weight solutes—such as the sugar trehalose, which protects cells against osmotic stress during desiccation—the authors also engineered the cells to express trehalose transporter (TRET1) to enable trehalose uptake. Cells were incubated in medium containing trehalose prior to desiccation. The authors then immediately rehydrated the cells and examined membrane integrity by microscopy. In the absence of trehalose and LEA proteins, the authors found no membrane integrity, but cells that contained trehalose and expressed either LEA protein showed 98% integrity. Moreover, cells containing LEA3 and trehalose proliferated 18-fold after 7 days in culture, whereas nondried controls proliferated 27-fold; cells expressing LEA2 with or without trehalose proliferated more slowly. The findings may aid the development of strategies for long-term storage of desiccated cells, according to the authors. — N.Z.

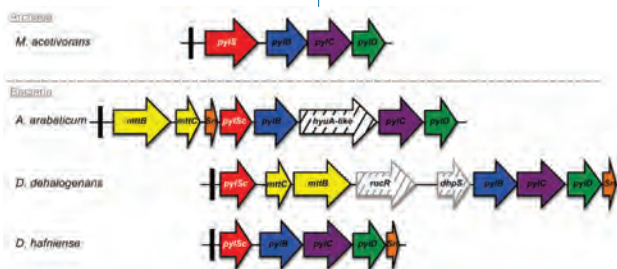


Salt-encrusted embryos of the brine shrimp *Artemia franciscana* from the shoreline of the north arm of the Great Salt Lake, Utah.

Bacterium expands its genetic code depending on carbon source

Some archaeal and bacterial species have evolved an expanded genetic code in which the stop codon UAG can encode the noncanonical amino acid pyrrolysine (Pyl), but little is known about the Pyl regulatory system in vivo. Laure Prat et al. (pp. 21070–21075) investigated the regulation of Pyl-decoding in three bacterial species that naturally contain the gene cassette required to synthesize and genetically decode the Pyl codon. The authors found that only one of the three species, *Acetohalobium arabaticum*, produced aminoacylated Pyl-tRNA^{Pyl}, which is required for Pyl incorporation into newly synthesized

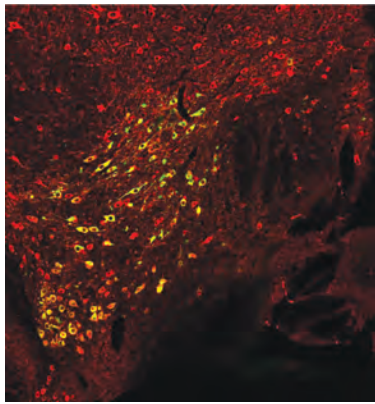
proteins. Further, *A. arabaticum* expressed aminoacylated Pyl-tRNA^{Pyl} only when cells were provided with trimethylamine as the energy source, but not when grown on pyruvate, suggesting that this organism modulates the size of its genetic code in response to the available energy source. In contrast to archaeal Pyl-decoding species that constitutively express the Pyl-decoding gene cassette, *A. arabaticum* downregulated the expression of genes in the Pyl cassette in the absence of trimethylamine, the authors found. In addition, Pyl-containing proteins were detected only in cells grown in the presence of trimethylamine, but not pyruvate. The findings suggest that the genetic code within a single cell may be more dynamic than previously recognized, according to the authors. — N.Z.



Genomic arrangement of genes required for Pyl decoding in archaeal and bacterial species.

Genetic factors underlying neural responses to alcohol

The brain's dopamine reward circuitry mediates the rewarding and reinforcing properties of alcohol and addictive drugs, but the genetic factors that control dopaminergic neuron activity and the responses to addictive drugs remain unclear. Previous studies have suggested a link between alcohol intake and genetic variation in the



Dopaminergic neurons in the ventral tegmental area, whose activity is dependent on the *RASGRF2* gene.

ras-specific guanine-nucleotide releasing factor 2 (RASGRF2) gene. David Stacey et al. (pp. 21128–21133) report that *RASGRF2* knockout mice showed reduced alcohol intake and preference compared with wild-type mice. Furthermore, the absence of *RASGRF2* prevented the otherwise normal ethanol-induced release of dopamine, and impaired the activity of dopamine-releasing neurons in a region of the midbrain called the ventral tegmental area. The authors also found that dopamine neuron excitability is con-

trolled by the activity of the signaling protein ERK, which is activated downstream of the Ras-GRF2 protein. Finally,

fMRI analysis of 663 14-year-old boys performing a reward-based task revealed that individuals with genetic variations in the *RASGRF2* gene display increased neuronal activity in the ventral striatum, a part of the dopamine reward circuitry. These genetic variations were associated with a high number of drinking

episodes in the same individuals at age 16. The findings suggest that *Ras-GRF2* may regulate dopaminergic neuron activity, reward sensitivity, and alcohol use in humans, according to the authors. — N.Z.

Groundwater flow drives ramification in spring-cut valleys

From vascular systems that circulate blood to watersheds that drain rivers, stream networks exhibit strikingly

similar geometries. Contemplated since at least the time of Leonardo da Vinci, ramification—the branching mechanism by which stream networks grow—remains an elusive phenomenon. To investigate the phenomenon, Olivier Devauchelle et al. (pp. 20832–20836) examined spring-cut valley networks in Florida and found that channels incised by groundwater seepage bifurcate at a characteristic angle of $2\pi/5$ or 72° . The authors determined this value by solving an expression for the theoretical angle at which two distinct branches emerge from a single valley head, based on well-established equations for how groundwater flows into springs and on simple assumptions about the direction in which spring-fed streams grow. The authors then analyzed nearly 5,000 bifurcated streams in a 100 km² groundwater field on the Florida Panhandle and found a mean bifurcation angle equal to $71.9^\circ \pm 0.8^\circ$, strongly supporting the model. The examination, which shows that groundwater flow alone predicts the average angle at which streams split in this Florida network, suggests that ramification occurs without regard to the water flow or sediment within the streams, according to the authors. — T.J.

Wildfire size and climate change

As Earth's climate warms, wildfire frequency and the amount of biomass burned are predicted to increase. But few fire prediction models have assessed how climate change may affect fire size. To address this question, Adam Ali et al. (pp. 20966–20970) used sedimentary charcoal records from nine lakes located in the eastern North American boreal forest to reconstruct the region's fire history over the last 7,000 years. The authors deduced the amount of forest cover lost to past fires, as well as past fire frequency, from variations in the rate of charcoal accumulation, and used these metrics to estimate fire size. The authors found that fire size has increased gradually during the last 7,000 years: Between approximately 3,000 and 7,000 years ago, the authors report that the region likely experienced numerous, small wildfires; by contrast, the last 3,000 years were characterized by larger, less frequent fires. The authors then compared these findings with reconstructions of the climate for the same time period, and suggest that fire frequency and total biomass burned were determined by the intensity of summer solar radiation and precipitation, whereas fire size depended on spring temperatures. The findings suggest that continued climate warming might lead to larger spring wildfires, according to the authors. — N.Z.



Image courtesy of Stéphane Chalifour (Société de protection des forêts contre le feu [SOPFEU], Québec City, Canada).

Charred particles released by wildfires can be used to investigate wildfire history.