

could improve prenatal care, especially in low-resource settings. By measuring the levels of certain placental RNA transcripts in maternal blood, Ngo *et al.* developed two noninvasive blood tests that provide a window into the progression of individual pregnancies. In a small proof-of-concept study, the first blood test predicted fetal age and delivery date with an accuracy comparable to that of ultrasound. The second blood test, also examined in a small pilot study, discriminated women at risk of preterm delivery from those who delivered at full term. The next step will be to assess the reliability of the tests in large, blinded clinical trials. —PAK

*Science*, this issue p. 1133

## PLANT GENETICS

### Sterility in rice via toxin and antidote

Crossing wild and domestic rice often results in hybrid sterility. Such genetic barriers can prevent the movement of potentially beneficial genes from wild rice into domestic varieties. To understand the barriers preventing gene flow, Yu *et al.* mapped a quantitative trait locus (QTL) that determines sterility between wild-type and domestic rice. This QTL encodes two open reading frames (ORFs) that are both expressed during gametogenesis. The ORFs encode a toxin, which affects the development of pollen, and an antidote,



Hybrid rice varieties produce sterile pollen.

which is required for pollen viability. Thus, selfish genetic elements can underlie evolutionary strategies that facilitate reproductive isolation. —LMZ

*Science*, this issue p. 1130

## ENVIRONMENTAL STUDIES

### Economic rationale for fishing the high seas

Economic evaluations of high-seas fishing have been lacking, in part owing to the scarcity of data on the costs and revenues of fleets that fish in these elusive waters. Sala *et al.* wanted to quantify high-seas fishing efforts globally and assess whether and when high-seas fishing makes economic sense. They used satellite data and machine learning to track the activity of more than 3600 fishing vessels in near real time. Patterns of fishing profitability varied widely between countries, types of fishing, and distance to port. As much as 54% of present high-seas fishing grounds would be unprofitable without large government subsidies, supporting recent calls for subsidy management reforms for the high seas. —PJB

*Sci. Adv.* 10.1126/sciadv.aat2504 (2018).

## DNA REPAIR

### DNA-bound ubiquitin coordinates repair

Ubiquitylation is a posttranslational modification that reversibly alters various protein properties. Liu *et al.* discovered that Lys<sup>63</sup>-linked polyubiquitin chains bound to the free ends of double-stranded DNA, bridged the broken ends of DNA, and recruited repair proteins. Ubiquitins with DNA-binding motif mutations were found in several types of tumors. When expressed in cultured cells, these mutant ubiquitins impaired the cellular response to DNA-damaging agents, suggesting that it might be possible to therapeutically exploit these mutations in some cancer patients. —LKF

*Sci. Signal.* 11, eaar2566 (2018).

## IN OTHER JOURNALS

Edited by **Sacha Vignieri** and **Jesse Smith**

Aerial view of a section of the San Andreas fault



## GEOPHYSICS

### The San Andreas creeps along the decade

The famous San Andreas fault in California is an excellent place to understand the behavior of faults. Khoshmanesh and Shirzaei used high-resolution satellite measurements to track surface deformation along the central portion of the fault over two decades. Accurate modeling of the deformation requires shifts in the time scale of the fault's aseismic creeping behavior from yearly to decadal. The different modes of creep are important for assessing seismic hazard and may provide some clues about fault rupture. —BG

*Geophys. Res. Lett.* 10.1002/2018GL077017 (2018).

## MOLECULAR BIOLOGY

### The long and short of RNA export

Circular RNAs (circRNAs) are back-spliced RNA products that have regulatory roles in gene expression, and most circRNAs are enriched in the cytoplasm. Huang *et al.* identified protein factors that are required to export circRNAs from the nucleus to the cytoplasm.

An RNA interference screen targeting some proteins that are known to export various linear RNAs in *Drosophila* cells showed that a RNA helicase is required for the cytoplasmic accumulation of circRNAs that are longer than 800 nucleotides. The two human homologs of this *Drosophila* helicase play similar roles in human cells. Surprisingly, one controls long (>1300-nucleotide)

Human-induced changes in Lake Baikal have resulted in the spread of a previously rare filamentous alga.



#### ECOLOGICAL INVASIONS

### An algal transformation in Lake Baikal

In central Siberia, Lake Baikal—the world's deepest freshwater lake—is undergoing ecological change. Volkova *et al.* report that species of the filamentous mat-forming alga *Spirogyra*, formerly present at low abundance in restricted areas of the lake, have proliferated and diversified in recent years. *Spirogyra* has invaded shallow-water zones of the lake, and several species have appeared in Baikal for the first time. These changes are likely to have been driven by a combination of factors, some of them anthropogenic, such as agricultural runoff and changing patterns of seasonal temperatures. The consequences may be hard to predict and control. —AMS

*Phycologia* **57**, 298 (2018).

and the other controls short (<350-nucleotide) circRNAs. Future investigation of pathways that measure and export circRNAs of different lengths will shed light on circRNA functions. —SYM

*Genes Dev.* 10.1101/gad.314856.118 (2018).

#### DNA METHYLATION

### Tissue-specific DNA demethylation after birth

Because of changes in their environment, including the need to repair tissue, cells cannot remain static. They must do their job even if conditions around them vary. One way to accommodate change in gene expression is through DNA methylation. The vast majority of this modification takes place during mammalian embryogenesis. Initially, methyl groups are

removed around implantation, and then de novo methylation occurs in specific tissues and at set times during cell differentiation. Using high-throughput and genetic analysis, Reizel *et al.* show that considerable post-natal demethylation also occurs. For example, hormone signaling triggers DNA demethylation at enhancer-like regions in the liver after birth in mice. These epigenetic changes give access to specific chromatin sites for proper hepatocyte gene expression and function. —BAP

*Nat. Comm.* 10.1038/s41467-018-04456-6 (2018).

#### PROTEIN STRUCTURE

### Not just a LARK

Many proteins involved in neurodegenerative diseases contain low-complexity domains (LCDs) that frequently exhibit no secondary structure but are

implicated in both functional reversible aggregation and pathological irreversible aggregation. Guenther *et al.* determined the structures of 10 peptide segments from the LCD domain of the RNA binding protein TDP-43. The LCD is implicated in the formation of stress granules, which disaggregate when stress is relieved, and of pathogenic amyloid fibrils. Six of the segments form structures characteristic of amyloid fibrils, whereas four form labile amyloid-like interactions, termed LARKs. Disease variants of TDP-43 convert the LARKs to irreversible aggregates. This raises the possibility that either mutagenesis or protein modifications such as phosphorylation may play a role in switching between functional and pathological aggregation. —VV

*Nat. Struct. Mol. Biol.* 10.1038/s41594-018-0064-2 (2018).

#### GENETICS

### Genomic crowdsourcing with privacy

Privacy concerns can be an obstacle to large-scale donation of the genetic material that is essential for understanding how genetic variants are associated with disease. Cho *et al.* have developed an approach that has the potential to be scalable to as many as a million genomes. Their system is based on dividing genotype and phenotype data from each individual among multiple servers in such a way that no one server can infer the original data. An attacker would have to hack all of the servers to extract the data. Computational approaches that simplified corrections for misleading correlations and sped up the system were used to reproduce three published genome-wide association studies representing 23,000 genomes and could make the process cost-effective. —BJ

*Nat. Biotechnol.* 10.1038/nbt.4108 (2018).

#### CLIMATE CHANGE IMPACTS

### Hurting the most vulnerable

The Paris Agreement set a goal of limiting global average anthropogenic climate warming to 1.5°C or less—cooler than the oft-cited target of 2°C that previously had been considered the threshold of dangerous consequences. Is the difference in impacts between the two goals meaningful, and who would be affected most by a failure to stay within the lower limit? King and Harrington find that exceeding the 1.5°C ceiling would affect tropical latitudes—which have a disproportionate share of poor populations—more than higher latitudes. Thus, if ways are not found to meet the global warming targets of the Paris Agreement, then the most vulnerable will experience the greatest consequences. —HJS

*Geophys. Res. Lett.* 10.1029/2018GL078430 (2018).

PHOTO: ANDREY NEKRASOV/ALAMY STOCK PHOTO