

In this issue . . .

Machine-learning approach identifies plants at risk of extinction

Plant biodiversity supports food chain diversity, helps counter natural disasters, and contributes to ecosystem productivity. The International Union for Conservation of Nature Red List of threatened species contains only a small fraction of extant species on Earth, partly because species assessments are expensive and time-consuming. Tara Pelletier et al. (pp. 13027–13032) developed a machine-learning approach to predict plant species at risk of extinction using open-source geographic, environmental, and morphological trait data for more than 150,000 land plant species. The authors identified various variables predicting extinction risk, including geographic and bioclimatic traits, and calculated the probability of a species being designated “at risk” based on the traits. The authors report that a large number of previously unassessed land plant species are likely at risk of extinction and may need to be considered for inclusion in the Red List. Further, the approach can be used to identify species at the highest extinction risk and to pinpoint geographic regions with the greatest need for conservation efforts by pairing GPS coordinates with risk probabilities. According to the authors, the approach can be used to guide policies aimed at allocating resources for biodiversity conservation. — T.G.



Artistic rendition of global conservation risk hotspots for land plant species. Image courtesy of Abbie Zimmer (Ohio State University, Columbus, OH).

Mitochondrial DNA is paternally inherited in humans

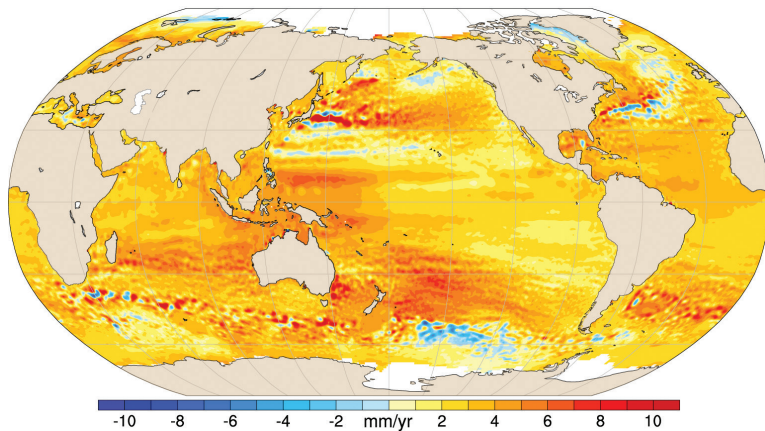
Mitochondria, which are the energy-producing organelles of cells, contain their own compact genomes that are separate from the nuclear genome. Mitochondria and mitochondrial DNA are generally thought to be maternally inherited in humans. In contrast to this widely held view, Shiyu Luo et al. (pp. 13039–13044) provide evidence of biparental inheritance of mitochondrial DNA in 17 members of three unrelated multigeneration families. The findings were independently validated using multiple approaches for whole mitochondrial DNA sequencing. The pattern of paternal inheritance of mitochondrial DNA appears to be determined in an autosomal dominant-like manner. The results suggest that the central dogma of maternal inheritance of mitochondrial DNA remains valid, but there are some exceptional cases wherein paternal mitochondrial

DNA could be passed onto offspring. According to the authors, the results may stimulate further study of mitochondrial DNA genetics that may provide insights into alternative mechanisms for the treatment of inherited mitochondrial diseases. — J.W.

Sea-level rise and climate variability

Satellite altimetry data have provided detailed and accurate data on sea-level rise since 1993. However, the extent to which observed changes in sea level reflect natural climate variations and long-term trends driven by external forcings, such as aerosols or greenhouse gas emissions, remains unclear. To address this question, John Fasullo and R. Steven Nerem (pp. 12944–12949) analyzed two large ensembles of 30–40 climate simulations, with each ensemble based on a single climate model. The authors calculated the forced response (FR) due to

external factors by averaging all of the simulations in an ensemble together, thereby canceling out the effects of internal variability. In both ensembles, spatial patterns of change during the altimeter era (1993–2018) in each of the individual simulations in



Altimeter era sea-level trends.

the ensemble correlated significantly with those due to the FR, much more so than in a control ensemble of unforced simulations. In addition, the altimeter era FR was significantly correlated with that simulated for 2020–2045. The results suggest that a significant amount of the trends in sea level measured by altimetry is due to external forcing and that such trends are likely to persist over the coming decades, according to the authors. — B.D.

Mechanisms of atopic dermatitis

Atopic dermatitis (AD) is a common skin disease in children, and its symptoms include inflammation and severe itching. Mutations in the transmembrane protein *Tmem79* are associated with a form of AD in both mice and humans. Joshua Emrick et al. (pp. E12091–E12100) used *Tmem79* knockout and reporter mouse lines to investigate the mechanisms underlying *Tmem79*-associated AD. The authors found that *Tmem79* is expressed in epithelial tissues, specifically in epidermal keratinocytes, as well as a subpopulation of sensory neurons. Loss of *Tmem79* in keratinocytes appeared to be responsible for most of the scratching phenotype, including a contribution from sensory nerve fibers. *Tmem79* knockout mice accumulated immune cells in the dermis, and treatment with cyclooxygenase inhibitors and an EP3 prostaglandin receptor antagonist reduced the accumulation and decreased AD-associated scratching. AD-associated itch involved histamine from mast cells acting through histamine receptors and appeared to be transmitted through TRPV1/TRPA1-negative H4R-positive nerve fibers. The authors suggest that *Tmem79* may help prevent the accumulation of harmful products of oxidative stress, and mutations in *Tmem79* thus lead

to a loss of protection from oxidative stress, resulting in the inflammation and severe itching seen in *Tmem79*-associated AD. According to the authors, the study suggests potential therapeutic targets in the prostaglandin and histaminergic signaling pathways that could help treat itching in *Tmem79*-associated AD. — S.R.

Pesticides and honey bee mass mortality

Mass honey bee mortalities occurred in France in the 1990s following the introduction of two pesticides, imidacloprid and fipronil. The former compound was initially thought to be the causal agent, but laboratory studies combined with modeling simulations point to the latter being more likely involved in honey bee deaths. Philippa Holder et al. (pp. 13033–13038) measured dose-dependent mortality rates for imidacloprid, fipronil, and two other widely used pesticides in bees from outdoor hives, and used the data to model colony-level effects in demographic simulations. The simulations predicted 4,000–9,000



Bee collecting pollen. Image courtesy of Wikimedia Commons/Jon Sullivan.

more bee deaths than control conditions during the first week of fipronil exposure, leading to colony collapse within 2 or 3 weeks. None of the other pesticides resulted in mortality sufficient to cause colony collapse. The authors employed two assays, recommended by proposed international regulatory guidelines, for determining the ability of potentially toxic compounds to bioaccumulate. Fipronil exhibited signs of toxic bioaccumulation in both assays, whereas the other pesticides showed no signs of bioaccumulation in either assay. The authors found that toxic fipronil metabolites from a single meal persisted in honey bees for at least 6 days. The results implicate fipronil as a likely cause of the mass honey bee mortalities in France in the 1990s and demonstrate the value of the proposed bioassays for identifying harmful bioaccumulative substances, according to the authors. — B.D.

