

Adam Ewing and Haig Kazazian at the University of Pennsylvania in Philadelphia used high-throughput sequencing to analyse the genomes of 25 individuals, including 15 people who were unrelated. They identified 1,139 insertion sites for the L1 retrotransposon family, of which 247 were previously unknown. They estimate that there are 3,000–10,000 relatively common L1 elements in the human population and that the rate at which a human genome gains a new L1 insertion is 1 in 140 births per generation. **C.L.**

NANOSCIENCE

Shifted shells

Phys. Rev. Lett. **104**, 207203 (2010)

Experimental findings confirm a theoretical prediction that certain chemically uniform nanoparticles have magnetically distinct cores and shells.

Using refined neutron-scattering techniques, Kathryn Krycka of the National Institute of Standards and Technology in Gaithersburg, Maryland, and her team probed the three-dimensional magnetic structure of magnetite nanoparticles nine nanometres wide. In the presence of an external magnetic field, they found a shell layer 1.0–1.5 nanometres thick in which magnetization was angled at 90° to the particle's core.

The findings indicate that nanoparticles cannot be assumed to have uniform magnetic moments — which could be useful in applications such as data storage. **D.P.C.**

GEOSCIENCE

Dam that water

Geophys. Res. Lett. doi:10.1029/2010GLO43462 (2010)

The coastal tide gauges that we rely on for information about sea-level rise may not be giving an accurate picture of the effects of climate change. This is because many of these instruments are located close to dams, which impound huge amounts of water on land. Dams depress sea levels globally, by taking some of the water out of the equation. However, the impounded water also depresses Earth's surface, gravitationally attracting more sea water and resulting in local sea-level increases.

Julia Fiedler and Clinton Conrad at the University of Hawaii in Honolulu analysed data from 674 of the world's largest reservoirs collected between 1900 and 2009. After accounting for the reservoir water, the location of tide gauges and variations in regional rise rates, the researchers estimate that global sea levels have increased by about 2.3 millimetres per year over the past century — around 20% faster than indicated by the tide gauges. **C.L.**

ECOLOGY

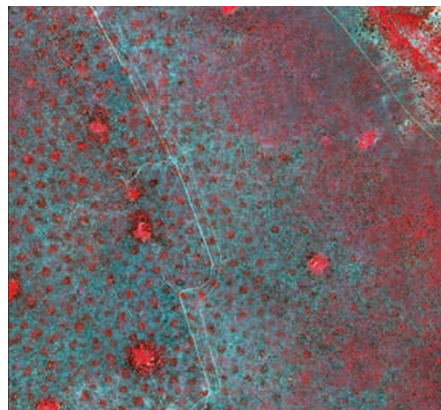
Mighty termite mounds

PLoS Biol. **8**, e1000377 (2010)

The regular 'polka-dot' arrangement of termite mounds in East Africa boosts ecosystem productivity, researchers say.

Robert Pringle at Harvard University in Cambridge, Massachusetts, and his team found that plants grow more quickly and animals are more abundant around the subterranean mounds of termites (*Odontotermes*) in Kenya. This is because the fungus-cultivating creatures make the soil more moist and nutrient-rich than that of the surrounding dry savanna. The even spacing of the mounds (pictured as small red circles in satellite image) means that all points in the local landscape are relatively close to a mound, maximizing the ecosystem's productivity.

Simulated landscapes with randomly arranged mounds were less productive than those with regularly spaced mounds. **N.G.**



R. M. PRINGLE ET AL.

NEUROSCIENCE

Sound learning

Neuron **66**, 610–618 (2010)

To be able to recognize the source of a sound — a flute or a train, say — we first have to learn that sound's acoustic characteristics. Scientists in France report that such learning is subconscious, rapid and remarkably robust.

Trevor Agus at the École normale supérieure in Paris and his colleagues asked 12 volunteers to listen to a series of short snatches of random noise, and to identify which of the snatches included repetitions. Their success rate was below 50%.

But when one specific snatch containing repetition was secretly and randomly interspersed at frequent intervals, the listeners quickly became near-perfect in detecting repetition — even when the snatch was compressed in time or reversed. Moreover, they retained the memory for several weeks. **A.A.**

JOURNAL CLUB

Petr Svoboda

**Institute of Molecular Genetics
AS CR, Prague**

A molecular biologist explores how new genomic tools can be applied to wild animals.

Some time ago, I learned about a bizarre cancer that is decimating populations of the Tasmanian devil (*Sarcophilus harrisii*), the carnivorous marsupial popularized by the cartoon character 'Taz'. Devil facial tumour disease (DFTD) is a rapidly progressive and metastasizing facial cancer caused by a genetically altered cell line that is transmitted between devils by biting.

Studying model organisms in the lab can make the ruthlessness of nature seem distant. But when nature is brought into the lab, one can see the power that modern tools hold for exploring a biological problem — and the limited options available for solving such problems.

Elizabeth Murchison, now at the Wellcome Trust Sanger Institute in Hinxton, UK, and her colleagues performed a comprehensive genomic analysis of the DFTD cells (E. P. Murchison *et al. Science* **327**, 84–87; 2010). They examined not only the nuclear genome, but also that of the mitochondria, cells' energy-generating organelles. And they performed high-throughput sequencing of RNA molecules, including small RNAs.

Their analysis confirms that DFTD is caused by the transmission of genetically identical cells. The authors also found that DFTD probably originated in Schwann cells, which wrap around neurons, and identified a set of genes that could contribute to DFTD pathology. This is an outstanding example of how next-generation sequencing technologies allow for in-depth analysis of a species that has been difficult to study using other genomic tools.

The data provide diagnostic and monitoring tools that will hopefully help in vaccine development. Until then, Taz's future lies in the hands of natural selection and conservation efforts that aim to protect healthy animals from DFTD carriers.

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