

## NEUROBIOLOGY

## Squeaking in tongues

*Cell* **137**, 961–971 (2009)

Mice carrying a humanized version of a gene considered key to the human capacity for speech show subtle changes in their brains and in the way they vocalize.

Wolfgang Enard of the Max Planck Institute for Evolutionary Anthropology in Leipzig, Germany, and his colleagues substituted two amino acids in the mouse *Foxp2* protein to generate the humanized version. The animals remained generally healthy, but calls made by isolated pups had a different structure from those of normal mouse pups.

The authors also found structural, neurochemical and neurophysiological changes to neurons in a brain circuit associated with speech in humans. They say it could represent the first investigation, in an animal model, of amino-acid substitutions that might be relevant to human evolution.

**For a movie about this work, see** <http://bit.ly/tLlFa>.

## CHEMISTRY

## Toxic toadstools

*Nature Chem. Biol.* doi:10.1038/nchembio.179 (2009)

A form of mushroom poisoning that leads to often-fatal breakdown of skeletal muscle tissue has been claiming unlucky victims in Japan since at least the 1950s. However, the toxin responsible has eluded mycologists owing to both its instability and confusion about the classification of the *Russula* mushrooms that it is associated with, say Kimiko Hashimoto of Kyoto Pharmaceutical

University in Japan and her colleagues.

They found that *Russula subnigricans* (pictured below) from Kyoto were toxic when fed to mice, whereas similar mushrooms from Miyagi prefecture were not. In addition, they identified the toxic compound responsible for the poisoning: cycloprop-2-ene carboxylic acid.

Extrapolating from data on mice, the researchers say that a serving of two to three mushroom caps (less than 200 grams) would kill most humans.

## GENETICS

## Filling mouse holes

*PLoS Biol.* **7**, e1000112 (2009)

Humans and mice have slightly less in common than was previously thought, reveals the international Mouse Genome Sequencing Consortium.

The team produced a more complete *Mus musculus* genome by sequencing DNA fragments and linking them back to a physical map of the genome. Earlier efforts used an efficient approach known as whole-genome sequence and assembly, which does

not require a physical map. This left many gaps owing to difficulty in assembling some regions, such as those containing repetitive DNA. Now researchers have filled more than 175,000 gaps and uncovered more than 139 million bases of overlooked DNA. Moreover, they identified more than 2,000 genes the sequences of which were missed or wrongly assembled before, more than half of which do not have an analogue in the human genome.

The results underscore the importance of complete genome sequences, and should lend more power to comparative studies in human biology, the authors suggest.

## QUANTUM PHYSICS

## Attack of the giant neutrinos

*Phys. Rev. Lett.* **102**, 201303 (2009)

Neutrinos are vanishingly small particles, but a theoretical analysis of neutrinos left over from the Big Bang shows that they could stretch across billions of light years.

Like all fundamental particles, the state and position of neutrinos can be described with a quantum-mechanical 'wavefunction'. George Fuller and Chad Kishimoto of the

University of California, San Diego, looked at the wavefunctions of neutrinos left over from the very beginning of the Universe. They found that these waves could extend for billions of light years. If true, that would mean that the individual neutrinos are effectively spread out over the same cosmic distances.

Disturbances could cause the wavefunction to collapse, and Fuller and Kishimoto postulate that gravitational effects or space-time itself might make the little particles pop into a single location.



K. HASHIMOTO

## JOURNAL CLUB

**Lucas N. Joppa**  
Nicholas School of the  
Environment, Duke University,  
Durham, North Carolina

**An ecologist calls for a  
citizen-science 'Wiki'.**

Where do species occur and why? What happens to ecological communities when species are removed or when alien species invade? And how will the answers shift as climates change? These questions span huge spatial and temporal scales, and involve

millions of species. By contrast, ecological field studies are generally of short duration, include few species and cover small areas. This means that getting data for the big questions is a tall order — impossible without harnessing a deeper reserve of people power.

Citizen science — in which qualified scientists oversee volunteers — is not new. The Audubon Society's Christmas Bird Count has run for 108 years and mobilizes about 60,000 volunteers across 1 million square kilometres of North America who count about 58 million individual

birds annually. Other citizen-science projects are under way around the world.

Dirk Schmeller at the Helmholtz Centre for Environmental Research in Leipzig, Germany, and his colleagues analysed 395 citizen-science projects across five European countries, involving more than 46,000 participants (D. Schmeller *Conserv. Biol.* **23**, 307–316; 2008). Volunteers donated more than 148,000 person-days per year, a figure inconceivable using professional scientists alone. Schmeller *et al.* found that volunteer-gathered data are reliable and unbiased,

with data quality determined less by 'volunteer' status, and more by survey design and methodology.

The rapid increase in citizen-science data sets can revolutionize what we know about the natural world. Wikipedia has shown that the public is willing to donate time, talent and knowledge, given a sufficient platform. Biodiversity data lack such a platform for input, integration, mapping and dissemination. This is a deficiency that the environmental community should address.

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