

PLANT GENETICS

Sweet potato is already a GM crop

The sweet-potato genome contains genes from bacteria, so is an example of a naturally occurring genetically modified (GM) plant.

While combing through the genome of the domesticated sweet potato (*Ipomoea batatas*), Jan Kreuze of the International Potato Center in Lima, Peru, and his colleagues stumbled on genes that originated from one or more *Agrobacterium* species. These bacteria infect plants and transfer DNA into their hosts' genomes, so are used by researchers to genetically modify many agricultural crops. The two stretches of bacterial DNA found in the sweet potato are expressed in various tissues, and one of the sequences is found only in cultivated sweet potatoes — not in closely related wild strains.

These genes could encode traits that were desirable for domestication of the crop, and were probably transferred into an ancient sweet-potato ancestor, the authors say.

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GLACIOLOGY

Antarctic ice shelf nears its demise

The remains of an ice shelf that collapsed spectacularly in 2002 may be headed for total disintegration.

The break-up of the Larsen B ice shelf was one of the largest and fastest melting events ever seen by glaciologists. Ala Khazendar of the Jet Propulsion Laboratory in Pasadena, California, and his co-workers studied satellite and airborne radar measurements of the heights and flow

speeds of glaciers feeding the remaining, southern section of Larsen B. They found that two of the glaciers thinned by 15–20 metres between 2002 and 2011, and one of them increased its flow speed by 55% from 1997 to 2012.

Modelling suggests that when most of Larsen B disintegrated, the remaining glaciers had less ice to buttress them in place, causing them to destabilize.

Earth Planet. Sci. Lett. 419, 199–210 (2015)



ROBERT CAPUTO/AURORA PHOTOS

MICROBIOLOGY

Bacterial bonanza far from the West

Members of an isolated Amazon tribe in Venezuela (pictured) have the most diverse gut bacteria ever documented in humans.

Maria Gloria Dominguez-Bello at New York University School of Medicine analysed oral, faecal and skin bacteria from 34 Yanomami villagers who had never met anyone from the West until 2009. The researchers found almost double the genetic diversity in the faecal bacteria compared with the microbiomes of US residents. The faecal and oral bacteria also carried genes for antibiotic resistance, even though the people had no known exposure to the drugs.

In a separate study, Jens Walter at the University of Alberta in Edmonton, Andrew Greenhill at Federation University Australia in Churchill and their colleagues looked at the gut microbiomes of people from two rural areas of Papua New Guinea. They found that the bacteria were extremely diverse and included lineages not seen in US populations. Using ecological modelling, the authors attributed the increased diversity to low sanitation levels, which increased the swapping of bacteria between people.

Science Adv. 1, e1500183 (2015);
Cell Rep. <http://doi.org/3vh> (2015)

CANCER BIOLOGY

Some mutations in cancer arrive late

Subpopulations of tumour cells can harbour unique mutations that crop up later in a tumour's lifetime, and these could lead to treatment resistance.

Tumours contain cells with distinct mutations. Charles Swanton of University College London and his colleagues analysed DNA sequence data from more

than 2,500 people with cancer to find out which mutations can fuel the expansion of subpopulations of tumour cells. The team found that mutations that drive cancer growth tend to emerge early in a tumour's evolution, and are typically found throughout the tumour. But the mutations can also develop later, in small subpopulations of cells.

The results suggest that some tumours become more resistant to therapy when small populations carrying resistance