

Angert of Cornell University in Ithaca, New York, and her colleagues have found that *Epulopiscium* cells also contain up to 250 picograms of DNA, compared with a human cell's 6 picograms, and have 50,000–120,000 copies of genes believed to occur only once in each genome.

Other bacteria contain multiple copies of their genomes, but so far none has been found to have nearly as many as *Epulopiscium*.

NANOTECHNOLOGY

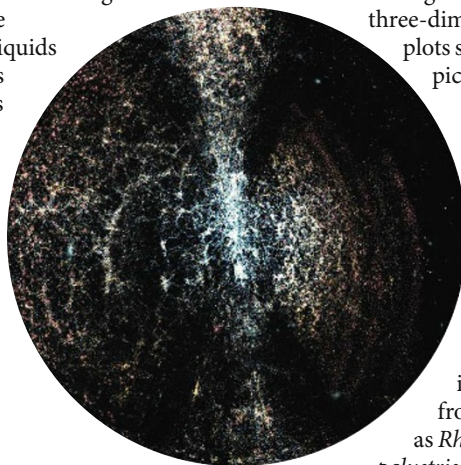
Tiny carbon workers

Nature Nanotech. doi:10.1038/nnano.2008.98 (2008)

Micromechanical devices are most commonly made from silicon; now it is time to welcome carbon-based wafers to the party. Kenji Hata at the Nanotube Research Center in Tsukuba, Japan, and his co-workers say wafers such as those that they have built could provide an inexpensive approach to making these microstructures.

The researchers constructed the wafers by growing an array of widely spaced, vertically aligned carbon nanotubes. These were then 'squeezed' together by introducing an alcohol solution; the surface tension of the liquids and strong interactions between the nanotubes pulled the tubes into a densely packed arrangement.

These wafers can be processed using the same lithographic techniques that are used to work on silicon. The team has made mini-cantilevers and a range of other structures.



CHEMICAL BIOLOGY

Maths and malaria

Nature Chem. Biol. doi:10.1038/nchembio.87 (2008)

A 'guilt by association' test can correctly pinpoint the function of proteins, reports a team led by Elizabeth Winzeler of the Scripps Research Institute in La Jolla, California. An algorithm the researchers wrote found that the malaria-causing parasite *Plasmodium falciparum* expresses a gene encoding CDPK1 — a protein with an unknown role — at the same time as some other genes involved in cell invasion and movement. These all become active as the parasite prepares for its sexual stage.

The authors then screened a chemical library for compounds that block CDPK1. One of these inhibited the protein and also prevented *P. falciparum* from entering its sexual stage, indicating that the bioinformatics algorithm had provided accurate clues to CDPK1's role.

ASTRONOMY

Galactic mapping

Astrophys. J. 678, 144–153 (2008)

Astronomers measure distance to galaxies in terms of 'redshift' — the far-off reddening of a galaxy's light as it zooms away from us. Current spectroscopic techniques measure at most a few hundred redshifts at once, but a new computer code can analyse larger batches of galaxies from digital images. It was developed by James Wray of Cornell University in Ithaca, New York, and Jim Gunn of Princeton University in New Jersey.

The algorithm works with general properties such as the colour and distribution of light across each galaxy. It gives good estimates of redshift when tested on 221,617 galaxies from the Sloan Digital Sky Survey, and could soon be used in the Sloan and other digital surveys to create three-dimensional galactic plots such as the one pictured left.

MICROBIOLOGY

Fuel cell

Environ. Sci. Technol. doi:10.1021/es800312v (2008)

Hydrogen is a useful and clean energy source, and it can be obtained from bacteria such as *Rhodospseudomonas palustris*. Bruce Logan of

Pennsylvania State University, University Park, and his collaborators have found that this bacterium has another potentially useful skill: it can produce an electric current.

The researchers extracted *R. palustris* from a microbial fuel cell — a device in which bacteria deliver electrons derived from the oxidation of foodstuffs to an electrode, thus producing current. After culturing, this strain did the job more efficiently on its own than it had in the mixed bacterial population from which it came. The work might lead to the development of systems that capture electricity or hydrogen from the same cultures.

M. SUBBARAO, R. LANDSBERG & D. SURENDRAN

JOURNAL CLUB

François Balloux

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A population geneticist looks back in time in search of human origins.

When and where anatomically modern humans evolved is arguably one of the most fundamental scientific questions. The issue also has philosophical and possibly even moral implications because it influences our definition of humanity. But I became involved in the subject for much more prosaic reasons. I was trying to make sense of the distributions among human populations of different versions of genes that imbue resistance to infectious diseases. It struck me that attempting to do this without a clear understanding of humans' past demography was bound to end in a muddle.

Despite decades of research, the origin of modern humans is still hotly debated. In a recent paper, Laurent Excoffier and his colleagues provide the first formal statistical evaluation of the likelihood for the various schemes that have been proposed (N. J. R. Fagundes *et al. Proc. Natl Acad. Sci. USA* 104, 17614–17619; 2007). They conclude that a recent expansion from a single African origin is better supported by the current geographical spread of human genes than a multi-regional scenario. The multi-regional hypothesis proposes that modern humans hybridized with archaic humans, such as *Homo erectus*, as they spread.

This result may seem unsurprising because most genetic evidence points to an African origin some 60,000 years ago with no or negligible hybridization with archaic humans. However, there is a twist. By far the best supporting evidence for hybridization between modern and archaic humans has been the observation that, looking back, the amount of time it takes to reach the most recent common ancestor of some genes largely predates the age of our species. The extensive simulations in this paper debunk that argument by demonstrating that such cases can arise if modern humans had a recent and single African origin.

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