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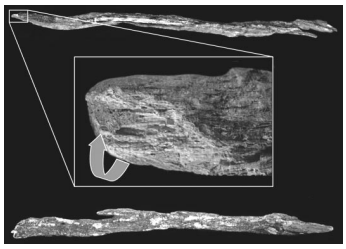
ANTHROPOLOGY

Chimpanzees use tools to dig for food

A report that chimpanzees use tools to dig up roots for food suggests that early humans could have used the same method. Previous research had speculated that such early use of tools allowed hominins to colonize arid savannahs and survive periods of food shortages. However, evidence has so far been confined to isotopic analyses of tooth-wear and fossils. Adriana Hernandez-Aguilar *et al.* suggest that early hominins could have used tools to dig for food. The researchers discovered 11 digging sites in the chimpanzee home-range in Tanzania. Although the authors were not able to film the animals in action, clues such as knuckle-prints, droppings, and chewed fibers showed that the excavations were the work of chimpanzees. At several sites, the researchers found sticks and shards of wood and bark that exhibit signs, such as impacted dirt, of having been used as digging tools. The tools were minimally worn, indicating that the chimpanzees used them simply to break through the hardened topsoil before excavating with their fingers. That chimpanzees use tools in this fashion shows that the same technology was within the reach of early human ancestors, the authors say. — K.M.



Digging tools used by chimpanzees.

"Savanna chimpanzees use tools to harvest the underground storage organs of plants" by R. Adriana Hernandez-Aguilar, Jim Moore, and Travis Rayne Pickering (see pages 19210–19213)

ANTHROPOLOGY

Rare great ape fossil discovered

Fossils of large hominoids in eastern Africa from the late Miocene period, when humans and the African great apes diverged, are so rare that some researchers have proposed that the last common ancestor actually returned from Eurasia. However, Yutaka Kunimatsu *et al.* now report the find of a fossil jaw in Kenya that they suggest represents a new great ape from this era. The discovery makes it more likely that the ancestor of humans and African great apes evolved in Africa. The last time a hominoid fossil of this period was found in Kenya was 1982. The new species, *Nakalipithecus nakayamai*, resembles the candidate formerly thought closest to a common ancestor: *Ouranopithecus macedoniensis* from Greece. Several details of the dentition indicate a less specialized diet than *Ouranopithecus*, placing *Nakalipithecus* in a genus of its own. The researchers found the fossil jaw, along with 11 isolated teeth, in volcanic mud flow deposits in the Nakali region of Kenya. Geological dating puts the age of the specimens between 9.80 and 9.88 million years. — K.M.

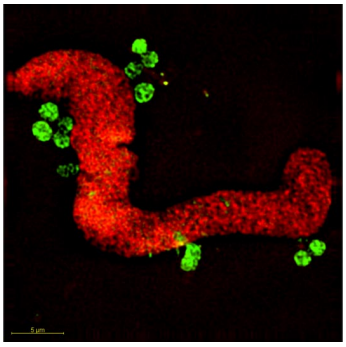
A jawbone discovered in a volcanic mud flow.

"A new Late Miocene great ape from Kenya and its implications for the origins of African great apes and humans" by Yutaka Kunimatsu, Masato Nakatsukasa, Yoshihiro Sawada, Tetsuya Sakai, Masayuki Hyodo, Hironobu Hyodo, Tetsumaru Itaya, Hideo Nakaya, Haruo Saegusa, Arnaud Mazurier, Mototaka Saneyoshi, Hiroshi Tsujikawa, Ayumi Yamamoto, and Emma Mbua (see pages 19220–199225)

EVOLUTION

A triple symbiotic team

When a species of bacteria adapts to symbiosis within another life form, its genome shrinks. Lost genes may be inserted in host DNA or may disappear entirely. With more than two symbionts, things get complicated. John McCutcheon and Nancy Moran studied the symbiosis between the glassy-winged sharpshooter, *Homalodisca vitripennis*, and two bacteria, *Baumannia cicadellinicola* and *Sulcia muelleri*, hosted in a specialized organ, the bacteriome. The authors sequenced the *Sulcia* genome and report that the two bacteria retained complementary genomes that enabled them to synthesize essential nutrients. McCutcheon and Moran collected *Homalodisca* from a lemon orchard and dissected out the bacteriomes, retaining only the fraction highest in *Sulcia*, which cannot be cultured outside of the host.



The dual symbionts of sharpshooters: *Baumannia* (green) and *Sulcia* (red).

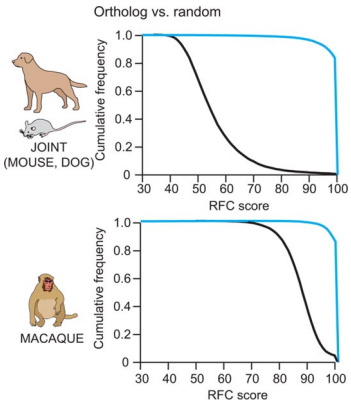
After sequencing the sample DNA, the authors subtracted material from the *Homalodisca* and *Baumannia* genomes to produce a 245-kb circular *Sulcia* genome. This genome encodes 228 protein genes and 31 tRNAs, making it the first highly reduced genome from the phylum Bacteroidetes. *Sulcia* appears to focus on amino acid production, complementing *Baumannia*'s synthesis of vitamins and cofactors, the authors report. *Sulcia* also produces homoserine and 2-ketovaline, which *Baumannia* converts to cysteine and coenzyme A, respectively. Together, the bacteria produce amino acids not available in plant xylem, *Homalodisca*'s food source. — K.M.

"Parallel genomic evolution and metabolic interdependence in an ancient symbiosis" by John P. McCutcheon and Nancy A. Moran (see pages 19392–19397)

GENETICS

Again, fewer genes for humans

Distinguishing protein-coding from noncoding genes is one of the essential, but surprisingly difficult, tasks of the post-genomic era. The number of protein-coding genes in the human genome is currently estimated to be ≈24,500. Michele Clamp *et al.* report that this number is too high and should be reduced to 20,500. The authors compared human open-reading frames (ORFs) with those in the dog and mouse genomes. They then compared the unique, nonconserved human ORFs with those of other primates and eliminated ≈4,000 ORFs that are not protein-coding genes, but are random occurrences in the human genome. This large revision to the human gene catalog gives a much more accurate picture of our protein-coding genes. The authors suggest that ORFs that do not show evolutionary conservation should be added to the catalog of known genes only if there is clear experimental evidence that a protein is produced. Clamp *et al.* also found that <200 totally new protein-coding genes, with no obvious relationship to any dog or mouse genes, have arisen in humans since our divergence from mice ≈75 million years ago. — P.D.



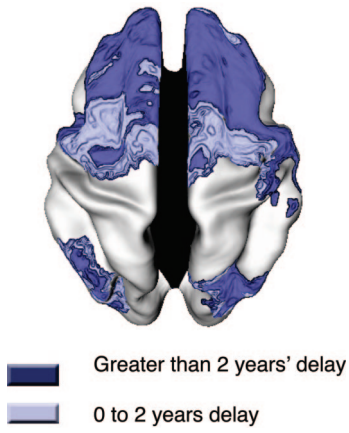
Reading frame conservation (RFC) scores comparing animal and human nucleotides.

"Distinguishing protein-coding and noncoding genes in the human genome" by Michele Clamp, Ben Fry, Mike Kamal, Xiaohui Xie, James Cuff, Michael F. Lin, Manolis Kellis, Kerstin Lindblad-Toh, and Eric S. Lander (see pages 19428–19433)

PSYCHOLOGY

Cortex development delayed in ADHD

The anatomical changes in brain development that underlie attention-deficit/hyperactivity disorder (ADHD) are hotly disputed. In particular, there is ongoing disagreement about whether ADHD results from a delay in brain development or from abnormal brain anatomy. Previous research provides evidence for both arguments. Using neuroimaging techniques, P. Shaw *et al.* determined the normal course of cortical development via measurements of cortical thickness. The authors estimated the cortical thickness at 40,000 cerebral points from 824 magnetic resonance scans from 223 children with ADHD and 223 controls. Shaw *et al.* found that brain development was similar in both groups, but also found that there was a delay in the cerebrum development of ADHD children. Children without the disorder showed peak thickness of the cerebrum by 7.5 years; children with ADHD did not reach this milestone until they were 10.5 years old. The delay was most visible in the prefrontal regions, which are vital for attention and motor planning. — B.T.



Areas of delayed maturation in ADHD brain.

"Attention-deficit/hyperactivity disorder is characterized by a delay in cortical maturation" by P. Shaw, K. Eckstrand, W. Sharp, J. Blumenthal, J. P. Lerch, D. Greenstein, L. Clasen, A. Evans, J. Giedd, and J. L. Rapoport (see pages 19649–19654)