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#### VOLUME 285

### Science www.sciencemag.org

NEWS

#### 6 AUGUST 1999

**COVER** Chuck Close's *Maggie* (1996). Oil on canvas, 30 by 24 inches (76.2 by 61.0 cm). Reduced to 44 percent of actual size and cropped. This painting demonstrates that the perception of shape depends on the size of the image. Compare its appearance from far to near, as the solid face collapses into flat squares. [Photograph of painting by Ellen Page Wilson. Courtesy of PaceWildenstein]





820 Getting together on fusion

### NEWS OF THE WEEK 810 SCIENTIFIC PUBLISHING: E-biomed Morphs to E-biosci, Focus Shifts to Reviewed Papers 811 SCIENTIFIC PUBLISHING: DOE Builds a Web

- Site for the Physical Sciences 811 MICROBIOLOGY: New Clues to Whooping
- Cough Pathology
- 813 RESEARCH FUNDING: House Panel Cuts Space Science, NSF Budgets
- 814 CELL BIOLOGY: Gene Linked to Faulty Cholesterol Transport

RESEARCH

862

864

867

870

874

- 816 NAVIGATION: GPS's 'Dress Rehearsal' for Year 2000 Problem
- 816 ENVIRONMENTAL SCIENCE: Science Board Floats \$1 Billion Trial Balloon

**REPORTS** TRACE Observation of Damped Coronal

Loop Oscillations: Implications for

Coronal Heating V. M. Nakariakov, L.

Magnetization Reversal C. H. Back, R. Allenspach, W. Weber, S. S. P. Parkin, D.

Weller, E. L. Garwin, H. C. Siegmann

Galileo Imaging of Atmospheric

W. H. Smyth, A. P. Ingersoll

Emissions from Io P. E. Geissler, A. S.

Ofman, E. E. DeLuca, B. Roberts, J. M. Davila

**Minimum Field Strength in Precessional** 

Current-Induced Switching of Domains in

Magnetic Multilayer Devices E. B. Myers, D.

McEwen, W. Ip, M. J. S. Belton, T. V. Johnson,

Quantitative Assessment of Reactive Surface Area of Phlogopite During Acid

Dissolution E. Rufe and M. F. Hochella Jr.

C. Ralph, J. A. Katine, R. N. Louie, R. A. Buhrman

#### 817 ENDANGERED SPECIES: A Plan to Save Hawaii's Threatened Biodiversity

NUMBER 5429

- 819 SPACE SCIENCE: U.N. Plans Its Future in Space
- 819 SYNCHROTRON RADIATION: France Takes Share in British Synchrotron

#### **NEWS FOCUS**

- 820 FUSION'S FUTURE: Common Ground for Fusion
- 821 FUSION'S FUTURE: Fusion Power From a Floating Magnet?
  - Many Shapes for a Fusion Machine FUSION'S FUTURE: JET Staff OKs Pay
- 823 FUSION'S FUTURE: JET Staff OKs Pay Settlement

Late Miocene Atmospheric CO<sub>2</sub>

Hf Isotope Evidence for Pelagic

Concentrations and the Expansion of C<sub>4</sub>

Sediments in the Source of Hawaiian

Grasses M. Pagani, K. H. Freeman, M. A. Arthur

Basalts J. Blichert-Toft, F. A. Frey, F. Albarède

Molecular Identification of a Eukaryotic,

Channel M. Kanzaki, M. Nagasawa, I. Kojima,

Phosphorylation of Histone H3 P. Sassone-

Corsi, C. A. Mizzen, P. Cheung, C. Crosio, L. Monaco, S. Jacquot, A. Hanauer, C. D. Allis

Relatedness B. J. Cole and D. C. Wiernasz

The Selective Advantage of Low

Stretch-Activated Nonselective Cation

C. Sato, K. Naruse, M. Sokabe, H. lida

**Requirement of Rsk-2 for Epidermal** 

**Growth Factor-Activated** 

825 ECOLOGY: A Long March to Save Africa's Dwindling Wildlands

DEPARTMENTS
NETWATCH
799
THIS WEEK IN
SCIENCE
801
SCIENCESCOPE
813

RANDOM SAMPLES 827

CONTACT SCIENCE 833 NEW PRODUCTS 940



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870

876

**879** 

882

886

891

Gleanings on Io's gaseous emissions

#### SCIENCE'S COMPASS

#### **EDITORIAL**

833 Staying Competitive D. A. Bromley

#### LETTERS

 835 How Women Contribute L. Schiebinger. "Macho Total Synthesis" C. Djerassi; J. Haseltine. Facts about Artificial Intelligence D. Proudfoot. Chimp Cultural Diversity D. S. Woodruff; N. G. Jablonski and G. Chaplin. DNA Discovery G. Wallis. Mitochondrial Recombination? (Continued) D. A. Merriweather and F. A. Kaestle. Protein Crystallization at NASA: Well Grounded M. R. Fiske. Corrections and Clarifications

#### ESSAY

839 A Tale of Two Cities: Architecture and the Digital Revolution W. J. Mitchell

#### BOOKS ET AL.

- 842 MATHEMATICS: *The Nature of Mathematical Modeling* N. Gershenfeld, reviewed by B. Sleeman
- 842 NEUROSCIENCE: The Nature of Cognition R. J. Sternberg, Ed., reviewed by C. R. Gallistel
- 843 Browsings

#### PERSPECTIVES

844 VISUAL SCIENCE: Close Encounters—An Artist Shows that Size Affects Shape D. G. Pelli



- ▼846 GEOPHYSICS: Hawaiian Plume Dynamics 879 J. Lassiter
- 847 PLANETARY SCIENCE & ASTRONOMY: Extrasolar Giant Planets and Brown Dwarfs A. Burrows
- \$62
   \$00 Content of the second se

#### REVIEW

851 EARTH AND PLANETARY SCIENCES: A Diamond Trilogy: Superplumes, Supercontinents, and Supernovae S. E. Haggerty



893 Landscape Structure and Biological Control in Agroecosystems C. Thies and T. Tscharntke

895 Signaling from Rho to the Actin Cytoskeleton Through Protein Kinases ROCK and LIM-kinase M. Maekawa, T. Ishizaki, S. Boku, N. Watanabe, A. Fujita, A. Iwamatsu, T. Obinata, K. Ohashi, K. Mizuno, S. Narumiya



Fas Ligand: A Sensor for DNA Damage Critical in Skin Cancer Etiology L. L. Hill, A. Ouhtit, S. M. Loughlin, M. L. Kripke, H. N. Ananthaswamy, L. B. Owen-Schaub

851

Time capsule

- 901 Functional Characterization of the S. cerevisiae Genome by Gene Deletion and Parallel Analysis E. A. Winzeler *et al.*
- 906 Early Neocortical Regionalization in the Absence of Thalamic Innervation E. M. Miyashita-Lin, R. Hevner, K. M. Wassarman, S. Martinez, J. L. R. Rubenstein

#### **TECHNICAL COMMENTS**

Genetics and Male Sexual Orientation D. H. Hamer. *Response* G. Rice, N. Risch, G. Ebers www.sciencemag.org/cgi/content/full/285/5429/803a

879

898

Traces of ancient crust in young island basalts

839

Breakthrough buildings



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#### 891

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#### **TRACING SOLAR LOOPS**

The solar corona, the outermost shell of the sun's atmosphere, is extremely hot (~2 million kelvin) and is the source of the solar wind that at its peak can disrupt communications and even power distribution on Earth.



Nakariakov et al. (p. 862; see the Perspective by Hudson and Kosugi) studied the oscillations in one coronal loop using the Transition Region and Coronal Explorer (TRACE) spacecraft to decipher how the corona is heated. The solar flare created transverse oscillations in an adjacent coronal magnetic loop. The period between oscillations rapidly increased, which damped the loop motions. They calculated that the rate of damping was consistent with classical models of coronal heating, such as viscous or resistive dissipation of magnetohydrodynamic (MHD) waves.

#### MAGNETIC SWITCHING WITH CURRENT PULSES

The switching of magnetic memories usually requires application of external magnetic fields. Two reports show how electric current pulses within small devices can be used to switch magnetic states. The rate at which magnetic data can be stored is limited by the time taken to reverse the magnetization orientation. In conventional methods, the reversal field is applied antiparallel to the outof-plane magnetization, and the switching speeds are limited to the nanoseconds. Back et al. (p. 864) show that this limitation may be overcome by switching the magnetization of thin, in-plane orientated ferromagnetic films using ultrafast focused current pulses from an accelerator. Although the magnetic fields generated were no greater than those of conventional recording heads, reversal times faster than 5 picoseconds were demonstrated. The electrical resistance of stacked layers of magnetic (ferromagnetic) and nonmagnetic materials depends greatly on the orientation of the magnetic moments in adjacent magnetic layers—if the moments are aligned, the resistance is low. Myers et al. (p. 867) show that the magnetic orientation in a single layer can be switched to be aligned or misaligned to a second magnetic layer by controlling the direction of an applied spin-polarized current pulse. Such switching may find application in fast, nonvolatile magnetic memories.

#### **GRASSLAND ORIGINS**

A dramatic increase in the abundance of grasslands that occurred about 7 to 8 million years ago may have had important effects on the evolution of mammals, including hominids. One explanation for this evolution has been that it was tied to a decrease in atmospheric CO<sub>2</sub> concentrations: Grasses have a photosynthetic pathway, known as C<sub>4</sub>, that is favorable at low CO<sub>2</sub> concentrations. Pagani et al. (p. 876) provide a CO<sub>2</sub> reconstruction based on analysis of alkenones in a sediment core which indicates that CO2 concentrations actually rose gradually during this time. They suggest that the rise of C4 plants may instead be tied to a period of global aridity.

#### **RECYCLED CRUST IN** HAWAIIAN BASALTS

The volcanic activity of the Hawaiian Island chain is thought to be associated with upwelling in Earth's mantle (a mantle plume). Examination of the chemistry of the volcanic rocks in Hawaii can provide information about the degree of mixing in Earth's mantle, why such voluminous magmatism occurs, and how deep these plumes extend. Blichert-Toft et al. (p. 879; see the Perspective by Lassiter) used an analysis of hafnium and lead isotopes to show that some of the Hawaiian magmas come from parts of the mantle that have incorporated but still preserved the chemical signature of ancient subducted oceanic crust-particularly the clay-rich upper part of the crust. Surprisingly, the data show that the contribution of what is normally thought of as the upper mantle to the magmas in Hawaii is minimal, which implies that the upwelling that forms the Hawaiian magmas is derived from deep in the mantle, where it has entrained ancient subducted crust.

#### **HISTONE PHOSPHORYLATION**

THIS WEEK IN SCIENCE edited by Phil SZUROMI

> One way in which gene transcription can be regulated is through remodeling of chromatin structure. Histone proteins are known to be modified through acetylation and deacetylation by enzymes recruited to specific promotors. Sassone-Corsi et al. (p. 886) provide evidence that another modification of histones-covalent phosphorylation-may also contribute to growth factor-induced gene expression. The authors show that histone H3 is phosphorylated in cells treated with epidermal growth factor (EGF) and that the kinase responsible appears to be the pp90 ribosomal protein S6 kinase Rsk-2. In human cells from individuals with Coffin-Lowry syndrome (which is associated with mutations in the RSK-2 gene), or in mouse cells in which the RSK-2 gene was disrupted, EGF-induced phosphorylation of histone H3 was not detected. The findings raise the possibility that phosphorylation of histones could influence chromatin structure and thus be part of the mechanism by which EGF alters gene activation.

#### **LIFE WITH FATHERS**

Can a figure be put on the advantage conferred by genetic diversity? It can for harvester ant colonies, thanks to a long-term study by Cole and Wiernasz (p. 891). The single queens that head these colonies may mate with one, two, or more males, resulting in worker populations that differ in average relatedness. Colonies with more fathers grow more quickly, have higher survival rates, and reach reproductive maturity sooner than those with fewer fathers-the difference in fitness can be a high as a factor of 35. Possible explanations include a greater resistance to pathogens or a greater range of specialized behaviors.

#### SPARE THE PLOW, SAVE THE CROP

Populations of pests of agricultural crops can be targeted chemically by pesticides or biologically through natural predators and parasites. It has long been supposed by ecologists, but not tested in any detail, that agroecosystems receive a major biological pest-control benefit from natural enemies inhabiting adjacent uncultivated land. In an experimental study conducted CONTINUED ON PAGE 803



MCF-7 breast cancer cell line



#### **AtlasImage Analysis**



AtlasImage 1.0 was used to compare hybridization patterns obtained with the Atlas Human Cancer 1.2 Array. Red indicates up regulation greater than 2fold and blue indicates down regulation greater than 2-fold.

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Illustration inspired by the art of Piet Mondrian (1872-1944).

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THIS WEEK IN SCIENCE

CONTINUED FROM PAGE 801

at different landscape scales in European agroecosystems, Thies and Tscharntke (p. 893) show a clear and positive effect of landscape complexity on parasite-induced mortality on the rape pollen beetle and a concomitant reduction in damage to the beetle's host plant, oilseed rape. This finding is directly relevant to recent efforts to determine the economic value of "ecosystem services" provided by natural and semi-natural habitat.

#### THE INDEPENDENT NEOCORTEX

Are neocortical areas naïve and thus in need of instructions from inputs, or are they preformed because they express certain molecules independently of specific afferents? This question represents a still unresolved issue in developmental neuroscience. Miyashita-Lin *et al.* (p. 906) studied mutant mice with a defect in thalamic differentiation. In the absence of thalamocortical innervation, the different neocortical regions still expressed their specific molecular signatures. This result strongly supports the hypothesis that there is an intrinsic patterning in the neocortex independent of afferent inputs.

#### BEYOND REPAIR

The skin is bombarded by ultraviolet radiation from the sun, which can induce chromosomal damage and mutated genes. Sunburn is thought to be a way of preventing the accumulation of mutations that could eventually result in a cancer in addition to DNA repair. The relative importance of apoptosis, as opposed to repair, in the elimination of DNA damage is not known because the original studies were done in p53-deficient mice (deficient in both pathways). Expression of the ligand for Fas (a cell death receptor), FasL, is controlled by p53. Hill *et al.* (p. 898) looked at FasL-deficient mice and found that such mice have much less epidermal apoptosis, but many more mutations in the p53 gene. Thus, FasL-dependent apoptosis and cellular elimination may be important mechanisms to maintain the chromosomal integrity of the epidermis, thereby reducing the probability of tumor progression.

#### GENE ANALYSIS BY THE BATCH

Exploiting the fruits of whole genome analysis will depend on the ability to rapidly and precisely characterize the function of the genes discovered. Winzeler et al. (p. 901) have used a strategy based on the polymerase chain reaction to induce precise deletions in each of 2026 open reading frames (ORFs) in Saccharomyces cerevisiae, which represents more than one-third of the ORFs in the yeast genome. "Bar codes" in the form of specific oligonucleotide sequences that were incorporated at both ends of an ORF during construction of the deletion allowed the analysis of the phenotypes of genes in batches of 500 at a time. Growth rates in minimal or enriched media were used to determine that more than 40% of the deletion strains had quantitative growth defects. There was no correlation observed between the level of expression of a gene under a particular growth condition and whether it was essential.

#### **TECHNICAL COMMENT SUMMARIES**

#### Genetics and Male Sexual Orientation

The full text of these comments can be seen at www.sciencemag.org/cgi/content/full/285/5429/803a

G. Rice *et al.* (Reports, 23 Apr., p. 665) studied a region on the genome—specifically, alleles at position q28 of the X chromosome—of 52 homosexual male sibling pairs from Canadian families, but did not find a link between those alleles and homosexuality. This result contradicts that made by D. H. Hamer *et al.* in a Research Article published on 16 July 1993, page 321.

D. H. Hamer comments that "(i) the family pedigree data [from the report by Rice *et al.*] actually support the Xq28 hypotheses; (ii) three other available Xq28 DNA studies did find linkage; and (iii) the heritability of sexual orientation is supported by substantial evidence independent of the X-chromosome linkage data."

In response, Rice *et al.* state, "we agree with Hamer that our results do not exclude the possibility of genetic effects underlying male homosexuality. But with the use of similar methods of family ascertainment, phenotyping, and genotyping, we were unable to confirm evidence for an Xq28-linked locus underlying male homosexuality." They state that "two independent replication studies" do not support the conclusions of the 1993 Research Article.

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