

spontaneously hypertensive rat's genome with the first rat genome to be sequenced, in 2004, and found that the two strains are about as different from one another as any two humans that have been sequenced so far. By contrast, mouse strains sequenced to date have much more variable genomes.

The team found 788 genes in the hypertensive rat that seem to be mutated enough to disrupt the function of the proteins that they encode. Many of these encode ion-channel proteins, such as those that regulate calcium and potassium, and may have a role in regulating blood pressure.

DRUG DEVELOPMENT

Virus knockdown

Proc. Natl Acad. Sci. USA doi:10.1073/pnas.0912186107 (2010)

The use of small RNA molecules called short interfering RNAs (siRNAs) to silence specific genes involved in disease has so far yielded few positive results in the clinic. John DeVincenzo at the University of Tennessee in Memphis and his colleagues report results from a phase II clinical trial that tested an siRNA on adults infected with respiratory syncytial virus (RSV), a major cause of respiratory infection in infants. The siRNA molecule blocks a viral protein involved in RSV replication.

In the 88-person study, volunteers received the siRNA daily by means of a nasal spray for two days before and three days after being experimentally infected with RSV. The team detected viral replication in 44.2% of people given the spray, compared with 71.4% of those receiving a placebo spray.

OPTICAL DEVICES

Organic light

Nature Mater. doi:10.1038/nmat2751 (2010)

Light-emitting transistors made from organic materials could become the next generation of low-cost display technologies. The organic light-emitting transistor (OLET), made by Michele Muccini and Raffaella Capelli at the Italian National Research Agency in Bologna and their colleagues, is 100 times more efficient at converting electricity into light than the equivalent organic light-emitting diode (OLED), the latest technology for thin, lightweight displays.

The OLET consists of a luminescent matrix sandwiched between two semiconductor layers, all stacked on a substrate. The architecture of these layers decreased or prevented the loss of photons and quenching of excitons — both particles responsible for the light emission — that are common in OLEDs.

MICROBIOLOGY

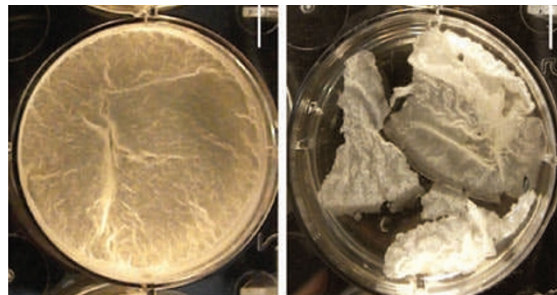
Bacterial break up

Science 328, 627–629 (2010)

A class of unusual amino acids that disperses films of bacteria might be used to make disease-causing species vulnerable to attack.

Biofilms are communities of bacteria that adhere to each other and are hard to eradicate, causing problems in hospitals and factories. Richard Losick of Harvard University in Cambridge, Massachusetts, and his colleagues found that the bacterium *Bacillus subtilis* can produce a mixture of D-amino acids that trigger the dispersal of its films. These amino acids are mirror images of the L-amino acids that are more commonly found in proteins.

Adding these D-amino acids to biofilms broke up *B. subtilis* communities (pictured), as well as films of the pathogenic bacteria *Staphylococcus aureus* and *Pseudomonas aeruginosa*. The D-amino acids were incorporated into bacterial cell walls, where they prevented attachment of the protein fibres that hold biofilms together.



COGNITIVE NEUROSCIENCE

Attention please!

J. Neurosci. 30, 6072–6079 (2010)

People can ignore the most attention-grabbing object in the room thanks to a neural circuit that dampens perception of such distractions.

Carmel Mevorach at the University of Birmingham, UK, and his colleagues asked 12 volunteers to perform a visual task in which they had to focus on a less prominent stimulus presented among more obvious ones. The authors used functional magnetic resonance imaging to monitor the left occipital pole, a part of the brain involved in visual processing in the task. They also used a technique known as transcranial magnetic stimulation to lower the activity in a brain region involved in attention, the left intraparietal sulcus.

The researchers show that this attention region directly suppresses activity in the visual-processing area when prominent distractions need to be ignored. This neural circuitry may be disrupted in attention-deficit disorders and even in ageing, the authors say.

SCIENCE/AAAS

JOURNAL CLUB

James Noonan
Yale University, New Haven,
Connecticut

An evolutionary geneticist looks at how small genetic changes can have big evolutionary effects.

Vertebrates are diverse in both form and function. What genetic alterations underlie this diversity? Evolutionary modifications in brain size or limb length, for example, involve changes in the complex developmental processes that give rise to these structures. Work in fish elegantly illustrates how a single genetic change can have profound effects on morphological evolution.

David Kingsley at Stanford University in California and his colleagues focused on threespine sticklebacks (*Gasterosteus aculeatus*), which exist in both marine and freshwater ecosystems (Y. F. Chan *et al.* *Science* 327, 302–305; 2010). Most bear pelvic spines on their underside; however, several freshwater populations have lost these structures.

In previous work, the authors suggested that the gene *Pitx1* is involved in pelvic reduction in these fish. Now they show that deletion of a sequence that activates *Pitx1* expression in the pelvis is directly responsible for the loss of pelvic spines in sticklebacks. In a simple but powerful experiment, they demonstrate that introducing the *Pitx1* gene to these pelvic-reduced fish, under the control of the intact *Pitx1* regulatory element, is sufficient to restore pelvic spines.

The *Pitx1* regulatory deletion has occurred independently in at least nine stickleback populations. This may be because the *Pitx1* regulatory element is in a particularly fragile region of the genome that is prone to deletion. Moreover, population-genetic evidence suggests that this recurrent loss of *Pitx1* pelvic expression confers a strong fitness advantage — possibly because insects that prey on sticklebacks can grab onto pelvic spines.

This study illustrates the power of laboratory genetics in understanding evolutionary mechanisms, and by doing so provides a conceptual basis for future functional studies of the evolutionary process.

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