

the tiles stick together, and the widths of Murata's ribbons are kept in check by special 'boundary' tiles.

The researchers have also programmed the tile-matching rules so that they embody computational cellular-automaton models. The arrangements that result resemble snakeskin belts under the microscope.

IMAGING TECHNIQUES

Heliomicroscopy

J. Microsc. 229, 1-9 (2008)

Electrons are commonly used to image materials at high resolution, but their negative charge and high energies can damage fragile samples. To get around this, a group of physicists used helium atoms instead, and successfully photographed a hexagonal copper mesh.

Bodil Holst at Graz University of Technology in Austria and her colleagues propelled helium through a nozzle and used a device known as a Fresnel zone plate to focus the beam onto the copper. This created an image with 2-micrometre resolution.

The experiment demonstrates that helium atoms can generate a picture even when fired at a sample much more slowly than would be required for electrons to produce an image. Holst says the technique might one day be used to image proteins and weak polymers.

MOLECULAR BIOLOGY

How to host HIV

Science doi: 10.1126/science.1152725 (2008)

To be able to infect human cells, HIV requires more than 250 host proteins, say researchers at Harvard Medical School in Boston, Massachusetts. Only 13% of these proteins have previously been implicated in HIV infection, and the collection could yield potential drug targets for anti-HIV therapies.

Stephen Elledge and his colleagues turned down the expression of more than 21,000 genes in human cell cultures. Each gene was silenced individually in a separate cell line, and all the lines were then tested for their ability to support HIV infection.

The proteins not previously known to have a role in HIV infectivity include some that transport vesicles between organelles, and components of a protein complex called Mediator, which regulates gene expression.

EVOLUTIONARY BIOLOGY

A twist in the tale

Biol. Lett. doi:10.1098/rsbl.2007.0602 (2008)

A snail with a shell that coils in four directions has been discovered in Malaysia. Reuben Clements of the conservation group WWF-Malaysia in Selangor and his team have described 38 examples of the gastropod — all with curves in similar positions — found in soil from a single limestone site. The creature came as a surprise because the majority of land snails' shells twist around one or two axes. Most species in the genus *Opisthostoma*, in which the new specimens fall, have three coiling axes.

Opisthostoma vermiculum, or 'little worm', as the authors have named the curvy creature (pictured below left), is the first of two species with bizarrely arranged coils that the team found.



R. CLEMENTS

GENETICS

Lethal matings

Science doi:10.1126/science.1151107 (2008)

When two strains of *Caenorhabditis elegans* mate, one-quarter of their grandchildren die during early development because of a weird genetic incompatibility that is maintained by natural selection.

Hannah Seidel,

Matthew Rockman and Leonid Kruglyak at Princeton University in New Jersey,

who discovered the incompatibility, crossed worms of the 'Bristol' strain with individuals from the 'Hawaiian' strain, then allowed the offspring to self-fertilize. Those embryos that lacked a gene called *zeel-1* — a deletion characteristic of the Hawaiian strain that is passed on in mendelian ratios — were sensitive to the product of another gene that is carried in sperm. A version of the latter gene from the Bristol strain arrested the development of such embryos.

Because Hawaiian and Bristol worms live together all over the world, the team propose that the incompatibility is not an example of incipient speciation. The genes involved probably confer some unknown benefit to counteract the reproductive cost, they add.

JOURNAL CLUB

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A geneticist reflects on DNA sequence variants that influence gene expression and disease risk.

Most people are familiar with the Human Genome Project and the HapMap, which catalogued the millions of DNA-sequence differences among humans. But which of these differences influence our risk of developing diseases remains unclear. This is particularly true for disorders such as heart disease that involve not only many genes but also the interactions among them. In addition, the effects of variations in DNA sequence are often subtle, such as altered levels of gene expression. Identifying those DNA sequences that determine levels of expression across individuals could have great medical potential.

One paper that illustrates this point looks at the two major contractile proteins of the human heart, the α - and β -forms of the myosin heavy chain (E. van Rooij *et al. Science* 316, 575-579; 2007). Here, Eric Olson and his team at the University of Texas in Dallas identify a microRNA, called miR-208, that regulates how much of the β -form heart cells produce.

A healthy heart requires a particular ratio of α - and β -heavy chains for its cells to function normally. When stressed, heart cells tend to make too much of the β -form, causing the organ to enlarge, replete with fibrous connective tissue, and less able to contract. This often happens in people with heart disease.

In finding miR-208, the researchers have determined a key component in the molecular basis of heart failure. The next step might be to look for sequence variants of miR-208 and of other gene-expression regulators that could explain why some people are more susceptible to heart disease than others. In this way, whole biological networks could be pieced together and common medical problems more fully understood.

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