RESEARCH HIGHLIGHTS

CANCER GENOMICS

Prognostic sign

Nature Med. doi:10.1038/nm.2174 (2010)

A tumour's genetic make-up holds important clues to its stage of development, and researchers are now closer to a tool that can 'read' this information.

Soft-tissue cancers called sarcomas are normally staged, or graded, largely according to the tumour cells' appearance under the microscope. This method is more than 20 years old and is not very reproducible from one pathologist to the next. Frédéric Chibon at the Bergonié Institute in Bordeaux, France, and his co-workers have teased out a signature pattern of gene expression, involving 67 genes, that better predicts the five-year metastasis-free survival rate for people with sarcomas.

The researchers analysed gene-expression patterns for 183 sarcoma samples and tested their prognostic signature in a separate set of 127 sarcomas. Almost all of the 67 genes are involved in cell division or maintaining chromosome integrity. Further validation is needed before this can be used in the clinic, the authors say. **C.L.**

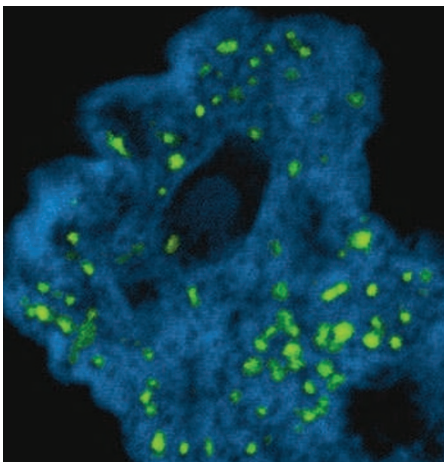
MICROBIOLOGY

Independent living

Mol. Microbiol. doi:10.1111/j.1365-2958.2010.07241.x (2010)

A group of bacteria that can multiply only in a host cell is less needy than scientists thought.

Members of the phylum Chlamydiae, which include human pathogens and symbionts of amoebae, were thought to be metabolically dependent on the cells they infect. Michael Wagner at the University of Vienna and his colleagues used Raman microspectroscopy to distinguish between the active and resting stages of the bacterium *Protochlamydia amoebophila* (pictured in green) on the basis of their chemical composition.



B. SIXT/UNIV. VIENNA

They expected resting bacteria to be metabolically inactive, but found that the cells took up the amino acid phenylalanine to produce proteins, even when outside their host cells. This uptake continued for up to three weeks, and the bacteria remained infective throughout. And the species was not alone: the human pathogen *Chlamydia trachomatis* also synthesized proteins independently of its hosts. **H.L.**

ASTRONOMY

No planetary X-ray pull

Astron. Astrophys. **515,** A98 (2010)

Planets seem to have no effect on the X-ray output of their parent stars, say Katja Poppenhaeger and her colleagues at the University of Hamburg in Germany.

Theorists have proposed that a planet's gravity could excite a star by causing it to bulge slightly or, similarly, that a planet's magnetic field could connect with that of its star and cause X-ray 'hotspots'. A previous study presented evidence for this effect.

Poppenhaeger *et al.* studied X-rays streaming from 72 nearby stars that host planets. In contrast to the earlier work, they find no obvious effect, and say that the phenomenon might appear in a few instances, for the most massive, close-in planets. **E.H.**

ECOLOGY

Don't damage dingoes

Ecol. Lett. doi:10.1111/j.1461-0248.2010.01492.x (2010)

Invasive species are often held responsible for driving native ones to extinction. Arian Wallach at the University of Adelaide in Australia and her colleagues propose that although invasives may drive biodiversity loss, a lack of ecosystem resilience is the ultimate cause of extinctions.

The authors assessed seven sites in Australia with differing levels of control of the top predator, the dingo (*Canis lupus dingo*; pictured). They found that harsh control actually promoted the spread of invasive species by disrupting dingo social structures and hence the resilience of the entire ecosystem. Relaxing control re-established biodiversity.

The team suggests that conservation managers should promote the inherent resilience of ecosystems rather than remove established invaders. **D.P.C.**

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IMMUNOLOGY

Gene plus virus

Cell **141,** 1135–1145 (2010)

Genes alone are rarely sufficient to cause disease. Researchers now report one possible explanation for this in Crohn's disease, a common inflammatory bowel disorder.

Thaddeus Stappenbeck and Herbert Virgin at Washington University in St Louis, Missouri, and their co-workers show that mice display some of the cellular abnormalities seen in Crohn's disease when they have a mutated Crohn's gene called *Atg16l1* and are also infected with a specific gut virus.

The results suggest that these abnormalities occur through mechanisms similar to those of Crohn's disease. The authors say that mutations in multiple genes combined with additional environmental factors may recreate the full range of Crohn's symptoms in mice. **C.L.**

GENETICS

Gene plus gene

Proc. Natl Acad. Sci. USA **107,** 10602–10607 (2010)

Hundreds of genetic variants are associated with complex diseases, but in most cases little is known about how the variants actually contribute to the disease.

Nicholas Katsanis at Duke University in Durham, North Carolina, and his colleagues have developed a model system using zebrafish (*Danio rerio*) to tease out such contributions to a rare genetic disorder known as Bardet–Biedl syndrome (BBS). Fourteen human genes have been linked to BBS, which has a range of symptoms, from retinal degeneration to mental retardation.

The researchers systematically replaced the fish versions of BBS genes with some of the 125 known human variants of the genes and observed developing fish embryos. Their technique revealed surprising quirks in the disease's inheritance, including interactions between genes that affect disease severity. The approach could be used to study the genetics of other diseases. **B.M.**

ORGANIC CHEMISTRY

Trifluoro triumph

Science **328,** 1679–1681 (2010)

Chemists would like to attach trifluoromethyl groups to organic molecules to improve their pharmacological properties, such as fat solubility or metabolic stability, but have struggled to find a simple way to add them to compounds containing aromatic rings.

Now Stephen Buchwald at the Massachusetts Institute of Technology in Cambridge and his colleagues have used a palladium catalyst to attach these groups to benzene-based aryl chloride molecules, under mild conditions.

Their method avoids the harsh conditions needed in previous methods and should allow the addition of trifluoromethyl groups to drugs at late stages in synthesis. **D.P.C.**

CANCER GENOMICS

Probing prostate cancer

Cancer Cell doi:10.1016/j.ccr.2010.05.026 (2010)

An in-depth genetic analysis has identified several gene alterations associated with prostate cancer.

Charles Sawyers and his colleagues at the Memorial Sloan-Kettering Cancer Center in New York analysed protein expression and the number of copies of genes in 218 prostate-cancer samples, including some that had metastasized to other parts of the body. They also analysed 12 prostate-cancer cell lines and sequenced 157 genes of particular interest from a subset of the samples.

The researchers identified three genes as potential tumour suppressors in some prostate cancers and found that differences in copy number of certain genes indicated clear subgroups of patients with high or low risk of tumour progression. **A.K.**

NEUROSCIENCE

Snakes on the brain

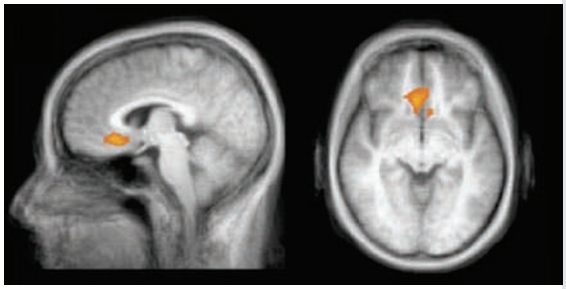
Neuron **66,** 949–962 (2010)

A hair-raising study has revealed a brain signal for acts of courage performed in the face of fear.

Yadin Dudai at the Weizmann Institute of Science in Rehovot, Israel, and his team used functional magnetic resonance imaging to scan the brains of volunteers as they decided whether to slide a live snake towards their heads.

In people fearful of snakes, a region called the subgenual anterior cingulate cortex (sgACC) was activated (pictured) if they mustered up the courage to move the snake closer. Skin conductance — an indication of bodily arousal — dropped as activity in the sgACC rose, even though the volunteers said that they still felt frightened.

The researchers propose that sgACC activation promotes courageous action and that manipulating its activity could help in treating fear disorders. **A.A.**



ELSEVIER

EVOLUTIONARY BIOLOGY

Meat-eating tadpoles

Proc. R. Soc. B doi:10.1098/rspb.2010.0877 (2010)

Exposure of ancient tadpoles to novel foodstuffs may have awoken genetic variation previously hidden from natural selection, leading to the evolution of new eating habits.

Cris Ledón-Rettig of the University of North Carolina at Chapel Hill and her team studied Couch's spadefoot tadpoles (*Scaphiopus couchii*), which eat algae and other organic material. The authors fed the tadpoles a shrimp diet resembling that eaten by tadpoles of the spadefoot toads (genus *Spea*), which probably evolved from ancestors similar to *S. couchii*. After feeding on the shrimps, the *S. couchii* tadpoles showed greater variation in growth and development speed than controls.

Similar results were seen in tadpoles treated with a hormone that is produced in response to dietary changes, suggesting that hormones may have mediated the *Spea* tadpoles' transition to carnivory. **J.F.**

JOURNAL CLUB

Marcelo A. Nobrega
University of Chicago, Illinois

A human geneticist explores the ways that genes are regulated.

Gene expression is the cellular process that decodes the genetic information in DNA and converts it into proteins. It is regulated at many levels: when messenger RNA is transcribed from DNA; when mRNA is translated into proteins; and at the epigenetic level, when the structure of chromatin, coils of DNA wound around histone proteins, is altered. Although most discussion of gene expression focuses on the regulation of transcription, the other components of the process are also crucial. Yet little is known about how they are integrated.

Work by Tom Misteli at the National Cancer Institute in Bethesda, Maryland, and his team provides a striking example of the integration of seemingly disparate components in gene-expression regulation (R. F. Luco *et al. Science* **327,** 996–1000; 2010). They describe how patterns of alternative splicing of newly made RNA, a key regulatory mechanism, can themselves be regulated by specific chemical modifications in the chromatin. They also found that a given set of modifications to histones predicts patterns of RNA splicing. The authors conservatively estimate that this mechanism occurs in dozens to hundreds of genes in the human genome.

This remarkable study makes a connection between a quintessential transcription-regulation mechanism, histone modification, and a post-transcriptional process, alternative splicing. It shows that chromatin can regulate not only how much of a protein, but also which protein, is made in a cell.

We have seen a surge of intriguing studies suggesting that molecules that were thought to regulate transcription also direct epigenetic modifications, modify alternative-splicing patterns and participate in the intracellular transport of RNA. These findings and the work of Misteli and colleagues provide insight into how the components of gene regulation are integrated.

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