

and thymus development in 13 species spanning the chordate phylogenetic tree. They paid special attention to the jawed vertebrates, which have a thymus, and jawless fishes such as lampreys, which do not. The authors conclude that the latter have many but not all of the genes required to develop a thymus. The study begins to show how the duplication and cooption of genetic pathways leads to the development of a complex organ.

BIOLOGY

Shell shocker

J. Zool. doi:10.1111/j.1469-7998.2009.00596.x (2009)
Big eggs risk being crushed by the big birds that sit on them. Eggshells must be sturdy, but not so sturdy that they entomb chicks. These conflicting demands placed on eggshells set the upper size limit for birds, according to Geoffrey Birchard of George Mason University in Fairfax, Virginia, and Charles Deeming of the University of Lincoln, UK. They are also, the authors suggest, the reason that females outweigh males in the largest of species.

The researchers analysed shell thickness, body mass and incubation behaviour for 968 species of bird. Having relatively small males do the incubating allows eggs to be bigger yet thinner-shelled. The largest specimens of extinct giants such as the 400-kilogram elephant bird might all be female, they speculate.

CHEMISTRY

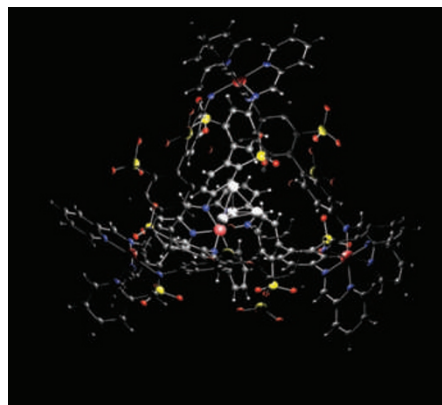
Fire boxed

Science 324, 1697-1699 (2009)
White phosphorus combusts violently in air, making it a dangerous agent, and one that has become controversial for its military uses.

Now Jonathan Nitschke at the University of Cambridge, UK, and his co-workers have constructed a molecular cage to defuse this version of phosphorus. The cage self-assembles in water from organic groups and iron ions. A solution of the cage can suck up solid white phosphorus, trapping its small, tetrahedral molecules within the cages' larger ones (pictured, below).

The cage doesn't prevent oxygen reaching the white phosphorus, but does stop it reacting because there isn't enough room within the cage for the normal products of the reaction to form.

Benzene can displace the incendiary molecule, releasing it from its confinement.



ASTRONOMY

Little neighbours

Astrophys. J. 699, 649-666 (2009)
How does one find dwarves in a crowd of giants? Evgenya Shkolnik at the Carnegie Institution of Washington in Washington DC and her colleagues searched X-ray data gathered by the now-defunct German satellite ROSAT for nearby M-class dwarf

stars less than 300 million years old.

Previous surveys placed greater emphasis on higher mass, higher luminosity Sun-like stars. The team identified 185 likely candidates before ruling out older interlopers by spectroscopy. The 144 remaining, some as small as 10% of the mass of the Sun, have a better chance than easier-to-spot, higher-mass stars of revealing the early formation of rocky Earth-like planets.

If any of the dwarves do host planets, their proximity to Earth (most are within 25 parsecs) will make them relatively easy to study in detail.

GENOMICS

Murky associations

Am. J. Hum. Genet. doi:10.1016/j.ajhg.2009.05.011 (2009)

Genome-wide association studies have been hailed for their ability to find genetic variations that may contribute to disease risk. But assigning meaning to these variations is more difficult. Peter Holmans of the MRC Centre for Neuropsychiatric Genetics and Genomics in Cardiff, UK, and his colleagues have developed an approach that they call ALIGATOR.

They look for gene ontology categories — agreed-upon terms used to define the function and activity of gene products — that regularly pop up in the candidates exposed by genome-wide association, reasoning that many associations in the same category signal functional relevance. For Crohn's disease, which is immunological in origin, overrepresented ontological categories included immune functions, as expected. For bipolar disorder, they included hormone activity and RNA splicing, processes with as yet unknown roles in the condition.

JOURNAL CLUB

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A biologist looks at the effect of a dynamic nuclear environment on gene expression.

In many organisms, including animals, genes are arranged linearly on chromosomes. But this linear order is largely meaningless during transcription, when RNA is made from DNA. Instead, a very different three-dimensional arrangement of genomic regions emerges in which structural flexibility and ability to

reorganize become crucial to gene expression. Some regions loop out dynamically, moving far from their neighbours. Genes can participate in 'transcription hotspots' in close association with genes from other chromosomes. But the question remains as to what leads this dance. Is the chromosomal reorganization a cause or a consequence of transcription?

Using *Hox* clusters — groups of genes important in development — Wendy Bickmore of the Medical Research Council in Cambridge and her colleagues start to answer this question. *Hoxb* and *Hoxd* have very different environments

in terms of their location on the chromosome and expression of their neighboring genes. The authors found that during tissue differentiation, *Hox* genes loop out and undergo active transcription. This reorganization then spreads from the *Hox* locus into adjacent genomic regions, but does not necessarily affect transcription of neighbouring genes (C. Morey *Genome Res.* doi:10.1101/gr.089045.108; 2009).

The authors propose that on activation, structural changes alter the constraints on genes' expression, allowing them to loop out and explore a much larger

transcriptional environment within the nucleus. The team concludes that positioning outside of a chromosomal region is important for, but not a driver of, transcriptional activation.

These findings have broad implications: first, dynamic reorganization of chromosome territories is necessary but not sufficient for activation. Second, this reorganization is associated with modification to DNA's structural packaging, which can permanently alter a cell's nature.

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