

Biophysics

How DNA avoids getting wound up

Preprint at <http://arxiv.org/abs/q-bio.SC/0404037> (2004)

There is only one way to untangle DNA from its tightly packed *in vivo* form, ready for transcription. Maria Barbi and colleagues reach this conclusion by studying the topological constraints on plant- and animal-cell chromatin fibres, in which DNA is wound around protein discs to form a string of bead-like nucleosomes. This is just one of the levels of hierarchical structure in chromatin (the DNA-protein composite of our genetic material), but its topological characteristics determine the way DNA becomes unpacked so that the genetic data are readable.

Chromatin fibres are typically organized into long loops pinned at each end, and provided that the fibre is not snipped apart by enzymes, unpacking part of a loop must preserve a topological quantity called the linking number, which depends on how the fibre is twisted around itself like a bundle of string. Barbi *et al.* show that there is just a single unwinding pathway that takes a fibre from a compacted form as dense as that seen in the cell to an open form, while conserving the linking number. Chromatin seems to have evolved precisely the nucleosome spacing that allows this unfolding pathway to be accessed. **Philip Ball**

Cardiovascular disease

The genetics of risk

*Hum. Mol. Genet.* **13**, 993–1004 (2004)

Our risk of developing cardiovascular disease is thought to depend partly on our levels of ‘good’ and ‘bad’ cholesterol (that is, on levels of high- and low-density lipoproteins, HDLs and LDLs, respectively). These concentrations in turn depend on both genetic and environmental factors. Hans Knoblauch *et al.* have found that most of the genetic differences in people’s cholesterol levels can be explained by changes in only 13 genes that are involved in lipid metabolism.

The authors measured the cholesterol levels of more than 1,000 people in 250 German families. They correlated these measurements with 93 variations, called single nucleotide polymorphisms (SNPs), in the 13 genes; these SNPs could be divided into groups, or haplotypes, that tend to be inherited together. Knoblauch *et al.* found that around one-third of the variation in cholesterol levels can be attributed to genes, and the rest to environmental factors. Variation in the haplotypes identified explained 67% of the genetic variation in LDL levels, 58% of that in HDLs and 99% of that in the HDL/LDL ratio.

Should the finding hold true in other populations, the next step will be to identify specific haplotypes that are linked to unhealthy cholesterol levels and that might be used to identify people at risk. **Helen Pearson**

Biomechanics

In a flap

*J. Fluid Mech.* **506**, 147–155 (2004)

Large flying animals, as well as some that swim, do so by flapping their forelimbs up and down. Microbes, in contrast, use tiny oars or spinning molecular motors to propel themselves along. Why the difference? The traditional answer is that larger creatures have to fight much harder against gravity. But how, then, do they create forward thrust while staying airborne?

Nicolas Vandenberghe and colleagues addressed the question by studying a model wing as it was moved up and down at varying frequencies in a tank of water. At low frequencies, the wing simply flapped vertically. But above a certain threshold it also began to move horizontally, and unidirectionally, during each stroke.

This process creates asymmetrical patterns of fluid movement on either side of the wing, giving it distinct ‘leading’ and ‘trailing’ edges. The authors acknowledge that animals will deliberately angle their wings or flippers. They nonetheless argue that, with increasing flapping frequency, there is a natural transition towards the development of thrust and the onset of horizontal motion, which occurs with even the simplest of wing motions. **Michael Hopkin**

Geochemistry

Ancient air not a fire hazard

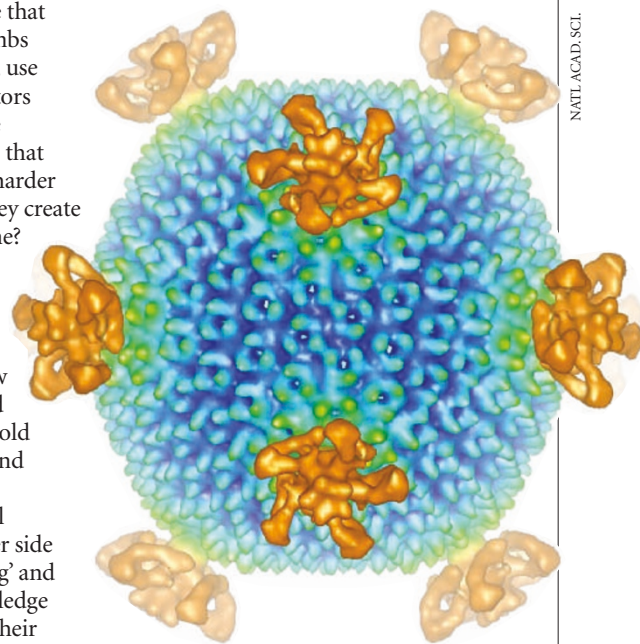
*Geology* **32**, 457–460 (2004)

Prehistoric forests may have been less combustible than has been thought, according to experiments by Richard A. Wildman Jr and colleagues. These findings challenge the notion that wildfires caused by high levels of atmospheric oxygen could have been catastrophic.

It has been argued that biological feedbacks tightly constrain both the upper and lower limits for the atmosphere’s oxygen content: too little, and aerobic respiration becomes untenable; too much (more than 25% or so), and natural wildfires, ignited by lightning, could devastate plant life. That idea sits uncomfortably with geochemical models that suggest the atmosphere contained up to 35% oxygen about 300 million years ago.

To resolve the issue, Wildman *et al.* looked at the effect of differing ambient oxygen levels on the burning of wood, foliage and moss chosen to approximate the vegetation of Carboniferous forests.

Under realistic fuel moisture conditions, the combustion rates and fire-spreading propensity do not seem to be sufficiently increased by oxygen contents of up to 35% for wildfires to have reached disastrous proportions. Previous experiments used paper, which burns more readily than moist vegetation, and so gave misleading results. **Philip Ball**



NATL. ACAD. SCI.

Virology

High-temperature infection

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There are three domains of life — the Archaea, Bacteria and Eukarya — and all three can be infected by specific viruses. Comparatively little is known about the viruses that infect the Archaea, a group of tiny microbes. But George Rice *et al.* have now analysed the genome and protein structure of a heat-loving archaeal virus (see picture) that lurks in the hot springs of Yellowstone National Park.

The authors isolated the virus from its host, *Sulfolobus solfataricus*, then extracted and sequenced its DNA and analysed its protein make-up. They found that the viral genes are quite different from those of other viruses and other organisms — perhaps indicating that this virus has a unique lifestyle compared with other species, or that it has been ecologically isolated for a lengthy period. But despite the genetic diversity, the structure of the viral ‘coat protein’ resembles that of bacterial and eukaryotic viruses.

The finding hints that some viruses may have a common ancestor that predated the split into the three domains of life more than 3 billion years ago. Analysis of this and similar viruses should, the authors say, allow new insights into the Archaea. **Helen R. Pilcher**