IN BRIEF

LIFESPAN

Lipoprotein genotype and conserved pathway for exceptional longevity in humans.

Atzmon, G. *et al. PLoS Biol.* **4**, e113 (2006)

This study took advantage of the limited genetic diversity among Ashkenazi Jews to identify a variant that might influence human lifespan. The authors genotyped offspring of 213 centenarians and an age-matched control group for variants in genes that have potential roles in cardiovascular disease. An allele of the apolipoprotein C3 (*APOC3*) gene, which encodes a protein that increases levels of harmful cholesterol, showed an association with parental longevity. Decreased APOC3 protein levels among carriers confirmed the variant as having a functional effect.

CHROMOSOME BIOLOGY

Telomere length as a quantitative trait: genome-wide survey and genetic mapping of telomere length-control genes in yeast.

Gatbonton, T. *et al. PLoS Genet.* **2**, e35 (2006)

Natural variation in a subtelomeric region of *Arabidopsis*: implications for the genomic dynamics of a chromosome end.

Kuo, H.-F., Olsen, K. M. & Richards, E. J. *Genetics* 17 March 2006 (doi:10.1534/genetics.105.055202)

Telomeric repeat number varies between and within species but excessively shortened telomeres have been linked with ageing. Gatbonton *et al.* carried out a deletion screen in *Saccharomyces cerevisiae* to identify genes that regulate telomere length. A large number of genes that encode various functions were identified. A subsequent genome-wide linkage analysis indicated that two loci accounted for 30–35% of telomere length variation between the strains under study. Combined with the observation that telomere length varies substantially among wild yeast strains, the authors concluded that polymorphisms at a large number of loci are likely to affect telomere length. Kuo *et al.* also studied natural variation but at the subtelomeric regions in *Arabidopsis thaliana*. Although expansion and deletion of blocks of repeats characterized proximal telomeres, DNA rearrangements such as inversions, deletions and transposon insertions characterized the distal subtelomeric regions. Therefore, diverse events ensure genomic variation at chromosome ends.

RECOMBINATION

Polymorphism in the activity of human crossover hotspots independent of local DNA sequence variation.

Neumann, R. & Jeffreys, A. J. *Hum. Mol. Genet.* 16 March 2006 (doi:10.1093/hmg/ddl063)

Variation of crossover activity in sperm can provide clues to how recombination hotspot activity is regulated. These authors analysed two nearby recombination hotspots on chromosome 1, one of which is considered to have only recently evolved. As well as providing the first direct evidence for rapid evolution of recombination hotspots in humans the authors show that hotspot activity might be regulated epigenetically or by distal regulators because men with active and suppressed hotspots have the same haplotypes around these sites.

TECHNOLOGY

Complexity on the nanoscale

Maps, smiley faces, triangles — these are not the sort of objects one normally associates with DNA. But nanotechnology has found many uses for DNA that are beyond this molecule's natural calling. In the most elaborate and remarkable example of these endeavours so far, Paul Rothemund reveals a way to fold a single strand of DNA into just about any two-dimensional shape imaginable.

The method is appropriately called 'DNA origami', which emphasizes the main innovation of this technique — the self-assembly of a single DNA viral strand into a predetermined shape. Attempts to create nanostructures rely either on manipulating individual atoms — a laborious and expensive approach — or on directing DNA strands to their position in the final structure by exploiting the complementarity of the component strands. Sequence complementarity also lies at the heart of the new method, but some innovations allow the structures to be more complex, easier to design and faster to create.

In DNA origami, the geometrical shape and the folding path that the ssDNA must take are first designed with the help of a computer. A 7 kb ssDNA molecule is then added to a surface, which is guided to the correct position by strategically placed 'staples' — that is, short strands of 200 kb that hold the long DNA strand in place. Once the ssDNA and the staples have been mixed together they assemble into the desired shape in a single step, all in under 2 hours.

By using this approach Rothemund has obtained DNA shapes (such as hexagons and snowflakes) that are 100 nm in diameter, achieving a complexity that is ten times as high as for any other assembled molecular pattern. There is clearly not going to be a lucrative market for tiny art of this sort, but the author's aim is to use these nanoscale structures for new applications in electronics and

GENE REGULATION

A closer look at conservation

In the hunt for regulatory elements that control gene expression, much emphasis has been placed on the conservation of non-coding regions at the sequence level over large evolutionary distances. A recent study demands a rethink of this approach, showing that such similarity is not enough to identify some key regulators, which might only be detectable using functional assays.

The expression pattern of the RET receptor tyrosine kinase is highly conserved in zebrafish and humans. By contrast, only part of the coding sequence of the gene shows similarity between the two species at the sequence level. So, sequence comparisons between zebrafish and human provide no clue to how patterns of *RET* expression have been maintained during evolution.

To identify non-coding regions that regulate *RET* expression, Shannon Fisher and colleagues looked for sequences in the region around the gene that are conserved at shorter evolutionary distances. They identified 38 such sequences that are conserved either between zebrafish and pufferfish, or between human and other non-primate mammals.

Using a transposon-based reporter vector, the authors looked at the patterns of expression that were driven by these sequences in zebrafish embryos. Surprisingly, almost all of the non-coding sequences — whether they were derived from zebrafish or human — directed expression in cell types