

IN BRIEF

GENOME INSTABILITY

DNA synthesis generates terminal duplications that seal end-to-end chromosome fusions

Lowden, M. R. *et al. Science* **332**, 468–471 (2011)

Shortened telomeres can lead to end-to-end chromosome fusions, which can result in genomic rearrangements that can contribute to tumorigenesis. These fusions have long been attributed to breakage–fusion–bridge cycles, but this work in *Caenorhabditis elegans* — in which end-to-end fusions can be transmitted stably through mitosis and meiosis because they have holocentric chromosomes — shows that fusions can occur by a mechanism that involves DNA synthesis. The authors suggest the involvement of a template-switching mechanism, similar to that proposed for interstitial duplications in humans.

EPIGENETICS

An epigenetic signature for monoallelic olfactory receptor expression

Magklara, A. *et al. Cell* 28 Apr 2011 (doi:10.1016/j.cell.2011.03.040)

This study changes the model of how neurons express single olfactory receptor (OR) genes. The authors show that, in the mouse olfactory epithelium, OR genes are marked by the histone modifications associated with constitutive heterochromatin (histone H3 trimethylated at lysines 9 and 20) and form compact and inaccessible chromatin domains, but have some functional characteristics of facultative heterochromatin. Unusually for constitutive heterochromatin, these marks occur at the OR genes in a tissue- and differentiation-specific manner and the silencing is reversed at individual OR genes.

GENOMIC VARIATION

Comprehensive assessment of array-based platforms and calling algorithms for detection of copy number variants

Pinto, D. *et al. Nature Biotech.* 8 May 2011 (doi:10.1038/nbt.1852)

These authors provide a comprehensive evaluation of copy number variation detection by different microarray platforms and analysis tools. They tested well-characterized control samples on 11 widely used arrays — including SNP and comparative genomic hybridization arrays — and analysed each data set with between one and five algorithms. Changing the platform or algorithm caused substantial differences among the results, which shows the importance of method choice and evaluation. These data will be a useful benchmark for testing new methods.

EVOLUTION

Experimental evidence supports a sex-specific selective sieve in mitochondrial genome evolution

Innocenti, P., Morrow, E. H. & Dowling, D. K. *Science* **332**, 845–848 (2011)

Because mitochondria are maternally transmitted, selection on the mitochondrial genome should only operate in females, and mutations that have deleterious effects that only occur in males are predicted to accumulate. This study supports this hypothesis. The authors looked at the effects of five mitochondrial variants on nuclear gene expression in *Drosophila melanogaster* and saw substantial changes in males only: almost 10% of transcripts were affected in male flies. These findings have broader implications for understanding the mutational load between the sexes in other species, including humans.