IN BRIEF

GENOME EVOLUTION

A burst of segmental duplications in the genome of the African great ape ancestor

Marques-Bonet, T. *et al. Nature* **457**, 877–881 (2009)

These authors generated maps of segmental duplications in the human genome and the genomes of three other primates: the macaque, orangutan and chimpanzee. The data reveal acceleration in the rate of duplication specifically on the branch of the primate lineage that includes humans and African great apes. In light of the slow rate of other types of mutation in the human lineage, these findings suggest that segmental duplications might have been major contributors to the rapid rate of phenotypic change that has marked human evolution.

SMALL RNAS

Pattern formation via small RNA mobility

Chitwood, D. H. *et al. Genes Dev.* **23**, 549–554 (2009)

Plant small interfering RNAs (siRNAs) are known to provide mobile signals during systemic antiviral gene silencing. Here, the authors show that small RNAs also provide mobile intercellular signals during plant development. They show that a class of *trans*-acting siRNAs (tasiRNAs) that are required for cell fate decisions in *Arabidopsis thaliana* form a gradient in the developing leaf, which extends outside the domain in which their biogenesis takes place. This finding has important implications for understanding the mechanisms by which small RNAs regulate pattern formation in plants.

RECOMBINATION

Genome-wide control of the distribution of meiotic recombination hotspots

Grey, C. *et al. PLoS Biol.* **7**, e1000035 (2009)

Trans-regulation of mouse meiotic recombination hotspots by *Rcr1*

Parvanov, E. D. *et al. PLoS Biol.* **7**, e1000036 (2009)

Meiotic recombination events tend to cluster at particular genomic regions, called hot spots. How and why hot spots form is poorly understood. Using mice carrying chromosomal segments from different strains, the authors of these two papers were each able to define a different locus that contains a *trans*-acting regulator of hot spot location and activity. In both cases, the *trans*-factor influences the initiation of recombination, probably by controlling the site of double-stranded DNA breaks.

GENE REGULATION

Drosophila Argonaute1 and Argonaute2 employ distinct mechanisms for translational repression

Iwasaki, S. *et al. Mol. Cell* 5 Mar 2009 (doi:10.1016/j.molcel.2009.02.010)

By using a new *in vitro* system the authors show that fly Argonaute 1 (AGO1) and AGO2 proteins both repress translation of their mRNA targets, but in different ways. These results contradict the model that only AGO1 represses translation and also reveal when AGO1 and AGO2 act: AGO1 shortens the poly(A) tail, and secondarily prevents a step after cap recognition; by contrast, AGO2 only inhibits cap function. The authors speculate that AGO1 induces a stronger response by triggering mRNA decay, whereas AGO2 preserves the mRNA and blocks translation transiently.