

IN BRIEF

GENOME EVOLUTION**Impact of replication timing on non-CpG and CpG substitution rates in mammalian genomes**

Chen, C.-L. *et al. Genome Res.* 26 Jan 2010 (doi:10.1101/gr.098947.109)

Mutation rates are heterogeneous across genomes, but it is unclear why. By genome-wide analysis of human and mouse replication timing, these authors showed that neutral substitution rates at both CpG and non-CpG sites increase with later replication. For CpG sites, the rate increase seems to be an indirect effect of higher DNA methylation levels in later replicating regions, but for non-CpG sites the effect seems to arise from decreasing DNA repair activity and fidelity during S phase.

PLANT GENETICS**Population resequencing reveals local adaptation of *Arabidopsis lyrata* to serpentine soils**

Turner, T. L., Bourne, E. C., Von Wettberg, E. J., Hu, T. T. & Nuzhdin, S. V. *Nature Genet.* 24 Jan 2010 (doi:10.1038/ng.515)

Associating genome-wide allele frequencies with environmental conditions is a powerful way of studying the genetics of local adaptation. The authors used pooled genotyping to investigate local adaptation of *Arabidopsis lyrata* to serpentine soil, which is characterized by high heavy metal content and low calcium/magnesium ratios. They found the strongest associations for polymorphisms in loci involved in heavy metal detoxification and calcium and magnesium transport, therefore revealing candidate genes for serpentine adaptation.

EPIGENETICS**A cellular memory of developmental history generates phenotypic diversity in *C. elegans***

Hall, S. E., Beverly, M., Russ, C., Nusbaum, C. & Sengupta, P. *Curr. Biol.* **20**, 149–155 (2010)

Experiences early in life affect adult phenotypes, but the mechanistic basis of such effects is poorly understood. These authors showed that adult *Caenorhabditis elegans* worms have distinctly different gene expression and histone modification profiles depending on whether the worm has gone through the stress-resistant dauer stage, and that these differences are dependent on chromatin remodelling. These findings offer a basis for exploring the role of epigenetic modification in providing a cellular memory of developmental or environmental effects early in life.

EVO-DEVO**Ancient animal microRNAs and the evolution of tissue identity**

Christodoulou, F. *et al. Nature* 31 Jan 2010 (doi:10.1038/nature08744)

This study reveals a close connection between microRNA evolution and the evolution of tissue identity and uses this connection to infer features of the protostome–deuterostome ancestor. The authors compared the expression pattern of microRNAs in extant protostome and deuterostome species to predict the initial sites of activity of these microRNAs, which seem to have been restricted to specific cell or tissue types. Based on these findings, the authors infer several features of the common bilaterian ancestor, such as a centralized nervous system.