IN BRIEF

CHROMATIN

Mapping accessible chromatin regions using Sono–Seq

Auerbach, R. K. *et al. Proc. Natl Acad. Sci. USA* **106**, 14926–14931 (2009)

Dynamics and function of compact nucleosome arrays

Poirier, M. G. *et al. Nature Struct. Mol. Biol.* **16**, 938–944 (2009)

These two papers use new approaches to explore how local chromatin features contribute to gene regulation. Auerbach and colleagues developed a simple new method, named Sono–seq, to identify locations of high chromatin accessibility. In Sono–seq, crosslinked chromatin is sonicated and subjected to size selection, then the DNA component is analysed by massively parallel short-read sequencing. When this method was applied to extracts from human cells, the sites that were identified corresponded to many known actively transcribed promoter regions and partially overlapped with, but were distinct from, those identified using DNase I hypersensitivity mapping. Poirier and colleagues used fluorescence resonance energy transfer (FRET) to analyse the dynamics of chromatin conformation on fluorescently labelled nucleosome arrays. They show that even when chromatin is compact it is highly dynamic and allows proteins to gain access to DNA that is contained within a nucleosome.

POPULATION GENETICS

A genome-wide view of *Caenorhabditis elegans* base-substitution mutation processes

Denver, D. R. *et al. Proc. Natl Acad. Sci. USA* 11 Sep 2009 (doi:10.1073/pnas.0904895106)

This study has characterized the genome-wide rate and distribution of hundreds of base substitutions that have accumulated in the genome of *Caenorhabditis elegans* over 250 generations. This feat, which was made possible by using two high-throughput sequencing methods, revealed a strong mutational bias from G/C to A/T nucleotides, indicating that many spontaneous mutations arise from oxidative stress. The transition/transversion ratio in these genomes is much lower than at the presumed neutral sequences of natural species, which argues for caution when using such regions to make generalizations about genomic mutation patterns.

CIRCADIAN RHYTHMS

The exosome regulates circadian gene expression in a posttranscriptional negative feedback loop

Guo, J. *et al. Cell* 10 Sep 2009 (doi:10.1016/j.cell.2009.06.043)

Transcription-based negative-feedback loops are known to be essential in eukaryotic circadian oscillators; this study shows that a post-transcriptional negative-feedback loop is also required for circadian regulation in *Neurospora crassa*. By deleting the *rrp44* gene, which encodes the catalytic subunit of the exosome (an exonuclease complex that regulates RNAs through degradation), Guo and colleagues showed that the exosome is required for normal clock function. Together with the FFC complex, which contains the frequency (FRQ) protein, the exosome regulates levels of the *frq* RNA to generate robust circadian oscillations. Because the mechanisms that drive circadian rhythms are highly conserved, similar post-transcriptional processes may operate in other organisms.