IN BRIEF

GENOME EVOLUTION

Ubiquitous internal gene duplication and intron creation in eukaryotes

Gao, X. & Lynch, M. *Proc. Natl Acad. Sci. USA* 19 Nov 2009 (doi:10.1073/pnas.0911093106)

Extensive, recent intron gains in *Daphnia* populations

Li, W. *et al. Science* **326**, 1260–1262 (2009)

Gene duplication is an important source of evolutionary novelty; however, most studies focus on duplication of complete genes. Gao and Lynch show that in six eukaryotic genomes duplication events that are internal to genes are common, and that a substantial proportion of these events gives rise to new introns. In their study of natural isolates of *Daphnia pulex*, Li *et al.* found that intron gain is more frequent than predicted by interspecies comparisons. Both studies suggest new avenues for exploring the evolution of gene architecture.

CHROMATIN

Chromatin profiling by directly sequencing small quantities of immunoprecipitated DNA

Goren, A. *et al. Nature Meth.* 29 Nov 2009 (doi:10.1038/nmeth.1404)

Current methods to analyse chromatin require large quantities of biological material and involve multiple steps. This paper describes a technique based on the direct single-molecule sequencing of chromatin-immunoprecipitated DNA. Reproducible and robust results could be obtained using as little as 50 pg of input DNA (approximately 25,000 cells). This method could be applied to limited cell populations, such as those derived from cancer tissues.

STRUCTURAL VARIATION

Donor–recipient mismatch for common gene deletion polymorphisms in graft-versus-host disease

McCarroll, S. A. *et al. Nature Genet.* **41**, 1341–1344 (2009)

This study reports a new mechanism by which human structural variation might affect clinically important phenotypes. The authors found that the risk of graft-versus-host disease after bone marrow transplantation is substantially increased (odds ratio of 2.5) when there is a mismatch between the donor and recipient for a common homozygous deletion of the gene *UGT2B17*, which encodes histocompatibility antigens. Future studies may identify other polymorphic deletions that result in such alloimmunity.

SMALL RNAS

Transgenic microRNA inhibition with spatiotemporal specificity in intact organisms

Loya, C. M., Lu, C. S., Van Vactor, D. & Fulga, T. A. *Nature Meth.* **6**, 897–903 (2009)

This is the first study to achieve precise spatial and temporal inhibition of microRNA (miRNA) function *in vivo*. MiRNA sponges (miR-SPs) are modified oligonucleotides that prevent miRNAs from regulating their normal targets. The authors introduced transgenic miR-SPs into *Drosophila melanogaster* using the modular GAL4–UAS system — which allows cell- and developmental stage-specific expression — and demonstrated the effectiveness of this method by determining the function of a miRNA in the formation of neuromuscular junctions.

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