TOOLS IN BRIEF

GENOMICS

Analysis of complex traits in rats

The Rat Genome Sequencing and Mapping Consortium has tackled the challenge of finding genetic variants that contribute to complex phenotypes by using a combination of genome sequencing and genetic mapping. They used over 1,000 outbred rats, descended from eight inbred progenitors, that were amenable to genetic mapping because their quantitative trait loci (QTL) could be resolved to high resolution, their genomes could be imputed from those of the founders and they had well-defined haplotypes. The researchers genotyped the outbred rats on a high-density single-nucleotide polymorphism array and measured 160 phenotypes for common disease models such as anxiety, diabetes and osteoporosis. They identified 355 QTLs for 122 phenotypes, and for 31 phenotypes they found the causal genes. Surprisingly, they also found that about half of all QTLs could not be attributed to a single variant; these QTLs may instead result from multiple alleles at closely linked loci.

Rat Genome Sequencing and Mapping Consortium *Nat. Genet.* **45**, 767–775 (2013).

CELL BIOLOGY

An optogenetic toolbox for yeast

The temporal and spatial precision of optogenetics makes it an ideal approach for protein localization and functional studies. The PhyB-PIF system is a light-inducible protein-protein interaction system that takes advantage of the light-controllable interaction between PhyB and PIF phytochrome fragments after conjugation with a small chromophore. The system has been used to recruit proteins to the plasma membrane, enabling control of the activation of intracellular signals, but to date it has not been optimized for the targeting of proteins to other organelles or cellular localizations besides the membrane. Yang *et al.* now report a library of constructs in which PhyB was fused to different anchoring sequences and localized to various subcellular places in budding yeast. The collection of probes includes tools for nuclear, endosome or peroxisome protein localization control. The researchers demonstrated the value of these tools for recruiting proteins to or away from their normal sites of action and for studying the effect on cell function.

Yang, X. *et al. Mol. Biol. Cell* doi:10.1091/mbc.E13-03-0126 (12 June 2013).

GENE EXPRESSION

An excision-only transposase

An attractive feature of the *piggyBac* system is that the transposon can be seamlessly excised from the genome; this system is therefore particularly useful as a vehicle for transient transgene expression. However, a substantial fraction of excised transposons reintegrate into the genome. Li *et al.* have now developed an excision-competent, integration-defective *piggyBac* transposase. Combining alanine-scanning mutagenesis of active-site residues with other known and newly identified mutants that modulate transposase activity, they generated transposase variants that are hyperactive at excision but lack integration activity in mammalian cells. Fusion to zinc-finger proteins that bind specific DNA sequences could rescue the integration activity of some variants, but not in a targeted fashion.

Li, X. *et al. Proc. Natl. Acad. Sci. USA* **110**, E2279–E2287 (2013).

MODEL ORGANISMS

Tools for salamander research

Salamander limb and tail regeneration has been a source of fascination for centuries; the relatively recent development of molecular genetic tools for use in this organism means that the salamander is now a viable model for studying the mechanisms of vertebrate regeneration. Khattak *et al.* have now substantially expanded the salamander toolbox. They report a collection of carefully screened germline transgenic lines with specific expression of a fluorescent reporter in neurons, glia, neural stem cells, muscle, cartilage or epidermis. Furthermore, they determined conditions to achieve tight spatiotemporal control of gene expression via inducible Cre recombinase. These tools should prove valuable for numerous types of experiments in this organism.

Khattak, S. *et al. Stem Cell Rep.* **1**, 90–103 (2013).

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