TOOLS IN BRIEF

SENSORS AND PROBES

More photoactivatable fluorescent proteins

The advent of super-resolution microscopy techniques that rely on fluorescent molecules that can be switched on and off or between two different colors, so as to localize subsets of tagged proteins and build up an image, has stimulated the development of new variants of photoactivatable fluorescent protein tags. Monomeric (m)Eos2, a protein that irreversibly switches from green to red when illuminated with violet light is one of the more popular ones. Chang *et al.* used targeted mutagenesis of mEos2 to eliminate the red form and make the green form reversibly switch off and on when illuminated with alternating violet and cyan light. This resulted in six reversibly photoswitchable monomeric green fluorescent proteins with different photophysical properties. These genetically encoded protein tags join a rapidly expanding toolbox of photoactivatable fluorescent proteins. A variety of choices is good, but researchers may now need help choosing among the available tools.

Chang, H. *et al. Proc. Natl. Acad. Sci. USA* advance online publication (28 February 2012).

EPIGENETICS

Sensing demethylation in cells

Epigenetic changes can affect gene regulation at mammalian genomic loci. For instance, inappropriate demethylation of the widespread *Line-1* retroelement has been associated with cancer gene expression. Huang *et al.* developed a non-integrating reporter to assay DNA accessibility at targeted loci in living cells. The biosensor consists of two independent zinc-finger proteins that recognize distinct 15-base-pair sequences in *Line-1*, bringing two halves of a luciferase reporter together. To help reduce background, each luciferase domain is joined to half of an intein, which excises when the parts are brought together. When both constructs are expressed in HeLa cells, the sensor shows brighter luminescence in the presence of DNA-demethylating drugs, suggesting increased access of the probe for binding in the absence of demethylation.

Huang, X. *et al. DNA Cell Biol.* advance online publication (7 February 2012).

GENETICS

A dual selection marker for *Drosophila*

To modify the fly genome, several rounds of genetic crosses are often required. Mutant progeny can be identified using the white gene, which produces flies with red eye color over a background of their siblings with white eye color. Visually inspecting the eyes of hundreds of flies can be time-consuming, however, particularly when the efficiency of the genetic modification is low and mutants are rare. Zhou *et al.* generated a dual genetic marker that can aid in this selection process. The group uses a white*::Neo* gene encoding a chimeric protein that confers resistance to neomycin as well as red eye color. The authors used white*::Neo* to screen for several fly mutants showing that the dual selection marker enriched the frequency of the targeting mutants by up to fifty times. The antibiotic can be fed to fly larvae, simplifying the mutant selection process.

Zhou, W. *et al. PLoS One* **7**, e31997 (2012).

GENOMICS

Yeast pan-genome

Not many other genomes are as well-studied as that of *Saccharomyces cerevisiae*; nonetheless, information on genomic variation in the species is scarce. Dunn *et al.* created a microarray platform, containing probes from *S. cerevisiae* and six other *Saccharomyces* species, to probe this diversity. They then collected 83 *S. cerevisiae* strains from different industrial and natural habitats and performed array comparative genomic hybridization. Almost all strains showed hybridization between strains and distribution of copy-number variation indicative of extensive cross-mating. This resource and generated data will be useful in determining regions important for adaptation to certain habitats.

Dunn, B. *et al. Genome Res.* advance online publication (27 February 2012).