IN BRIEF

DEVELOPMENT

Dynamics of Dpp signaling and proliferation control

Wartlick, O. *et al. Science* **331**, 1154–1159 (2011)

A new mechanism is proposed to explain how tissue growth can occur uniformly in response to a morphogen concentration gradient. By monitoring the expression dynamics of a Decapentaplegic (DPP)–GFP reporter in fly imaginal discs, the authors built a quantitative model that suggests that cells divide when DPP concentration increases by ~50%. Cells would therefore seem to respond not to the slope of the gradient or to mechanical constraints, as previously suggested, but to the relative temporal variation in DPP sensed by cells as the tissue grows.

GENE NETWORKS

Mapping of signaling networks through synthetic genetic interaction analysis by RNAi

Horn, T. *et al. Nature Methods* 6 Mar 2011 (doi:10.1038/nmeth.1581)

Mapping synthetic genetic interactions in yeast and bacteria has proved to be highly informative about how genes function in networks, but similar approaches in metazoans have been challenging to implement. These authors successfully used RNAi in cultured *Drosophila melanogaster* cells to map synthetic genetic interactions for 93 genes involved in signalling. Important aspects of the approach included robust experimental design to account for off-target effects of RNAi, stringent statistical analysis of interaction data and the use of automated microscopy for phenotyping, independently of pathway-specific read-outs.

STEM CELLS

Role for Dpy-30 in ES cell-fate specification by regulation of H3K4 methylation within bivalent domains

Jiang, H. *et al. Cell* **144**, 513–525 (2011)

In embryonic stem cells (ESCs), many developmental genes have so-called 'bivalent' chromatin marks — that is, histone H3 lysine 4 (H3K4) and H3K27 methylation, which are associated with gene activation and repression, respectively. To test the functional importance of H3K4 methylation, these authors knocked down components of the complexes that catalyse this mark in mouse ESCs. They show that H3K4 methylation is not essential for ESC self-renewal but is important for differentiation, and they present a revised model for the effects of bivalent marks.

EVOLUTION

Human-specific loss of regulatory DNA and the evolution of human-specific traits

McLean, C. Y. *et al. Nature* **471**, 216–219 (2011)

As a way to explore the genetic basis of human-specific traits, McLean *et al.* identified genomic regions that have been lost is humans but are conserved in chimpanzees and other mammals. They found 510 such human-specific deletions, all but one of which map to non-coding regions. The deletions are enriched near genes involved in neural function and steroid hormone receptor signalling, and the authors discuss functional effects of the deletion of several enhancers, including changes in morphology and tissue size.