IN BRIEF

DEVELOPMENT

Initiation of proximal-distal patterning in the vertebrate limb by signals and growth

Cooper, K. L. *et al. Science* **332**, 1083–1086 (2011)

Diffusible signals, not autonomous mechanisms, determine the main proximodistal limb subdivision

Roselló-Diez, A., Ros, M. A. & Torres, M. *Science* **332**, 1086–1088 (2011)

These studies support of a model of vertebrate limb development in which proximal–distal patterning is directed by signalling rather than a cell-autonomous clock. In chick limb-bud, both groups show that a balance between retinoic-acid signalling at the proximal end and distal fibroblast growth factor activity maintains limb progenitors and directs patterning.

STEM CELLS

Reprogramming of mouse and human cells to pluripotency using mature microRNAs

Miyoshi, N. *et al. Cell Stem Cell* **8**, 633–638 (2011)

Highly efficient miRNA-mediated reprogramming of mouse and human somatic cells to pluripotency

Anokye-Danso, F. *et al. Cell Stem Cell* **8**, 376–388 (2011)

A new method for generating induced pluripotent stem cells is reported, in which human and mouse somatic cells were reprogrammed by expression of microRNAs (miRNAs) alone. Miyoshi *et al.* used direct transfection of mature miRNAs, whereas Anokye-Danso *et al.* expressed miRNA clusters from a lentiviral vector. The lentiviral method was two orders of magnitude more efficient than standard reprogramming.

CHROMATIN

The specificity and topology of chromatin interaction pathways in yeast

Lenstra, T. L. *et al. Mol. Cell* **42**, 536–549 (2011)

The authors used gene-expression analyses in 165 yeast strains that carry deletions of single chromatin machinery subunits to construct a network of their functional interactions. The network was branched but highly interlinked, indicating that despite substantial functional overlap among subunits, almost all of them have unique roles. These findings also indicate a finer control of gene expression than is suggested by the broad genomic distributions of chromatin marks and modifiers.

COMPLEX TRAITS

Genome partitioning of genetic variation for complex traits using common SNPs

Yang, J. *et al. Nature Genet.* **43**, 519–525 (2011)

To investigate the genetic architecture of human complex traits such as height and body-mass index, the authors analysed 586,898 common SNPs in 11,586 unrelated individuals. By considering all SNPs cumulatively — rather than focusing only on the most statistically significant SNPs at the expense of many false negatives — they generated increased estimates for the phenotypic variance explained for the traits that were studied. Analysis of the genomic distribution of SNPs provided further insights: for example, SNPs that were in or near genes explained more variation than intergenic SNPs.