

IN BRIEF

STEM CELLS

Large intergenic non-coding RNA-RoR modulates reprogramming of human induced pluripotent stem cells

Loewer, S. *et al. Nature Genet.* **42**, 1113–1117 (2010)

This study found that numerous large intergenic non-coding RNAs (lincRNAs) are up- or downregulated in human induced pluripotent stem cells (iPSCs) and embryonic stem cells compared with fibroblasts. Knockdown of one lincRNA that is particularly enriched in iPSCs resulted in decreased ability to reprogramme somatic cells to iPSCs, whereas its overexpression increased reprogramming ability. This lincRNA — lincRoR — is regulated by the core pluripotency network and might function by associating with chromatin-modifying complexes.

DEVELOPMENT

Genetic control of organ shape and tissue polarity

Green, A. A. *et al. PLoS Biol.* **8**, e1000537 (2010)

Quantitative control of organ shape by combinatorial gene activity

Cui, M.-L. *et al. PLoS Biol.* **8**, e1000538 (2010)

By combining experimental and modelling approaches in the snapdragon, two papers have highlighted regulatory changes that might underlie the evolution of diverse shapes. Green *et al.* found that as well as controlling local rates of tissue growth, shape genes influence organizers of tissue polarity. Cui *et al.* quantified flower shape in plants with a range of transcription factor mutations and integrated this information with other data. They show that transcription factors act in combinations in local regions and that shape evolution is probably driven by 'tinkering' with local growth properties.

SMALL RNAs

mRNA turnover rate limits siRNA and microRNA efficacy

Larsson, E., Sander, C. & Marks, D. *Mol. Syst. Biol.* **6**, 433 (2010)

This paper offers an explanation for why mRNAs are not equally regulatable by RNAi. The authors used reporter and expression analyses to show that the mRNAs with the highest turnover rates are the least responsive to RNAi-mediated silencing. This is likely to be due to the prevalence of other degradation mechanisms already acting on these mRNAs. MicroRNA target prediction could be improved by accounting for mRNA turnover rates.

GENE REGULATION

Tissue-specific disallowance of housekeeping genes: the other face of cell differentiation

Thorrez, L. *et al. Genome Res.* 18 Nov 2010 (doi:10.1101/gr.109173.110)

A new study reveals that housekeeping genes are not always ubiquitously expressed, but can be selectively silenced in certain tissues. The authors compared gene expression across 21 differentiated mouse tissues and identified *Mct1* and *Oxct1* as selectively silenced in pancreatic islets and liver, respectively, which is consistent with the specialized metabolic roles of these genes and tissues. Gene repression occurred concurrently with histone H3 lysine 9 methylation and microRNA expression, suggesting potential silencing mechanisms.