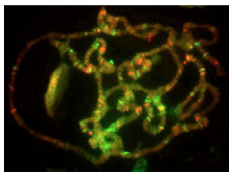
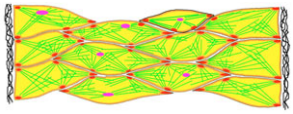


Transcriptional regulation: PcG and trxG take a separate approach

Polycomb group (PcG) and trithorax group (trxG) proteins control the transcription of Hox and other target genes during development by binding to their respective response elements, which cluster in regulatory regions called maintenance elements (MEs). But do PcG and trxG proteins act synergistically at MEs? Not in most cases, claim Petruk et al., who have examined how trxG and PcG proteins associate with the ME of the *bxd* regulatory region of an *Ultrabithorax* (*Ubx*) transgene in individual *Drosophila* salivary gland cells in vivo (see p. 2383). Multiple trxG and PcG proteins, they report, act through the same or at juxtaposed sequences in the *bxd* ME. However, trxG or PcG proteins, but not both, associate with the ME of an activated or repressed *Ubx* transgene, respectively. Only the PcG protein Asx and the trxG protein Ash1 require Trithorax to bind to their targets. These results provide new insights into how PcG and trxG proteins might regulate transcription during development and during pathogenic processes such as cancer.

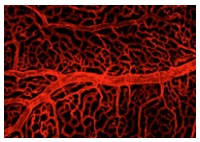


Myosin IIB: a force for morphogenesis

Two tissue movements – convergence and extension – are essential for axial morphogenesis in vertebrate and invertebrate embryos. But what generates the tensile forces that drive the intercalation of cells that underlies these two movements? On p. 2435, Skoglund and colleagues report that in *Xenopus laevis* embryos, convergence and extension at gastrulation require a myosin IIB-dependent cortical actin network. Using morpholino knockdown, they show that myosin IIB (a cytoskeletal myosin that crosslinks actin filaments and acts as a molecular motor) is needed during gastrulation to maintain a stereotypical cortical actin cytoskeleton. This network is polarized relative to the embryonic axis, the researchers report, and cyclically lengthens and shortens during gastrulation. Depletion of myosin IIB also results in the loss of the polarized protrusive activity usually seen in intercalating cells, the loss of cell-cell and cell-matrix adhesion, and failure of blastopore closure. Together, these findings reveal how a molecular-scale motor protein can generate the tensile forces that drive tissue-scale embryonic morphogenesis.

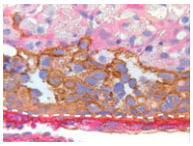
Notch not numbed by Numb

The membrane-localized intracellular protein Numb is known to antagonize Notch signalling in several developmental contexts, such as during mesodermal development in *Drosophila*. But now, surprisingly, Range and co-workers report that the sea urchin homologue of Numb (LvNumb) regulates Notch signalling positively during the specification of non-skeletal mesoderm (NSM) cells in sea urchin embryos (see p. 2445). The researchers show that LvNumb protein localizes to the presumptive NSM cells in early embryos. By injecting LvNumb RNA and antisense morpholinos, they demonstrate that LvNumb is needed for the specification of all the NSM cell types. The authors also show that LvNumb acts synergistically with Notch during NSM specification and that, unlike in other systems, LvNumb does not need to interact with the endocytic machinery to regulate Notch signalling. Numb might, the researchers speculate, regulate Notch positively by binding to other unknown factors, the identification of which could provide new insights into Notch and Numb signalling and shed light on the changing role of Numb during evolution.



c-Myc essential for haematopoiesis

The transcription factor c-Myc regulates the expression of numerous genes involved in many aspects of cellular function and its deregulation is associated with a wide range of human tumours. However, the physiological role of c-Myc during development is poorly understood. Now, two papers in this issue suggest that c-Myc functions primarily in haematopoiesis during mammalian development. First, on p. 2467, Rong Wang and colleagues report that c-Myc expression in the haematopoietic lineage indirectly controls angiogenesis (the growth of new blood vessels from pre-existing vessels). *c-myc*-null mouse embryos, which die by embryonic day (E) 10.5, have many severe developmental abnormalities, including a lack of elaborate blood vessels. To study the role of c-Myc in vascular development, the researchers deleted the *c-myc* gene in selected cell lineages using Cre-*lox*-mediated recombination. To their surprise, the elimination of c-Myc in most endothelial cells in mouse embryos did not abrogate the de novo differentiation of endothelial cells (vasculogenesis) or their proliferation, survival and migration. The mutant embryos also survived to beyond E12.5. By contrast, the elimination of c-Myc in haematopoietic lineages alone caused defects in both haematopoiesis and angiogenesis, suggesting that hematopoietic defects can disrupt angiogenesis. Further insights into the role of *c-myc* during development are also provided by Andreas Trumpp and colleagues on p. 2455, who show that the severe abnormalities previously seen in *c-myc*-null embryos are largely absent when *c-myc* is eliminated specifically in the epiblast, which suggests that the *c-myc*-null mutant phenotype results mainly from placental insufficiency. Although the epiblast-restricted c-Myc deficient embryos, which express c-Myc in placental but not in embryonic cells, appear surprisingly normal, they still die around E12, the researchers report. Specifically, these embryos have non-functional haematopoietic stem cells, are anaemic because of apoptosis of erythrocyte precursors, and have defective livers. Interestingly, the elimination of c-Myc in the hepatoblast lineage alone did not affect liver or haematopoietic development, but the elimination of c-Myc in the haematopoietic lineage affected both liver and blood development. Thus, both these papers unexpectedly show that c-Myc function is not required ubiquitously during development, but instead is specifically essential for haematopoiesis, which then supports vascular and liver development.



Jane Bradbury

IN JOURNAL OF CELL SCIENCE

Actin makes a move with annexin A2

The dynamic remodelling of the actin cytoskeleton is crucial for cell adhesion and motility, and can be triggered by stimuli that activate the insulin receptor (IR) and other receptor tyrosine kinases. IR activation promotes cell motility by disrupting cell-substrate contacts, but many steps in this signalling cascade are unknown. In *Journal of Cell Science*, Konietzko et al. now identify a key stage in the pathway – the tyrosine phosphorylation of the phospholipid- and actin-binding protein annexin A2. In kidney cells that overexpress the human IR, they show that annexin A2 is tyrosine phosphorylated in response to insulin and that annexin A2 and the IR co-immunoprecipitate, indicating that the IR phosphorylates annexin A2 directly. Rho/ROCK signalling, the authors show, mediates insulin-induced morphological changes, and knocking down annexin A2 inhibits insulin-triggered Rho activation and actin rearrangements. From their findings, the authors propose that annexin A2 tyrosine phosphorylation links IR activation to Rho/ROCK-mediated actin rearrangement and cell adhesion.

Konietzko, V. et al. (2008). Tyrosine phosphorylation of annexin A2 regulates Rho-mediated actin rearrangement and cell adhesion. J. Cell Sci. 121, 2177-2185.