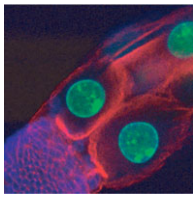
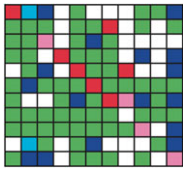


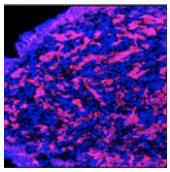
Sunspot shines new light on Wnt signalling

In many organisms, the Wingless (Wg)/Wnt signalling pathway regulates developmental processes through Armadillo (Arm)/β-catenin, which activates target gene transcription through the TCF transcription factor family. Now, Tetsu Akiyama and colleagues have identified a new interaction partner for Arm in *Drosophila*, called Sunspot (Ssp), which acts independently of dTCF (see p. 1755). Using mutant fly lines, the researchers report that Ssp is required for the proliferation of imaginal disc cells, salivary glands and the central nervous system in fly larvae. Ssp controls the transcription of genes involved in proliferation, they report, but although this requires Arm, it is independent of dTCF. By using overexpression studies, the authors also show that Wg negatively regulates Ssp signalling by controlling its subcellular location: Wg expression directs Ssp to the nuclear envelope, away from its targets, in a process that also requires Arm. Given that Wnt signalling is highly conserved, the researchers suggest that Ssp regulation by Wg and Arm might be a general signalling mechanism.



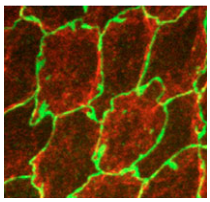
ChIPping away at gene regulatory networks

Although the gene regulatory networks (GRNs) that control various developmental processes have been mapped in different organisms, the exact interactions that exist between transcription factors and their gene targets are not always known. Now, on p. 1613, Yutaka Satou and colleagues have mapped the binding profiles of the core transcription factors during early embryonic development of *Ciona intestinalis*. The researchers had previously identified 11 transcription factors central to embryonic specification events during early *Ciona* development. In the present study, they used ChIP (chromatin immunoprecipitation) to identify the interactions between these transcription factors and genomic DNA. They confirmed that most previously identified genetic interactions in *Ciona* development are direct interactions between the transcription factor and the target gene's cis-regulatory region. They also integrated the ChIP data with the known gene expression network to study several tissue-specific gene regulation pathways. The researchers estimate that over 50% of the direct interactions found in the ChIP assay contribute to gene expression regulation, thus expanding our knowledge of GRNs in *Ciona* development.



Hedgehog signals gut growth

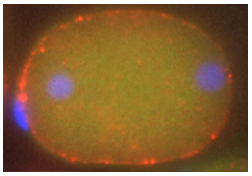
Vertebrate digestive tract development requires hedgehog (Hh) signalling, but the exact mechanisms by which Hh regulates gut development are not known. Andrew McMahon, Junhao Mao and colleagues now report, on p. 1721, that Hh signalling is required for the proliferation of mesenchymal progenitor cells in the developing mouse gut. By conditionally inactivating the expression of sonic hedgehog (Shh) and Indian hedgehog (Ihh) in the early gut endoderm, the authors observed a decrease in the size of the digestive tract and a reduction in the development of the mesenchyme compared with controls. Through a combination of in vivo and in vitro experiments, they showed that Hh proteins act as mitogens required for the proliferation of mesenchymal progenitors in the mouse embryo, including those progenitors that develop into gut smooth muscle cells. Based on their results, the researchers propose that a similar mechanism might be involved in postnatal gut homeostasis. In addition, they suggest that this mechanism could be key to elucidating the function of Hh in digestive tract tumours.



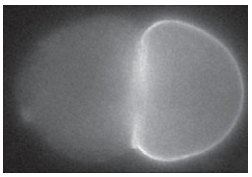
PARs on par with cytoskeletal dynamics

The PAR proteins are best known for their conserved roles in establishing cell polarity during development. Four studies now shed light on their cytoskeletal interactions in contrasting developmental contexts.

Apical constriction, powered by actomyosin (AM) contractility, drives cell internalisation during morphogenesis. To investigate PAR complex (Par-6, aPKC and Bazooka/Par-3) protein functions in apical constriction, Tony Harris and colleagues studied dorsal closure (DC) in *Drosophila*, in which amnioserosal cells undergo pulsed contractions (see p. 1645). By performing live imaging on GFP-tagged embryos, they observed amnioserosal cells undergoing repeated cycles of (apically restricted) AM network assembly and disassembly during DC. As these networks form, they interact transiently with an apically localised Par-6/aPKC/Par-3 PAR complex, report the authors, with each assembly event driving apical constriction. Strikingly, their live imaging results combined with genetic interaction tests reveal that different PAR proteins regulate distinct phases of the assembly/disassembly cycle, with Par-3 promoting the network's duration and Par-6/aPKC promoting the lull time between pulses. Together, these findings reveal how the PAR complex regulates the mechanics of AM contractility during apical constriction.



The *C. elegans* zygote is also a classic model for studying cell polarity, in which cortical flows created by AM network contractions mobilise the anterior PAR proteins (PAR-3, PAR-6 and PKC-3) away from the future posterior end of the embryo, as marked by the sperm centrosome and the posterior PAR-1 and PAR-2. The Rho-GEF ECT-2 is central to establishing these early cortical flows. Now Geraldine Seydoux's lab report that a second, parallel and redundant, PAR-2-dependent pathway can polarise the zygote in the absence of ECT-2-dependent cortical flows (see p. 1669). They show that PAR-2 localises to the cortex nearest the sperm centrosome, even when cortical flows are absent, where it antagonises the PAR-3-dependent recruitment of myosin. This creates myosin flows that transport the anterior PAR complex away from PAR-2 in a positive-feedback loop. The authors propose that this second polarity pathway strengthens the robustness of the initial polarity cue provided by the sperm centrosome. In a separate study of early embryo polarisation on p. 1765, Daniel St Johnston and colleagues report that in a new *Drosophila Par-3* mutant, oocyte polarity is, surprisingly, normal but axis formation is not. Importantly, they show that when Par-3 is absent, the main anteroposterior and dorsoventral axis determinants are mislocalised. From their findings, the authors propose that a Par-1-activating kinase cascade, rather than cortical contractions, generate the initial AP asymmetry in fly embryos.



Finally, Carrie Cowan and colleagues, on p. 1743, highlight in *C. elegans* embryos the role of PAR proteins in asymmetric cell divisions, in which the boundary between the anterior and posterior PAR domains is matched to the site of cell division to ensure the correct segregation of cell fate determinants to daughter cells. They report that cell polarity and cell division are coordinated by a novel mechanism involving the repositioning of the PAR-2 boundary via a Gα pathway that repositions the boundary between the PAR domains to match the cytokinesis furrow. It does so by regulating microtubule-cortex interactions to cause large-scale cortical reorganisation that moves PAR-2 towards the furrow. This mechanism, the authors suggest, could also exist in asymmetric divisions of more complex systems.