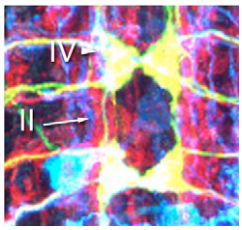
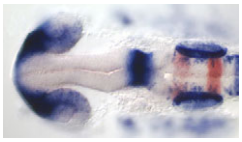


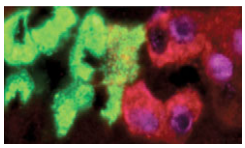
Linking dendrite structure to neuronal function

Neuronal dendrites and axons have distinct functions and morphologies, and, to wire up the nervous system correctly, their development must be coordinated. On p. 55, Grueber and colleagues provide an analysis of axon projections from different types of dendritic aborization (da) sensory neurons in *Drosophila* and identify some new genes involved in axon and dendrite development. These neurons, which lie just below the transparent body wall in *Drosophila,* form four classes based on their dendritic morphology. The researchers use mosaic cell-labelling techniques to analyze da neuron axon projections in embryonic and larval stages. They report that the axons in da neurons in different dendritic classes have distinct morphologies and organize into different layers of the CNS, a novel finding that suggests that each class has a distinct function. They also use forward genetic screening to identify loci that are involved in sensory dendrite and/or axon patterning. This new information provides a firm foundation for understanding the similarities and differences in the morphogenesis of axons and dendrites.



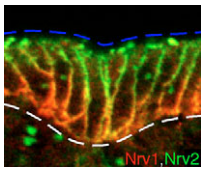
Degrading uniformity in hindbrain patterning

Retinoic acid (RA) plays an essential role in establishing anterior-posterior patterning in the hindbrain, where a spatio-temporal gradient of RA is believed to generate domains of RA-responsive gene expression. Given this, it is puzzling that a uniform concentration of exogenous RA can rescue RA-depleted embryos. Cecilia Moens and co-workers now resolve this puzzle by showing that Cyp26 enzymes (which degrade RA) generate the RA-response gene expression patterns required for zebrafish hindbrain development (see p. 177). The researchers first documented dynamic spatio-temporal expression domains for the three zebrafish cyp26 genes – *cyp26a1*, *cyp26b1* and *cyp26c1* – in the developing hindbrain. They then showed that, in embryos depleted of all three enzymes, the entire hindbrain expresses RA-responsive genes that are normally restricted to the posterior hindbrain. Finally, they report that cyp26 genes are responsible for the ability of exogenous RA to rescue embryos depleted of endogenous RA. Given these results, the researchers propose a 'gradient-free' model for hindbrain patterning in which Cyp26 activity establishes sequential RA-responsiveness boundaries.



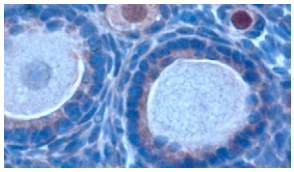
Gastric cell differentiation: from the neck down

In the mammalian stomach, digestion is initiated by acids, digestive enzymes (zymogens) and mucus secreted by different types of gastric epithelial cells. These cells are constantly replenished from adult stem cells but, strangely, zymogenic cells (ZC) seem to arise from mucus-secreting neck cells instead of directly from stem cells, a route that probably involves dismantling the secretory apparatus of neck cells. On p. 211, Ramsey and co-workers confirm that this unlikely conversion occurs, and that it requires the transcription factor Mist1. The researchers analyzed gene expression in gastric cells purified from mouse stomach by laser capture microdissection and identified *Mist1* as a potential ZC regulatory factor. Their detailed study of gastric unit differentiation in *Mist*$^{-/-}$ and wild-type mice indicates that ZC progenitors arise as neck cells that become transitional cells with characteristics of both mature cell types. This new information about ZC differentiation should help researchers discover why this developmental pathway is aberrant in precancerous lesions of the stomach.



Transport free Na,K-ATPase role at a junction

Cell junctions provide important adhesion, diffusion barrier, polarity and signalling functions during epithelial development. In *Drosophila*, claudin-containing septate junctions (SJs) provide a diffusion barrier and control the size of tracheal tubes. The formation of SJs requires the heterodimeric Na,K-ATPase ion transporter but not, as Paul and co-workers now report, its ion-pump activity (see p. 147). By investigating the localization and function of wild-type and chimeric isoforms of the single-transmembrane Na,K-ATPase β-subunit, the researchers show that the extracellular domain of the Nrv2 isoform of this subunit is specifically required for both SJ functions. Similarly, only some isoforms of the ten-transmembrane α subunit, which contains the ATPase activity, support SJ function. Unexpectedly, mutations that inactivate the ATPase do not compromise SJ function, which indicates a pump-independent role for Na,K-ATPase in SJ formation and activity. Finally, because the rat α1 isoform completely rescues *Atpα*-null *Drosophila* mutants, the authors suggest that the Na,K-ATPase has an evolutionarily conserved role in epithelial junctions.



Foxo3a: support signal from oocyte to follicle

During mammalian oestrous cycles, ovarian follicles support the development and release of oocytes. But this is not just one-way support, as oocytes also contribute to follicle development. On p. 199, Liu and colleagues report that oocyte-specific expression of the transcription factor Foxo3a negatively regulates oocyte growth and follicular development. The researchers' previous work had suggested that the suppression of Foxo3a in oocytes – through activation of the phosphatidylinositol 3-kinase pathway – might be needed for follicular development and oocyte growth. To test this idea, the researchers generated transgenic mice that express constitutively active Foxo3a in their oocytes. The female transgenic mice, they report, are infertile because of retarded oocyte growth and follicular development, and anovulation. They also show that constitutively active Foxo3a causes reduced oocyte-specific expression of proteins that are required for follicle development. Overall, the researchers conclude that Foxo3a is an important intra-oocyte signalling molecule and suggest that their results might provide clues to the causes of premature ovarian failure in humans.

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IN JOURNAL OF CELL SCIENCE

Green approach to G-protein signalling

Heterotrimeric G proteins are important signal transducers. In mammals, activated G-protein coupled receptors exchange GDP bound to the Gα subunit for GTP. The Gα and Gβγ subunits then dissociate and activate various effectors. Gadella and co-workers now provide the first evidence of a heterotrimeric G protein in a dicot plant, which behaves differently to mammalian G proteins. Lipid modifications are important for mammalian G-protein function. To discover their role in plant G-protein heterotrimer formation and localization, the authors measured fluorescence resonance energy transfer in cowpea cells transfected with GFP-tagged *Arabidopsis* G-protein subunits. The localization of Gα (GPα1) and two Gγ (AGG1 and AGG2) subunits to the plasma membrane, they report, requires lipid modification of two motifs in each subunit. They also show that GPα1-AGβ1-AGG1 heterotrimers at the plasma membrane do not dissociate upon GPα1 activation, indicating that plant cells regulate G-protein signalling in a novel way.

Adjobo-Hermans, M. J. W., Goedhart, J. and Gadella, T. W. J., Jr (2006). Plant G protein heterotrimers require dual lipidation motifs of Gα and Gγ and do not dissociate upon activation. *J. Cell Sci.* **119**, 5087-5097.