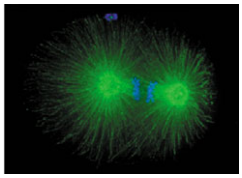
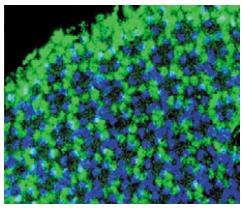


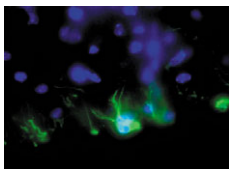
CDC-42 takes a cell polarity PARtner

The establishment of polarity is an important developmental event. In *C. elegans*, the segregation of different PAR proteins into anterior and posterior cortical domains establishes anteroposterior polarity in one-cell embryos. PAR protein segregation is coupled to rearrangements of the embryo's acto-myosin cytoskeleton. Schonegg and Hyman now report that the Rho family GTPases CDC-42 and RHO-1 coordinate acto-myosin contractility and PAR protein localization during polarity establishment in these embryos (see p. 3507). Using live imaging of GFP-tagged PAR proteins and RNAi depletion of *rho-1* and *cdc-42*, the researchers show that RHO-1 activity helps to localize CDC-42 to the anterior of the embryo by participating in the early organization of the myosin cytoskeleton. CDC-42 then stabilizes the acto-myosin network and localizes PAR-6 to the anterior cortex. Although these results differ from other data that indicate that CDC-42 helps to maintain but not establish polarity, they provide important new insights into how RHO-1 and CDC-42 might interact during developmental cell polarization events.



A Snail trail to Wg-induced death

The periphery of the fly eye is a good place to study the final stage of positional signalling. Here, Wingless (Wg) signalling induces concentrically arranged cellular specializations, such as the pigment rim, which shields the eye from extraneous light. The pigment cells that form this structure originally surrounded the peripheral ommatidia of the eye, which die during pupal eye development. On p. 3529, Lim and Tomlinson report that three Snail family transcription factors – Worniu, Snail and Escargot – and the enzyme Notum are Wg signalling targets at the edge of the fly eye. Notum limits the extent of Wg signalling, but Snail gene expression, they report, is required for removing the peripheral ommatidia and for forming the peripheral rim. Because Snail family proteins are expressed only in a subset of ommatidia cells, not in the photoreceptors that die, Lim and Tomlinson propose that a death signal released from the Snail-family-expressing cells directs the death of the photoreceptors.

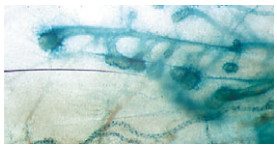


Developmental plasticity of adult human brain revealed

Contrary to expectations, recent work has indicated that some regions of adult rodent brains contain neurogenic cells. But what about in the adult human brain? On p. 3671, Dennis Steindler and colleagues describe how they derived multipotent astroglial neural progenitors that can proliferate extensively from adult human brain tissue. The researchers took tissue from patients undergoing surgery for temporal lobe epilepsy. By applying culture conditions that favour the growth of neural stem cells, they isolated a population of adult human neural progenitor cells – identified by morphology and the expression of markers such as nestin – from multiple forebrain regions traditionally thought to be non-neurogenic. These cells divided for more than 300 days and generated both glial and neuronal cell types, in vitro and after transplantation into immunodeficient mice. These results therefore suggest that cells in the adult human brain retain considerable developmental plasticity. In addition, the astroglial neural progenitors isolated by the researchers could provide a source of cells for treating neurogenerative disorders or damage to the nervous system.

Translational regulation moves upstream

Gene expression during development is regulated both transcriptionally and translationally; however, relatively few examples of translational regulation are known. On p. 3575, Imai and colleagues describe for the first time how an upstream open reading frame (uORF) mediates translational control during plant development. Loss-of-function mutants of *Arabidopsis ACAULIS 5* (*ACL5*), which encodes spermine synthase, have a dwarf phenotype because of a defect in stem elongation. To find out how *ACL5* regulates stem elongation, the researchers isolated a dominant suppressor mutant of the *acl5* phenotype – *sac51-d*. They show that *sac51-d* disrupts a short uORF of *SAC51*, which encodes a bHLH transcription factor. Other experiments indicate that this disruption might increase the translation of *SAC51*. Thus, the researchers suggest that the uORF-encoded protein normally prevents the initiation of *SAC51* translation, and that *ACL5* acts directly or indirectly (possibly through spermine's effects on protein synthesis) to activate *SAC51* translation and subsequent stem elongation.



Mammary development: no Hedgehog required

Hedgehog (Hh) signalling is essential for the development of many vertebrate epidermal appendages, including hair and teeth. Another epidermal appendage that shares a common origin is the mammary gland. But, as Hatsell and Cowin now report, positive Hh signalling is absent throughout the embryonic and postnatal development of mouse mammary glands (see p. 3661). In mammals, three Gli transcription factors act downstream of Hh: the activator Gli2 induces the expression of Gli1, which antagonizes the repressor activity of Gli3. The researchers show that although *Gli2* and *Gli3* are expressed during embryonic mammary development, Hh target genes are not expressed. Furthermore, whereas mammary gland development is normal in mice that lack *Gli1* or *Gli2*, two pairs of mammary buds are missing in $Gli3^{xt/xt}$ mouse embryos, which do not make Gli3. Misactivation of the Hh pathway by targeted expression of *Gli1* in $Gli3^{xt/+}$ mice also induces mammary bud loss. Thus, the researchers conclude, Gli3-mediated repression of Hh signalling is required for normal embryonic mammary development.

MicroRNA signals time for phase change

The role that microRNAs – short, single-stranded RNAs that bind to mRNA – play in gene regulation during plant and animal development has only recently begun to emerge. Now, Wu and Poethig report that the microRNA *miR156* promotes the vegetative phase change in *Arabidopsis* by temporally regulating the transcription factor *SPL3*, and probably also *SPL4* and *SPL5* (see p. 3539). In plants, the shoot apex progresses through juvenile and adult phases of vegetative development before switching to reproductive development. Wu and Poethig show that all three *SPL* genes promote the vegetative phase change and the switch to flowering, and that their effect on development is strongly repressed by *miR156*. The juvenile-to-adult transition, they report, is accompanied by a decrease in the level of *miR156* and an increase in *SPL3* mRNA abundance; other experiments indicate that the decrease in *miR156* is responsible for this increased *SPL3* expression. Thus, conclude the researchers, temporal variation in microRNA expression plays a regulatory role in developmental timing in plants.

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