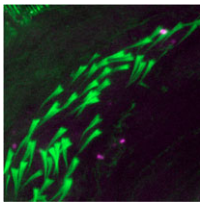
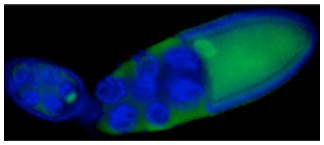
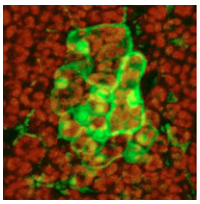


Germline transcription gets the message

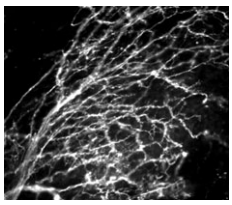
Although the transcription of new genes drives many processes during development, it is generally accepted that the late stages of both male and female germline development in *Drosophila* occur in the absence of transcription. Now, two papers in this issue of *Development* provide important new insights into how the gene expression necessary to drive spermiogenesis and oogenesis in *Drosophila* is controlled. On p. 1897, Barreau et al. reveal that, although the mRNAs for most of the proteins involved in late spermiogenesis are transcribed before the spermatocytes undergo meiotic division to form spermatids, some genes are transcribed post-meiotically. The researchers identify 24 genes whose mRNAs are most abundant in elongating spermatids, and use quantitative RT-PCR to show that these genes are transcribed post-meiotically, just before histone-to-protamine chromatin remodelling occurs. They show that these post-meiotically transcribed mRNAs are localized to the distal elongating end of the spermatid bundles and report that at least one of them (*scotti*) is required for late spermiogenesis. Further studies on this and the other post-meiotically transcribed genes should provide insights into the mechanisms of genetic control of sperm maturation. Turning to the maturation of oocytes, on p. 1969, Benoit et al. report that two distinct poly(A) polymerases regulate the translation of stored maternal mRNAs at different stages of *Drosophila* oogenesis. Cytoplasmic polyadenylation plays an essential role in activating maternal mRNA during oogenesis and early development. Previous studies have shown that the canonical poly(A) polymerase (PAP) interacts with Orb, the *Drosophila* homolog of the vertebrate CPEB RNA-binding protein, to control cytoplasmic polyadenylation during mid-oogenesis. These researchers now report that an atypical GLD-2 poly(A) polymerase is required for the polyadenylation of specific mRNAs during late oogenesis and early embryogenesis. They show that this female germline GLD-2 is encoded by *wispy*, that Wisp (the protein encoded by *wispy*) is required for meiotic progression in mature oocytes, and that Wisp interacts with Orb. Thus, because Orb forms complexes with both PAP and Wisp, it seems that the same pool of mRNAs is regulated by two different poly(A) polymerases at different stages of oogenesis.





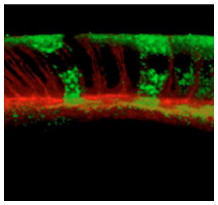
Complexities of trichome patterning

In plants, the regular pattern of trichomes (leaf hairs) is thought to be generated during development through intercellular communication. That is, trichome inhibitors, which are activated by self-enhanced trichome activators, move between cells to determine the trichome pattern. On p. 1991, Zhao and colleagues refine this model, which is largely based on data obtained from the root hair system, through a detailed analysis of the TTG1-bHLH-MYB complex, which activates trichome initiation and patterning in *Arabidopsis*. By co-precipitation, they confirm that the WD40 repeat protein TTG1 associates with the bHLH protein GL3 and the R2R3-MYB protein GL1 in vivo. They identify the trichome activators *GL2* and *TTG2*, and repressors *CPC* and *ETC1* as being transcriptional targets of this complex by showing that GL1 and TTG1 bind to their promoters in vivo. Finally, they provide the first direct evidence that the trichome repressor CPC moves between cells in developing leaves. Thus, they conclude, the TTG1-bHLH-MYB complex affects trichome patterning by directly regulating downstream targets and the movement of trichome repressors.



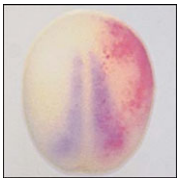
The muscle behind synaptic patterning

During the innervation of mammalian muscles, neuromuscular (NM) synapses form at specific sites on muscle fibres. For years, it has been thought that ingrowing nerves determine these synaptic sites. However, on p. 1957, Liu and colleagues challenge this 'neurocentric' view by reporting that the γ-subunit of the acetylcholine receptor (AChR), which is expressed in embryonic muscle but is replaced after birth by the ε-subunit, plays an essential role in NM synaptic patterning. In wild-type mice, pre-patterned AChR clusters form on muscle cells early in NM synaptogenesis but their subsequent role in synapse development is unclear. The researchers show that deletion of the AChR γ-subunit gene delays the formation of these clusters, which are also more broadly distributed than normal. Furthermore, the presynaptic nerves in the γ-null mice contact a broader region of the muscle than those in wild-type mice. These results indicate that the AChR γ-subunit is required for the formation of pre-patterned AChR clusters, which, in turn, determine the pattern of NM synaptogenesis.



Endocytosis: shaping the Gurken gradient

In the *Drosophila* ovary, different levels of Egfr signalling establish the axis of the egg and the future embryo. A dorsal-ventral gradient of the morphogen Gurken, an Egfr ligand, is thought to control Egfr activation; but what is the precise shape of this gradient and how is it regulated? Using a horseradish peroxidase (HRP)-Gurken fusion protein, Chang and colleagues now report that the gradient of Gurken is directly regulated by Cbl, a protein that downregulates Egfr signalling by mediating its endocytosis (see p. 1923). They show that HRP-Gurken is internalised with Egfr into follicle cells and passes through the Rab5/7-associated endocytic pathway to the lysosome for degradation. Loss-of-function and overexpression studies show that Cbl facilitates this internalisation. Finally, the researchers show for the first time that the Gurken gradient extends from its source at the anterior/dorsal side of the egg to the ventral follicle cells, which suggests that Gurken is a long-range morphogen that directly determines the fate of these cells.



FoxM1: linking cell division and neuronal differentiation

During vertebrate embryogenesis, the formation of the nervous system from the ectoderm begins with neural induction, a process that involves the inhibition of BMP signalling. The resultant neuroectoderm cells proliferate briefly before differentiating into neural cells. But what stimulates this proliferation and is it essential for neural differentiation? Ueno and co-workers now report that the Forkhead transcription factor FoxM1 is required for both proliferation and differentiation of neural precursors in early *Xenopus* embryos (see p. 2023). They show that FoxM1 expression in the neuroectoderm is required for cell division in this embryonic region, and that BMP inhibition induces the expression of FoxM1 and also of the cell-cycle regulators it targets. Importantly, they show that FoxM1-dependent cell division is required for neuronal differentiation but not for the specification of the neuroectoderm. These results reveal how cell division and neuronal differentiation are linked in early *Xenopus* embryos, but also suggest that BMP signalling may regulate cell proliferation, as well as cell fate, in many developmental situations.

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