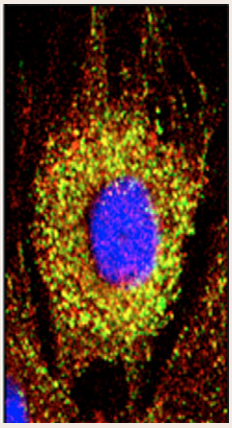
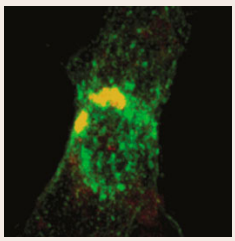
In this issue

by Jane Bradbury



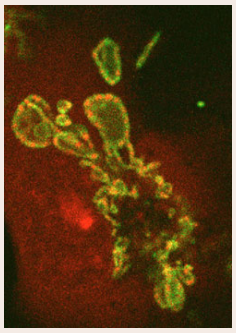
High FYVE for BMP signalling

Signalling by the transforming growth factor β (TGFβ) receptor superfamily involves second messengers called Smad proteins. These bind to the receptor complex, become phosphorylated and then translocate to the nucleus. The FYVE-domain protein SARA (Smad anchor for receptor activation) facilitates TGFβ and activin/nodal signalling by recruiting unphosphorylated Smad2 and Smad3 to membranes. Now, Xu Cao and co-authors report that another FYVE-domain protein – endofin – acts as a Smad anchor during bone morphogenetic protein (BMP) signalling (see p. 1216). The authors show that endofin binds preferentially to Smad1 and enhances its phosphorylation and nuclear translocation upon BMP stimulation. RNAi studies indicate that endofin is required for BMP-dependent Smad1 phosphorylation. Furthermore, mutating the membrane-anchoring FYVE domain of endofin reduces BMP-responsive gene expression in cell cultures and *Xenopus* ectodermal explants. Finally, the authors show that endofin also recruits protein phosphatase 1, which dephosphorylates and inactivates the type 1 BMP receptor. Thus, they conclude, endofin both positively and negatively regulates BMP signalling.



Synapsin makes sweet moves

Glucose transport in adipocytes is controlled by regulating the number of glucose transporters – particularly the Glut4 isoform – at the cell surface. In response to insulin, Glut4 moves from an intracellular, vesicular pool to the plasma membrane. This insulin-stimulated exocytosis uses many proteins involved in other aspects of membrane trafficking but, as Cynthia Corley Mastick and colleagues report on p. 1168, it also involves synapsin IIb, a protein that helps to organize a reserve pool of synaptic vesicles in neuronal cells. The authors show that adipocytes express synapsin IIb and that it colocalizes with Glut4. Then, because phosphorylation of synapsins affects their function in synaptic vesicle trafficking, the authors use a non-phosphorylatable mutant (S10A synapsin IIb) to investigate whether synapsins are involved in Glut4 trafficking. They report that expression of S10A (but not wild-type) synapsin IIb in adipocytes increases the level of Glut4 on the basal cell surface fourfold. Together with other results, this finding indicates that synapsin IIb plays an important role in Glut4 traffic in adipocytes.

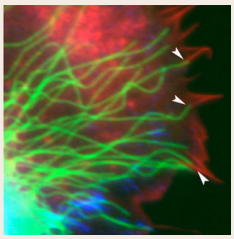


SUMO wrestling in mitochondria

Mitochondria undergo regulated fission and fusion events that are necessary for metabolic stability. One protein that helps to control these events is DRP1. This GTPase can be post-translationally modified by addition of the ubiquitin-related molecule SUMO; so might SUMOylation help to regulate mitochondrial function? On p. 1178, Heidi McBride and colleagues provide evidence that it does by showing that the SUMO protease SENP5 is needed to maintain normal mitochondrial morphology and to control intracellular levels of reactive oxygen species (ROS). Overexpression of SUMO1 increases fragmentation of mitochondria and stabilizes DRP1. The authors show that overexpression of SENP5 reduces the amount of SUMO1 conjugation and DRP1 levels and rescues SUMO1-induced mitochondrial fragmentation. By contrast, knocking down SENP5 by RNAi stabilizes DRP1, increases mitochondrial fragmentation, and increases ROS production. Finally the authors report that knocking down DRP1 rescues the effects of SENP5 downregulation. Their data represent the first report of a function for a SUMO protease in the regulation of mitochondrial dynamics and reveal a new mechanism for the regulation of mitochondrial morphology and metabolism.

Dawn arrival for condensin

During mitosis, interphase chromatin is reorganized into condensed, rigid chromosomes. This morphological change and the subsequent segregation of chromosomes requires the association of condensin I and II – protein complexes containing two ATPases of the structural maintenance of chromosomes (SMC) family and three non-SMC subunits – with the chromosomes. But what controls this? On p. 1245, Jan-Michael Peters and co-workers report that for condensin I (but not condensin II) the answer is Aurora B – a kinase that controls various stages of chromosome segregation. Using quantitative time-lapse imaging of human cells expressing GFP-labelled condensin subunits, the authors show that the loading of condensin I on to chromosomes in prometaphase and its maintenance on the chromosomes as mitosis proceeds requires Aurora B. The three non-SMC subunits of condensin I, they report, are phosphorylated by Aurora B in vitro and their phosphorylation during mitosis requires Aurora B. The authors conclude, therefore, that Aurora B contributes to chromosome rigidity and segregation during mitosis by promoting the binding of condensin I to chromatin.



Microtubules talk filopodia into turning

Cross-talk between the microtubule and actin cytoskeletons is involved in many cellular processes. Joseph Schober, Gary Borisy and co-workers have been investigating how the interaction between microtubules and filopodia (fine actin cytoskeletal projections) is involved in one of these, cell motility. They now report that microtubules make contact with filopodia and stimulate their reorganization in melanoma cells and fibroblasts (see p. 1235). Microtubules grow, through polymerization, from the centre of the cell to its periphery, where their plus ends interact with several sites (including filopodia) that help to coordinate cell movement. The authors' analysis of digital fluorescence images reveals that contact between microtubules and filopodia correlates temporally with filopodia turning and merging and that nocodazole-induced depolymerization of microtubules decreases merging of filopodia and increases their density. Because other results indicate that neither several plus-end-binding proteins nor focal adhesion sites are involved in targeting of microtubules to filopodia, the authors conclude that microtubules participate in directed cell motility by interacting directly with filopodia to alter their dynamics.

Development in press

Shrooming into shape

Cell shape changes brought about by apical constriction and apicobasal elongation are a common feature of morphogenesis. Although the basis of apical constriction is becoming clearer, the molecules that govern apicobasal elongation remain a mystery. Now, in a paper appearing in *Development*, John Wallingford and colleagues report that Shroom3 – an actin-binding protein – is required for the apicobasal elongation of neuroepithelial cells during *Xenopus* neural tube closure. Surprisingly, Shroom3 redirects the apical distribution of the microtubule (MT) regulator γ-tubulin, causing apicobasal MT arrays to form. It is already known to act in apical constriction and thus appears to be required for both types of neuroepithelial cell shape change during neural tube closure. The demonstration that Shroom3 can direct γ-tubulin redistribution reveals a novel conserved function for Shroom proteins. By combining their data with those from earlier studies, the authors are able to propose a model in which Shroom3 controls epithelial cell shape changes.

Lee, C., Scherr, H. M. and Wallingford, J. B. (2007). Shroom family proteins regulate γ-tubulin distribution and microtubule architecture during epithelial cell shape change. *Development* **134**, 1431-1441.