

TORC2 secures dendrite tiling

In the nervous system, the TOR complex 1 (TORC1) is involved in cell size control, synaptic plasticity and dendrite arborization, whereas no neuronal function has been identified for the TORC2 complex, which is composed of Rictor, LST8 and Sin1. Emoto and colleagues now report that TORC2 is essential for dendritic tiling of *Drosophila* sensory neurons (*EMBO J.*, doi:10.1038/emboj.2009.312; 2009).

Class IV neurons achieve complete and non-redundant coverage of the receptive field through tiling of their dendrites. Tiling relies on homotypic repulsive interactions between dendrites and requires signalling from the NDR family kinase Tricornered (Trc). By screening for genes involved in this process, Emoto and colleagues found that *sin1* and *rictor* mutants display inappropriate overlapping of the dendritic fields, and that Sin1 and Rictor interact genetically in controlling repulsion between dendrites in the same or adjacent neurons. TORC2 components interacted genetically and physically with Trc, and were responsible for direct Trc phosphorylation on Thr 449, a critical event in the regulation of Trc kinase activity.

Together with previous evidence of TORC1 function in dendrite growth and branching, these findings point to a fundamental role of TOR in dendrite physiology. Given the involvement of mammalian TOR in neuronal diseases

such as neurodegeneration and schizophrenia, it will be important to assess whether this function of TORC2 is conserved in vertebrates. SG

Mind the gap

How organisms compensate for the death of cells in a tissue is not well understood. In the vicinity of dying cells, reorientation of the division axis is now shown to maintain tissue homeostasis (*Curr. Biol.*, doi:10.1016/j.cub.2009.09.023; 2009). In mosaic clones of *Drosophila* imaginal discs, Minute mutant cells that have a reduced ribosomal dosage and decreased growth rate are progressively killed by wild-type cells, a phenomenon known as cell competition. Nick Baker and colleagues noticed that in this situation, the spindles of dividing wild-type cells in direct contact with the boundary of mutant clones are reoriented so that their progeny fill the gap left by the death of mutant cells. Overexpression of the apoptotic inhibitor p35 and of a dominant-negative form of the caspase Dronc in the mutant clones prevented spindle reorientation in wild-type neighbours, indicating that this event involved a signal from dying cells. When apoptosis was triggered via a mutation that does not involve competition, wild-type cells also reoriented their division towards the mutant clone boundary. Planar cell polarity (PCP) has been linked to mitotic orientation during normal wing development and the authors showed that mutations in several

PCP genes, such as *Dachsous*, *Fat* or *Atrophin*, which encodes a transcription factor acting downstream of Fat, impair this reorientation. How dying cells induce spindle repositioning in wild-type cells and whether a similar mechanism accounts for tissue homeostasis in response to cell death in other organisms remain to be investigated. NLB

Haematopoiesis: novel role for β -arrestin1

β -Arrestin1 has a well-established role in internalization and desensitization of G-protein-coupled receptors. Nuclear β -arrestin1 has previously been shown to act in gene transcription. Pei and colleagues (*Cell* **139**, 535–546; 2009) have now identified a role for β -arrestin1 in zebrafish haematopoiesis, by relieving Polycomb-mediated repression of *hox* genes that are important for haematopoiesis.

Depletion of zebrafish β -arrestin1 leads to defects in primitive haematopoiesis and down-regulation of *Cdx4* — a haematopoietic transcription factor that regulates *hox* genes — and *hox* gene expression. Expressing *Cdx4* or certain *Hox* family members restored haematopoietic marker gene expression in zebrafish depleted of β -arrestin1, indicating that the *cdx4* and *hox* genes are key downstream regulators of β -arrestin1. The authors identified YY1, a factor known to recruit the repressive Polycomb complexes PRC1 and PRC2 to *hox* gene promoters, as a β -arrestin1 interactor. Depleting β -arrestin1 resulted in increased binding of YY1 and a PRC2 component to *hox* gene promoters and enhanced repressive chromatin marks; these changes could be reversed by expressing wild-type β -arrestin1, but not a mutant β -arrestin1 that is unable to bind YY1. Moreover, YY1 or PRC2 loss of function rescued the haematopoietic defect seen upon β -arrestin1 depletion, indicating that β -arrestin1 is a negative regulator of YY1 and PRC2. The authors also implicate FGF signalling in being upstream of β -arrestin1 in haematopoiesis. SS

Inhibition in naked mole-rats

Normal cells in culture stop proliferating when in close contact with one another, whereas cancer cells are refractory to contact inhibition. The naked mole-rat has a life-span of over 28 years and is resistant to cancer. Gorbunova and colleagues suggest that one mechanism by which naked mole-rat cells are protected from transformation is a hypersensitivity to contact inhibition (*Proc. Natl Acad. Sci. USA*, doi:10.1073/pnas.0905252106; 2009). They found that fibroblasts from the naked-mole rat become contact inhibited at a much lower density than mouse and human fibroblasts, and that this growth arrest differs from normal contact inhibition in mouse and human cells. It requires the activities of both pRb and p53 (unlike mouse cells where pRb does not have a major role) and is associated with increased levels of the cyclin-dependent inhibitor p16 (rather than p27, which is induced in contact-inhibited mouse and human cells). Notably, a cell clone that had lost the hypersensitive response retained a contact inhibition response with p27 induction. Thus, cells from this unusual animal possess an extra layer of contact inhibition. How sparse cell–cell contacts can trigger a cell-cycle block in naked mole-rat cells remains to be determined. Long-lived rodents may be useful models to study anticancer strategies. CKR

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