Bud14 — actin' in formin displacement

The formin family of actin regulators catalyse actin polymerization and associate with growing filament ends through their FH2 domains, protecting them from capping proteins which block actin subunit binding. Goode and colleagues (*Dev. Cell* **16,** 292–302; 2009) now identify Bud14 as a new formin-displacement factor in yeast. Bud14 was found in a screen for regulators of mother-cell actin cables and its depletion leads to formation of abnormally long and bent actin filaments. Genetically Bud14 was shown to function upstream of the formin Bnr1 and, although Bud14 has no affect on *in vitro* actin assembly on its own, it inhibits the activity of Bnr1. Bud14 binds the Bnr1 FH2 domain directly and prevents actin assembly in the presence of capping proteins, suggesting that it displaces the FH2 domain of Bnr1 from actin. In agreement with a role for Bud14 in the control of actin architecture, actin-dependent secretory vesicle transport is impaired in Bud14 depleted cells. A previously demonstrated role of Bud14 in dynein-dependent microtubule sliding along the cell cortex is shown here to be separable from its role in actin organization. How the two functions of Bud14 are coordinated are topics for the future, as is the question of whether a similar class of formin inhibitors exists in mammals. CKR

Nucleosome organization drives gene expression divergence

Low nucleosome occupancy of gene promoters correlates with higher gene expression. Evolutionary changes in yeast species have now been linked to variations in nucleosome occupancy by Segal and colleagues (*Nature Genet.,* doi: 10.1038/ng.324; 2009). The authors compared the transcription program and nucleosome distribution of the aerobic human pathogen *Candida albicans* with those of the anaerobic *Saccharomyces cerevisiae*, in which expression of respiratory genes is low under typical growth conditions. Using the large datasets available for both species and a computational approach to assess nucleosome occupancy at the promoters of protein-coding genes, they classify genes according to their expression relative to that of cytoplasmic ribosomal protein (CRP)-coding genes, which usually correlates with cellular growth. In both yeasts, expression of genes required for basal cellular growth correlated highly with that of CRPs and with low nucleosome occupancy. Conversely, genes involved in response to specific environmental conditions did not correlate with CRPs and were predicted to show high nucleosome occupancy. Interestingly, genes required for respiration correlated with CRPs and low nucleosome occupancy in the aerobic *C. albicans* but not in the anaerobic *S. cerevisiae*, suggesting that nucleosome occupancy was linked to diversity in terms of metabolism. These predictions were verified by mapping nucleosome positions *in vivo* and by reconstituting nucleosomes on naked DNA from both species *in vitro*. The same correlations between gene expression and nucleosome occupancy were predicted in 12 additional yeast species, suggesting that phenotypic diversity is linked to nucleosome organization in promoters through changes in DNA sequence. NLB

A complex DNA damage response complex

The tumour suppressor and breast cancer susceptibility gene BRCA1 is engaged in several multiprotein complexes, and has key roles in the DNA damage response by regulating DNA repair, transcription and ubiquitylation. A complex containing Abra1/Abraxas/CCDC98, RAP80, BRCC36 and BRE/BRCC45 is implicated in the recruitment of BRCA1 to DNA double-stranded breaks through a damage signalling pathway involving the kinase ATM, the histone variant γ-H2AX, Mdc1, the ubiquitin ligase RNF8 and the conjugating enzyme Ubc13. Three groups independently identified a new component of this stable complex called MERIT40 or NBA1 through a shRNA screen (Wang et al.; *Genes Dev.,* doi: 10.1101/glad.1739609; 2009) or affinity purification schemes (Feng *et al.*; *Genes Dev.,* doi: 10.1101/glad.1770609; 2009 and Shao *et al.; Genes Dev.,* doi: 10.1101/glad.1770309; 2009). All three papers show MERIT40/NBA1 regulates localization of complex components as well as BRCA1 to DNA breaks. The new component of the BRCA1 complex mediates resistance to ionizing radiation and it is essential for the G2/M DNA damage checkpoint. MERIT40/NBA1 is recruited by directly interacting with BRE. Indeed, MERIT40 and BRE are required to maintain stability of the complex and Abra1 seems to serve as a central organizing adaptor. The complex appears to interact with a spectrum of ubiquitin chains through four different ubiquitin-binding domains. Shao *et al.* also show MERIT40 is required for the known Lys 63 de-ubiquitylation activity of BRCC36, which is implicated in both the checkpoint and resistance to ionizing radiation. Interestingly, Wang *et al.* point out that a structural model of the complex resembles the 19S lid of the 26S proteasome. BP

Re-growing out of the niche

In plants, apical stem-cell niches sustain the indeterminate growth of roots and shoots. A study by Birnbaum and colleagues now reveals that plants are able to regenerate these organs in the absence of a functional stem-cell niche (*Nature* **457,** 1150–1153; 2009). Following root-tip excision and removal of the niche quiescent centre, regeneration was analysed in *Arabidopsis thaliana* by tracking the re-establishment of the different cell types through time-lapse high resolution imaging of cell-identity markers and concomitant analysis of cell-type-specific transcriptional profiles. This demonstrated that, at regeneration sites, cell identities were re-specified within hours of excision, and that fully functional specialized cells were restored before recovery of the stem-cell niche. Moreover, regeneration and functional specification of roots still occurred in plants with mutations that cause root growth defects due to impaired stem-cell niche maintenance. Further marker analysis indicated that the competence to regenerate might be a feature of differentiating cells sharing a common set of stem-cell-like properties. These properties are therefore not restricted to niches, but rather widely dispersed in plant meristematic tissues, a characteristic that could explain the high regenerative capacity of plants. SG

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