DOI:
10.1038/nrm2464

IN BRIEF

CELL POLARITY

Polarization of the *C. elegans* embryo by RhoGAP-mediated exclusion of PAR-6 from cell contacts.

Anderson, D. C. *et al.* *Science* **320**, 1771–1774 (2008)

The *Caenorhabditis elegans* embryo polarizes radially when cell contacts restrict PAR-6 and other polarity proteins to the contact-free outer surfaces of early embryonic cells. Anderson *et al.* now show how this PAR asymmetry is achieved. The Rho GTPase-activating protein (RhoGAP) PAC-1 is recruited to the inner surfaces by cell contacts and locally inhibits the Rho GTPase CDC42, thereby restricting active CDC42 to outer surfaces. Active CDC42 binds the semi-CRIB domain of PAR-6, which is required for the stable interaction of PAR-6 with the outer cell cortex, thereby creating an 'inner–outer' asymmetry in PAR-6 localization. So, PAC-1 provides a molecular link between cell contacts and PAR proteins that polarize embryos radially.

MEMBRANE TRAFFICKING

Beclin1-binding UVRAG targets the class C Vps complex to coordinate autophagosome maturation and endocytic trafficking.

Liang, C. *et al.* *Nature Cell Biol.* **10**, 776–787 (2008)

The autophagic and endocytic pathways share similar features and are thought to interconnect. The authors provide evidence for this hypothesis by showing that the Beclin1-binding autophagic tumour suppressor UVRAG interacts with the class C Vps tethering complex — a key component of the endosomal fusion machinery. This interaction promotes autophagosome maturation as well as endocytic vesicle trafficking, which suggests that the two processes may share similar vesicle fusion machineries. The UVRAG–class C Vps interaction is distinct from the UVRAG–Beclin1 interaction, which promotes autophagosome formation. So, UVRAG functions in two separate steps in the autophagic pathway and may couple autophagosome formation and maturation.

CHROMATIN

Fungal Rtt109 histone acetyltransferase is an unexpected structural homolog of metazoan p300/CBP.

Tang, Y. *et al.* *Nature Struct. Mol. Biol.* **15**, 738–745 (2008)

An old HAT in human p300/CBP and yeast Rtt109.

Bazan, J. F. *Cell Cycle* **7**, 1884–1886 (2008)

The yeast-specific histone acetyltransferase (HAT) Rtt109 modifies histone H3 Lys56 (H3K56) and has an important role in genome stability. Tang *et al.* determined the X-ray structure of Rtt109 from budding yeast in complex with the acetyl-CoA cofactor and demonstrated a substantial structural homology to the metazoan HAT p300/CBP. The structure reveals an autoacetylated Lys residue, the *in vivo* significance of which is unknown. The structural similarity is not matched by an overlap in key catalytic residues, as shown by mutagenesis studies, and there is no evidence that H3K56 is a substrate for p300/CBP. In addition, Rtt109 is thought to use the histone chaperones Asf1 and Vps75 for targeting its substrate, whereas p300/CBP uses an alternative mechanism. Altogether, these data suggest that Rtt109 and p300/CBP are structural but not functional homologues. In a second paper, J. F. Bazan proposes an evolutionary relationship between Rtt109 and p300/CBP on the basis of structural prediction studies.