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# In This Issue

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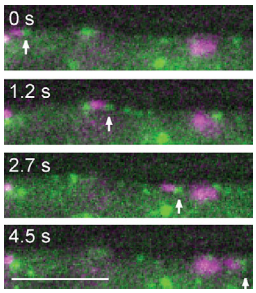
## PxdA helps peroxisomes hitch a ride




**This time-lapse series shows a peroxisome (magenta) trailing an early endosome (green) as it moves along a microtubule.**

Salogiannis et al. identify a linker protein that helps peroxisomes hitchhike through the cell on early endosomes.

In most eukaryotic cells, organelles and other cargoes move through the cytoplasm along microtubules, using specific adaptor molecules to recruit microtubule-based motor proteins such as cytoplasmic dynein or plus end–directed kinesins. Following up on a genetic screen for genes involved in the transport of various organelles through the multinucleate cells of the filamentous fungus *A. nidulans*, Salogiannis et al. studied the function of PxdA, a protein specifically required for the bidirectional movement of peroxisomes.

In the absence of PxdA, peroxisomes clustered at hyphal tips instead of dispersing throughout the cell, whereas the motility and distribution of other organelles, including early endosomes, was unaffected. Surprisingly, however, PxdA mainly localized to early endosomes. Salogiannis et al. found that the protein links these highly motile organelles to peroxisomes, potentially allowing peroxisomes to move through the cell without recruiting their own set of motor proteins. PxdA's central coiled-coil domain was necessary and sufficient for the protein's localization and organelle linker function. Senior author Sam Reck-Peterson now wants to investigate how PxdA interacts with both early endosomes and peroxisomes.

In a recent *JCB* paper, Guimaraes et al. revealed that not only peroxisomes, but also lipid droplets and ER membranes, hitchhike on early endosomes in the pathogenic fungus *U. maydis*. Reck-Peterson says it will be important to determine if PxdA links these other organelles to early endosomes, and whether this phenomenon occurs in animal cells as well.

Salogiannis, J., et al. 2016. *J. Cell Biol.* http://dx.doi.org/10.1083/jcb.201512020

## Yeast chromatin takes global action on carbon

Changing growth conditions prompt large-scale rearrangements of budding yeast chromosomes, Dultz et al. reveal.

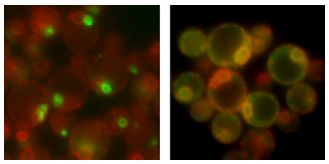
Genes can change their position within the nucleus when they are activated or repressed. The *GAL* locus on budding yeast chromosome II, for example, is transcriptionally activated and relocated to the nuclear periphery when glucose in the cells' growth medium is replaced with galactose. Whether the repositioning of individual genes is accompanied by larger scale changes in chromosome organization is unclear, however, so Dultz et al. developed an automated imaging protocol to analyze how the location of different, fluorescently labeled chromosome regions changed under varying growth conditions.

Glucose withdrawal induced the relocation of not just the *GAL* locus but also many additional regions of chromosome II to the nuclear periphery. Loci on other chromosomes also moved to the nuclear envelope in the absence of glucose. Computer modeling combined with experimental analyses showed that this global chromatin reorganization depends on several tethering sites located throughout the yeast genome.

To understand how the nuclear position of these sites might be regulated, Dultz et al. conducted a genetic screen for mutants affecting *GAL* repositioning. The screen identified several components of histone deacetylase complexes; deleting these genes or inhibiting deacetylase activity with the drug trichostatin A blocked the relocalization of *GAL* and other chromosomal loci to the nuclear periphery. The histone acetyl transferase activity of the SAGA complex was also required for global chromatin reorganization in response to changing carbon availability. Dultz and colleagues note that the targets of these enzymes, and the functional consequence of blocking chromatin rearrangements, remain unclear.

Dultz, E., et al. 2016. *J. Cell Biol.* http://dx.doi.org/10.1083/jcb.201507069

## Sorting out peroxisome biogenesis



**Pex2 (green) localizes to peroxisomes in wild-type cells (left) but is dispersed throughout the ER (red) in cells lacking Pex3 (right).**

Agrawal et al. describe how different peroxisomal membrane proteins (PMPs) are sorted into distinct vesicles that bud from the ER during de novo peroxisome biogenesis.

Peroxisomes can be generated by the growth and division of preexisting organelles or by a de novo pathway in which preperoxisomal vesicles (ppVs) bud from the ER before fusing to form mature peroxisomes. In the growth and division pathway, newly synthesized PMPs are delivered to peroxisomes by the chaperone Pex19 and its peroxisomal membrane receptor Pex3. Pex19 is also required for ppV budding during de novo biogenesis, but whether Pex3 is involved in this process remained unclear.

Agrawal et al. analyzed how two types of PMP are packaged into ppVs in the yeast *P. pastoris*. Pex3 and Pex19 were both required to sort the RING-domain PMPs Pex2 and Pex12 (and likely Pex10) to a specialized ER domain called the preperoxisomal ER (pER), where ppVs are formed. Pex3 contains a sorting signal that targets it to this domain. Pex19 linked the RING-domain PMPs to Pex3, allowing them to be co-sorted to the pER and subsequently packaged into two distinct ppVs. In contrast, the docking complex PMPs Pex13, Pex14, and Pex17 were sorted to the pER independently of Pex3 and Pex19, though Pex19 was still required for their incorporation into ppVs.

In mature peroxisomes, the RING-domain and docking complex PMPs form the importomer, which transports peroxisomal matrix proteins into the organelle's lumen. However, the two types of PMP seemed to occupy slightly distinct regions of the pER, and they weren't all packaged into the same ppVs, thereby preventing the importomer from assembling prematurely. The researchers now want to investigate the protein and lipid composition of ppVs in more detail.

Agrawal, G., et al. 2016. *J. Cell Biol.* http://dx.doi.org/10.1083/jcb.201506141