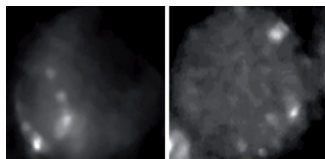


## Ubiquitylation keeps the nucleus moving



The dynein light chain (white) is normally recruited to NPCs (left), but recruitment is inefficient when Nup159 can't be ubiquitylated (right).

Hayakawa et al. reveal that many components of the yeast nuclear pore complex (NPC) are ubiquitylated and describe how this modification helps segregate the nucleus during mitosis.

NPCs and their constituent nucleoporin proteins control several cellular processes, including molecular transport

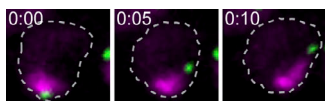
between the nucleus and cytoplasm. These functions can be regulated by phosphorylation, but the effects of other posttranslational modifications, such as ubiquitylation, are less well understood. Hayakawa et al. systematically analyzed all 30 nucleoporins in the budding yeast *S. cerevisiae* and found that half of them were either mono- or polyubiquitylated.

The researchers focused on Nup159, a nucleoporin involved in mRNA export that is monoubiquitylated on a specific lysine residue by the SCF E3 ubiquitin ligase. Blocking this ubiquitylation didn't affect Nup159's localization or mRNA transport, but it did reduce the nucleoporin's ability to recruit the dynein motor light chain to the nuclear envelope. In yeast, dynein attaches to NPCs and helps to orient the mitotic spindle and move the nucleus to the bud neck at the beginning of mitosis. Spindles were often misaligned and nuclear migration delayed in cells unable to ubiquitylate Nup159 and recruit dynein to NPCs. These defects became much more severe in cells that also lacked an alternative spindle orientation pathway involving the APC protein Kar9.

Senior author Catherine Dargemont now wants to investigate how ubiquitylation regulates the functions of the many other nucleoporins that undergo this posttranslational modification.

Hayakawa, A., et al. 2012. *J. Cell Biol.* <http://dx.doi.org/10.1083/jcb.201108124>.

## How meiotic chromosomes meet their match



Pairing centers (green) on oocyte X chromosomes (magenta) dance around the nucleus in early meiosis.

By imaging homologous chromosome movements in living nematodes, Wynne et al. describe how they pair up during meiosis to facilitate recombination.

In *C. elegans*, homologue pairing relies on DNA sequences near one end of each chromosome called pairing centers. These regions bind zinc finger proteins that link chromosomes to a pair of nuclear membrane proteins called SUN-1 and ZYG-12 that span the nuclear envelope and connect to microtubule-based dynein motors in the cytoplasm. The motors are thought to drag chromosomes around the inner surface of the nucleus until they meet their homologous partner.

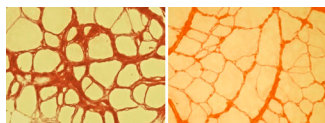
Wynne et al. followed the movements of individual pairing

centers and ZYG-12 molecules in living worm oocytes. Chromosomes were relatively immobile before meiosis, but, soon after meiotic entry, pairing centers and their nuclear envelope linker proteins showed two different modes of movement: rapid translocations in a single direction interspersed with periods of slower, more meandering motions on the nuclear surface. The faster, directional movements were inhibited if microtubules were depolymerized or dynein was depleted, but the slower motions continued in the absence of dynein, which may explain why dynein knockdown delays, but doesn't prevent, homologue pairing.

Dynein is required, however, for synapsis—the stable association of homologous chromosomes after their initial coupling. Senior author Abby Dernburg now wants to expand the live imaging approach to investigate how the motor protein contributes to this process.

Wynne, D., et al. 2012. *J. Cell Biol.* <http://dx.doi.org/10.1083/jcb.201106022>.

## A firmer understanding of muscle fibrosis



Muscle from an aged *mdx* mouse (left) contains large collagen deposits (red), but these are reduced when miR-21 is inhibited (right).

Ardite et al. describe how increased production of a microRNA leads to progressive muscle deterioration in Duchenne muscular dystrophy (DMD) patients.

As DMD patients age, their damaged muscle cells

are gradually replaced by collagen-rich fibrous tissue. This muscle fibrosis is partly induced by TGF- $\beta$ , which is highly activated in DMD patients, though exactly how this cytokine promotes fibrogenesis is unclear. Ardite et al. examined the role of miR-21, a microRNA whose production is stimulated by TGF- $\beta$  signaling.

miR-21 was upregulated in the collagen-producing fibroblasts of both DMD patients and muscular dystrophy model (*mdx*) mice. Inhibiting miR-21 reduced collagen levels and prevented, or even reversed, fibrogenesis in diseased animals, whereas *mdx*

mice overexpressing the microRNA produced more collagen and developed fibrotic muscles at earlier ages.

Ardite et al. also discovered that TGF- $\beta$  activity and miR-21 production were regulated by the balance of two extracellular factors: uPA—a protease that activates TGF- $\beta$ —and its inhibitor PAI-1. *mdx* mice developed fibrotic muscles more quickly in the absence of PAI-1, but these symptoms could be reversed by inhibiting uPA with a drug or a specific siRNA. In addition to producing more collagen, PAI-1-null fibroblasts also proliferated rapidly because the extra miR-21 induced by active TGF- $\beta$  inhibited the tumor-suppressive phosphatase PTEN.

TGF- $\beta$  inhibitors prevent muscle fibrosis but have damaging side effects; this study suggests that uPA or miR-21 may make attractive alternative targets. Senior author Pura Muñoz-Cánoves now wants to investigate the function of miR-21 in other cell types that influence muscle homeostasis, such as the macrophages involved in tissue repair.

Ardite, E., et al. 2012. *J. Cell Biol.* <http://dx.doi.org/10.1083/jcb.201105013>.