In This Issue

Repair at the nuclear periphery

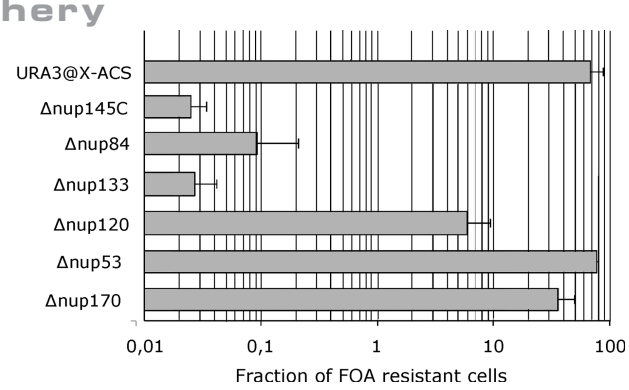
Telomere association with nuclear pores is critical not only for transcriptional silencing but also for efficient repair of double-stranded breaks in the subtelomeric region of budding yeast chromosomes, according to Therizols et al. (page 189).

As in many organisms, yeast telomeres localize to the nuclear periphery. To determine whether nuclear pore proteins are involved in telomere tethering, Therizols et al. looked for telomere localization in cells lacking functional Nup84 complexes, which are essential components of the pore. They found that the telomeres no longer associated with the nuclear periphery in these mutants.

As might be expected from previous work on transcriptional silencing, transgenes located in the subtelomeric region were no longer silent in Nup84 complex mutants, indicating that localization of the telomere to the nuclear periphery was functionally important.

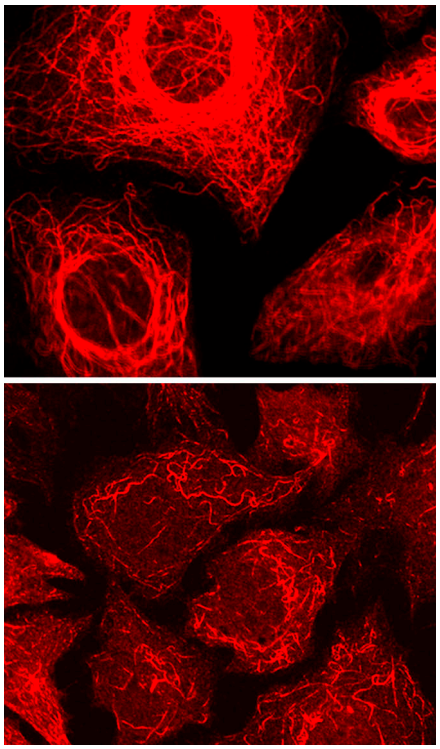
Surprisingly, when double-stranded breaks were introduced into subtelomeric sites in the mutants, DNA repair efficiency dropped significantly relative to wild-type cells. The efficiency of break repair in central regions of chromosomes did not differ between wild-type and mutant cells.

The DNA silencing and repair phenotypes were separated in cells mutant for Esc1p, a protein located at the nuclear periphery but which is not directly involved in the pore. In this case, telomere localization and DNA repair were disrupted, but silencing remained intact.



Cells lacking some nucleoporins die on FOA because they derepress a telomeric URA3 gene.

The researchers conclude that anchoring telomeres to the nuclear pore is important for efficient DNA double-stranded break repair in the subtelomeric regions, though it is not yet clear why this is true. Because silencing remained intact in the Esc1p mutants but repair was disrupted, it appears that chromatin structure itself is not the problem. One possibility is that clusters of repair proteins may be concentrated near groups of tethered telomeres, thereby facilitating rapid repairs. JCB



Microtubules (top) get chewed up when Stat3 is missing (bottom).

Stat3 stabilizes microtubules

The STAT proteins are well-known as signaling proteins and transcription factors. But Ng et al. (page 245) report that Stat3 also functions in the cytoplasm, stabilizing microtubules by directly binding to and inhibiting the activity of a microtubule-destabilizing protein.

Stat3 functions in a variety of processes, including proliferation, survival, tumorigenesis, and migration. In each case, except migration, the protein works via transcriptional control of downstream effector proteins. How the protein controls migration is uncertain, though it is clear that cells lacking Stat3 do not migrate efficiently in vivo or in vitro.

Ng et al. found that Stat3 binds to stathmin, a protein that accelerates depolymerization of microtubules by binding to tubulin subunits. Stat3 bound stathmin via stathmin's tubulin-binding domain, blocking its depolymerizing activity.

Cultured cells lacking Stat3 showed a disordered microtubule network. However, expression of a transcriptionally inactive form of Stat3 rescued the phenotype, suggesting that nuclear signaling by Stat3 was not required. Moreover, down-regulation of stathmin partially rescued the Stat3 migration phenotype, but did not affect phosphorylation or transcriptional activity of Stat3 in normal cells.

The team is now looking to find out exactly how Stat3 affects microtubule dynamics. Because stathmin down-regulation only partially rescues the Stat3-null phenotype, Ng et al. hypothesize that Stat3 has another, as yet undiscovered, role in migration. Regardless of what comes next, the work demonstrates that the Stat3 previously detected in the cytoplasm is not just waiting to enter the nucleus. JCB

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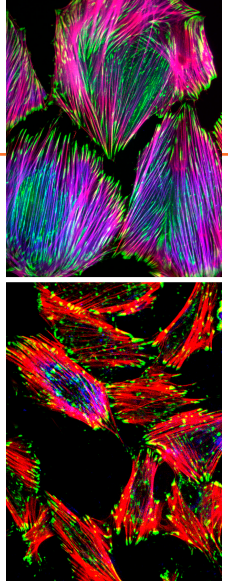
Sometimes size does matter

During myofibroblast differentiation in vitro, "supermature" focal adhesions (FAs) arise due to increased physical stress, report Goffin et al. (page 259). Additionally, increased tension induces accumulation of α-smooth muscle actin (α-SMA) in stress fibers that are anchored at these FAs.

In vivo, the extracellular matrix rearranges and increases in rigidity in response to wounding. This change, along with the release of growth factors, induces fibroblasts to take on a contractile phenotype, including expression of α-SMA. The question remains, however, as to what triggers incorporation of α-SMA into stress fibers in these cells.



α-smooth muscle actin (blue) joins stress fibers that are under a lot (top) but not less (bottom) tension.

When differentiated myofibroblasts were cultured on flexible substrates, FAs remained relatively small. However when the cells were grown on rigid substrates, supermature FAs formed. Once formed, supermature FAs were able to withstand substantially larger physical forces and generated higher intracellular tension than did FAs of a more typical size. This higher tension in turn triggered α-SMA recruitment to stress fibers, which did not occur in cells with smaller FAs.

The team is working to identify the cellular component that senses the increased tension in stress fibers and recruits α-SMA. In the meantime, they are convinced that tension and size are intimately linked in the formation of supermature FAs and α-SMA stress fibers. JCB

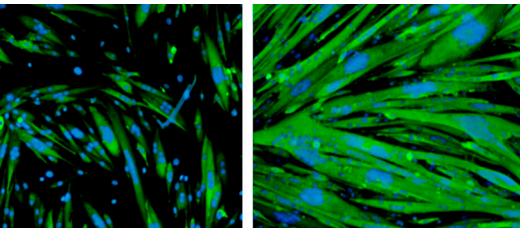
NO induces myoblast fusion

Nitric oxide (NO) functions at numerous points in muscle development and function. On page 233, Pisconti et al. add one more item to that list: NO stimulates myoblast fusion via cGMP signaling and follistatin. Increasing NO in vivo stimulates muscle fiber formation, which suggests a potential therapeutic approach for muscular dystrophy.

Addition of an NO-releasing compound to cultures of embryonic myoblasts or satellite cells, which function as stem cells in adult muscles, stimulated cell fusion. Conversely, addition of an inhibitor of nitric oxide synthase blocked fusion.

When the team added NO to cells but blocked production of cGMP, a known mediator of NO signaling, fusion was inhibited in a cGMP-reversible manner. Significantly, prolonged exposure of the myoblasts to a nonhydrolysable analogue of cGMP induced the formation of abnormally large muscle fibers in culture. A similar effect was not observed with extended exposure to an NO donor.

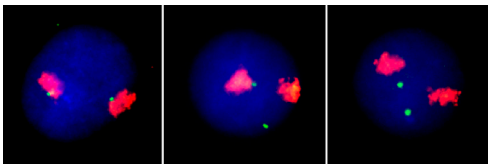
RT-PCR analysis of NO-treated myoblasts showed that follistatin, a protein known to trigger myoblast fusion, was up-regulated relative to untreated cells. Another fusion-promoting protein, insulin growth factor-1 (IGF-1) was not increased.



Muscle cells (left) fuse when treated with cGMP (right) or NO.

The results suggest that NO donors may be valuable as therapies for muscular dystrophy. Preliminary testing in animal models supports that idea. JCB

Mobile genes



α-globin genes (green) can stay near (left) or stray away (right) from their home territories (red).

On page 177, Brown et al. follow the nuclear positioning of the globin genes during erythroid differentiation and find that they are often close to each other during active transcription. However, such associations do not appear to be a requirement for transcriptional regulation, but rather a consequence of it.

The α- and β-globin genes are highly transcribed for a brief time during the maturation of red blood cells, with each gene producing about the same amount of mRNA. But the chromosomal contexts for the genes are very different. The human α-globin genes lie in a gene-dense subtelomeric region that is constitutively in an open chromatin conformation. The β-globin genes are in an AT-rich region that is open only during erythroblast development.

At the point of maximal transcription, the α-globin genes were frequently decondensed and distinct from their chromosomal territories. By contrast, the β-globin genes remained close to their native chromosome arms, as did the mouse α-globin genes, which lie in a less gene-rich region than their human counterparts.

Moreover, the human α-globin alleles associated near one another in approximately half of the transcribing cells examined, as did α- and β-globin alleles. β-globin alleles, in contrast, were almost never in close proximity to each other. Finally, the α-globin alleles were more likely to be in contact with large aggregates of splicing factors called speckles.

Thus, despite the functional similarities of human and mouse α- and β-globin genes, the loci show differing patterns of nuclear localization and interaction. Brown et al. conclude that gene positioning in the nucleus depends on multiple factors, including gene density and chromosomal location. They hypothesize that rapidly transcribed genes—or at least those that are potentially mobile—can be pulled near one another as large aggregates of transcription and processing factors accumulate in their vicinity. Already, they have seen similar associations between other coexpressed genes. JCB