In This Issue

**Shockingly localized**

Upon activation by stress, heat shock factor 1 (HSF1) accumulates at a specific heterochromatic locus on human chromosome 9, according to Jolly et al. (page 775).

The final target of HSF1 is DNA, in the form of the heat shock element (HSE), and this binding event is known to activate transcription of adjacent heat shock protein (hsp) genes. But heat shock also causes HSF1 redistribution into nuclear loci known as HSF1 granules. Jolly and colleagues have now shown that the granules are located at chromosomal DNA sites that are distinct from RNA polymerase II transcription sites, meaning they are unlikely to be related to transcriptional activation. The HSF1 granules were found on the 9q11 region, which is primarily composed of heterochromatic satellite III repeats.

What could transcriptional activators be doing at heterochromatic regions following heat stress? Jolly hypothesizes that heterochromatic localization may provide a buffer to avoid over-activation of HSF1, which can be toxic to the cell. Alternatively, she suggests, the transcription factor may have a secondary role as a protective agent for the locus, preventing damage to a DNA region known to be prone to chromosomal rearrangements.

**Actin to completion**

The actin cytoskeleton is alone on the cytokinesis stage no longer. The final step of cytokinesis cannot be completed without interactions between actin and a microtubule-interacting protein, CHO1, according to a new study by Kuriyama et al. on page 783.

Organization of microtubules into the central spindle is achieved in part by the MKLP1 microtubule-binding motor protein. Kuriyama has determined that alternative splicing of MKLP1 generates CHO1, which has an additional 100 amino acids in the COOH-terminal tail. The group shows that MKLP1 and CHO1 are coexpressed within mammalian cells, both tightly associated with microtubules.

Although CHO1 associates with microtubules, Kuriyama et al. show that it is not required for chromosome separation. The unique CHO1 region imparted an unexpected actin-binding activity both in vitro and in vivo. Inhibition of this actin binding did not impair early steps in cytokinesis, but did prevent the final stage. Although the daughter cells initially appeared to separate completely, within hours the two had merged.

**The bud is all in the timing**

A new study by Schenkman et al. on page 829 reveals that the subcellular localization of yeast budding proteins can be determined by the time the genes are expressed.

The genes BUD8 and BUD9 are required for establishment of the bipolar budding pattern in normal diploid cells, in which both poles are specified as potential bud sites. Although the two proteins are similar in structure, they show distinct subcellular localizations, consistent with functions as markers of the distal and proximal poles of daughter cells.

Using promoter swap experiments, Schenkman et al. now show that the timing of gene expression determines the localization of Bud8p and Bud9p. The localization of the proteins is probably determined by the direction of the general secretory vesicle traffic at the stage of the cell cycle when the protein is delivered. Although new Bud8p is delivered shortly before or concurrent with bud emergence, and thus will be found at the distal end of the bud, new Bud9p is deposited to the bud side of the neck very late in the cell cycle, and is thus found at the proximal pole of new daughter cells.

The group’s analysis also determined that the peak in transcription of the BUD8 and BUD9 mRNAs precedes the delivery of the corresponding proteins to the cell surface by about an hour. This could be accomplished by a delay in either the translation of the protein or the trafficking of the protein to the cell surface.