Cohesin gets pushed around

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Lengronne, Frank Uhlmann (Cancer Research UK, London, UK), Katsuhiko Shirahige (Tokyo Institute of Technology, Yokohama, Japan), and colleagues now suggest that cohesin rings get pushed to their final resting places by transcription complexes.

Cohesins are known to bind a heterochromatin protein at centromeres, but previous reports of cohesin localization on chromosome arms were incomplete. The authors did a comprehensive survey of four budding yeast chromosomes and two fission yeast chromosomes using chromatin immunoprecipitation. In budding yeast, 91% of cohesin sites were between converging genes, and cohesins were bound to 84% of the 328 convergent intergene regions.

Earl Glynn, Jennifer Gerton (Stowers Institute, Kansas City, MO) and colleagues gathered similar data for budding yeast. They suggest that transcription displaces cohesin from the DNA of active genes, and that the chromatin in convergent intergenic regions may be a stickier substrate for cohesin.

But Uhlmann's group favors the sliding model. Looking earlier, they saw that cohesins initially load at sites defined by the loading protein Scc2. These sites are most often in highly transcribed regions, but soon after loading the cohesin moves toward the intergenic regions. This would get the cohesin away from the loading proteins, which may have an opening activity that can also promote unloading.

Cohesin that was seen in the middle of several dormant genes later moved downstream when the genes were turned on during either meiosis or heat shock. Passive pushing is conceivable, says Uhlmann, because proteins bound to RNA polymerase and its nascent transcript "make the transcription machinery quite enormous." Pushing would prevent transcripts from getting stuck in the rings. The replication machinery may, however, slip through the cohesin rings, which are loaded well before DNA replication starts. ■

References: Lengronne, A., et al. 2004. *Nature*. 10.1038/nature02742. Glynn, E.F., et al. 2004. *PLoS Biol*. 10.1371/journal.pbio.0020259.

Flat-out pushing by actin

amellipodia are almost flat, whereas many model systems for actin-based Imany model systems for actin-based
propulsion involve the convex surfaces of beads, vesicles, or bacteria such as *Listeria*. Thus, it is reassuring that actin pushing against a flat surface can lead to productive movement even in these model systems, as demonstrated by Ian Schwartz, James McGrath, and colleagues (University of Rochester, NY) using squashed beads.

Actin at the leading edge of moving cells has been suggested to work as a tethered ratchet. Thermal fluctuations lead to the bending of actin filaments away from the cell surface, freeing them for lengthening by polymerization. As these bent, and thus strained, longer filaments relax by straightening, they exert a forward force on the cell surface.

Bead-based experiments have, by contrast, led to the elastic propulsion model. In this

model, new layers of actin laid down near the bead surface force expansion of and thus induce compressive stresses in the older, outer layers. The bead shoots forward like a marble squeezed between finger and thumb.

But the absence of obvious convex curvature at the leading edge made McGrath wonder if the elastic propulsion model, and the assay systems used to study it, held any relevance for moving cells. "Maybe [the beads] are operating by a completely different mechanism than what is happening in cells," he says. "That's a problem if we want to understand the cell's mechanism."

McGrath's new experiments do not resolve whether spherical objects move using elastic propulsion. But they do show that an in vitro system can recapitulate movement via actin action at a flat surface. The

Actin can move objects by pushing on a flat surface.

Rochester group saw squashed beads move in directions that could only result from force against the flat, not curved, portions of their beads. McGrath hopes in the future to pattern actin polymerizing proteins only on the flat surfaces.

Reference: Schwartz, I.M., et al. 2004. *Curr. Biol.* 14:1094–1098.