**ClpX eats randomly**

ClpXP is an ATP-powered eating machine. Its ring of six ClpX ATPase modules feeds substrates to the ClpP protease. The ClpX subunits have been suggested to fire all at once or in a sequential, piston-like sequence. But now Andreas Martin, Tania Baker, and Robert Sauer (MIT, Cambridge, MA) find that the hexamer functions even if only one subunit can hydrolyze ATP. They suggest that the the order of firing of the subunits may be not deterministic but probabilistic—all the better to manhandle half-digested protein substrates whose features protrude haphazardly.

Martin wanted to test the models by mixing and matching functional and non-functional ClpX subunits. But the six subunits are identical, so coexpression of wild-type and mutant subunits would yield only messy mixtures. “If you were going to make headway you needed to connect the subunits” into a single unit, says Sauer. Martin set to work, but “progress was not encouraging,” says Sauer. “After six months there were only insoluble proteins. I was encouraging him to think of other projects, but he refused to give up.” As a last attempt Martin deleted a nonessential part of ClpX. The deletion—which was done “because we could,” says Sauer—worked.

The resulting construct of six linked subunits could be reassorted at will. Amazingly, activity per functional subunit barely decreased as more mutants crept in. Hexamers with only two active subunits had almost a third of the activity and ATP efficiency of a fully active hexamer. With only one active subunit the hexamers fell down further in activity assays, but still showed impressive digestive powers.

Reference: Martin, A., et al. 2005. *Nature*. doi:10.1038/nature04031.

**Divided identities in the niche**

To maintain a stem cell niche at a fixed size, the niche exerts control over both cell differentiation (how many cells functionally leave the niche) and cell division. G. Venugopala Reddy and Elliot Meyerowitz (Caltech, Pasadena, CA) now show that, in the growing shoots of plants, these two control points are separable in both time and space.

Their model was the shoot apical meristem (SAM). The SAM has a central zone (CZ) of stem cells plus various surrounding cells that make the transcription factor WUSCHEL. Although WUSCHEL creates a signal that promotes stem cell identity back in the CZ, it also induces these stem cells to produce CLAVATA3 (CLV3), an extracellular ligand that keeps WUSCHEL repressed centrally. This forces the inducing ring to keep its distance from the induced stem cells.

Reddy and Meyerowitz turned on a RNAi-inducing transcript that knocked down CLV3. As others have found, the end result was more WUSCHEL activity, and thus more promotion of stem cell identity and an expanded CZ and SAM. Unfortunately, says Reddy, any such terminal phenotype is the sum of changes in multiple interacting components of a network. The function of individual genes, he suggests, is best understood via a transient perturbation that allows changes in cell identities and cell division to be observed as the phenotype develops.

To see this kind of dynamics, the pair used GFP-labeled cell markers and transient induction of the CLV3 RNAi. Soon after this treatment the CZ expanded, via the dedifferentiation or respecification of surrounding cells. Only later was there an increase in the division rate of cells more distant from the stem cell area, but still within the SAM.

The separable effects point to a complicated system of signaling. WUSCHEL is no doubt part of the answer, but real-time analysis of a few more genes will probably be necessary to understand fully how plants keep a group of stem cells at a buffered and consistent size.

Reference: Reddy, G.V., and E.M. Meyerowitz. 2005. *Science*. doi:10.1126/science.1116261.