

Research Roundup

Antagonistic drivers share BuMPy pathway

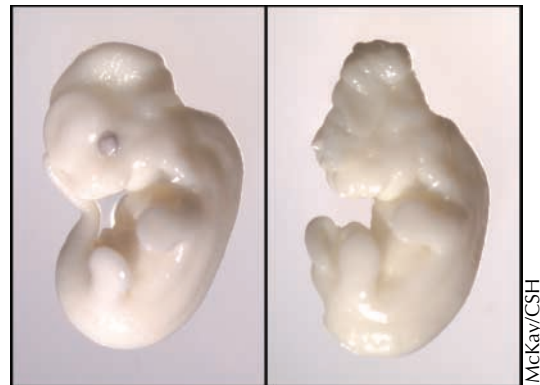
Seemingly confounding and contradictory, the ability of bone morphogenetic proteins (BMPs) to promote both proliferation and terminal differentiation (and even apoptosis!) of neuronal stem cells—to both expand and limit precursor cell numbers—now makes perfectly good sense. At least it does in light of the conclusions drawn by Ronald McKay, David Panchision, and colleagues (National Institutes of Health, Bethesda, MD), who postulate a mechanism by which BMP ligands control both the production and fate of neural precursor cells.

Panchision attributes this “dynamic process” to the sequential and linked expression and function of two BMP receptors, BMPR-IA and BMPR-IB. In this model, “the BMP-mediated induction of receptor IB accounts for features of stem cell proliferation, identity, differentiation, and death,” says McKay.

Expression of mutant BMP receptors in CNS stem cells in vitro and in transgenic mice led to the startling discovery of a

“feed-forward” mechanism. Activation of the BMPR-IA receptor early in development promotes proliferation of neural precursor cells and determines their dorsal identity. But BMPR-IA also induces the expression of *Bmpr-1b*. BMPR-IB activation then mediates mitotic arrest, resulting in either apoptosis (early in development, perhaps to control cell numbers) or terminal differentiation (later in development, for those cells that are left). Additional competence signals must be required to interpret the BMPR-IB signal into an apoptotic or differentiation response.

An induction–termination sequence could, suggests Panchision, be a general property of signaling in stem cells. It is unclear whether this self-limiting sequential mechanism, which dead-ends at terminal differentiation or cell death, could be reactivated on demand to regenerate



McKay/CSH

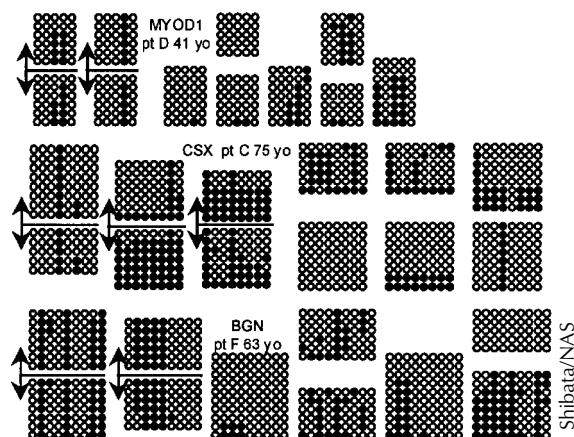
Too much BMPR-IB (right) causes widespread cell death.

tissues, say during wound healing or limb amputation. McKay envisions using knowledge of the linked receptor model to control stem cell proliferation and differentiation, with an eye toward potential applications in cell therapy and cancer therapeutics. ■

Reference: Panchision, D.M., et al. 2001. *Genes Dev.* 15:2094–2110.

Tales from the crypt

How many stem cells reside in a human colonic crypt and how do they divide and regenerate? According to the deterministic theory, a small number of “immortal” stem cells haunt a crypt, and when they divide, each generates a single replacement stem cell. The stochastic model, in contrast, contends that a crypt niche harbors many stem cells, and each cell division randomly generates one, two, or no new stem cells. In this model, stem cell lines may be lost over time, and “bottlenecks” will eventually develop in which all stem cells in a niche will diverge from a recent, common ancestor.



Each methylation tag (horizontal line) shows variation within a crypt (each group of circles).

A new and clever strategy for studying stem cell dynamics, devised by Darryl Shibata and colleagues (University of Southern California, Los Angeles, CA), uses DNA methylation tags as markers of stem cell fate. The authors applied this technique to track changes in methylation patterns among stem cells in human colonic crypts and to test the two competing models of stem cell dynamics. Their conclusion: the data support the stochastic model, as demonstrated by the similarity of methylation patterns within individual crypts and the large variability in the numbers of unique tags per crypt.

These findings lend credence to the theory that crypt niches contain multiple long-lived stem cells that self-renew most of the time through asymmetric division. Loss of methylation tags occurs as random stem cells fail to generate replacements and bottlenecks develop. One implication of these bottlenecks for stem cell dynamics is that the periodic death of stem cells might eliminate potentially cancerous cells.

Perhaps the most surprising outcome, in Shibata’s view, is that “a population genetics type of approach worked for human crypts,” and that epigenetic patterns, in this case methylation, can serve as a marker of cell fate. The ability to map stem cell fate in human tissues and cancer cells could offer a glimpse into the process of cell aging, by allowing the construction of cell fate maps that detail which cells survive longest. ■

Reference: Yatabe, Y., et al. 2001. *Proc. Natl. Acad. Sci. USA.* 10.1073/pnas.191225998. <http://www.pnas.org/cgi/content/full/191225998>