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Urchin, meet starfish

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Comparative genomic analysis is increasingly used to provide evidence for phylogenetic relationships and the relative importance of both coding and noncoding DNA sequences. However, simple sequence comparison may not reveal all the relationships among organisms, particularly when they have been separated by vast amounts of evolutionary time. By viewing the interactions of genes as integrated multitasking networks, Veronica Hinman and colleagues at the California Institute of Technology report in the October 27 Proceedings of the National Academy of Sciences USA that a gene regulatory network (GRN) architecture controlling embryonic endomesoderm development in the sea urchin is strongly conserved in the starfish, despite half a billion years of divergent evolution. Such networks, the authors report, provide another tool for the understanding of genomic regulatory control, functions of noncoding DNA sequences, and mechanisms in evolution (*Proc Natl Acad Sci USA* 2003, DOI:10.1073/pnas.2235868100).

Hinman *et al.* used genes involved in endomesodermal specification in the early embryo in the sea urchin, *Strongylocentrotus purpuratus*, including krox, otx, gatae, foxa, and brachurya (bra), to isolate and clone orthologues in the starfish (*Asterina miniata*) genome. Using quantitative reverse transcription polymerase chain reaction and antisense oligonucleotides, the authors quantified effects of perturbation of individual genes within the group and enabled a map of positive and negative interactions, and feedback loops, to be constructed for each organism. Examining these GRN architectures revealed the conservation of a three-gene feedback loop fundamental for endoderm specification in the sea urchin that is almost identical in the starfish, even though their morphologies are quite distinct.

"This evidence for shared conserved GRN features goes far beyond the observations commonly used to support conserved evolutionary roles, namely, apparently similar patterns of gene expression and morphology of knockout phenotypes," the authors write. "Whereas these kinds of phenomenological observations are necessary first steps, they can provide only weak evidence for conservation of function, compared with the direct identification of GRN linkages. The criterion for true evolutionary homology in apparently similar processes is that they descend from a common ancestor that used the same process."

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