



INTRODUCTION

The Glorious Sea Urchin

Sea Urchin Genome

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See also related News story page 908; Poster; Podcast; Science's STKE material on page 887 or at www.sciencemag.org/sciext/seaurchin/

ANYONE WHO HAS SPENT ANY TIME TAKING COURSES IN DEVELOPMENTAL BIOLOGY has heard about the sea urchin. It has been a major experimental model for over a century, and the elucidation of its genomic sequence described here will be of interest to communities studying everything from economics and ecology in marine ecosystems to fundamental questions in evolution and development.

Davidson (p. 939) introduces us to this organism and to the reasons for its importance. Vertebrates share specific features of embryonic development with the sea urchin (which is the basis for their classification as deuterostomes). The sea urchin genome represents the first full sequence of a nonchordate deuterostome, and as such, makes it possible to identify genes that are truly vertebrate innovations and others that have been lost during evolution. Although much is known about developmental gene regulatory modules, a more detailed picture of these genetic elements and underlying principles of gene regulation that may apply across phyla is now possible. [For further discussion, see *Science*'s Signal Transduction Knowledge Environment site (STKE; www.stke.sciencemag.org)].

To help you visualize the history of sea urchin research and this latest achievement, the section contains a poster, done with the scientific input of A. Cameron and E. Davidson and sure to enrich many walls. An interactive version of the poster, including additional images, video, and Web resources, was created by T. Marathe and S. Wills with images assembled by A. Ransick (www.sciencemag.org/sciext/seaurchin/).

Initial analyses of the 814-megabase genome led to an outpouring of insights, which can be found here in *Science* (Sea Urchin Genome Sequencing Consortium, p. 941), with additional details appearing in a special issue of *Developmental Biology* on 1 December. See also the News article by Elizabeth Pennisi (p. 908). Some of the most striking findings from the sea urchin genome sequence relate to immunity, as described by Rast *et al.* (p. 952). These include an expansion of some innate immune receptors by more than an order of magnitude relative to vertebrates. To complement the genomic sequencing effort, Samanta *et al.* (p. 960) used high-resolution custom tiling arrays to generate a picture of the repertoire of genes expressed during embryogenesis. Having this picture proved to be very valuable to the community in the annotation process.

One fascinating trend is the creative ways in which genomic data can be combined with data from very different disciplines to yield new insights. By examining sequence data for extant sea urchins and combining this information with what is known from the fossil record, it is possible to speculate about the genes that underlie the structural composition of the earliest echinoderms that appeared during the early Cambrian Period. As described by Bottjer (p. 956), paleogenomic analyses of the sea urchin provide insight into genes participating in the generation of fossil-recorded structures. Pearse (p. 940) describes the cause and effect of population fluctuations in this animal, which has economic value as a fishery resource and is a vital component of marine benthic ecosystems. The sequence of the purple sea urchin (and sequences we hope are to come of related species) will help in understanding the basis for variations that affect the cycle between rich kelp forests (on which the urchin grazes) and sea urchin-filled "barrens." The sequencing of the sea urchin moves us a further step away from the past, when the analysis of an individual gene was a breathtaking achievement, toward a future where we will be following multidimensional changes in gene networks and relating them to the world around us.

—BARBARA R. JASNY AND BEVERLY A. PURNELL

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