The sea urchin joins the genome era

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Abstract

The first stages in the sea urchin genome project have been reported.

Significance and context

This paper represents the culmination of two years of work by five laboratories, making the first inroads on the problem of deciphering the sea urchin genome. These spiny ocean denizens occasionally serve as a model organism in developmental biology and are sometimes used to study gene regulation. As echinoderms, they also have a potentially informative phylogenetic relationship to chordates, and thus to the vertebrates. The California purple sea urchin, *Strongylocentrotus purpuratus*, was the organism selected for this genomic study.

Key results

The cornerstone of the sea urchin project was the construction of a contiguous set of bacterial artificial chromosomes (BACs) spanning the entire genome. To create a genomic scaffold, BAC clones were aligned using overlapping end sequences and additional sequence-tagged sites, then checked by comparing restriction enzyme digests. Analysis of the end sequences allowed the authors to estimate that the sea urchin genome contains about 27,000 genes, consistent with the urchin's genome being about one quarter the size of a human's. In addition to the BAC map, cDNA libraries were generated from several developmental stages and from particular organs. Each library was arrayed onto filters that are now available for hybridization screening. The genome project also includes a cDNA database that will expand as data from analyzed cDNAs become available.

Links

Further information about the Sea urchin genome project is available.

Reporter's comments

   The good news is that a complete BAC map of the genome makes the sea urchin ready for whole-genome sequencing. Unfortunately, it is not clear if such an effort will be undertaken any time soon. As the sea urchin genome is large - about a quarter the size of the three billion bases of the human genome - determining its entire sequence would require a significant effort. So far, only widely used model organisms such as the nematode *Caenorhabditis elegans* and the fruit fly *Drosophila melanogaster* have received so much attention. The latest focus is on the human genome, with the mouse likely to be next. Where the sea urchin fits into these sequencing schemes is uncertain. Despite a few particular advantages as a model research organism, the urchin is now rarely used as such, and its popularity is unlikely to increase in the near future.

   One major feature of interest, however, is the sea urchin's phylogeny, as echinoderms are more closely related to chordates, and thus to the vertebrates, than are other invertebrate groups. Although only very distantly related, we and the sea urchin are both deuterostomes unlike protostomes such as *Drosophila* and *Caenorhabditis*. The difference between these classification groups lies in the symmetry of the embryonic divisions and the formation of the body cavity. By comparing vertebrate and echinoderm genomes, it should be possible to determine how the original gene set of an early deuterostome ancestor diverged over the course of evolution to create such different creatures. To this end, the *S. purpuratus* Genome Project is undertaking an in-depth, full-sequence analysis of the sea urchin's lone Hox gene cluster. The Hox genes regulate important aspects of animal development and are highly conserved between different organisms. Comparing the Hox gene clusters from sea urchins and other species is the first step in comparative genomics using these prickly little animals.

Table of links

   Proceedings of the National Academy of Sciences of the United States of America

   Sea urchin genome project

References

1. Cameron RA, Mahairas G, Rast JP, Martinez P, Biondi TR, Swartzell S, Wallace JC, Poustka AJ, Livingston BT, Wray GA, et al: A sea urchin genome project: sequence scan, virtual map, and additional resources. Proc Natl Acad Sci U S A. 2000, 97: 9514-9518. 0027-8424

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