GENERAL SCIENCE NOTE

GENOMES AND DESIGN

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In recent years the publication of new genomes has become almost routine. During November of 2006, *Science* published the genome of the purple sea urchin, *Strongylocentrotus purpuratus*.[1] Because of the purported relationship between sea urchins and chordates, this creature's genome is of particular interest due to the information it brings to bear on the origin of these creatures and their genetic makeup. Current taxonomies classify echinoderms, including sea urchins, with the deuterostomes which also include hemichordates and chordates. Within a Darwinian framework, this means that all genes shared by humans and sea urchins must have been present in a common ancestor shared sometime before Cambrian strata, which contain both chordate and echinoderm fossils, formed.

Perhaps the most surprising discoveries during comparison of the *S. purpuratus* genome with other sequenced genomes have been the number of genes present and the similarity between those genes and the genes of other deuterostomes. The estimated number of genes in *S. purpuratus* is 23,300, which is very similar to estimates from other genomes including the human genome. This is particularly surprising from an evolutionary perspective because two whole genome duplications resulting in four copies of the ancestral genome are thought to be necessary to account for the chordate genome. Because genome duplications are not invoked in echinoderms, the number of genes must be accounted for by a different mechanism in which many small duplications occurred. Thus, the Darwinian explanation for gene number similarity results in an explanation that is unparsimonious despite the similarity in the gene number estimates.

Comparison of gene families between the *S. purpuratus* genome and genomes of other deuterostomes reveals a remarkable lack of novelty. "[T]he distribution of proteins among those conserved families shows the trend of expansion and shrinkage of the preexisting protein families, rather than frequent gene innovation or loss."[2] This means that the truly difficult task of inventing new kinds of genes must have occurred before the split between chordates and echinoderms. Within a conventional framework, this removes over half a billion years from the time available for genes shared among deuterostomes to evolve via the neo-Darwinian mutation-selection mechanism.

It has been shown that gene duplication is not a viable mechanism for production of genes with new functions, even within gene families.[3] Presumably this means that creation of the truly novel genes from which the various gene families are supposed to have developed via duplication and modification would be a significantly more difficult achievement. Thus, production of the original genes from which Darwinists hypothesize gene families are derived must be that much further beyond the capacity of Darwinian processes. The truly surprising finding is that *S. purpuratus* shares genes thought to be vertebrate specific. These include genes involved in adaptive immunity and virtually the entire set of genes involved with Usher syndrome, a genetic disorder affecting hearing, balance and sight. But the situation is made worse by comparison of the *S. purpuratus* genome with protostome bilaterians. It turns out that "bilaterian genes are more broadly shared"[4] than previously thought, further reducing the window of time for mutation and selection to produce these genes.

Some genes are unique to *S. purpuratus* and a subset of these provide unique opportunities to examine the time available for their evolution within a Darwinian framework. Among the most informative of these unique echinoderm genes are those involved in forming stereom, the distinctive endoskeletal tissue found in all echinoderms.[5] It is now proposed that "the specific sereom matrix gene battery (i.e., the variety of structural functions encoded in its diverse proteins, plus its regulatory controls) must have been assembled as such in Early Cambrian time."[6] The time span suggested for evolution of this suite of genes and its regulatory controls is from 542 – 520 Ma or approximately 22 million years. This brings much more focus to questions about how much time and what has to be achieved given Darwinian assumptions of mechanism and time. Publication of this genome allows for more realistic evaluation of what the neo-Darwinian mechanism is claimed to have achieved, even within a framework of long ages.

An unusual aspect of publication of this particular genome was the co-publication of papers detailing when specific genes are active in the genome.[7] This was made possible in part by the fact that *S. purpuratus* has been a model organism for the study of development for some time. This study revealed that about half the identified genes in this organism are active during embryogenesis. On the surface this might appear to support the hypothesis of Lynn Margulis that creatures may expand their genomes by "fusing" their genomes with those of other organisms. Thus "Acquired traits can be inherited not as traits but as genomes."[8] In developing this "symbiotic" version of evolutionary history, she embraces the ideas of Donald I. Williamson who explains organisms that have distinctly different larval and adult stages as the product of blended

genomes of two distinctly different organisms and specifically cites sea urchins as an example of an organism which acquired the genes for its larval stage from another organism.[9] The problem is that certain classes of genes, (e.g., most transcription factors and signaling proteins) are expressed during embryogenesis,[10] making the theory that genes from one genome are expressed early in development while those from the "adult" genome are expressed later untenable.

Since publication of the first multicellular eukaryotic genome, *Caenorhabditis elegans*, in 1998,[11] publication of each successive genome has invariably revealed findings which are surprising within a Darwinian framework and almost unavoidably described in terms of design. The sea urchin genome is no exception to this. For Biblical creationists, "unexpected sophistication in the urchin genome"[12] is expected, not unexpected. The idea that in different organisms "the same [genes] are used in different ways,"[13] much as engines and pumps may use pistons in different ways is unlikely to leave those familiar with how machines are designed "scratching their heads."

Most creationists will be impressed with the design language used when describing the sea urchin genome. The *S. purpuratus* genome will help us "understand on sight the logic functions they execute in response to the sets of transcription factors in given cells at given times." "The sea urchin genome will directly contribute to solving the principles of design of gene regulatory networks for embryonic development." "Such principles can only be obtained by comparing network architecture in different animals developing in similar or different ways." "The genome will not only provide the 'code' for development but will also contribute to linkage between gene regulatory networks and the actual realization of developmental events." "It remains to connect the genes that execute these functions to the control circuitry that specifies their occurrence."[14] As with previously published genomes, the sea urchin genome makes Darwinian explanations appear significantly less tenable while at the same time exhibiting the characteristics of a brilliantly designed creation.

ENDNOTES

1. Sea Urchin Genome Sequencing Consortium. 2006. The genome of the sea urchin *Strongylocentrotus purpuratus*. Science 314:941-952.
2. Ibid., p 943.
3. Behe BJ, Snoke DW. 2004. Simulating evolution by gene duplication of protein features that require multiple amino acid residues. Protein Science 13:2651-2664.
4. Sea Urchin Genome Sequencing Consortium, p 950.
5. Bottjer DJ, Davidson EH, Peterson KJ, Cameron AR. 2006. Paleogenomics of Echinoderms. Science 314:956-960.

6. Ibid., p 958.
7. See the December 1, 2006 issue of Developmental Biology 300:1-496.
8. Margulis L, Sagan D. 2002. Acquiring Genomes: A theory of the origins of species. Basic Books, p 41.
9. Williamson DI. 2006. Hybridization in the evolution of animal form and life-cycle. Zoological Journal of the Linnean Society 148:585–602.
10. Samanta MP, Tongprasit W, Istrail S, Cameron RA, Tu Q, Davidson EH, Stolc V. 2006. The transcriptome of the sea urchin embryo. Science 314:960-962.
11. *C. elegans* Sequencing Consortium. 1998. Genome sequence of the nematode *C. elegans*: a platform for investigating biology. Science 282:2012-2018.
12. Pennisi E. 2006. Sea urchin genome confirms kinship to humans and other vertebrates. Science 314:908-909.
13. George Weinstock quoted in Pennisi E. 2006. Sea urchin genome confirms kinship to humans and other vertebrates. Science 314:909.
14. All quotes in this paragraph are from column 3 on p 939 of Davidson EH. 2006. The sea urchin genome: Where will it lead us? Science 314:939-940.