

electronic levels of the quantum dots — to produce recombination luminescence. There is another explanation, that energy is transferred directly from the excited states of molecules in the surface region of the ETL or HTL. But the data collected by Coe *et al.* support the model of direct electron-hole capture and emission within the nanocrystals, and, from the perspective of high efficiency and stability of emission, this is very promising. In addition, the spread, or bandwidth, of the emission spectrum from these devices has an almost perfect gaussian profile and is determined by the uniformity of the quantum-dot size, which can be accurately controlled during fabrication. And by varying the actual size of the quantum dots, the luminescent spectrum can be tuned to particular wavelengths.

The authors also mention another advantage of this quantum-dot LED. In fluorescent materials, including the polymers used in conventional LEDs, the restrictions of statistical mechanics mean that fewer than half of the electron-hole recombinations result in light emission. This is the principal reason for the low quantum efficiency of

such devices⁹. But in inorganic nanocrystals every electron-hole recombination can produce a photon. So, in addition to the newly discovered possibilities of phosphorescent emitters¹⁰, building quantum-dot LEDs with simple inorganic nanocrystals opens a new route towards achieving a quantum efficiency of 100% at any visible wavelength. ■

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Genomics

Return of a little squirt

Henry Gee

The draft sequence of the genome of a dim and distant relation of vertebrates will allow closer inspection of vertebrate origins. Some people have been waiting more than a hundred years for this.

The sea squirt *Ciona intestinalis* is an unassuming creature whose wider significance lies largely in its ancestry: it is a deuterostome, a member of the great group of multicellular animals that also includes the vertebrates, and so ourselves. The draft sequence of its genome, published last week in *Science*¹, promises to shed light on the evolutionary origins of vertebrates and their relationships with other creatures.

Of the animals whose genomes have been published, the roundworm *Caenorhabditis elegans* and the fruitfly *Drosophila melanogaster* are protostomes, members of the other great group of multicellular animals, and therefore only remotely related to vertebrates. Humans, mice and the puffer fish *Fugu rubripes* are all bona fide vertebrates, and so their genomes can tell us little about the sequence of events that led to the evolution of the extraordinary suite of features that make vertebrates so distinctive. These include the heart, the nervous system and lymphocyte-based adaptive immunity — features that are so characteristic, and in many ways so complex, that tracing their origins among the altogether simpler invertebrates has proved an insurmountable challenge.

What is required is the genome sequence of an animal that is a deuterostome but not a vertebrate, and which shared an ancestry with vertebrates that excludes protostomes. Enter *Ciona* (Fig. 1, overleaf), the first non-vertebrate deuterostome to have its genome published in any form. The sequence is preliminary, and mapping data are too sparse to allow the sequence to be placed on *Ciona*'s 14 chromosomes. But the researchers¹ can say that *Ciona* has just under 16,000 genes, comparable to the number for *Caenorhabditis* (19,000) and *Drosophila* (14,000) but less than the 30,000-plus seen in vertebrates. And with a genome of around 160 million base pairs — a twentieth the size of the human genome — genes in *Ciona* are as densely packed as they are in protostomes.

The main message is that the sea-squirt genome looks like a vertebrate genome, only simpler. *Ciona* has single copies of genes that are not found in protostomes, but which in vertebrates have diversified into entire families involved in cell signalling and developmental regulation: families such as the fibroblast growth factors, Smads and T-box genes. *Ciona* contains similar genes to those that, in vertebrates, direct distinctively



100 YEARS AGO

Though Jupiter has been unfavourably placed for European observers during the present year, his surface markings have been extremely interesting, of great variety and in plentiful numbers. The English climate, even at its best, can scarcely be said to suit astronomical work in an eminent degree, but its characteristics in 1902 have proved unusually bad... The most noteworthy incident in connection with recent studies of Jupiter is to be found in a very pronounced acceleration of motion in the great red spot. This first made itself evident in 1901, but it has been intensified during the past summer. For about twenty-three years, uninterruptedly, this singular marking had exhibited a constantly increasing retardation, which caused its rotation period to lengthen from about 9h. 55m. 34s. to nearly 9h. 55m. 42s. But in 1901 it declined to 9h. 55m. 41s. and during the present year the rate has been about 9h. 55m. 39¹/₂s. And this increase in velocity has been contemporary with the outbreak of a large, irregular or multiple marking of a dusky hue, in the same latitude of the planet.

From *Nature* 18 December 1902.

50 YEARS AGO

The existence of discrete sources of extra-terrestrial radio-frequency radiation is now well established and the positions of more than one hundred sources have been published. Attempts to identify these sources with any particular class of visual object have so far failed, and the origin of the radiation remains unexplained. One of the fundamental requirements in the study of these sources is a knowledge of their apparent angular size, and although attempts to make this measurement have been made by several observers, it has proved to be beyond the resolving power of their equipment. The present communication gives a preliminary account of a successful attempt to measure the angular size of the two most intense sources... The measurements are not yet adequate to define satisfactorily the shape of the sources or the distribution of intensity across their disks. Further observations are now being made... We wish to thank Dr. R. Q. Twiss for his assistance with the mathematical theory, and Prof. A. C. B. Lovell for making the necessary facilities available and for his interest in the investigation.

R. Hanbury Brown, R. C. Jennison
& M. K. Das Gupta

From *Nature* 20 December 1952.

vertebrate processes of development, such as formation of the nervous system and heart. All of this suggests that the sea squirt retains a primitively simple complement of genes that would have been found in the last common ancestor of sea squirts and vertebrates, more than 550 million years ago.

The converse is also true — *Ciona* has had plenty of time to evolve its own, non-vertebrate peculiarities. Sea squirts have some interesting physiological quirks, the most bizarre of which is the manufacture of cellulose for their distinctive outer coverings, or 'tunics'. Some of the enzymes involved in cellulose metabolism are undoubtedly home-grown, but the report¹ of a cellulose synthase gene, previously found in plants, is unique for animals and might have been an import from nitrogen-fixing bacteria.

Genomes of other non-vertebrate deuterostomes will be required to fill in the fine details of the order in which the various distinctively vertebrate developmental and physiological features were acquired. In this context, the genome of the lancelet *Bran-chiostoma* — a vaguely fish-like creature even more closely related to vertebrates than is *Ciona* — would be especially welcome.

What we have is a splendid start — or rather restart. This story really began in the 1880s with the frustration of one young researcher at the general inability to get to grips with the issue of vertebrate origins. With nothing to go on but basic embryology and comparative anatomy, schools of researchers devised a variety of explanations for vertebrate origins, not all of which were compatible, and with no way of deciding which ones were more likely to be correct.

This was the last straw for our hero. "Out of the same facts of anatomy and development men of equal ability and repute have brought the most opposite conclusions," he wrote. "To take for instance the question of the ancestry of the Chordata, the problem on which I was myself engaged, even if we neglect fanciful suggestions, there remain two wholly incompatible views as to the lines of Vertebrate descent, each well supported and upheld by many. From the same facts opposite conclusions are drawn. Facts of the same kind will take us no further. The issue turns not on the facts but on the assumptions."

He then proceeded to burn his boats in spectacular fashion: "Surely we can do better than this. Need we waste more effort in these vain and sophistical disputes?"

Six years after publishing these lines², the author coined a word for an entirely new discipline that promised to put hard facts in place of vacuous speculation. He was William Bateson, and the word was 'genetics'. Across the Atlantic, Thomas Hunt Morgan was also leaving old-fashioned evolutionary biology for experimental science, abandoning various worms for the fruitfly, on whose narrow and bristly shoulders rests a century

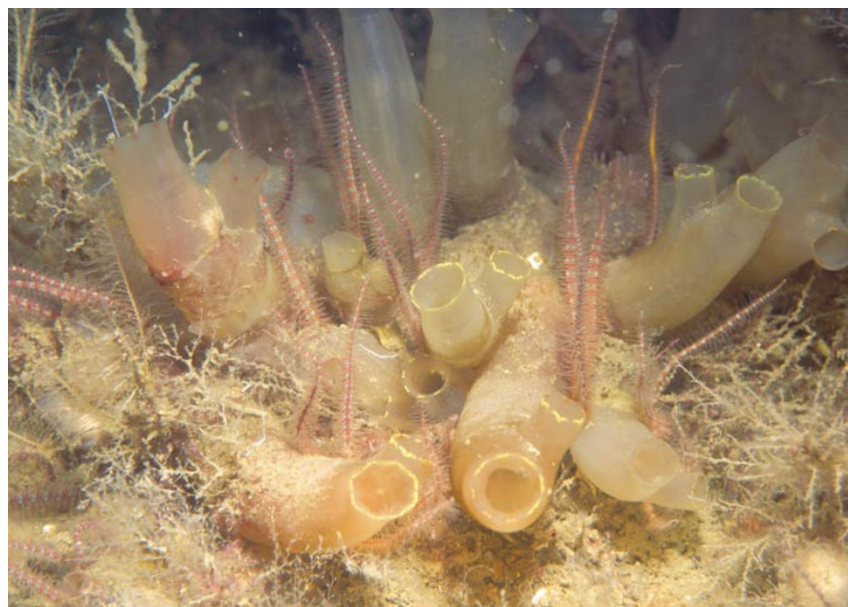


Figure 1 Object of taxonomic affection — *Ciona intestinalis*, the tube-like organisms seen in this underwater display.

of work on comparative developmental biology. The work on the genome of *Ciona* can thus trace its lineage to Bateson and Morgan and the very foundations of genetics.

The origin of vertebrates may seem like a question straight out of some dusty zoology textbook. But we owe the existence of genetics, genomics and, arguably, a large part

of molecular biology to the frustration of two young men unable to coax the secrets of evolution from creatures such as *Ciona intestinalis*. Welcome back, little squirt. ■
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Computational biology

Evolution plays dice

Philip Gerrish

In computer simulations, initially identical populations of organisms growing in identical environments follow very different evolutionary trajectories. Mutational interdependence is a key factor.

Because of the long timescales involved, evolution has principally been a historical or retrospective science, relying in large part on a sparse fossil record. This constraint makes drawing inferences about evolutionary processes very difficult, but it does not apply to systems where evolution happens fast. With such systems, evolution ceases to be a strictly historical science and becomes amenable to experimentation, allowing hypotheses about evolution to be tested directly. Notably, fast evolution has been studied in laboratory populations of microbes^{1,2}, and really fast evolution has been studied in *in silico* populations of virtual organisms³. Virtual organisms are self-replicating, mutable computer programs, and as Yedid and Bell show on page 810 of this issue⁴, they provide a powerful way of addressing fundamental questions about evolution.

One such question, remarkably, continues to confound evolutionary biologists. Is evolution governed mainly by chance or is its outcome largely predetermined? With microbial or *in silico* systems, this question can be addressed experimentally as follows. Create several parallel populations with identical organisms; let them evolve independently in identical environments for a period of time; then see whether the evolved organisms are the same or not. If evolution is governed solely by chance, each population will follow a unique evolutionary trajectory and the evolved organisms will all be different. If evolution is completely deterministic, each population will follow the same trajectory and the evolved organisms will be the same.

This simple experiment has been performed with different microbes^{5–7}. Yet even with today's sophisticated biotechnological