Scientists spin a gripping yarn

Fishing line and sewing thread can be twisted into artificial “muscles” that are much more powerful than their human equivalents. They could be used to make robots, prosthetic limbs, and clothing with pores that open and close to keep their wearer warm or cool.

Scientists have previously tried to make artificial muscles from other materials such as metal or carbon. But these materials are expensive and hard to control. An international team led by Ray Baughman of the University of Texas at Dallas in Richardson, US, has investigated using low-cost polyethylene and nylon fibres as alternatives. The team twisted the fibres into very tight coils that they then wove into braids or textiles. The extreme twisting of the fibres allowed the artificial muscles to lift loads 100 times heavier than a human muscle of equivalent size could (*Science*, **343**: 868-872, 2014).

The artificial muscles can be made to expand or contract by changes in temperature, so they can be controlled by a small heating element, or allowed to respond to changes in the environment.

(176 words)

Molecular evidence of anteroposterior patterning in adult echinoderms

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Abstract

The origin of the pentaradial body plan of echinoderms from a bilateral ancestor is one of the most enduring zoological puzzles. Since echinoderms are defined by morphological novelty, even the most basic axial comparisons with their bilaterian relatives are problematic. Here, we used conserved antero-posterior (AP) axial molecular markers to determine whether the highly derived adult body plan of echinoderms masks underlying patterning similarities with other deuterostomes. To revisit this classical question, we used RNA tomography and *in situ* hybridizations in the sea star *Patiria miniata* to investigate the expression of a suite of conserved transcription factors with well-established roles in the establishment of AP polarity in bilaterians. We find that the relative spatial expression of these markers in *P. miniata* ambulacral ectoderm shows similarity with other deuterostomes, with the midline of each ray representing the most anterior territory and the most lateral parts exhibiting a more posterior identity. Interestingly, there is no ectodermal territory in the sea star that expresses the characteristic bilaterian trunk genetic patterning program. This suggests that from the perspective of ectoderm patterning, echinoderms are mostly head-like animals, and prompts a reinterpretation of the evolutionary trends that made echinoderms the most derived animal group.

Introduction and results

Echinoderms, defined by their calcitic endoskeleton, unique water vasculature system, and perhaps most strikingly by their pentaradial body plan[1,2], are among the most enigmatic animal phyla. Since echinoderms are phylogenetically nested within the deuterostomes[3-5] (echinoderms, hemichordates, and chordates), their pentaradial organization was evidently derived from a bilaterian ancestor. Yet, despite a rich fossil record, comparative morphological studies have come to conflicting conclusions regarding the axial transformations that led to pentamery from the ancestral bilaterian state[2,6]. Among bilaterians, the deployment of the gene regulatory network that specifies ectoderm AP polarity is highly conserved and represents a suite of characters that is often more conserved than the body plans they regulate[7-14] (Fig.1a). The deployment of this AP regulatory network could therefore provide an alternative way to test hypotheses of axial homology in cases such as echinoderms where morphological characters are too divergent to reconstruct ancestral states[15].

Detailed comparisons between chordate and hemichordate axial patterning have established the ancestral deuterostome AP patterning program[11-14]. The fate of this conserved network and its role in patterning the adult body plan of extant echinoderms could provide key insights into the evolution of echinoderm axial properties, with two distinct scenarios. First, the ancestral deuterostome AP patterning network could have been dismantled and reassembled into novel conformations during the radical body plan modifications along the echinoderm stem lineage. In this scenario, expression of transcription factors in derived morphological structures without conservation of relative spatial expression across the network would imply co-option into novel developmental roles[16,17]. Alternatively, conservation of spatially coordinated expression of this network during the elaboration of the echinoderm adult body plan would provide a molecular basis for testing hypotheses of axial homology with bilaterians, and establish regional homologies masked by divergent anatomies[15,18] (Fig.1b).

Four main hypotheses have been proposed to relate the echinoderm body plan to other bilaterians (Fig.1c). The bifurcation[19] and the circularization[19,20] hypotheses can be ruled out, since they require a unique molecular identity for each of the five echinoderm rays that is inconsistent with molecular data[18,21]. In the duplication hypothesis[19,22], each of the five echinoderm rays is a copy of the ancestral AP axis, and in the stacking hypothesis [2,6,23,24] the oral-aboral axis of adult echinoderms is homologous to the ancestral AP axis. While broad bilaterian comparisons of AP axis patterning are typically based on ectodermal expression domains, the stacking hypothesis was proposed largely on the basis of nested posterior Hox gene expression in the posterior mesoderm of the bilateral larval stages in holothuroids (sea cucumbers), crinoids (sea lilies), and echinoids (sea urchins)[25-31], and need to be tested based on ectodermal expression.

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Zoology

Starfish are actually flattened heads with no bodies

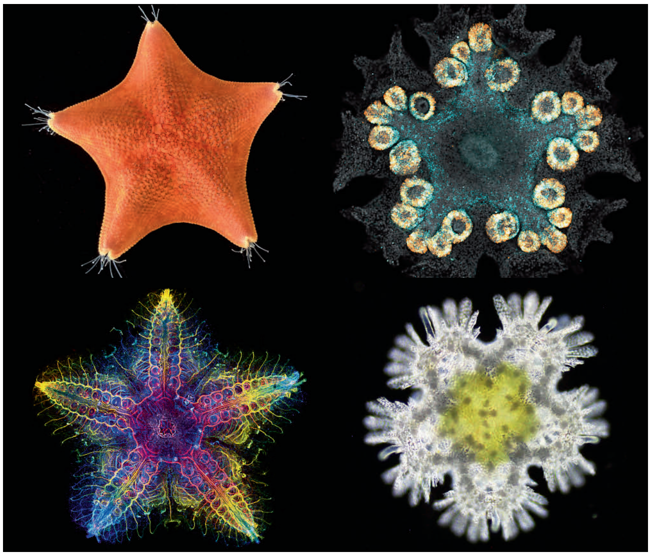
Claire Ainsworth

SCIENTISTS trying to work out where a starfish's head is have come to a startling conclusion: it is effectively the whole animal. As well as solving this long-standing mystery, the finding will help us understand how evolution generates the dramatic diversity of animal forms on Earth.

Starfish, also known as sea stars, belong to a group of animals called echinoderms, which includes sea urchins and sea cucumbers. Their strange body plans have long puzzled biologists. Most animals, including humans, have a distinct head end and tail end, with a line of symmetry running down the middle of their body, dividing it into two mirror-image halves. Animals with this two-sided symmetry are called bilaterians.

Echinoderms, on the other hand, have five lines of symmetry radiating from a central point and no physically obvious head or tail. Yet they are closely related to animals like us and evolved from a bilaterian ancestor. Even their larvae are bilaterally symmetrical, later radically reorganising their bodies as they metamorphose into adults.

Fluorescent stains labelling various tissues in a starfish



LAURENT FORMERY (WITH OLYMPUS/EVIDENT IN LOWER LEFT ONLY)

> **"The body of an echinoderm is essentially a head walking about the seafloor on its lips"**

These profound differences make it hard for scientists to find and compare equivalent body parts in bilaterians to work out how echinoderms evolved. "The morphology cannot tell you anything, almost," says Laurent Formery at Stanford University in California. "It is just too weird."

Formery and his colleagues decided to look at a set of genes known to direct the head-to-tail organisation of all bilaterians. In these animals, the genes are turned on, or expressed, in stripes in the outer layer of the developing embryo. The genes that are expressed in each stripe define which point on the head-to-tail axis it will become.

The idea was to see if the gene expression patterns would reveal a "molecular anatomy" hidden in echinoderms. "This particular suite of genes is just good for exploring animal diversity in its most extreme forms," says team leader Chris Lowe, also at Stanford University. "I think echinoderms represent a really extreme experiment in how to use that bilateral network to produce a very, very different body plan."

To the team's surprise, the genes that determine the head end in bilaterians were expressed in a line running down the middle of each arm on the underside of a starfish. The next "head-most" genes were expressed on either side of this line, and so on (*Nature*, DOI: 10.1038/s41586-023-06669-2).

Even more strangely, the genes normally expressed in the trunk of bilaterians were missing in the outer layer of the animal. This suggests that starfish have jettisoned their trunk regions and freed up the outer layer to evolve in new directions, says Formery.

The findings show that "the body of an echinoderm, at least in terms of the external body surface, is essentially a head walking about the seafloor on its lips", says Thurston Lacalli at the University of Victoria in Canada. Animals like us may have kept their trunks to escape predation by swimming away. "Echinoderms hunkered down and armoured themselves, so they didn't need a trunk," says Lacalli. ▮

Chicken Genome Analysis Unlocks Secrets of Mammalian and Bird Evolution

An international consortium of researchers, including a geneticist at the University of California, Davis, uncovered a treasure trove of data when they analyzed the recently sequenced chicken genome, a development that will benefit research in basic biology and medicine for years to come.

Their analysis of the chicken genome -- the first genome of a livestock or bird species to be sequenced -- is the cover story in the Dec. 9 issue of the journal *Nature*.

"The draft sequence of the chicken genome and the findings provided in this first-level analysis truly revolutionize what research can be accomplished with this agriculturally and biomedically important species," said Mary Delany, a geneticist in UC Davis' Department of Animal Science and a co-author and a coordinator for the analysis....

Chicken genome analysis will benefit human health and agriculture

We may soon be thanking Michigan State University chicken No. 256 for better treatments or even new vaccines for the flu and other human ailments.

As the first bird and the first agricultural animal to have its genome sequenced, the chicken is paving the way for research on human diseases, as well as studies on chicken breeding to benefit agriculture. An international consortium of scientists that includes a researcher from Michigan State University analyzed the chicken genome and published a paper in the Dec. 9 issue of the British science journal *Nature*.

The first draft of the chicken genome was placed into free public databases for use by researchers around the world in March 2004.

The bird whose genome was sequenced, a red jungle fowl (*Gallus gallus*) known by her wing band number, 256, still lives on the MSU campus in a facility that serves the lab of Jerry Dodgson, professor of microbiology and molecular genetics at MSU, who has worked on mapping the chicken genome for the past 17 years. At 7, she’s quite old for a chicken and is oblivious to the importance of her contributions to science....

Strange quark contribution to proton structure yields surprising result

Scientists seeking to confirm earlier measurements of the strange quark's contribution to the proton's magnetic moment have found several surprises, instead.

As reported in the Dec.15 issue of the journal *Science*, physicists who combined results from two measurements have calculated a lower strange quark contribution, and provided evidence for the existence of a parity-violating electromagnetic effect known as the proton's anapole moment.

In experiments with the SAMPLE apparatus at the MIT/Bates Linear Accelerator Center, scientists used the weak magnetic force to uncover the contributions of the up, down and strange quarks. "The parity-violating nature of the weak force provides a powerful tool to unravel the international structure of the proton," said Doug Beck, a physics professor at the University of Illinois and a collaborator on SAMPLE. "The basic ideas is to study the preference for the proton's interaction with electrons spinning counterclockwise, over those spinning clockwise."...

Electron is surprisingly round, say Imperial scientists following ten year study

Scientists at Imperial College London have made the most accurate measurement yet of the shape of the humble electron, finding that it is almost a perfect sphere, in a study published in the journal *Nature* today.

The experiment, which spanned more than a decade, suggests that the electron differs from being perfectly round by less than 0.000000000000000000000000001 cm. This means that if the electron was magnified to the size of the solar system, it would still appear spherical to within the width of a human hair.

The physicists from Imperial's Centre for Cold Matter studied the electrons inside molecules called Ytterbium Fluoride. Using a very precise laser, they made careful measurements of the motion of these electrons. If the electrons were not perfectly round then, like an unbalanced spinning-top, their motion would exhibit a distinctive wobble, distorting the overall shape of the molecule...
