all their faults, provide a type of subtlety that you don't get in more objective measures." Paraphrasing Winston Churchill's views on democracy, he says that reputational rankings of academic quality "are the worst method for assessing the comparative quality of U.S. research universities—except for all the others."

Don't forget the students

Focusing on reputation, however, ignores the question of how to calibrate many of the other complex elements that make up a graduate education. "The previous [NRC] survey was misnamed," says the AAU's Vaughn, echoing the views of many. "It was an assessment of the quality of research faculty, not of graduate programs. And we don't really know how to measure the quality of graduate education." Kuh plays down the distinction. "I don't think you can separate the two," she insists, adding that she thinks previous surveys got it right in emphasizing research.

Still, many administrators feel that the next NRC survey must do a better job in exploring the quality of education. That includes such factors as the time to degree, dropout rate, and starting salary of graduates, as well as such intangibles as the quality of mentoring, opportunities to attend meetings, and the extent of career advice offered students. "It's not easy to do, but without it the community support [for the next survey] will vanish," says Debra Stewart, vice chancellor and graduate dean at North Carolina State University in Raleigh, who served on the advisory panel for the 1995 study and who in July becomes CGS president.

Joseph Cerny, vice chancellor for research and dean of the graduate division at the University of California, Berkeley, and his Berkeley colleague, Maresi Nerad, took a first crack at the issue by surveying some 6000 graduates a decade after they received their Ph.D. The study, carried out in 1995 and still being analyzed (*Science*, 3 September 1999, p. 1533), surveyed graduates on the quality of the training they received and whether they would do it again, among other questions. The results were quite different from when the NRC asked peers to rate the quality of both faculty and programs.

"The [NRC] found an almost perfect correlation," says Cerny, who as a member of the advisory panel lobbied unsuccessfully for outcome data to be collected in the 1995 survey. "But when we asked graduates to rank such things as the quality of the teaching, the graduate curriculum, and the help they received in selecting and completing their dissertation, we got dramatic differences. Instead of a slope of 45 degrees, indicating a perfect fit, we got a 20% fit. The graph looked like it had come out of a shotgun."

The data on whether students would repeat their training are also eye-opening. "Computer science ranked the highest, at 85%, and biochemistry was the lowest, at 69%," he says. And the performance of individual programs varied wildly, including two biochemistry programs that scored 100% and one that received only 15%.

Kuh argues that such ratings from graduates have limited value because the information quickly becomes dated and doesn't take into account the variation among students. She adds that a stressful graduate experience could still lead to a successful career. Cerny argues, however, that even stale information on student outcomes would be extremely valuable to the university administrators who run the programs—and to the federal agencies that fund graduate training. "I'd certainly want to know if I was the dean at a school [where only 15% of students would redo their training]," he says. "Even if you consider 60% to be a passing grade, we found that only one-third of the programs scored at or above that level."

Ultimately, say Kuh and others, the key to a successful assessment is giving customers something they need. Bell and Webster of Oklahoma State say that the NRC and *U.S. News* surveys have had little impact on their university's research policies not because they fared badly but because the yardstick—the research reputation of its faculty—was seen as tangential to the university's main mission of educating students. "It's like MIT's [the Massachusetts Institute of Technology's] reaction to the weekly Associated Press football polls," says Webster. "We're just not a big player in that sport." Kuh hopes that the next NRC survey is good enough to generate as much interest at Oklahoma State as it does at MIT or Yale, setting the standard for anybody interested in assessing graduate education. "The U.S. is at the top of the world in higher education," says Graham, "and it's too important a topic to produce reports that aren't used."

–JEFFREY MERVIS

MEETING

An Integrative Science Finds a Home

ATLANTA—This year's annual meeting of the Society for Integrative and Comparative Biology (SICB), held here earlier this month, marked a milestone for the fledgling discipline known as evo-devo biology. Beginning about a decade ago, modern biologists realized that they might glean clues to how organisms evolved by studying the genes that control development (*Science*, 4 July 1997, p. 34). Now, the discipline is so strong that last year it gained its own division within SICB and was invited to present its inaugural symposia in Atlanta. Prominently featured were new findings on the genes needed for butterfly wing development and on the homeobox genes, a key group of developmental genes involved in organizing animal body plans.

Hox and the Simple Hydra

Evolution, like development, entails a transformation of shape and form, but on a much longer time scale. The discovery by developmental biologists that the *Hox* (for homeobox) genes play a major role in guiding this transformation in fruit fly and vertebrate embryos posed an intriguing question. Researchers wondered whether the appearance and proliferation of these genes 550 million years ago made possible the transformation of early life into the wide range of complex shapes and forms seen today. Results presented at the meeting supported this idea.

***Hox* history.** Hydras seem to need *Hox* genes to define their body axis.

CREDIT: G. OLIVER/VISUALS UNLIMITED

The work, which comes from the labs of two independent investigators, John Finnerty of Boston University and Hans Bode of the University of California, Irvine, deals with the homeobox genes of cnidarians. These animals—a group that includes corals, hydra, sea anemones, and jellyfish—resemble the fossils of some relatively simple pre-Cambrian creatures that existed before the large-scale diversification took place. Both groups of organisms lack a key feature of most modern animals—bilateral symmetry, a balanced shape that distributes the body in mirror-image halves along a line drawn from head to tail. However, in contrast to the simplest multicellular organisms, such as sponges, cnidarians do have a body axis: They have a top, defined by the mouth, and a bottom. And the new results suggest that the *Hox* genes may have been instrumental in establishing that axis.

Whereas sponges have at most one *Hox*-like gene, Finnerty has found that sea anemones and other cnidarians can have seven, a mix of *Hox* genes and related *paraHox* genes. The *Hox* genes also appear to be organized much as they are in vertebrate genomes. Bode's results suggest that the genes have similar functions in primitive and advanced organisms, such as helping establish the head region. Taken together, Finnerty suggests, these molecular data say that "[cnidarians] are much closer to bilateral organisms than we have thought. I think these genes are absolutely required for the establishment of the body axis in all animals above a sponge-grade construction." Later in evolution, the genes may also have helped organize tissues along that axis into discrete and ever more complex body regions.

The new findings come from a collaboration involving Finnerty and Mark Martindale, formerly at the University of Chicago and now at the University of Hawaii, Honolulu. They conducted an exhaustive search for *Hox* genes in two sea anemone species and also searched the literature for cnidarian *Hox*-like genes. Based on an analysis of the sequences of 13 candidate genes, Finnerty and Martindale concluded that seven are either *Hox* or *paraHox* genes. Their studies also showed that the sea anemone *Hox* genes are clustered closely together in one chromosomal location, much as they are in vertebrates.

The sea anemone is less richly endowed, however. Whereas vertebrate *Hox* gene clusters can have up to 13 genes, and even simple invertebrates such as flatworms have at least seven, the sea anemone has only four. By assessing the degree of similarity between each cnidarian *Hox* gene and *Hox* genes in other organisms, Finnerty was able to match the cnidarian genes with their equivalents in bilateral animals and figure out which were missing. And as far as he can tell, Cnidaria "lack central *Hox* genes," the ones that guide the establishment of the central part of the body. That's logical, Finnerty added, because, "In Cnidaria, the center part of the body is relatively unspecialized." Overall, he concluded, Cnidaria "seem to be at an intermediate stage of evolution" between organisms with no *Hox* genes and bilaterally symmetrical species.

There is some evidence that *Hox* genes carry out similar functions in cnidarians and higher organisms. Bode has identified six *Hox*-like genes in hydras and finds that at least two are involved in determining where and when the tentacled head of the hydra forms. In earlier work, for example, he reported that a gene called *Cnox2*, which is active in the body column but not in the cells of the head, appears to suppress head formation. If you expose the hydra to a chemical that seems to shut this gene down, he says, "you get tentacles in the wrong places and heads along the body."

More recently, he found that a gene called *Cnox3* has the opposite expression pattern. It is weakly expressed in newly formed young cells in the body column, but as the tissue approaches the top of the hydra, where the tissue stops dividing and begins to differentiate, *Cnox3* gets more active. "[Expression] is very strong just below the tentacle," he reported. Combined with the activity of another gene that turns on briefly at about the same time, the *Cnox3* activity, he says, may coordinate tentacle development.

Because *Cnox3* looks like the head-defining *Hox* gene in other organisms, Bode thinks that it's playing a similar role in the hydra. If so, it would mean that even before organisms had evolved strongly defined head, thorax, and tail regions, homeobox genes might have been working as they do in higher organisms—sequentially, in a "head-to-tail" way.

Other researchers aren't so sure, however. The work in cnidarians "shows *Hox* genes have always had a role in specifying cells, but [they] might not have been [used to] specify the body axis," cautions evolutionary developmental biologist Rudolf Raff of Indiana University, Bloomington. Moreover, the body parts may not be parallel: The head of a hydra might not really correspond to the head of a lizard. Nevertheless, Finnerty notes, "we are starting to get enough comparative data that we can fill in the details of the evolution of the clusters." And that, says John Postlethwait of the University of Oregon, Eugene, is what makes cnidarian work "great."

Genetic Diversion, Evolutionary Diversity

When Sean Carroll set out more than 5 years ago to find out how the buckeye butterfly got its spots, he had only a slight inkling of what this tale could contribute to an emerging discipline called evo-devo. But he soon discovered that the eyespot that adorns many butterflies' wings—where it helps confuse predators looking for a tasty snack—evolved through the reuse of genes already known to be important for the development of the wing. Because this result demonstrated that nature could co-opt genes for completely different purposes, the work guaranteed the story a place in the evo-devo history books.

Since then, the plot has become even more intriguing. About a year ago, Carroll, an evolutionary developmental biologist at the University of Wisconsin, Madison, and his team showed that not just single genes, but an entire developmental control pathway involving a suite of genes—the one through which the key gene *hedgehog* exerts its effects—had been recruited to specify where eyespots would appear. This suggested that evolution of new features doesn't require the evolution of new genes or pathways, just a change in how those pathways are used.

In new results presented at the meeting, Carroll and his colleagues have now taken the work a step further, identifying some of the genes that take over after the eyespot location has been established to determine the sizes, and, very likely, the colors, of the central spot and any surrounding rings. The work fills in a "missing link" in understanding how the butterfly sets up the details of spot formation, says Scott Gilbert, a developmental biologist at Swarthmore College in Pennsylvania.

Evo-devo classic. Thanks to the eyespots of this East African butterfly, researchers are seeing how genes make diversity possible.

CREDIT: HOWARD HUGHES MEDICAL INSTITUTE

The results show that some of the same genes involved in determining the eyespot locations are called upon again, this time to set up the exact eyespot pattern. There's also a great deal of flexibility in how the genes are used. Whereas all four butterfly species studied appear to use the same patterns of gene expression to set up a spot, they each use the genes differently to determine the spot's details. "Everything looks very fixed and conserved to a certain step, and then there's a little riot going on," Carroll said.

For the current work, Carroll and Wisconsin's Craig Brunetti decided to track the activity of three genes, called *engrailed*, *spalt*, and *Distalless*, during the stage of development when the outlines of the spot and its rings are actually defined. They just happened to pick those genes from among the many that help the wing form. "We got really lucky," Carroll reported, as all three proved active at this time.

The genes' expression patterns indicated that they help define the spots and rings. For example, in the East African butterfly, *Bicyclus anynana*, all three genes are active in what becomes the white center of the spot, while just *spalt* and *Distalless* are turned on in the black ring flanking it. And in the outer ring, only *engrailed* was active.

In contrast, in the buckeye butterfly, *Distalless*, *spalt*, and *engrailed* are turned on in both the central white spot and its adjacent ring, leaving it up to another, still unidentified, gene to set up the ring. The combinations of active genes were different yet again in two other species examined. "What we've lifted the lid on is a very flexible system," Carroll concluded.

He suggested that such flexibility in gene usage is tolerable because the butterfly has already set up the wing and other critical aspects of its body, so it can tolerate deviations in more superficial characteristics, such as the appearance of the wing decorations. What results is a rapid and continual experimentation with new eyespots and eyespot patterns, some of which persist because, in the context of entire populations, one distracts predators better than another.

Despite the progress, many questions remain about eyespot evolution. For one, Carroll has yet to identify the mutations that enabled butterflies to co-opt the same genes for so many different functions. Still, he and others are pleased with what's been learned so far. "[The work] is a very good example of comparative developmental studies and how it is now possible to do detailed studies down to the molecular level in nonmodel organisms like butterflies," notes Lennart Olsson, an evolutionary developmental biologist at Uppsala University in Sweden. "Studying later parts of development will become more common, I hope, [because] from an evolutionary perspective, later parts of development are more interesting because this is where the viable variation occurs." **–ELIZABETH PENNISI**

ASTROPHYSICS

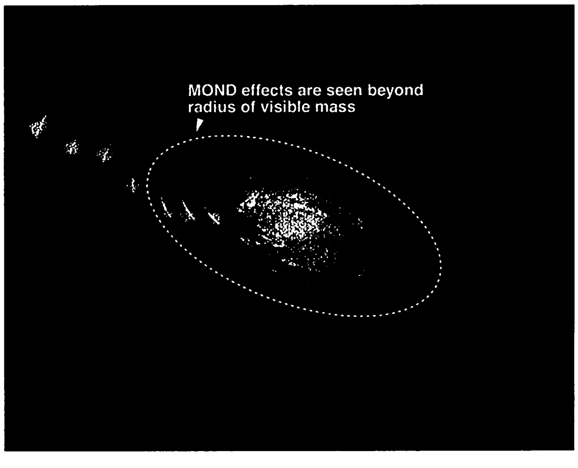
Heretical Idea Faces Its Sternest Test

Upcoming studies of the big bang's afterglow should make or break MOND, an equation that many cosmologists love to hate

When Vera Rubin began mapping massive hydrogen gas clouds that swarm around spiral galaxies like sluggish electrons around a nucleus, the astronomer at the Carnegie Institution in Washington, D.C., had a good idea of what she should find. Moving out from the galactic center, the gravitational pull of the ever-larger amount of mass within a cloud's orbit should make the cloud wheel faster and faster around the hub. But very distant clouds, orbiting beyond a certain radius that encompasses virtually all of the galaxy's mass, should chug more slowly, as the galaxy's gravitational pull diminishes with distance. Although Rubin did see the predicted rise in cloud velocity away from the center, the farthest clouds—to her astonishment—never did slow down.

To Rubin and most other experts, the explanation for this curious behavior, first noticed more than 20 years ago, had to lie in the presumption that galaxies are far more massive than meets the eye. Indeed, they say, the gravitational pull of invisible dark matter—thought to make up as much as 90% of the universe's mass—should account for the zippiness of clouds skirting the fringes of galaxies. But an alternative notion says that dark matter has nothing to do with this phenomenon. Instead, it argues that when mass is spread thinly across space, the local gravitational force—that exerted by a galaxy, say—is stronger than Newton's law of gravity predicts it should be. This gravitational fudge factor, called Modified Newtonian Dynamics (MOND), flies in the face of modern physics. But to the horror of many scientists, "it works amazingly well," says Princeton University cosmologist David Spergel.

It *was* working well, anyway, until researchers took a closer look at a new class of lightweight galaxies. There, they have found, clouds are trucking along more slowly than they should be according to MOND. "I wouldn't say it is a death blow," says astronomer Julianne Dalcanton of the University of Washington, Seattle, "but MOND is staggering and bleeding." The coup de grâce—or MOND's resurrection—may arrive after what could be a decisive test: measurements of fluctuations in the faint afterglow of the big bang, the cosmic microwave background, that should force scientists to choose between a universe dominated by dark matter and one that obeys the weird rules of MOND.



Fringe idea? Scientists hope to soon settle a debate over what keeps distant galactic clouds moving faster than can be explained by a galaxy's visible mass.

CREDIT: (PHOTO) NASA/JPL

At stake is a pillar of modern physics, Einstein's hallowed special theory of relativity. According to Newton and Einstein, gravity is a simple creature. An object's gravitational attraction, they showed, is proportional to its mass divided by the square of the distance from the object. To calculate gravitational force, all you need is the number that reflects the proportion: the gravitational constant, which holds true anywhere in the universe.

Challenging that fundamental idea about gravity, Moti Milgrom, an astrophysicist at the Weizmann Institute of Science in Rehovot, Israel, proposed MOND in 1983 as a way to explain the surprising speed of Rubin's clouds without having to resort to cramming galaxies full of invisible dark matter. Milgrom conceived another universal constant, the MOND critical acceleration. The idea is that instead of diminishing with the square of the distance, the pull of gravity—once it falls below a threshold, the critical acceleration—declines less precipitously, in direct proportion to distance. Milgrom and others have pegged a minuscule value for the critical acceleration: about one-trillionth the force of gravity we feel on Earth.

Needless to say, most cosmologists hate the idea. Not only does it fly in the face of Einstein's theory, but unlike general relativity, MOND offers no insights into how the rapidly accelerating early universe evolved, says Spergel. And cosmologists are