EVOLUTIONARY BIOLOGY

Morphologists Learn to Live With Molecular Upstarts

PARIS—Pity the poor elephant shrew. For much of this century, taxonomists, at a loss over how to classify this small, bug-eating African mammal, put it with the insectivores, an order that includes moles and hedgehogs. Then, in the late 1980s, a reevaluation of mammalian fossil evidence led some experts to suggest that this lowly animal—with its long, flexible snout resembling a tiny elephant's trunk—was closer to rodents and rabbits on the evolutionary tree.

If new data presented at a recent meeting* here are correct, the elephant shrew's identity crisis may now be resolved. A comparison of molecular sequences from a dozen mammalian species suggests that it is much more closely related to its mighty namesake, the elephant, than to hedgehogs or rats.

The new classification of the elephant shrew, part of a thorough revamping of mammalian ancestry, was one of several revelations at the Paris gathering, which brought together 200 biologists to look back over the past decade of progress in systematics—the discipline devoted to putting taxonomy on solid scientific ground. In recent years, systematists have been struggling to reconcile classical "morphological" methods of reconstructing evolutionary trees—based on anatomical similarities and differences between living species or their extinct relatives, such as the shape of a molar or the intricate details of a bone—with an avalanche of new molecular data on genetic variation among organisms (*Science*, 22 February 1991, p. 872).

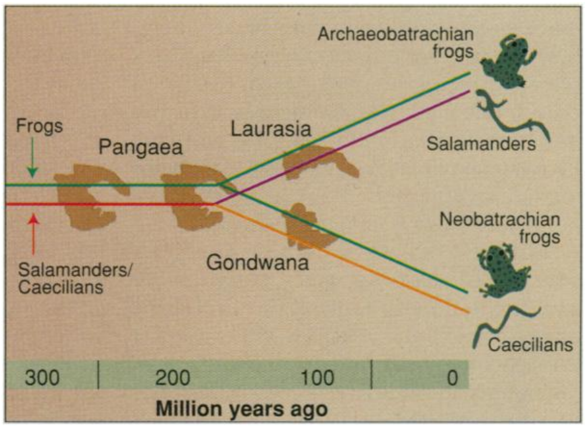
In the past, the face-off between proponents of molecules and those of morphology was sometimes bitter—particularly on the many occasions when the two methods gave different answers. While some presentations at the Paris meeting continued to fan those flames, there were encouraging signs that the two camps have moved much closer together—and that systematists of all stripes are coming to appreciate the important roles that both molecular and morphological evidence must play in sorting out the many remaining puzzles in the field.

And puzzles there are. Few groups of plants or animals have had their evolutionary, or phylogenetic, trees worked out with complete confidence. Debates still rage over when and how flowering plants split off from their nonflowering ancestors, the relations among orders of amphibians, the origins of rodents, and a host of other issues. And while a number of talks at the meeting showed the considerable power of molecular data to tease out elusive phylogenetic relations, there were also warning signs that molecular evidence can lead to misleading and embarrassing errors.

Nor were the questions tackled at the Paris meeting of only academic interest. "Systematics is the entire underpinning for evolutionary biology," says Colin Patterson, a fossil-fish expert at London's Natural History Museum. "You can't even start to think about evolution without it."

North-south split. While molecules and morphology often agree, they sometimes collide head-on. This rivalry is particularly sharp when it comes to classifying the amphibians. There are three living orders of these cold-blooded vertebrates: frogs, salamanders, and caecilians—burrowing, wormlike animals with small eyes and no limbs. Most morphological studies of living and fossil amphibians over the years have concluded that frogs and salamanders are closely related "sister groups" that split off from the caecilian line some 250 million years ago. But more recently, this neat grouping has been severely disrupted by molecular studies, which suggest that salamanders and caecilians are the sisters and that frogs are the more distant relatives of both.

In a talk at the Paris meeting, evolutionary biologist Blair Hedges of Pennsylvania State University suggested that the conflict might be resolved by looking at the geographical distribution of living species and correlating it with current views of early Earth geology. The amphibians are thought to have arisen at a time when there was just one supercontinent, Pangaea. About 200 million years ago, Pangaea split into a northern continental mass, Laurasia, and a southern mass, Gondwana, both of which later broke up into the northern and southern continents we know today.



SOURCE: B. HEDGES

Continental divide. Early Earth history supports molecular data on amphibian relations.

If the morphological point of view is correct, Hedges argues, frogs and salamanders would have branched off from caecilians early in amphibian history, before Pangaea split. Today, then, we would expect to find frogs, salamanders, and caecilians in both the northern and southern hemispheres, but this is not the case. Modern salamanders live almost entirely in the north and caecilians almost entirely in the south. Hedges says that this geographical distribution better fits the scenario supported by the molecular data, in which salamanders and caecilians are sister groups that diverged from an early ancestor at about the same time as the Pangaean split—one branch going north and the other south.

Hedges concludes that when molecules and morphology are in conflict, the sequence data are usually a more reliable measure of phylogeny. The reason, he argues, is that morphological features are much more susceptible to "adaptive convergence"—what systematists call homoplasy—in which features that seem similar enough to derive from a common ancestor actually have an independent origin. Hedges maintains that trees should be built with molecular data alone and the morphological characters "mapped" onto the branches. The result, he concludes, would be a more accurate picture of how the morphological features changed over the course of evolution.

Hedges's proposal split the delegates along traditional lines. One participant privately referred to Hedges's suggestion as "blatant molecular chauvinism." But it struck a chord with other proponents of molecular methods, including Morris Goodman of Wayne State University in Detroit. His decades-long contention that molecular data prove humans are more closely related to chimpanzees than to gorillas has achieved wide acceptance only in recent years. Says Goodman: "I believe that in the long run, as we learn to extract all the phylogenetic information stored in the DNA sequences of genomes, these sequences will prove to be more reliable than morphological characters when the two are in conflict."

Taming of the shrew. The tale of the elephant shrew garnered another point for the molecular team, this time in a longstanding debate over the phylogenetic relations among placental mammals. More

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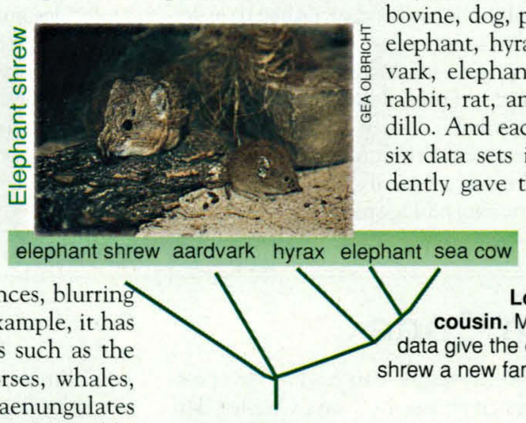
* "Molecules and Morphology in Systematics," Paris, 24–28 March 1997.

than 50 years ago, the American paleontologist George Gaylord Simpson divided the class *Mammalia* into a bewildering array of subclasses, infraclasses, cohorts, and superorders, based on morphological and fossil evidence. But despite Simpson's brave attempt, the exact relations among the 18 living orders of placental mammals have remained elusive, possibly because they evolved very rapidly after diverging from a common ancestor about 100 million years ago. This period of rapid evolution meant that organisms that once resembled each other quickly developed significant morphological differences, blurring relations among species. For example, it has long been unclear how groups such as the ungulates (which include horses, whales, and cattle) are related to the paenungulates (including elephants and sea cows). In addition, there are major questions about where aardvarks, rodents, and bats fit on the evolutionary tree.



Long-lost cousin. Molecular data give the elephant shrew a new family tree.

SOURCE: WILFRIED DE JONG

In recent years, most systematists have turned to cladistics, a method of phylogenetic analysis first developed in the 1950s by the German entomologist Willi Hennig. Cladistics arranges species together in special groupings, called clades, based on their inheritance of specific morphological features, such as feathers, fur, or flowers. If two species share modified versions of the same features—referred to as "shared derived characters"—it is assumed that they also share a common ancestor. And the extent to which these characters differ can be used to estimate how closely related are species or whole groups of organisms to one another.

Cladistics, which grounds classification schemes strictly on organisms' evolutionary history, has revolutionized systematics. For example, the technique allows the use of computers to compare a large number of characters from different taxonomic groups, and it is not restricted to morphological characters: Variations in molecular data—such as changes in the nucleotide or amino acid sequences of genes or proteins—can be treated as characters and plugged into phylogenetic analyses. Moreover, cladistic methods allow direct comparisons between morphological and molecular data.

Yet, despite this progress, mammalian phylogeny has remained muddled because of frequent discrepancies between and even among morphological and molecular data sets. At the Paris meeting, however, biochemist Wilfried de Jong, of the Catholic University of Nijmegen in the Netherlands, presented molecular data from his own and other labs that may point the way out of this morass.

De Jong and his colleagues, including postdoc Ole Madsen and Michael Stanhope's team at Queen's University in Belfast, used computerized cladistics programs to compare the nucleotide or amino acid sequences of six different genes or proteins taken from 12 species, each representing a different order of placental mammals. They are: human, horse, bovine, dog, pangolin, elephant, hyrax, aardvark, elephant shrew, rabbit, rat, and armadillo. And each of the six data sets independently gave the same surprising answer: The elephant shrew, the elephant, and the aardvark were all closely related members of the paenungulate clade. Also joining this group was the hyrax, a small mammal with molars like those of a rhinoceros but incisors like a rodent's; its classification had long been controversial.

"Their data show a bizarre phylogenetic relationship among a bunch of mammals that theoretically shouldn't be related," says Timothy Crowe, an evolutionary biologist at the University of Cape Town in South Africa. But de Jong says that this clade "is so strongly supported that it's amazing it has never been recognized at the morphological level." He adds that "It seems molecules can really tell us something."

Indeed, most scientists at the meeting found the story of the elephant shrew and its paenungulate cousins particularly convincing, because de Jong and his team used genes and proteins with widely different structures and functions to construct their proposed phylogenies. These included a protein that aids water transport across cell membranes, a component of the lens of the eye, and a blood-clotting protein.

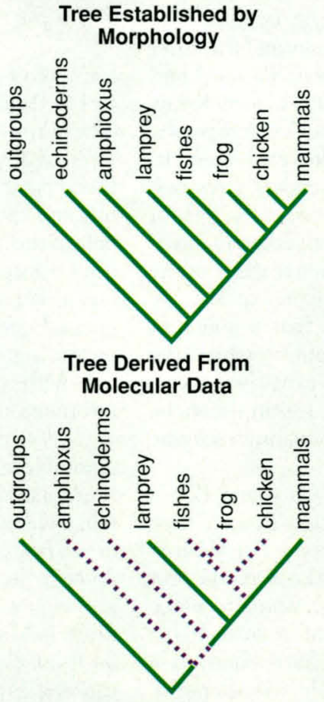
De Jong and his colleagues believe their work may ultimately help untangle other branches of the mammalian tree as well. For example, their molecular data also suggest that the ungulates and paenungulates are not closely related, as had long been assumed. Rodents and rabbits also appear to be close cousins. Says London's Patterson: "De Jong and Stanhope are chopping the phylogenetic tree to bits and reshaping it."

Misleading molecules. Although the elephant shrew and amphibian stories may turn out to be triumphs for molecular analysis, a sobering presentation by evolutionary biologist Gavin Naylor of Yale University provided a wake-up call for evolutionary biologists who might be tempted to put too much stock in the molecular approach. Naylor's talk—which Patterson says received "the closest thing to a standing ovation during the meeting"—showed that sequence data can sometimes mislead or even give an entirely wrong answer.

Naylor, together with Wesley Brown of the University of Michigan, decided to see how well molecular data would reconstruct the universally accepted phylogenetic relations among the major groups of vertebrates and their close evolutionary relatives—relations based on strong morphological and fossil evidence. The pair compared DNA nucleotide sequences from the mitochondria of 19 different taxa. Using a computer to crunch the numbers, Naylor and Brown aligned the sequences of 13 protein-coding mitochondrial genes from the 19 groups—a total of 12,234 nucleotide sites—and calculated the phylogenetic relations that best fit the data.

The result, Naylor told the meeting, gave "really quite impressive" statistical support—for what was clearly the wrong answer. For example, the molecular tree clustered frogs and chickens in a clade with fish, even though these three species do not derive from a common ancestor. To make matters worse, echinoderms (which include the sea urchin and the starfish) branched closer to the vertebrates than did amphioxus, a primitive marine chordate that is well established as the closest living relative of the vertebrates. "I think this talk was fairly distressing for many people," says de Jong. And Diethard Tautz, a developmental biologist at the University of Munich, comments, "It has become clear that the analysis of molecular data is not as straightforward as many would have wished."

To figure out what was going wrong, Naylor and Brown looked more closely at the 12,234 nu-



Wrong answer. Molecules fail to reconstruct "true" vertebrate tree.

SOURCE: GAVIN NAYLOR

cleotides, to see which ones were providing accurate information about the expected phylogenetic tree and which were causing the problems. "We wanted to see what makes a good site good and a poor site poor," Naylor says. The results were very instructive. For example, when they grouped the nucleotides into codons—nucleotide triplets that code for specific amino acids—they found that codons corresponding to the hydrophobic (water-hating) amino acids gave an "absolutely rotten" fit to the tree. On the other hand, codons for amino acids that are hydrophilic (water-loving) or carry an electric charge provided a much better fit. But the best fit of all came from amino acids that seemed to be critical for determining the proteins' three-dimensional structure.

When the analysis was rerun using only the nucleotide sites corresponding to these amino acids, the expected phylogenetic tree reemerged with considerable statistical support. Naylor concluded that rather than trying to build better trees by sequencing more and more genes—an approach common among molecular phylogeneticists—"our efforts are probably better spent investigating which kinds of sites best reflect actual historical, phylogenetic signals." Michael Nedbal, an evolutionary biologist at the Field Museum in Chicago, says Naylor's talk was "an especially important message to those in molecular phylogenetics. Just like morphologists, molecular systematists must investigate how their characters are evolving before subjecting them to phylogenetic reconstruction."

While the debate over the relative merits of molecules and morphology—and how to get the most out of each data set—is far from over, the take-home message from the Paris meeting was that each side ignores the other at its peril. Says zoologist Tim Littlewood of London's Natural History Museum: "We are all searching for a Tree of Life we can agree on."

–Michael Balter

PHYSICS

Flaw Found in a Quantum Code

With a basic principle of physics on its side, quantum cryptography seemed foolproof. Because the very act of observing a quantum system—a single photon or particle—disturbs it, any effort to crack quantum secrecy should leave a detectable trace. Or so physicists thought. In the 28 April issue of *Physical Review Letters*, researchers report with regret that another principle of quantum mechanics could undermine one quantum-cryptography scheme. The threatened scheme has never been put into practice, and the threat depends on technologies that don't exist yet outside theorists' minds. But like any blemish on something thought to be flawless, the finding has unsettled quantum cryptographers.

"I'm very disappointed with this result," says Claude Crepeau of the University of Montreal. The papers, one by Dominic Mayers of Princeton University and the other by Hoi-Kwong Lo of Hewlett-Packard and H. F. Chau of the University of Hong Kong, do not affect a basic quantum-cryptography stratagem called quantum "key exchange." In this stratagem, Alice (the sender) gives Bob (the receiver) a secret password in the form of a string of photons polarized in different directions. Any eavesdropper trying to measure the polarizations would alter them. But Mayers, Lo, and Chau have found that a quantum principle called entanglement, in which the state of one photon in a pair can reveal everything about its counterpart, can in theory be used to undermine a second quantum scheme called bit commitment.

Bit commitment gives Alice and Bob a way to exchange information even if they don't trust each other. "Suppose Alice wants to prove that she can make a prediction about the stock market, but wants to make sure that Bob can't use the information to his advantage," explains Richard Hughes, a physicist at Los Alamos National Laboratory in New Mexico. That requires a way for Alice to transmit a message to Bob while retaining control over when he can read it. "It's post–Cold War cryptography," says Charles Bennett, a cryptographer at the IBM Thomas J. Watson Research Center in Westchester County, New York. "There are no enemies anymore, but you don't trust your friends."

"[The discovery] is a big disappointment for anyone interested in cryptography."

—Dominic Mayers

In a bit-commitment scheme proposed in 1984, mistrustful Alice sends a string of photons, all of them polarized diagonally, at 45 or 135 degrees, or rectilinearly at 0° or 90°. The entire string represents either a 1 (say, a series of diagonal polarizations) or a 0 (rectilinear polarizations). Bob receives each photon and randomly chooses to determine its polarization with a rectilinear or a diagonal filter. Only the correct filter will give a real measurement, but Bob can't tell when he has guessed correctly. Using the wrong filter—measuring, say, rectilinearly polarized photons with a diagonal filter—will destroy the information in the photons and yield a string of random diagonal measurements, indistinguishable from real ones.

As a result, Bob gets no information until Alice chooses to reveal whether she sent a 1 or a 0. Bob can then verify, after the fact, that Alice really sent what she claims, by looking at the photons he measured with the correct filter. If Alice has told the truth, his readings for those photons will agree with hers. Alice can't lie, saying she sent diagonally polarized photons when they were actually rectilinear, because she has no idea what Bob saw when he used a diagonal filter. She has to guess—and because Bob randomly saw a 45° or 135° polarization, Alice will be wrong about half the time. Thus, Alice has to commit herself to a value for the bit when she sends it, but doesn't need to show her hand until later.

But there's a hole in this and all other bit-commitment schemes, the new work shows. Instead of producing each photon individually, Alice can prepare them as Einstein-Podolsky-Rosen (EPR) pairs: two photons whose polarizations are intimately linked—entangled—even as they travel in different directions. Sending a rectilinearly polarized photon to Bob, Alice stores the other without measuring it. Bob does the measurements as usual. Normally, this would mean that Alice was committed to a 0. But thanks to entanglement, she's not.

Alice can change her commitment from a 0 to a 1, or vice versa, simply by measuring each stored photon with a diagonal filter. Because her photon and Bob's make up an EPR pair, measuring one tells her all about the other; Alice thus knows what Bob's diagonal measurements were. Alice can now claim she sent a 1—a string of diagonal polarizations—and there is no way Bob can tell that she is cheating.

This scenario is still an academic exercise. For one thing, it requires the ability to store a photon without affecting its quantum state, something researchers in quantum computation are only taking the first steps toward doing. But "it's a big disappointment for anyone interested in cryptography," says Mayers, adding that it threatens a host of post–Cold War protocols designed to keep Alice, Bob, or—in some cases—both of them in the dark about parts of the information being transferred.

"It's the foundation stone which held up a useful part of quantum cryptography," agrees Bennett. "Now, it's gone, and there's no way to fix it."

–Charles Seife

Charles Seife is a writer in Riverdale, New York.