

Morphology: The Shape of Things to Come

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Centuries before Mendel played with his peas, before Watson and Crick described a double helix, and before PCR (polymerase chain reaction) machines came in desktop models, people were trying to understand how the world worked by scrutinizing the plants and animals around them. The first account of this endeavor can be found in the Book of Genesis, in which Adam's initial task is to name the animals in the Garden of Eden. In ancient Greece, Aristotle spent a great deal of time studying and classifying various plants and animals—an early systematic attempt to categorize Earth's many inhabitants. Centuries later, Linnaeus devised a formal classification system. This coincided with a collecting fury that sent Europeans all over the globe in a frenetic attempt to document the variety of living creatures. Museums filled up, and herbaria sprang to life.

As scientists forced order onto these discoveries, some relationships seemed quite apparent. An Easter lily was obviously more akin to a ficus tree than, say, to a small rodent. But with species that are more closely related, kinships became a little tricky. And then there were bizarre exceptions such as whales, marine animals that nurse their young and have skeletons resembling those of terrestrial mammals. As for fossils, well, who knew?

In the 1950s, Willi Hennig proposed grouping species by clades. This system



Barbara Thiers is director of the New York Botanical Garden's herbarium. Her research on the Lejeuneaceae family of bryophytes takes her to tropical rain forests all over the world. Photograph: Tori Butt.

is known as phylogenetic systematics, or cladistics, and is based on hypothetical shared lineages. The idea is that a trait—a certain bone or a plumage pattern—can be used to determine relatedness. For instance, mammals have a quadrate bone and so do amphibians and birds. Researchers can track how these groups have evolved by noting, for instance, that the quadrate bone in birds is in the lower jaw, while in mammals it is part of the

middle ear. However, although this provides a fascinating example of evolution, it doesn't help scientists if they want to compare distantly related organisms. At that point the morphologies are too dissimilar.

When sequencing technology arrived a few decades ago, scientists realized they had a quick and easy way to understand phylogenetics without the time-consuming need to study museum

specimens. Comparing sequences of nucleic acids—denoted as A, T, C, and G—is much simpler than scrutinizing plumage pattern, pelt color, or skeletons. Furthermore, these four letters are easily converted to binary code, squishing the whole complexity of systematics into simple 1s and 0s and opening up possibilities for powerful statistical analysis. Genomic comparisons capture the public's attention and can lead to simplistic, catchy statements like “humans are 98 percent chimpanzee.” Or, as one British scientist explained, “We are 40 percent banana.”

“I knew PCR was going to be important,” says Joel Cracraft, curator in charge of the Department of Ornithology at the American Museum of Natural History (AMNH). In fact, when he was at the University of Illinois Medical School in the early 1980s, he had a PCR machine before his colleagues in the genetics department did. “When I was learning this technique, there were 15 papers on PCR and we had every one of them. Within six months, there were hundreds. Now they're in every journal.”

Didn't your grandfather do taxonomy?

It's hard to separate morphology—the way something looks—from taxonomy. During Darwin's famed adventure, he gathered notes, drawings, and specimens of creatures he encountered during the *Beagle's* voyage. But he was just one of many scientists collecting specimens in exotic locations, which made for one problem. Where do you keep all the stuff? More important, what do you really need to keep and what can you throw away?

Given the powerful attraction of reducing life forms into sequences of four letters, it's no wonder people migrated to genetics. While taxonomists working with traditional morphology may need to refer to plant specimens collected in the 1500s by someone at the medical school in Salerno, Italy, today's researchers also have libraries of genetic information that grew up with computers. In fact, most molecular information is usually only a mouse-click away.

“I think science moves forward in two steps,” says Diana Lipscomb, director of



These mantis shrimp specimens are preserved in ethanol in bell jars and paraffin-capped sample vials in the American Museum of Natural History's invertebrate zoology collection. Mantis shrimp, or stomatopods, are crustaceans that burrow in marine sediments and breathe through gills on their abdominal appendages. Photograph: Denis Fennin.

the Tree of Life program at the National Science Foundation (NSF). “When we have a breakthrough in technology, then things move forward rapidly.” With PCR, she says, scientists suddenly had access to large amounts of easily manipulated data and began pushing the technology.

As molecules became more important, traditional taxonomy, with its reliance on large specimen collections, became an antiquated backwater. It recalled too many memories of 20th century naturalists, butterfly catchers, and John Steinbeck's “Doc”—a marine biologist who collected specimens off the rocks on Cannery Row. Many of the gene jockeys questioned whether taxonomy was ever a science at all.

As if in response to this growing consensus, financing for taxonomy took a nosedive. Traditional taxonomists, those who have full knowledge of a single taxon, are now in short supply. When NSF began funding research in 1950, fully 10 percent of its initial 97 awards granted were for systematics research. Today the number has dropped to less than 1 percent.

But molecular work can only tell you so much. Eventually you have to figure

out what all those Cs, Gs, As, and Ts really mean. “You can build a tree out of sequence, but it will tell you nothing about how an animal looks or behaves,” says Cracraft. “But morphology in the analysis puts some flesh and bones on the tree. Because if sequence tells you that flamingos and grebes are very closely related, you can look at the two and see that there have been some huge changes in evolution.”

Problems with morphology: How do you press a cactus?

There are numerous things working against morphology. First, it's slow. Instead of downloading sequences off the Web, you have to personally handle a large number of specimens. Of course, this is much easier if you have access to all the specimens in the first place, which is rarely the case. Scientists who work on morphology are serious globetrotters. Studying tyrannosaurs requires knowledge of specimens at the AMNH in New York, the Field Museum in Chicago, the British Museum of Natural History in London, and some collections in Montana and Poland. The money for these trips has to come out of grants.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25
<i>kirki</i>	2	0	1	0	0	1	0	1	1	0	1	0	0	2	?	?	0	0	0	0	1	1	3	1	0
<i>typicalis</i>	2	0	1	0	0	1	0	1	1	0	1	0	0	2	0	1	0	0	0	0	1	1	1	1	0
<i>jugalis</i>	2	0	1	1	1	1	0	1	?	0	1	0	0	2	?	?	0	1	0	0	?	?	?	?	1
<i>subula</i>	0	1	0	0	1	1	1	1	0	0	1	1	0	1	1	1	0	0	0	0	1	1	1	0	0
<i>maritima</i>	0	1	0	0	1	0	1	?	0	0	1	1	0	1	1	1	0	0	0	0	?	?	?	?	0
<i>hamula</i>	0	1	0	1	1	0	0	1	0	0	1	1	0	1	1	1	0	0	0	0	?	?	?	?	0
<i>triangulata</i>	3	1	0	1	1	0	0	1	0	0	1	1	1	1	1	1	0	0	0	0	1	0	1	2	0
<i>leonensis</i>	3	1	0	1	1	0	0	1	0	0	1	1	0	1	1	1	0	0	1	0	0	1	2	2	0
<i>carinata</i>	1	0	2	1	1	0	0	0	0	0	1	1	1	2	2	0	1	0	0	1	?	?	?	?	0
<i>bulbosa</i>	1	0	0	1	1	0	0	0	0	0	1	1	1	2	2	0	0	1	0	0	?	?	?	?	0
<i>prima</i>	1	0	2	1	1	0	0	0	0	0	2	1	0	2	?	?	0	0	0	1	2	0	4	?	1
<i>punctata</i>	1	0	0&2	1	1	0	0	0	0	0	2	1	0	2	?	?	0	0	0	1	2	0	4	1	1
<i>depressa</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Costs limit the number of photographs that can be placed in a paper, making it difficult for the reader to discern which parts of a specimen are being referenced. Clarity could be improved by publishing electronically, allowing for more images, different perspectives, and even video recordings, but Adrain says that there is some resistance to this.

“The problem is that the international code of zoological nomenclature, now in its fourth edition, is written by people of a certain age, and they are hostile to the naming of new taxa in journals that are only electronic,” he says. “So the underlying rules are still wedded to paper journals.”

Some journals have made a run around this rule by producing CD-ROMs, which are placed in libraries, but this backdoor maneuver does not address the need for a fundamental change in nomenclature rules.

“Using the old-fashioned methods of exploring, collecting, then identifying and describing—the old Linnaean classification—is very laborious and slow,” says E. O. Wilson. He argues for a fundamental change in the whole process. Speed it up by placing everything online, speeding information collection, increasing access, and dramatically lowering costs. “I just finished a detailed monograph of all the biological information we have for 625 species of ants, only 20 percent of the known species in the Western Hemisphere,” he continues. “It was a very singular effort that took, off and on, 12 years of my time.”

Virtual herbarium

Opening a cabinet door, Barbara Thiers, director of the herbarium at the New York Botanical Garden (NYBG), randomly selects a folder from a shelf and brings it over to the observation bench. We are in a climate-controlled, humidity-stabilized, low-light preservation room where NYBG keeps its valuable collection of specimens.

“From the red color of the folder, you can tell that this is a type specimen,” she explains. “For every new organism

This matrix compares different traits in extinct trilobites to determine their relationships. The left column lists a number of species in the family Ptychaspidae from the Late Cambrian period in North America. The top row indicates different morphological characters, for which each species is scored. For example, the traits for character 21 refer to the shape of the tail, or pygidium: 0, transversely semielliptical; 1, subelliptical to subtriangular; 2, elongate, subtriangular. From J. M. Adrain and S.R. Westrop, “Stratigraphy, Phylogeny, and Species Sampling in Time and Space,” pp. 291–322 in J. M. Adrain, G. D. Edgecombe, and B. S. Lieberman, eds., Fossils, Phylogeny, and Form: An Analytical Approach (New York: Kluwer Academic/Plenum Press, 2001).

Once the specimens have been analyzed, you have to give a code to different physical traits—calling a bump on the end of a bone “trait X,” for example. This throws a great deal of subjectivity into the analysis, and in a journal article it can make it tough to understand what the author finds important or even what is being discussed.

“You can sometimes tell what someone is talking about by reading the text of the paper, but eventually you need a picture,” say Christopher Brochu, assistant professor of geoscience at the University of Iowa. He adds that because papers often do not have enough visual information, morphological studies are often criticized for a lack of clarity and for the difficulty others have trying to repeat the work. This makes much of taxonomy useless, according to some researchers. “It’s not that the observations are not repeatable,” Brochu says, “but they are not described in enough detail to be repeated without consulting the original scientist.”

Analyses based on physical characteristics can have critical gaps, too, which don’t emerge until after comparisons are made between many different species. Specific characters are selected initially and placed into a matrix for comparative purposes, but if this first analysis raises further questions, as often happens, it isn’t easy to switch gears. Attempts to in-

clude a new character, perhaps another bone, may require a whole new round of trips to museums and laborious recoding of specimens.

Phylogenetic analysis based on gene sequences does not have half these problems. Sequences for known genes are readily identifiable and referred to by name, so everybody can tell which genes are being used in a matrix. Also, genetic information is stored online, and there is no need to resequence a genome to pick different genes or add more species. This removes confusion and cuts down on subjectivity.

“Even the same investigator will look at morphology differently over time,” says Cracraft. “As you learn and mature, your philosophy on how to code will change. This affects variation since even the same investigator will change how they code things over time. I know I have.”

Genetic research is also less expensive. You don’t have to travel to do genetic work, and you don’t have to keep filing cabinets of sequences. By contrast, even the publishing side of morphology is fraught with expense and lack of access. Publishing costs eat up most of a journal’s budget, which limits the number of pages, explains Jonathan Adrain, an assistant professor at the University of Iowa and current editor of the *Journal of Paleontology*.

discovered, one example has been designated the type and kept in a repository so that others can refer to it and question the author.”

Inside the folder is a pressed specimen of *Dortmannia*, which was collected by Otto Kuntze in 1892, a time that predates NYBG. The bottom right corner of the paper has the original tag (a barely legible scrawl by Kuntze, noting that the plant was collected in Chile) along with numerous other stamps, tags, and even a bar code.

On the paper’s bottom left corner, “Carnegie” has been stamped on the paper to document the specimen’s purchase by Andrew Carnegie, one of the early benefactors of NYBG. There is also a stamp by the Field Museum of Chicago.

“When [the Field Museum] borrows a specimen, they photograph it and stamp it,” says Thiers. “This stamp gives the reference number of the photograph in their collection.” The Field Museum started this practice back at the turn of the century, which means that they have the only records of many specimens from Berlin that were destroyed during World War II.

To the left of the specimen is a new label glued to the century-old paper. Dated 1997, the label disputes Kuntze’s taxonomic judgment. In the view of the expert who annotated the specimen, this plant does not represent a new species but in fact is the same as a plant originally described by Linnaeus a century earlier.

“Kuntze described a lot of species unnecessarily,” says Thiers. Even back in the 1800s, she explains, scientists were overwhelmed with the growing catalog of plant species, and some scientists chose to describe the plants they couldn’t identify as new rather than to make an exhaustive search of the literature and the world’s herbaria looking for a match with a previously described species.

Today, scientists estimate they have named a mere 10 percent of all the planet’s species. Still, the world’s more than 3000 herbaria hold, at a minimum, several thousand herbarium specimens each, resulting in a staggering storage problem. NYBG has 90,000 types and over 7 million specimens. Its new state-of-the-art herbarium contains about 2000



The New York Botanical Garden’s type specimen of Dortmannia bicarata, a tropical-looking bellflower in the Campanulaceae family, was collected in Chile in 1892. This photographic record can be found in the NYBG’s virtual herbarium (www.nybg.org/bsci/vh/) by searching the catalog of vascular plant types.

steel cabinets installed in a compact storage system so the cases can be moved apart like an accordion-style storage folder. There are five floors in the building, each with an identical warehouse.

This storage issue is the reason for the bar code stuck to the lower end of the specimen. It documents that the specimen has been archived in the garden’s online specimen warehouse. The virtual herbarium shrinks five floors of climate-controlled rooms into three small mainframe computers, lowering

the cost of international travel to the price of an Internet hookup.

Down the hall, three technicians make up a botanical garden bioinformatics group. Specimen documentation has been automated to create a self-service system complete with a light box and digital camera calibrated with two lights. The captured image is fed into a computer and placed into a customized database with over 700,000 online specimens.

The system allows a field researcher to carry all the herbarium’s specimens



Some mollusks from the American Museum of Natural History's mollusk collection, estimated to be the fifth largest in the world. The collection is worldwide in scope but most strongly represents western Atlantic and tropical Pacific marine species.
 Photograph: Denis Fennin.



*The American Museum of Natural History has a large collection of *dasylbe*, a fossil fish from the Cretaceous period, 65 million to 144 million years ago. They are often called "broken neck fish," because their heads hang down as if their necks were shattered.*
 Photograph: Denis Fennin.

on a laptop. Any discoveries in the field can be instantly referenced and documented with a digital camera. Much as gene banks operate, the herbarium's database allows a specimen to be easily annotated. "Often a researcher exploring the database will realize that something is named incorrectly," says Tony Kirchgessner, leader of the bioinformatics group. "So it allows us to correct our own information and document the history of that annotation."

Thiers adds that the information also opens up research possibilities to scientists without funds or with an unfortunate geographic location. The botanical garden has about 10,000 plant type specimens collected during expeditions to

Brazil. "You really can't do much research on Brazilian plants without consulting the New York Botanical Garden Herbarium," Thiers says.

Brazilians don't have the funds to visit New York very often, and although the garden pays to ship specimens, the Brazilians cannot always afford the two or three dollars per specimen for the return postage. Such funding paucity makes it difficult to take your research to a scholarly level.

The virtual herbarium cuts through the cost of shipping, international plane fare, and time-intensive searches across five floors of specimens. "Our colleagues working on the flora of São Paulo State tell us all the time how the virtual

herbarium has expedited their work by making the data they need so easily available," says Thiers.

Entering the matrix

The NYBG's virtual herbarium is just one of many Web-based archives designed to centralize and speed access to image data. The Fairchild Tropical Garden also has a virtual herbarium, and others are found at the University of California–Davis and the Illinois Natural History Museum. The University of Trieste in Italy even has a virtual herbarium devoted specifically to lichens. While each herbarium uses its own database software, making it difficult to integrate information, Thiers says that Web-based software is being developed to simplify searches between different sites.

Tim Rowe, a paleontologist at the University of Texas, has started DigiMorph, an online catalog of digital x-ray images and videos. Users can compare the skull of a human side by side with that of a chimpanzee, or view three-dimensional images of an extinct fossil. In Europe, a Swedish group has also started morphobank.net, a visual catalog of various wasp species.

Recently funded by NSF, a group of paleontologists, including AMNH paleontologist Mark Norell, will soon debut a Web site devoted to theropods—birds and their dinosaur predecessors. The site will use an Oracle database (the same powerful program used in financial, communications, and information sectors) and a user-friendly interface with images of various taxa. This should cut down on the confusion about the choices that have to be made when constructing a matrix of species and character traits. "We're creating the next generation of matrices where each cell has a picture from the specimen so you can evaluate the scoring," says Norell.

The idea has also been captured by the biomedical community, which has various Web sites devoted to microscopic images, videos of fluorescently tagged proteins moving in cells, and pictures of embryonic development. The European Commission has funded a project called BioImage to store pictures from the scientific literature. And with images of

knockout mice, Rockefeller University is creating an atlas of the genes that form the nervous system.

What all these systems will need is some way to integrate their software, ensuring that information does not become walled off. What scientists studying morphology need is an all-encompassing Web site where all the information comes together, speeding access and uniting images, text, and data.

In November 2001, NSF hosted a workshop at AMNH titled "MorphoBank." Scientists from across the United States attended, and all were interested in creating a new Web-based portal to comparative anatomy. MorphoBank is the most ambitious project yet conceived and would involve linking a single species to all the data that have been collected on it. Such a project would help not only in functional morphology but also in conservation biology, ecology, and even education. NSF declined to fund Morpho-

Bank, but many scientists feel it will inevitably become reality and receive financing when the idea matures.

"MorphoBank equals GenBank," says Maureen O'Leary, assistant professor in the Department of Anatomical Sciences at Stony Brook University in New York. What researchers want is for technology to do for morphology what it did for genetics. In many ways, the PCR machine has created a false dichotomy, much like the "nature versus nurture" debate, in which one side must win at the expense of the other. "People want morphology to integrate with the molecular, so that you can better interpret the information," says O'Leary.

This line of thought leads back to a paper that appeared 50 years ago in *Nature*. Announcing what is now celebrated as the breakthrough of the century, James Watson and Francis Crick told the world that they had solved science's most important genetic problem. What they

had found, however, was not a string of Cs, Gs, As, and Ts. Nor was it the genetic sequence of mouse or man. What they announced in the paper was the structure of the molecule that encodes the genetic information of every living cell. And the shape of this molecule, which could not be made clear in text with fewer than a thousand words, was elegantly revealed in a drawing by Odile Crick, artist and wife of Francis Crick. "The gene is the most important molecule in the cell," said Watson in a BBC interview this past February. "And finally we saw the gene." In years to come, powerful programs such as MorphoBank may reopen scientists' eyes to the importance of visual imagery.

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