

Evolving Similarities—Between Disciplines

A remarkable recent meeting at Cold Spring Harbor brought biologists and social scientists together to see how well the principles of evolution fit disparate areas of research

NIGHT IS FALLING IN GABON, AND YOU'RE A male hammerheaded bat looking for a mate. But females are hard to find, because they're flying far and wide in the jungle, in search of figs to eat. So what's a lonely boy bat to do? One answer: Join the guys and hang out in a lek—a breeding ground that's a sort of bat "disco" where females fly in, select a mate, and then depart when the night's mating dance is over.

Bats are not the only species who engage in this bizarre behavior: Sage grouse in the Great Basin of Nevada, Jackson widow birds in Kenya, and Uganda kob antelopes are among the diverse species who like to lek. "It's a bizarre system that's rare overall," says Jack Bradbury, a behavioral ecologist at the University of California at San Diego. "So my question is how do you get identical behavior in such different species—how do you get leks in a nocturnal frugivore, a diurnal herbivore, and a savanna-living granivore?"

On a more general level, that question—how similarities evolve in separate entities (be they genes, species, or cultures)—was a central theme at an unusual symposium on "Evolution: Molecules to Culture" held at Cold Spring Harbor Laboratory on 24 to 27 September. The idea for the meeting came

from lab director James Watson, who's been giving a lot of thought to the evolution of his own institution as part of its centennial celebrations (see story by Leslie Roberts on page 496).

Watson called on Jared Diamond, a physiologist at the UCLA School of Medicine, and Oxford University zoologist Richard Dawkins to pull off an ambitious feat: bring together 40 scientists from a wide array of disciplines, from molecular genetics to cultural anthropology, to see how the principles of evolution are being applied in their fields. "The reason for bringing together all these different approaches and disciplines," explained Diamond, "is that all these fields are concerned with the evolution of similarity, but the people in these fields usually don't think of each other as sharing related problems."

Diamond thinks that by the end of his and Dawkins' whirlwind tour through a half dozen discrete disciplines, most attendees concluded that there is a "general science of evolution." The meeting also seemed to prove that Darwinian evolution, now more than 100 years old—and its more contemporary modifying principles—have infiltrated every discipline that deals with living beings, their behavior, and their artifacts.

But it also was clear that this general science has made more progress in the areas where it originated—the development of species—than it has in such farflung areas as the analysis of cultural artifacts. And as a result, the meeting organizers found themselves surrounded by scientists as different from one another as, say, long separated subspecies of songbirds.

To make sure the participants were at least attempting to speak the same language, Diamond suggested a general approach, which he encouraged the speakers to follow: Try to identify which of three mechanisms is responsible for the similarities observed in the researcher's area of work. The first is the most familiar feature of Darwinian evolution: descent from a common ancestor, with both entities retaining and modifying the inherited trait or structure—such as two proteins that have descended from a master molecule.

The second mechanism, also well established, is convergence—in which separate organisms, such as birds and bats, independently develop a similar trait or behavior (wings, say) even though they did not inherit that structure from a common ancestor. The third mechanism is borrowing, and it involves the direct transfer of structures or information from one entity to another (apart from inheritance)—such as one person learning a language from another.

The symposium opened with the molecular biologists, who took a crack at the problem of similarity at the molecular level. Once they set the stage at this basic level, other scientists analyzed similarities in increasingly complicated systems, moving from animal behavior and functional morphology to ethnology, archeology, and linguistics.

Right from the start, the similarities between proteins were startling. When protein chemists compare the sequential arrangements of the 20 amino acids that are the building blocks of protein chains, they find that the odds are 50-50 that a newly sequenced protein will be similar to a previously sequenced protein. Why?

In many cases, the reason is that similar proteins are descended from a common ancestor, a master molecule whose key parts

HOT SESSIONS AT COLD SPRING HARBOR

Primate Evolution—in Slow Motion

In a session entitled "Molecular Evolution," Morris Goodman of Wayne State University noted that molecular evolution has slowed over time, in primate history. One possible reason: better DNA repair mechanisms in the long-lived higher primates, which lower the number of mutations passed to progeny.

The Big Boom in the Cambrian

In a session on "Functional Morphology," Simon Conway Morris of the University of Cambridge asked what triggered the Cambrian explosion in species—550 million years ago—that led to the rise of all major animal body plans now in existence. He thinks Cambrian creatures inherited a few good designs from their ancestors, those designs, some workers say, may have been elaborated through large-scale gene transfer.

A Better Yardstick—for Fossils

At the session on functional morphology, Carole S. Hickman of the University of California at Berkeley said more precise, standardized ways of analyzing fossil forms are now emerging. That will answer a basic requirement: "We need to introduce more rigor into how we measure similarity in form and function."

Social Register

At a session on "Human Society," the anthropologists

worked to fit their ideas into an evolutionary framework. Henry Wright considered emergence of centralized states in Madagascar as an example of a process that has happened independently and convergently a dozen or more times in human history since the Neolithic. Patrick Kirch discussed the radiation of Polynesian societies founded on different islands, followed by independent convergence toward population control and intensified food production.

Creatures Great and Small

At a session on "Animal Behavior," Timothy Clutton-Brock of the University of Cambridge noted that large males in polygamous species get more females, but pay a price for their success (and size): they die sooner and they do in their mothers faster than female offspring. His examples were drawn from red deer and birds.

Apples and Oranges?

At a session entitled "The Comparative Method," Oxford University zoologist Paul Harvey described recent improvements in the methods biologists use for deducing family trees and reconstructing ancestral states, even when surviving branches are represented by very different numbers of species. One example: a computer program called MacClade, which was described at the session by Wayne Maddison of the University of Arizona.

were used as the template for new proteins—such as one of the functional domains of epidermal growth factor. “The EGF domain is found in all animals and plants,” says Russell Doolittle, of the University of California at San Diego. “It evidently has very good binding or recognition qualities,” making it what Doolittle calls a “Chevrolet-type” protein that is so durable that it has survived eons of natural selection. “The number of fundamental master proteins from which others are derived is 1000 to 2000,” according to Cyrus Chothia, of the MRC Laboratory of Molecular Biology in Cambridge, England.

While molecular biologists can trace the ancestry of similar sequences of proteins in a fairly straightforward way, it’s often trickier to deduce the cause of similarities in the physical attributes or the behavior of animals. In the case of leks, it was clear to Bradbury from the beginning that the diverse species he saw lekking must have evolved the same strange mating habits through convergence: A sage grouse and a hammerheaded bat living on opposite sides of globe last shared a common ancestor so long ago that it is unlikely they inherited the trait from it, and they certainly didn’t learn the behavior from each other.

But why would such different creatures adopt the same unusual mating ritual? Bradbury thinks leks are due, in part, to the females’ independent behavior. In all the lekking species he’s observed, females roam over large, overlapping home ranges—usually in search of food. As a result, they are dispersed over a wide territory, which may make it difficult for males to find them. A second common factor is that the males do not participate in raising the young, so it’s all right for the females to love ’em and leave ’em—unlike monogamous females who are dependent on the males’ aid and protection. Add the two features together, and it may be more efficient for these species to lek.

Once the biologists had looked at similarities in proteins, genes, and species, the social scientists took over: they tried applying the same evolutionary framework to their fields—with varying results. One of the

most heated sessions at the symposium was one where linguists claimed that just as gene and protein sequences are alike in separate species, so too are many words in languages that have gone their separate ways for many thousands of years.

The linguists are intent on trying to figure out which words are inherited from a common ancestral language—a proto-language that was a sort of Eve of tongues. They also see signs of convergence where two languages will come up with a similar sounding word with a similar meaning by accident. But unlike the situation in the biological sciences, the linguists also find that many words are similar because one culture has “borrowed” them from another. The challenge for linguists is to sort out the newer borrowed words from the core language that has been passed down through generations.

As appealing as the analogies between linguistics and genetics are, the session left many symposium participants skeptical, including co-organizer Dawkins who declared, “What we’ve had here is an orgy of borrowing.” He warned

that borrowing concepts from evolutionary biology could sometimes be misleading.

If the conference had been like most others, the linguists would have been left to debate within their own world and indeed, a major battle might have been waged had traditional linguists who have rejected such notions as an ancestral “mother tongue” for all languages been present. But this meeting was exceptional, because biologists had been inveigled to stay through the talks of this particular group of linguists with two goals in mind: to see if they could draw something from the kinds of problems and solutions the linguists spoke of for their own work—and to determine if geneticists might have something to offer the linguists.

In this particular case, the answer is yes in one respect: the influence of the “harder” sciences has stimulated a small group of linguists to study the evolution of language with statistical methods normally used to trace the inheritance of similar genes or traits among different species. The area where these methods are applied is known as glottochronology. “We can pull almost

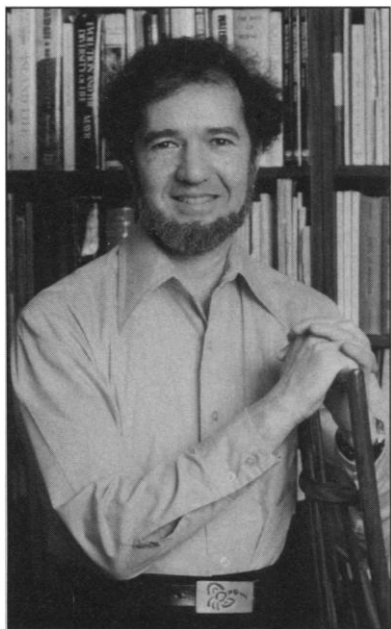
without change these models from biology and apply them to linguistics,” says Mark Pagel, an Oxford University evolutionary biologist who recently has applied statistical and mathematical methods used for reconstructing phylogenies of species to do the same in linguistics. “I think the potential is there for an explosive change in linguistics.”

S. A. Starostin of the Institute of Oriental Studies in Moscow has been a pioneer in the use of such statistical methods to build what he calls “linguistic genealogical trees.” Those methods essentially try to trace phonetic similarities in modern languages to a common ancestor. Starostin, for example, takes the phonetic similarities between Nostratic languages (including Indo-European, Kartvelian, Uralic, and Altaic languages) and traces their origins to one language spoken about 10,000 years ago—what he calls proto-Nostratic. And that language, in turn, was derived from an earlier one—Pre-Nostratic which was spoken around 12,000 B.C. and was also the parent of the Dravidian languages, according to Starostin.

Another linguist at the meeting, Merritt Ruhlen, an independent scholar in Palo Alto, was intrigued by a software program used by University of Arizona evolutionary biologist Wayne Maddison to build phylogenetic trees. Maddison uses MacClade to build trees that reconstruct how genes and traits are passed from a common ancestor to different species, Ruhlen thinks the same method will be useful for tracing the lineage of languages. “I’m in favor of this,” says Ruhlen. “I think linguistics has been under statistified.”

But the importation of these statistical methods into linguistics is still highly controversial. Even John Maynard Smith, a University of Sussex biologist who has written on the application of evolutionary theory to many fields, has his doubts: “I don’t think you can take the whole of linguistics and genetics and say the algorithms are the same.” And Diamond noted that the linguists at the symposium were by no means statistically representative of their field; they were selected for their receptiveness to applying evolutionary theory to their work. “They’re definitely a nonrandom sample. They’re interested in evolution and pushing the field to the limits,” he said.

Another group who are pushing their field to its limits consists of the anthropologists who are struggling to apply evolutionary principles to the development of cultural artifacts in different societies. This attempt is by no means entirely novel. A familiar debate has been whether similar structures, such as the pyramids in the Old World and New World or megalithic monuments such as Stonehenge in England



Highly evolved. Jared Diamond was an organizer of the interdisciplinary Cold Spring Harbor meeting.

and other parts of Europe, were invented independently or were the result of cultural diffusion—borrowing, in short.

During the discussions, however, it became clear that the evolution of cultural traits is too complex to be explained by the simple framework of Neo-Darwinian theory. “Darwinian evolution, with its emphasis upon common ancestry, offers an ineffective framework for the analysis of cultural diversity,” says Colin Renfrew, a professor of archeology at the University of Cambridge. Renfrew argued that so far it has been too difficult to measure cultural similarities precisely and objectively enough to know the value of the comparison. Just because two structures happen to look alike, for example, it doesn’t mean that they were built according to similar principles of construction learned from a common ancestor.

What anthropologists need, says Renfrew, is greater intellectual sophistication. Instead of merely borrowing Darwinian mechanisms, they need to elaborate their own theory of how changes arise in different societies. That theoretical backbone would then serve as a reference point for analyzing complicating effects such as population migration and diffusion, ethnicity, the development of production, wealth and technology, and the emergence of power hierarchies. “I’m sure we do have a lot to learn from the analogies between different fields, but I believe we’re straining when we try to explain culture in Neo-Darwinian terms.”

Others agreed. “There really is no need for some of us to be here: I know all of the archeology and linguistics I need to know,” remarked Maynard Smith, after listening to the sessions on the social sciences. He warned that drawing analogies between such disparate fields can be misleading, if not dangerous—particularly when the conclusions from one field don’t apply to another. “The question of the conference is whether any of the similarities between the human sciences and the biological sciences are sufficiently close to be useful in a formal way,” he said.

But the answer for some was clearly yes. Indeed, the evolutionary biologists and linguists found parallels between their disciplines so compelling that they are planning a follow-up meeting in a year or so. Other participants said the hallway talk suggested new ideas or provided new tools. And a few biologists were pleased to see social scientists be so open-minded about applying evolutionary theory to their work—after years of skepticism. For most, however, the symposium’s ambitions remain plausible, but not yet realized. “One can now say there is a general science of evolution,” concluded Diamond. “Is it going to be useful? That remains to be seen.” ■ ANN GIBBONS

Playing Tetherball in the Nervous System

A simple “ball and chain” model turns out to explain a key feature of how some ion channels work in nerve cells

IMAGINE A PROTEIN TETHERBALL, DANGLING by a protein cord on the inside of a nerve cell’s outer membrane: while the tetherball floats free, ions pass into or out of the cell; but when the ball pops into the mouth of a pore, the ion flow stops. Sound too cartoon-like to be taken seriously as a scientific model? Two articles in this issue of *Science* provide evidence that this “ball and chain” model of channel inactivation—a notion first proposed 13 years ago but for which there was little hard data—does in fact explain how some of the ion channels that control electrical excitability in nerve cells work (see papers on pages 533 and 568).

Not only is this work—by Stanford neurophysiologist Richard Aldrich, with postdocs Toshinori Hoshi and William Zagotta—generating great excitement on its own, it is also being heralded as the most elegant application to date of a molecular genetic technique that may be the realization of a 40-year-old dream in neuroscience. In that technique, called site-specific mutagenesis, researchers make specific mutations in an ion channel and then observe the effects of those mutations. The technique has already begun to make it possible to understand, for the first time, the precise relations between structure and function in these essential nerve-cell proteins.

“These are really a beautiful set of very trenchant experiments,” says Chris Miller, a physiologist at Brandeis University who studies ion channels, of Aldrich’s work. “They make the case that there is actually a ball and there is a chain; and the ball actually flops in and [blocks] the channel.”

The application of site-specific mutagenesis to ion channels has been made possible largely by the cloning in the last few years of the genes for the ion channels. The channels are membrane-spanning proteins that contain pores through which specific ions can pass. But the pores are not open all the time. Instead, they are “gated”—primed to open and close under certain conditions. Some channels respond to changes in voltage across the membrane, others to the binding of neurotransmitters.

The opening and closing of these channels have potent consequences. For example, the action potential—the electrical



Molecular confirmation. Rick Aldrich applied molecular genetic methods to confirm a 13-year-old model for how some ion channels are inactivated.

impulse that travels the length of neurons—depends on the precisely timed opening and closing of voltage-sensitive channels for sodium and potassium ions. Other voltage-dependent ion channels, including calcium and chloride channels and a variety of more specialized potassium channels, play modifying roles in nerve cell function, altering the nature of a nerve cell’s action potentials or the timing of their firing.

But how does the molecular structure of a channel enable it to carry out these functions? It is assumed that the proteins making up the channel snake back and forth many times across the cell membrane to form the channel’s functional parts. The sequence of amino acids in the channel proteins supports that notion: stretches of amino acids that would be at home in membranes alternate with stretches of residues that would be more stable surrounded by water.

Beyond these vague assumptions, however, no one knows what precise shape the channel proteins take in the membrane, how they form pores that select one type of ion over another, how voltage changes cause the pores to open and close, or how inactivation—which seems independent of voltage—occurs. One problem is that no one