

Evolution's New Look

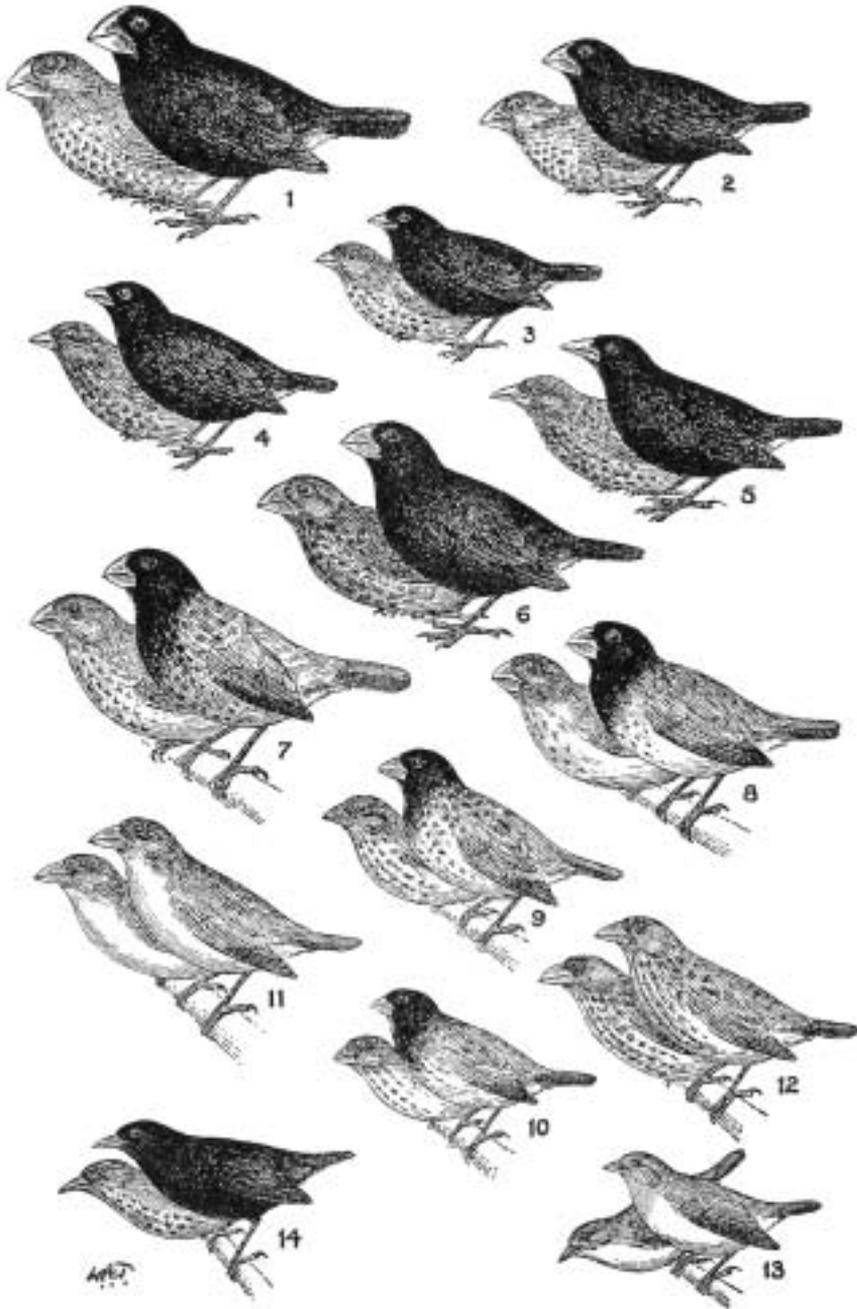
From the sudden spread of West Nile virus in the United States to the discovery that Galápagos Island finches are evolving by unexpected means, there are signs that the natural world does not function quite as we thought. A variety of scientific findings now point to the need for a radically revised understanding of the way evolution itself works.

by *Michael L. Arnold and Edward J. Larson*

Ever since Darwin's day, most evolutionists have envisioned the evolutionary process as a tree of life with radiating branches that never cross. The pattern appears in the only illustration Charles Darwin included in the original 1859 edition of *Origin of Species*—a rough sketch of species branching over time from a few thin lines at the bottom into many more as they move upward. Some lines terminate in extinction, but none of them ever reconnect. Darwin's most influential 19th-century disciple, German morphologist Ernst Haeckel, captured the concept in his drawing of a towering tree with many twigs emerging from broad branches and a sturdy trunk. Each twig is distinct and bears the name of a separate species, with “man” at the tree's apex.

This tree-of-life notion of evolution attained near-iconic status in the mid-20th century with the modern neo-Darwinian synthesis in biology. But over the past 15 years, new discoveries have led many evolutionary biologists to conclude that the concept is seriously misleading and, in the case of some evolutionary developments, just plain wrong. Evolution, they say, is better seen as a tangled web of long-term and extensive breeding across species lines.

What's crucial about this new model of evolution is that it incorporates an increased recognition by biologists that new species can arise through hybridization—crossbreeding between purebred individuals of two distinct kinds that results in an individual, a hybrid, that is more fit (at least in some cases) than the original, nonhybrid parents. Darwin knew that some species could interbreed, of course, but he thought that the offspring would be either sterile (like mules) or less fit than purebreds; in either case, the hybrids would die out, unless artificially propagated by humans. Darwin did not know about genes or DNA. Now that we do, biologists find examples (often involving microorganisms) of gene exchanges across species lines without the intermediate step of sexual reproduction. Viral infec-



The finches Charles Darwin observed on the Galápagos Islands were later grouped into neatly defined species, shown here in male-female pairs. But research reveals that the birds are still evolving rapidly, and doing so by the un-Darwinian means of hybridization.

tion or even close contact between microorganisms will do the trick in some cases. The process can resemble the laboratory techniques of genetic engineers.

The emerging new look of evolution is not merely a matter of having a better image or metaphor to explain the origin of species. It has profound consequences for our understanding of what happened in the distant past, what's happening around us today, and what's happening *to* us in the era of West Nile virus and HIV/AIDS.

The tree-of-life metaphor sometimes blinded us to important realities. It told us that lineages should diverge and keep diverging from one another, and that

genetic interactions, if they occur, should have only transient and trivial consequences. The evolutionary web metaphor points to a very different understanding. We are beginning to see that gene exchange is so rampant that every aspect of nature is affected by the shuffling and reshuffling of genomes.

Earlier this year, for example, a team of Smithsonian Institution biologists, led by Dina Fonseca, reported in *Science* that the recent outbreaks of sometimes deadly West Nile virus in parts of the United States might have result-

THE TRADITIONAL
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ed from the rise of a new species of hybrid mosquitoes. West Nile virus incubates mainly in birds and is carried to other hosts by mosquitoes. In the Mediterranean regions of Europe and North Africa, where the virus is endemic, one type of mosquito feeds mostly on birds, while another favors mammals such as us. That interruption in the channel of transmission ensures that the virus rarely

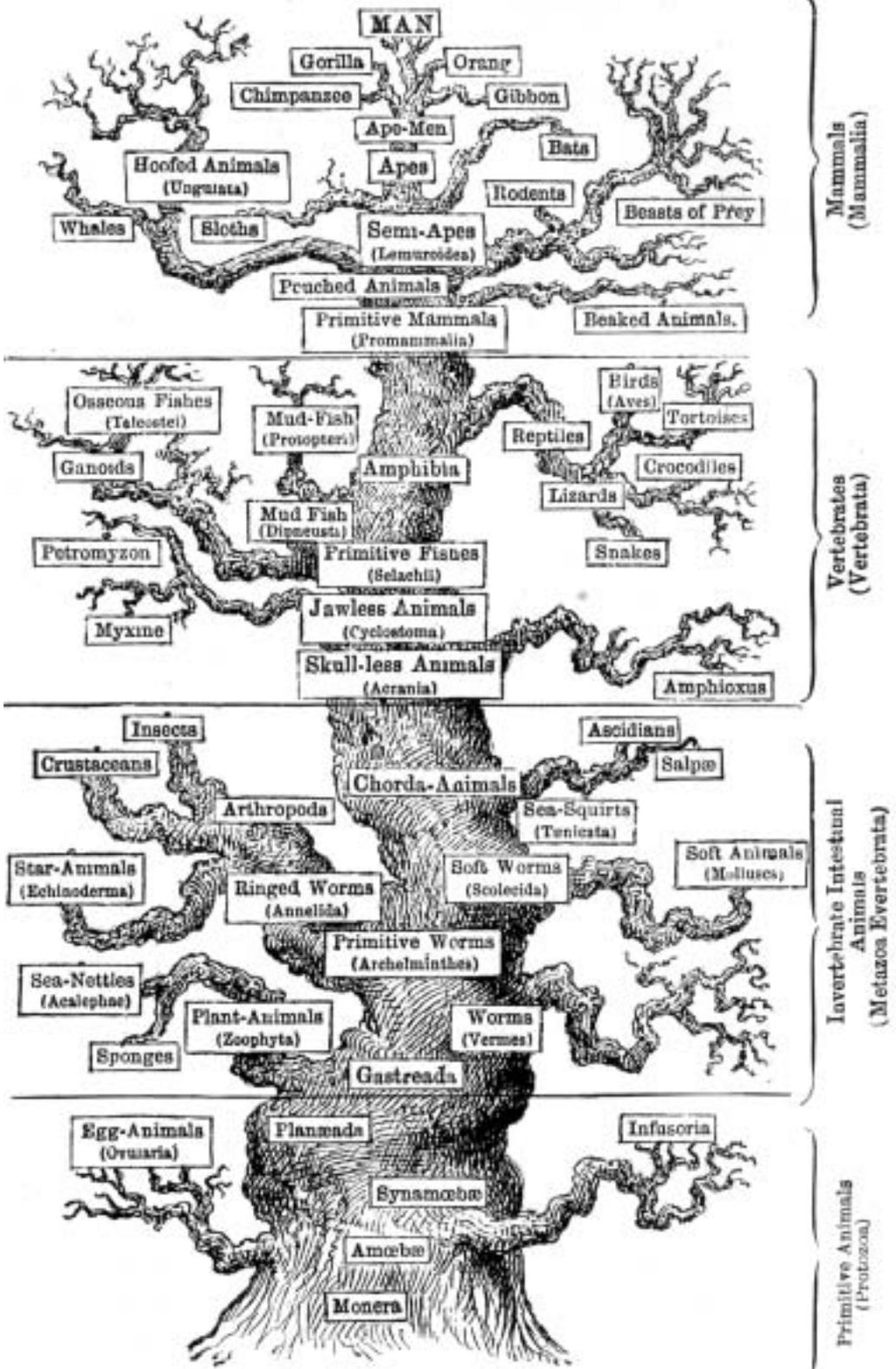
finds its way from birds to humans. In the United States, however, the two types of mosquitoes have crossed to create a hybrid that appears to bite both birds and humans. The consequence? From the first cases reported in New York City during 1999, when seven people died, the disease has spread steadily across the continent; nearly 10,000 cases in 46 states were reported last year, and more than 250 deaths.

A branching evolutionary tree could not have produced this outbreak of disease, even if we assume that the two types of mosquitoes had a common evolutionary ancestor. The bird-biting mosquitoes should have kept diverging from the human-biting mosquitoes (like two twigs growing from a common branch) and not shared their genetic traits through crossbreeding.

Fonseca and her collaborators stumbled on the hybrid explanation for West Nile transmission only after working initially with the assumptions of the traditional model of evolution. They weren't looking for the new explanation. Indeed, when Fonseca began researching the outbreak of West Nile virus in America, she thought she was dealing with a single type of Old World mosquito long resident in the United States—the human biters. She analyzed the DNA of U.S. mosquitoes and compared it with that of both Old World types and other mosquitoes from around the world. That gave her an extensive database of mosquito DNA. Then, University of London biologist Colin Malcolm proposed that this database be used to investigate the evolutionary origin of a distinct type of pesky,

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PEDIGREE OF MAN.



Ernst Haeckel's "Pedigree of Man" (1866) captures the classic Darwinian vision of evolution, with species following separate lines of development that never cross.

human-biting mosquito that had taken up residence in sewers, subway tunnels, and other warm underground spaces of northern European cities during the past century.

Though the two traditional Old World types of mosquitoes act differently and tend to live apart, they look alike to us. The bird biter, *Culex pipiens*, inhabits an extensive portion of Europe (as far south as the Mediterranean coast) and is dormant in winter; the people biter, *C. molestus*, dominates in the Mediterranean regions of North Africa and remains active year-round. During the 1700s, scientists gave these mosquitoes different names based on their biting preferences, but their physical similarities led many later researchers to view them as two varieties of a single species and to call them both by the older name, *C. pipiens*.

Malcolm and Fonseca wanted to find out whether the human-biting underground dweller that had appeared in northern European cities in the 20th century had evolved independently out of the local *pipiens* population or represented a colonial extension of the North African *molestus*. Evolutionary biologists maintain that genetic differences increase along with the amount of time that has elapsed since divergence, so that the greater the similarity between the DNA of two types, the closer the two types' kinship will be. In the case of *pipiens* and *molestus*, Fonseca found that, though the two species look alike on the outside, each has its own distinctive DNA signature or fingerprint. The DNA of the underground mosquitoes turned out to be so similar to that of the North African type that the under-



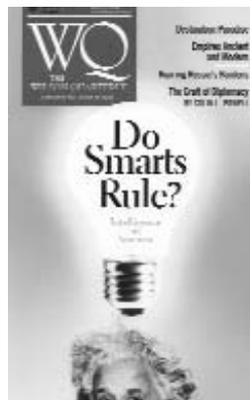
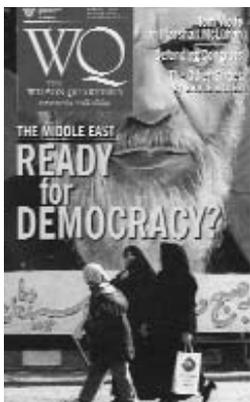
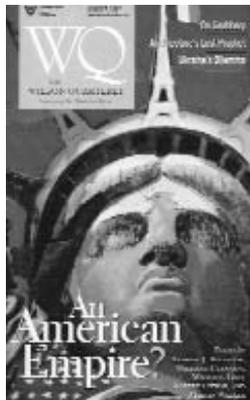
A new species of mosquito with a taste for both birds and humans may be responsible for the recent outbreaks of West Nile virus. Not yet named, the mosquito is a hybrid of Culex pipiens (shown) and Culex molestus.

ground mosquitoes must have come from *molestus* stock.

That finding had important implications for Fonseca's work on the outbreak of West Nile virus in America. Mosquitoes tend to spread. Transported in cargo or by other accidental means, *pipiens* and *molestus* mosquitoes now live in many places, including the United States. By studying their DNA, Fonseca discovered that, except for those living in America, the two types typically segregate in breeding. In the United States, however, she found many hybrids with a mix of DNA markers characteristic of both types of mosquitoes. Fonseca proposed that these opportunistic American mosquitoes, combining the preferences of their hybrid ancestry, bite both birds and humans, and thereby serve as a bridge carrying the virus from birds to humans, whom it can infect and kill. A disease that existed for years in Mediterranean regions, typically without any significant threat to the human population, became a dreaded killer once introduced into America. An evolutionary web of life explains this development in a way that a branching evolutionary tree could not: If the mos-



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quitoes did not crossbreed and produce viable hybrids, they would not pose any greater threat of spreading the West Nile virus in the United States than they do in Europe.

Mating is not the only means by which the evolutionary web is woven. Genes, and even entire genomes, can be captured by one organism as it feeds upon, infects, or otherwise associates intimately with another organism. The process, known as horizontal gene transfer or lateral gene transfer, can link species from different branches of the evolutionary tree. To the organisms involved in the transfer, the process is beneficial; to other species with which they come into contact—us, for example—the results can be innocuous, beneficial, or disastrous. As Darwin taught us nearly 150 years ago, that is how the struggle for existence operates—and nothing in the new view of evolution repeals the “law” of natural selection.

A dramatic example of horizontal gene transfer was reported this year in the *Proceedings of the National Academy of Sciences*. The case involved an unnamed patient infected with *Bacillus cereus*, a bacterium that normally causes little more than a bad case of food poisoning. But the patient became deathly ill with a form of pneumonia associated with anthrax. No one knows how the patient was infected, but he sought medical care two days after exhibiting symptoms (chills, fever, nausea, and vomiting) resembling those suffered by victims of the 2001 bioterrorist anthrax attacks. He fought for his life during 44 days of

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mechanical ventilation, treatment with five separate antimicrobials, and the partial removal of a lung. When researchers performed an after-the-fact analysis of a *Bacillus cereus* strain isolated from the patient, they discovered that it had acquired toxin-producing genes from *Bacillus anthracis*. The acquired genes made the strain as deadly to humans as anthrax—a chance natural occurrence, apparently,

that may not pose any continuing threat. The researchers found only four suspiciously similar, but perhaps unrelated, cases in the medical literature.

There are still other ways for organisms to exchange portions of their genomes. The virus that causes influenza, one of the most devastating of all pandemic diseases to humans, exists in various forms and uses many avenues to assimilate and reassemble its genome. Pigs, chickens, ducks, and geese are among the living reservoirs within which different influenza strains are collected, and exchanges and rearrangements occur. Certain genetic combinations allow the virus to attack our species. Sometimes, as in 1918, 1957, and 1968, millions of us die, but in any severe flu season, thousands perish. The DNA fingerprints tell a tale of reas-

sortments between many players in many hosts. From ducks to chickens to geese to pigs to humans, and back again, the virus migrates and reassorts, then migrates and reassorts once more.

In 1997 and 2002, for example, deadly outbreaks of bird flu among humans in Hong Kong and southern China occurred when a previously harmless strain of the virus, long endemic in ducks, acquired gene segments from viruses in quail and geese, then jumped to chickens and, ultimately, humans. This new strain was not the product of mutations at individual DNA bases, as the classical Darwinian model would suggest, but a result instead of genetic recombinations across species lines, such as scientists perform in biotechnology labs. The sojourning and changing take place because the virus is part of the web of evolutionary interactions. In this example, the web acts somewhat like a terrorist sleeper cell: Hidden units immigrate and reassort but are destined ultimately to destroy their hosts.

Disease-causing insects and microorganisms are not the only species invested in—and vested by—this web of genetic interactions. For many people, British ornithologist David Lack's studies of finches on the Galápagos Islands, culminating in his landmark 1947 book, *Darwin's Finches*, captured the essence of neo-Darwinism's metaphor of a tree with never-crossing, ever-diverging branches. Lack concluded that, despite their obvious similarities, the finches fell into 13 distinct species, which would not hybridize. Distinguished mainly by their beaks, these species had evolved to eat different plant foods in the isolated, arid archipelago. A diagram in George Gaylord Simpson's influential 1957 college text *Life: An Introduction to Biology* shows these finch species diverging ever outward from a common ancestor in a classic neo-Darwinian process known as adaptive radiation, with no imaginable end to the divergence as each became ever more finely tuned to exploit its feeding niche. Similarly, a model high school biology text published in 1963 by the federally funded Biological Sciences Curriculum Study pictures Darwin's finches perched neatly on separate branches of the metaphorical tree of life. Even today's most widely used college text on the topic, Douglas Futuyma's *Evolutionary Biology*, first published in 1979 and periodically revised thereafter, depicts the evolution of these birds as an ever-branching, never-crossing tree of diversity.

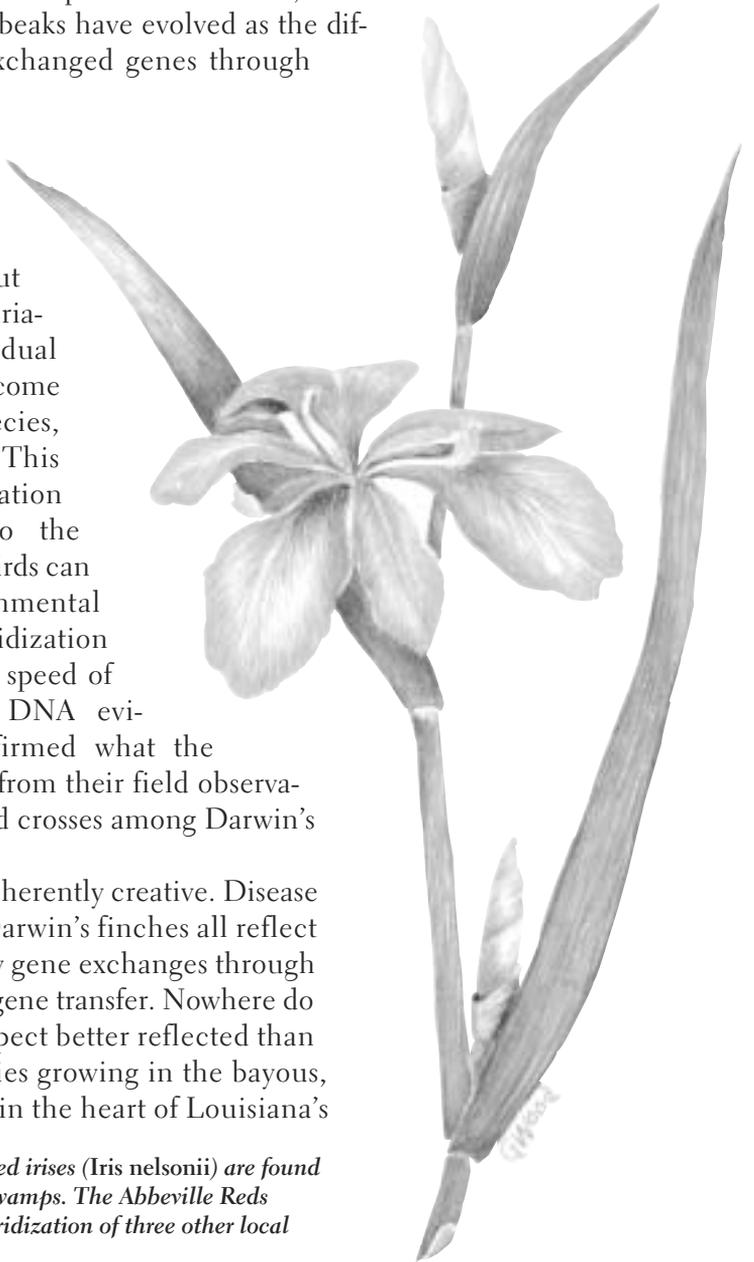
The ongoing field study of Galápagos finches by Princeton University ornithologists Peter and Rosemary Grant, made famous by the 1993 best-seller *Beak of the Finch*, paints a different picture: a tangled web of long-term and extensive breeding across species lines, with some hybrids more fit than their original, nonhybrid parents. At the best of times, the environment is harsh for the finches that inhabit the few acres of arid, cone-shaped oceanic protuberance known as Daphne Major, where the Grants have carried out the bulk of their fieldwork since 1976. In the course of the three decades the Grants have been keeping watch, marked annual fluctuations in rainfall have periodically altered the type and amount

of seeds available for the finches to eat. The evolutionary response to these severe pressures has not been the total extinction of the unsuited species. Rather, the finch species' beaks have alternately become more similar to or different from one another as the birds adapt to their available food.

The shifts are stunning in their speed—no gradual changes over millions of years here. Under the classic neo-Darwinian view of evolution, this appears to be a simple and elegant example of the effects of natural selection at work on distinct species. But according to the Grants, such a conclusion, based as it is on the tree-of-life metaphor, is simply wrong. The different finch species have not changed solely as a result of selective breeding within their own kind, with only the fittest of each species surviving, as Darwin postulated. Instead, at least in some cases, the birds' beaks have evolved as the different species have exchanged genes through hybridization. Beneficial changes have been preserved through natural selection, just as Darwin proposed, but some of the genetic variation feeding individual species' evolution has come from other finch species, not from their own. This source of added variation surely contributes to the speed at which these birds can adapt to environmental changes, just as hybridization may contribute to the speed of evolution generally. DNA evidence has now confirmed what the Grants first suspected from their field observations: successful hybrid crosses among Darwin's finches.

The web of life is inherently creative. Disease vectors, viruses, and Darwin's finches all reflect the novelty afforded by gene exchanges through matings or horizontal gene transfer. Nowhere do we see this creative aspect better reflected than in a group of iris species growing in the bayous, swamps, and marshes in the heart of Louisiana's

Louisiana's rare Abbeville Red irises (Iris nelsonii) are found in only a few of the state's swamps. The Abbeville Reds arose out of the natural hybridization of three other local iris species.



Cajun country. The various species, known colloquially as Louisiana Irises, cross to produce floral colorations and body forms that span the range of the parents' floral hues (lavender, blue, and red) and sizes (from flower stalks that barely rise above the forest floor to stalks that tower seven feet high). Though the creative processes at work among Louisiana Irises are not limited to gene exchanges, such exchanges had a central role in generating this wonderful plant.

The region's human inhabitants long knew about one particular, though rarely seen, type of Louisiana Iris so distinctive that they called it "Abbeville Red," after its brilliant color and only known habitat. During the 1960s and 1970s, a series of studies by botanist L. F. Randolph confirmed what local residents had tacitly recognized all along: The Abbeville Reds represented a distinct species. Yet to proclaim the Abbeville Reds a separate species, *Iris nelsonii* (named to honor Ira Nelson, a professor of horticulture who taught at what is now the University of Southwestern Louisiana), posed a problem for tradition-minded taxonomists, because the evolutionary origin of the Reds clearly involved hybrid matings. The species was declared a hybrid at a time when Darwinian doctrine still maintained that species arise from diverging branches, not from the crossing of diverging branches.

To make matters worse, Randolph concluded that his proposed species derived from hybridization between not two but three different species of Louisiana Irises, *I. fulva*, *I. brevicaulis*, and *I. hexagona*. And just to make the conclusion harder to swallow, these were not some lowly microorganisms that might be expected to interchange their genomes more easily than complex organisms such as the "higher" plants. There the story paused for a quarter-century, awaiting the merger of technological advances that would allow the fine-scale genetic dissection of the Louisiana Iris genome by a group of evolutionary biologists interested in reexamining even the most basic Darwinian doctrines. Fieldwork done by one of us, Mike Arnold, in the late 1980s, here becomes part of our larger account.

HYBRIDIZATION HAS HELPED
GALÁPAGOS FINCHES EVOLVE
WITH STUNNING SPEED.

Mike arrived in the Louisiana town of St. Martinville to meet his soon-to-be-guide to the *I. nelsonii* populations, Tim Hebert, in the Café Thibodaux. Tim quickly spotted Mike, the lone tourist, and the two headed off in Tim's pickup truck to a point some 10 miles or so from the marshes that hedge the bottom of the state. Their course led to a swamp owned by a Cajun family whose matriarch was Anna Mae Butaud. As Anna Mae smiled through her screen door, she explained that over the years many people had carted off—first in wagons, then in trucks—thousands of iris plants for use in the horticultural trade. She frowned as she said, "I just don't know if there are any Abbevilles left back there."

So it was with diminished hopes of finding the nearly mythical plant that Mike and Tim stepped through the border of brush into the twilight-tinged, moisture-filled air of a perfect bald cypress swamp. To their delight, the gray and deep green of the cypress trunks and palmetto fronds were accented by splashes of color from the large, brick-red flowers of *I. nelsonii*. Mike wondered silently whether Randolph's hypothesis was correct—that bumblebees and hummingbirds, the pollinators of

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the Louisiana Iris species, had acted as the pollen vectors between *I. fulva*, *I. brevicaulis*, *I. hexagona*, and their hybrids, resulting in the evolutionary origin of the remarkable *I. nelsonii*.

Mike surfaced from his musings, and he and Tim got to work collecting fragments of leaves from a subset of the plants. This material, and specifically the DNA from the *I. nelsonii* cells, would give them the molecular clues to solve the evolutionary mystery. Several days later, as Mike stared at the DNA fingerprints from *I. fulva*, *I. brevicaulis*, *I. hexagona*, and *I. nelsonii*, arrayed side by side under ultraviolet light, he had the answer. Not only was *I. nelsonii* a hybrid species, it was indeed a tripartite hybrid species—and a profound illustration of why the web-of-life metaphor is needed to define accurately the evolutionary process.

Organisms need not be as closely related as the irises to participate in genetic exchanges that generate genomes reminiscent of a patchwork quilt. *Haemophilus influenzae*, for example, is one of the most common bacterial species in the upper respiratory tract of humans. It is normally benign. Only when it gets into the eye, causing the mild reddish irritation known as conjunctivitis, or “pink-eye,” do we commonly notice its presence. So no one suspected a role for *H. influenzae* when a novel, lethal, meningitis-like disease called Brazilian purpuric fever began to afflict Brazilian children in the 1980s; the death rate among its victims was an astounding 70 percent. Researchers began the hunt for isolates of the unknown organism causing the deadly infection, and they were initially baffled when they recovered instead “pinkeye” bacteria, species *H. influenzae*. But subsequent confirmation that this novel form of *H. influenzae*, biogroup *aegyptius*, was indeed the deadly pathogen forced researchers to the obvious conclusion that *H. influenzae* had acquired the genes necessary to yield meningitis.

As we now know, such exchanges between highly divergent microorganisms are common. The increase in pathogenicity of *H. influenzae* reflects the acquisition of a novel adaptation and is conceptually the same as the adaptation that led to the increase in ecological tolerance in Darwin's finches in the Galápagos. However, unlike what occurred with

the finches and in other cases of natural hybridization, the acquisition of a new adaptation in *H. influenzae* was a consequence of horizontal gene transfer rather than sexual recombination. Nonetheless, we are led back once again to the same conclusion: The web of life is a better metaphor than the tree of life for understanding evolutionary phenomena.

The most devastating plague of our generation, HIV/AIDS, continues to gain much of its vehemence from processes associated with the web of life. Known as SIV, or simian immunodeficiency virus, the virus that now gives rise to AIDS was originally lodged in chimpanzees and sooty mangabeys. Ancient recombination among various forms of this virus possibly contributed to the extreme variability seen in the HIV that strikes humans today. The web of genomic interactions produces an ever-changing array of virus types. There is not just one AIDS-causing virus; their number is legion, which makes fighting the disease all the more difficult. The enemy keeps changing. But so do we. That is the essence of organic evolution. It generates diversity in life, to our benefit or our detriment.

Thus far we've highlighted some of the frightening results—frightening for humans, that is—of gene exchanges through hybridization and horizontal transfers. But we should also mention some delightful ones. We need look no farther than the dog curled up at our feet. The ties that have bound this diverse and adaptable species to our own over thousands of years have not kept dogs from mating (or backcrossing) with their wild relatives in the canine genus—the wolf, the jackal, and the coyote. Molecular research confirms what was long suspected: Dogs are opportunistic breeders. Diverging evolutionary “trees” cannot fully account for the genome of the modern dog.

Although each canine species has a distinct and identifiable DNA fingerprint, biologist Robert K. Wayne of the University of California, Los Angeles, found that domestic dogs still carry bits and pieces of DNA imported from wolves after the supposed separation of the two species. Other geneticists have detected similar links caused by mating between dogs and coyotes and between wild canine species. Such hybrid crosses probably contributed to the extremely high level of genetic variation that has blessed dog fanciers with breeds as divergent as the French poodle, the German shepherd, the Cuban havanese, the Mexican Chihuahua, the Great Dane, the Siberian husky, and the English bulldog.

But the benefits to humans of gene flow from interspecies crosses may have been far more direct than is reflected in our appreciation of the many breeds of dogs. Interspecies crossing may also have helped to create *us*. Although their speculations remain tentative and controversial, some researchers propose that our hominid ancestors may have interbred, and

LOUISIANA'S SWAMPS YIELD A
PROFOUND ILLUSTRATION OF
THE EVOLUTIONARY WEB.

that the vaunted *Australopithecus robustus*, which many paleontologists place in the main line of human evolution, may itself have had a hybrid genome. More recently in our pedigree, members of the Neanderthal species may have bred with early *Homo sapiens* and passed along some of their genes to us.

Two opposing models of modern human origins have emerged within the scientific community. The “complete replacement” hypothesis holds that approximately 40,000 years ago modern humans, migrating out of Africa, displaced all archaic human populations without gene exchange. This neo-Darwinian version of the human family tree regards *H. neanderthalensis* and *H. sapiens* as separate branches radiating from the *H. erectus* trunk, incapable of crossbreeding successfully because they were distinct species. *Sapiens* then won the struggle for existence.

The “multiregional evolution” hypothesis counters that, like domestic dogs, modern humans are a hybrid between two different *Homo* species. If this hypothesis is correct, our hybrid ancestry dates from the time when immigrating *sapiens* from Africa encountered and mated with the resident *neanderthalensis* individuals living in Eurasia. In light of all the other examples we have discussed, it would be logical to conclude that a geographic and temporal overlap between modern and archaic forms of humans could have resulted in some level of gene flow through crossbreeding. That’s just what Washington University evolutionary biologist Alan Templeton concluded after examining mitochondrial and nuclear DNA fingerprints taken from human lineages. Templeton’s genetic evidence shows that there was at least some gene exchange as *sapiens* occupied *neanderthalensis* territory. The resulting hybrids were the modern *sapiens* that have spread to the uttermost parts of the earth, including back to Africa.

Fossil remains also support the hypothesis of genetic admixture between modern and archaic humans. The evidence includes individual fossils with a mixture of traits of the older and newer human forms, as well as entire populations preserved in the fossil record that appear to blend archaic and modern physical structures. Neanderthals may not have gone quietly into the night, as paleontologists long thought, but instead mated and produced children with *H. sapiens*.

Evidence involving various species, then, suggests that evolution is best depicted by closely or distantly related strands of a web that diverge, converge, and intersect. Yet humans are not mere passive actors caught in this web. For millennia, through crop and animal breeding, we have actively contributed to the process of hybridizing closely related species. Most recently, with the advent of genetic engineering and biotechnology, we have begun to contribute as well to the web process of horizontal gene transfer. Whether transferring “delayed ripening” genes from a disease of bacteria (i.e., a bacteriophage) into cantaloupe to prevent our breakfast from going mushy too quickly, or splicing a gene for pesticide resistance from bacteria into corn to keep insects from feeding on the plants in a field, or implanting the gene for human interferon into the DNA of chickens so that their eggs contain the pro-

tein used to battle hepatitis C, or introducing the gene for a red fluorescent protein from a sea anemone into zebra fish so that they look more attractive to us in an aquarium, biotech researchers now move genes between species so unrelated to one another that it's difficult to imagine the natural web of life ever accomplishing the same task. Yet these researchers' work perfectly represents how evolution has proceeded through the ages to produce the diversity of life on earth. Different evolutionary strands have been brought into association, either through hybridization or genetic capture, and the result has been mosaic genomes.

Perhaps there's a warning for us in the web-of-life metaphor. Before we fully accept genetic engineering, with its cornucopia of genetically modified crops and farm animals, we should consider the take-home message of the popular science-fiction movie (and novel) *Jurassic Park*, which features self-absorbed geneticists bringing dinosaurs back to life on a jungle island.

To ensure that viewers don't miss the point, one of the movie's heroes scolds the architect of this mad scheme: "Your scientists were so preoccupied with whether or not they *could* that they didn't stop to think if they *should*." Should we be as concerned that the engineered genes of transgenic corn and melon plants will make it into their wild relatives, which still grow near them throughout the cultivated world? Is it a problem that these wild relatives might become "superweeds," resistant to natural pests that previously controlled their population? "Of course it's a risk," say many scientists. Is it probable that delayed-ripening genes added to food crops might end up in their wild relatives as well — causing a lack of seed production in them and leading to the extinction of the native forms? Again, some scientists are concerned that the answer is yes. And what of the glowing zebra fish that's flushed down the toilet when its owner grows tired of its radiance? Once introduced into the novel ecosystem of a North American city's lakes or streams, will the fish threaten the resident flora and fauna? The risk, though small, is real.

If we think in terms of an evolutionary web of life, we'll be more alert to the prospect that gene transfer can cause unforeseen consequences to unfold quickly in nature — much more quickly than if evolution occurred only through the gradual accumulation of gene mutations envisioned by a neo-Darwinian tree of life. Evolution could not have produced the current diversity of life in the time available to it without employing every source of genetic variation open to it. But once we begin to radically modify the genetic systems that we know as species, the outcome may be a blessing or a bane. Only time and experience will teach us which. In many cases, the outcome is likely to be a bit of both. □

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