Breakthrough of the Year

Equipped with genome data and field observations of organisms from microbes to mammals, biologists made huge strides toward understanding the mechanisms by which living creatures evolve

Evolution in Action

The *big* breakthrough, of course, was the one Charles Darwin made a century and a half ago. By recognizing how natural selection shapes the diversity of life, he transformed how biologists view the world. But like all pivotal discoveries, Darwin's was a beginning. In the years since the 1859 publication of *The Origin of Species*, thousands of researchers have sketched life's transitions and explored aspects of evolution Darwin never knew.

BREAKTHROUGH ONLINE
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Today evolution is the foundation of all biology, so basic and all-pervasive that scientists sometimes take its importance for granted. At some level every discovery in biology and medicine rests on it, in much the same way that all terrestrial vertebrates can trace their ancestry back to the first bold fishes to explore land. Each year, researchers worldwide discover enough extraordinary findings tied to evolutionary thinking to fill a book many times as thick as all of Darwin's works put together. This year's volume might start with a proposed rearrangement of the microbes at the base of the tree of life and end with the discovery of 190-million-year-old dinosaur embryos.

Amid this outpouring of results, 2005 stands out as a banner year for uncovering the intricacies of how evolution actually proceeds. Concrete genome data allowed researchers to start pinning down the molecular modifications that drive evolutionary change in organisms from viruses to primates. Painstaking field observations shed new light on how populations diverge to form new species—the mystery of mysteries that baffled Darwin himself. Ironically, also this year some segments of American society fought to dilute the teaching of even the basic facts of evolution. With all this in mind, *Science* has decided to put Darwin in the spotlight by saluting several dramatic discoveries, each of which reveals the laws of evolution in action.

All in the family

One of the most dramatic results came in September, when an international team published the genome of our closest relative, the chimpanzee. With the human genome already in hand, researchers could begin to line up chimp and human DNA and examine, one by one, the 40 million evolutionary events that separate them from us.

The genome data confirm our close kinship with chimps: We differ by only about 1% in the nucleotide bases that can be aligned between our two species, and the average protein differs by less than two amino acids. But a surprisingly large chunk of noncoding material is either inserted or deleted in the chimp as compared to the human, bringing the total difference in DNA between our two species to about 4%.



Chimp champ. Clint, the chimpanzee whose genome sequence researchers published this year.

Somewhere in this catalog of difference lies the genetic blueprint for the traits that make us human: sparse body hair, upright gait, the big and creative brain. We're a long way from pinpointing the genetic underpinnings of such traits, but researchers are already zeroing in on a few genes that may affect brain and behavior. This year, several groups published evidence that natural selection has recently favored a handful of uniquely human genes expressed in the brain, including those for endorphins and a sialic acid receptor, and genes involved in microcephaly.

The hunt for human genes favored by natural selection will be sped by newly published databases from both private and public teams, which catalog the genetic variability among living people. For example, this year an international team cataloged and arranged more than a million single-nucleotide polymorphisms from four populations into the human haplotype map, or HapMap. These genetic variations are the raw material of evolution and will help reveal recent human evolutionary history.

Probing how species split

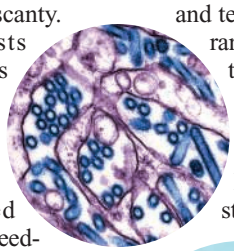
2005 was also a standout year for researchers studying the emergence of new species, or speciation. A new species can form when populations of an existing species begin to adapt in different ways and eventually stop interbreeding. It's easy to see how that can happen when populations wind up on opposite sides of oceans or mountain ranges, for

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example. But sometimes a single, contiguous population splits into two.

Evolutionary theory predicts that this splitting begins when some individuals in a population stop mating with others, but empirical evidence has been scanty. This year field biologists recorded compelling examples of that process, some of which featured surprisingly rapid evolution in organisms' shape and behavior.



For example, birds called European blackcaps sharing breeding grounds in southern Germany and Austria are going their own ways—literally and figuratively. Sightings over the decades have shown that ever more of these warblers migrate to northerly grounds in the winter rather than heading south. Isotopic data revealed that northerly migrants reach the common breeding ground earlier and mate with one another before southerly migrants arrive. This difference in timing may one day drive the two populations to become two species.





Two races of European corn borers sharing the same field may also be splitting up. The caterpillars have come to prefer different plants as they grow—one sticks to corn, and the other eats hops and mugwort—and they emit different pheromones, ensuring that they attract only their own kind.



Biologists have also predicted that these kinds of behavioral traits may keep incipient species separate even when geographically isolated populations somehow wind up back in the same place. Again, examples have been few. But this year, researchers found that simple differences in male wing color, plus rapid changes in the numbers of chromosomes, were enough to maintain separate identities in reunited species of butterflies, and that Hawaiian crickets needed only unique songs to stay separate. In each case, the number of species observed today suggests that these traits have also led to rapid speciation, at a rate previously seen only in African cichlids.

Other researchers have looked within animals' genomes to analyze adaptation at the genetic level. In various places in the Northern Hemisphere, for example, marine stickleback fish were scattered among landlocked lakes as the last Ice Age ended. Today, their descendants have evolved into dozens of different species, but each has independently lost the armor plates needed for protection from marine predators. Researchers expected that the gene responsible would vary from lake to lake. Instead, they found that each group of stranded sticklebacks had lost its armor by the same mechanism: a rare DNA defect affecting a signaling molecule involved in the development of dermal bones and teeth. That single preexisting variant—rare in the open ocean—allowed the fish to adapt rapidly to a new environment.

Biologists have often focused on coding genes and protein changes, but more evidence of the importance of DNA outside genes came in 2005. A study of two species of fruit flies found that 40% to 70% of noncoding DNA evolves more slowly than the genes themselves. That implies that these regions are so important for the organism that their DNA sequences are maintained by positive selection. These noncoding bases, which include regulatory regions, were static within a species but varied between the two species, suggesting that noncoding regions can be key to speciation.

That conclusion was bolstered by several other studies this year. One experimental paper examined a gene called *yellow*, which causes a dark, likely sexually attractive, spot in one fruit fly species. A separate species has the same *yellow* gene but no spot. Researchers swapped the noncoding, regulatory region of the spotted species' *yellow* gene into the other species and produced dark spots, perhaps retracing the evolutionary events that separated the two. Such a genetic experiment might have astonished and delighted Darwin, who lamented in *The Origin* that "The laws governing inheritance are quite unknown." Not any longer.

To your health

Such evolutionary breakthroughs are not just ivory-tower exercises; they hold huge promise for improving human well-being. Take the chimpanzee genome. Humans are highly susceptible to AIDS, coronary heart disease, chronic viral hepatitis, and malignant malarial infections; chimps aren't. Studying the differences between our species will help pin down the genetic aspects of many such diseases. As for the HapMap, its aims are explicitly biomedical: to speed the search for genes involved in complex diseases such as diabetes. Researchers have already used it to home in on a gene for age-related macular degeneration.

And in 2005, researchers stepped up to help defend against one of the world's most urgent biomedical threats: avian influenza. In October, molecular biologists used tissue from a body that had been frozen in the Alaskan permafrost for almost a century to sequence the three unknown genes from the 1918 flu virus—the cause of the epidemic that killed 20 million to 50 million people. Most deadly flu strains emerge when an animal virus combines with an existing human virus. After studying the genetic data, however, virologists concluded that the 1918 virus started out as a pure avian strain. A handful of mutations had enabled it to easily infect human hosts. The possible evolution of such an infectious ability in the bird flu now winging its way around the world is why officials worry about a pandemic today.

A second group reconstructed the complete 1918 virus based on the genome sequence information and studied its behavior. They found that the 1918 strain had lost its dependence on trypsin, an enzyme that viruses typically borrow from their hosts as they infect cells. Instead, the 1918 strain depended on an in-house enzyme. As a result, the reconstructed bug was able to reach exceptionally high concentrations in the lung tissue of mice tested, helping explain its virulence in humans. The finding could point to new ways to prevent similar deadly infections in the future.

Darwin focused on the existence of evolution by natural selection; the mechanisms that drive the process were a complete mystery to him. But today his intellectual descendants include all the biologists—whether they study morphology, behavior, or genetics—whose research is helping reveal how evolution works.

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CREDITS: C. GOLDSMITH/CDC (AVIAN FLU); W. A. CRESKO *ET AL.*, *PNAS* **101**, 6050 (2004) (STICKLEBACK); DAVID SCHARF/PETER ARNOLD (*DROSOPHILA*); ANDY BRIGHT (EUROPEAN BLACKCAP)