EVOLUTIONARY BIOLOGY

Will Molecular Data Set The Stage for a Synthesis?

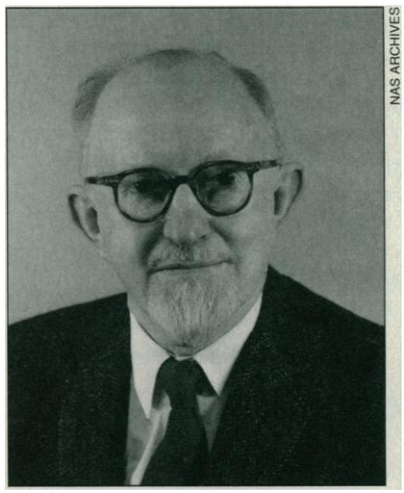
Fifty years ago, the great evolutionary biologist George Gaylord Simpson, then at the American Museum of Natural History, published a classic volume called *Tempo and Mode of Evolution*. In that book, Simpson, a leader in what became known as the "modern synthesis" movement in evolution, attempted to combine the results of classical paleontology with those of the rapidly expanding field of genetics to give an overview of evolutionary theory. Fifty years later, 250 leading evolutionary theorists gathered in Irvine, California at a symposium in Simpson's honor.* Appropriately, the aim of the symposium was to provide a Simpsonian overview of the field, and the conclusion was that its tempo of change is rapid, and one of the main modes of change is the acquisition of new data from molecular biology.

As one presentation after another confirmed, molecular biology is offering researchers a multitude of new genetic clues about evolutionary change. "We have a tremendous explosion of discovery now," says Francisco Ayala, a molecular evolutionist at the University of California (UC), Irvine, who cochaired the meeting with UC Irvine's Walter Fitch. The challenge facing scientists in the field is to make sense of those discoveries, to fit diverse pieces of evidence into more comprehensive patterns. "We know we need the data from everyone else," says paleontologist William Schopf of the University of California, Los Angeles. "We know it's another arrow in our quivers."

This isn't an easy task, and often it raises questions as fast as it answers them. Ford Doolittle of Canada's Dalhousie University, who studies the genetics of primitive single-celled organisms called archaebacteria, explained that molecular biology has reshaped his field in the last decade but that the new shape is hard to discern. In a talk called "The Root of Life," Doolittle said molecular comparisons of living organisms have rewritten the textbook story that the first cells were prokaryotes (cells without a nucleus), which in turn gave rise to nucleated eukaryotes.

The first deep wrinkle in this smooth fabric came more than a decade ago, Doolittle noted, when Carl Woese of the University of Illinois at Urbana-Champaign sequenced RNA from the ribosomes of a variety of organisms (ribosomes being the cellular structures that make proteins). Comparisons of the ribosomal RNAs led Woese to divide prokaryotes into two groups—archaebacteria and eubacteria—and to suggest that they are as distinct from each other as they are form eukaryotes.

More recently, said Doolittle, the popular notion that the three lineages diverged from a common ancestor, called a progenote, has been put on thin ice by studies of the distinctive genome organization in archaebacteria. "Many of us have quietly been saying goodbye to the progenote concept," Doolittle said. "The root is back up in the air again." And with an upended root, it's anybody's guess as to how to draw these three branches on an evolutionary tree.



NAS ARCHIVES

Search for a synthesis. George Gaylord Simpson argued in 1944 that evolutionary biology should draw from many diverse disciplines.

Molecular techniques are also raising new insights about where, exactly, humans fit on the evolutionary tree. UC's Ayala described how analyses of DNA from the human leukocyte antigen (HLA) are casting additional doubt on the disputed "mitochondrial Eve" theory of human origins, which, based on DNA analysis of mitochondria—cells' energy-producing organelles—holds that all humans today descended from a single lineage passed on by one woman some 200,000 years ago in Africa (*Science*, 7 February 1992, p. 686).

The "Eve" hypothesis came from the University of California, Berkeley's Rebecca Cann, a student of the late Allan Wilson, in 1987. HLA analysis, however, contradicts that tale. HLA is a key immune-system molecule that helps to distinguish between "self" and "nonself." DNA comparisons of HLA molecules reveal that some chimpanzee leukocyte antigens are actually closer to human sequences than some human antigens are to each other, indicating a tremendous diversity among human HLA alleles (slightly varying versions of the same gene). And in genetics, such diversity means the alleles have been in existence for a long time, since it takes millennia for genes to diverge by accumulating mutations.

Using computer simulations that model human populations and their genes over time, Ayala finds that a population bottleneck, such as the one hypothesized in the Eve concept, is "outright impossible"—because an Eve-type genetic bottleneck would have eliminated the wide range of existing HLA alleles.

Not all questions are going unanswered, of course. The powerful tools of molecular biology have also been supplying the missing pieces of longstanding evolutionary puzzles. John Avise of the University of Georgia described at the meeting how he and his former graduate student, Brian Bowen, are using genetic sequences to explore evolution within a single species.

In order to understand the dynamics of intraspecies evolution in the green turtle, researchers need to know whether mothers return to the rookeries where they were born to lay their eggs. Tagging the turtles, which was for a long time the only available technology for tracking the creatures, is an impractical way to answer this question, because it takes some 20 years before hatchlings return and nest.

Avise and Bowen exploited the fact that mitochondrial DNA (mtDNA) provides stable genetic markers that can link related animals together. The researchers, who began with a small sample of turtle colonies (*Science*, 11 May 1990, p. 724), have now expanded their sample by analyzing mtDNA patterns from more than 200 rookeries. The mtDNA patterns seem unique to each colony, indicating that females do seem impelled to return to their own natal sites for nesting. "This links mitochondrial genetics and population demography," said Avise. "And it can be applied to any creatures structured along maternal lines."

At the meeting, there were many other examples of the influx of molecular results into evolutionary theory. And the attendees were left with the feeling that the next task for the field is to integrate them into a synthesis of the kind Simpson tried to achieve. At the moment, however, that fusion seems far off. "Whether we'll have a synthesis of the magnitude seen in Simpson's era, I don't know," said Ayala at the meeting's end. Yet he argued that, as a result of the new findings, "the grounds are there."

–Jon Cohen

* 28-29 January, "Tempo and Mode in Evolution," sponsored by the National Academy of Sciences, Beckman Center, Irvine, California.