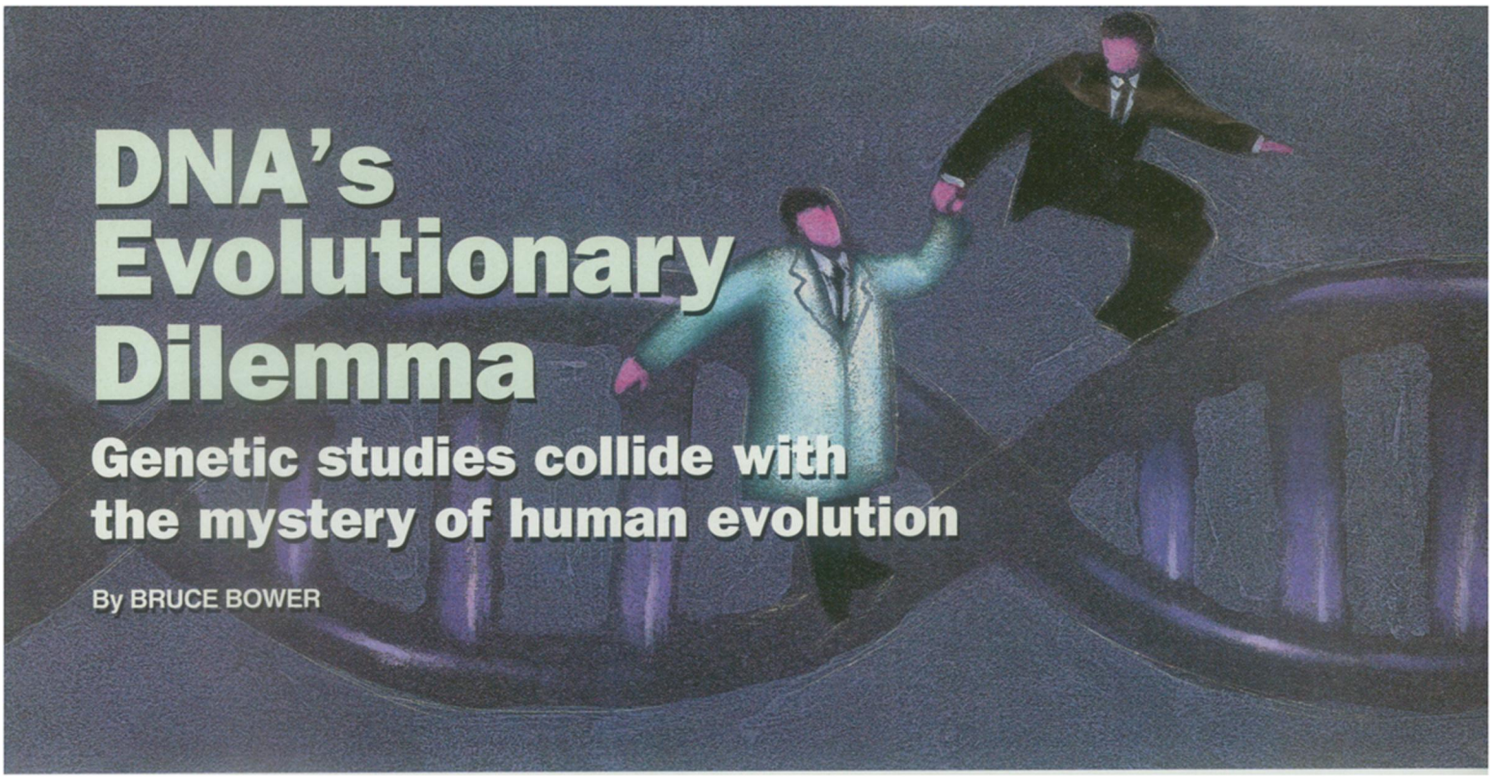

# DNA's Evolutionary Dilemma

## Genetic studies collide with the mystery of human evolution

By BRUCE BOWER

Just a few years ago, genetic researchers assumed the status of a scientific Supreme Court in the debate over humanity's prehistoric roots. The coils of human DNA appeared to have hardened into a molecular gavel with which these scientists could issue a final ruling on how best to explain the evolution of modern *Homo sapiens*.

During the late 1980s, initial studies of global DNA diversity encouraged a vigorous bout of gavel pounding. One after another, investigators concluded that modern humans probably arose in Africa around 200,000 years ago and then spread elsewhere, replacing Neandertals and any other species in our evolutionary past. Analyses of mitochondrial DNA—inherited only through the maternal line—in people from different parts of the world traced the origin of these genes back to one or a few African women dubbed "mitochondrial Eve."

Decades of anthropological debate over modern human origins that was based on interpretations of measurements and a host of bumps and grooves on ancient fossils teetered on the verge of irrelevance.

However, even some admirers of mitochondrial Eve now say that the jury is out on whether state-of-the-art DNA studies can live up to their early billing. Accumulating data prove compatible with either of the two main theories of how *H. sapiens* came about.

The recent African-origin model championed by many genetic researchers relies on genetic findings that fit just as easily into a contrasting multiregional model. That is, populations of *H. sapiens* living in different parts of Africa, Asia, and Europe interbred enough over at least the past 1 million years to evolve collectively as a single species. The various populations around the world derived from even older ancestors of *H. sapiens* in this scenario.

Practitioners of what has been dubbed anthropological genetics now operate with a sense of caution and a hunger for better explanations of how evolutionary forces produce genetic diversity among individuals and groups.

"A lot of us have been too eager to assume that a strict out-of-Africa model is correct because it's compatible with the genetic data, without considering that the data also fit with the multiregional theory," says anthropologist John H. Relethford of the State University of New York at Oneonta. "It's time to go back to the drawing board on this issue."

A fundamental conflict between the two current theories—each of which has several proposed variations on its theme—lies in their differing assumptions about the evolutionary significance of genetic differences among individuals and populations, Relethford asserts. DNA analyses appear unable to determine which perspective proves superior, he says.

According to the more common assumption, which supports recent African origins for humanity, DNA disparities between modern populations arose as prehistoric populations split into distinct regional groups, which then rarely interbred. Computer programs retrace this tree-like evolutionary pattern back to a common genetic ancestor, based on estimates of the presumed rate at which particular DNA regions undergo change.

Such reconstructions of an evolutionary tree branching from a single ancestor have hinged on evidence that sub-Saharan Africans have accumulated more variations in their genetic makeup than any other geographic group. According to the theory, they therefore have existed as a relatively separate population for a longer time. Moreover, African DNA diverges in particularly pronounced ways from the genetic material of people living elsewhere in the world, the presumed result of a longer period of African evolution.

Beginning with the first reported branching analysis in 1987, directed by Rebecca L. Cann of the University of Hawaii at Manoa in Honolulu, evolutionary trees portray all modern *H. sapiens* populations as descendants of a single African population living 100,000 to 200,000 years ago. At some more recent time, part of the original African group departed its homeland and trekked into Asia. Further splits, migration, and occasional interbreeding between some human groups yielded distinctive human populations now found throughout the world.

Only about 10,000 breeding adults comprised the founding block of *H. sapiens*, according to these investigations. That number could not have supported the network of interbreeding populations proposed in the multiregional model.

The alternative perspective on these same genetic data, however, favors the multiregional picture of human evolution. It holds that genetic variation within and among groups arises from low but consistent levels of interbreeding combined with the buildup in regional groups of random changes in the makeup of DNA.

Proponents of this view argue that Africa's greater genetic diversity arose because more people inhabited Africa than

any other continent during the rise of *H. sapiens*, not because the African population is older. DNA determinations of ancient population sizes represent conservative estimates that may turn out to be unreliable, these scientists argue.

The standoff between contrasting genetic perspectives shows no signs of resolution, Relethford contends. Attempts to confirm presumed splits of prehistoric human populations face particular difficulty, he says. However our species originated, it's likely that interbreeding has occurred among dispersed human populations during the past 100,000 years. The resulting jumbling of DNA traits and patterns has diminished the reliability of reconstructed evolutionary trees and estimates of their ages, in Relethford's view.

Researchers have for decades studied DNA diversity in the composition of genes linked to specific blood groups, proteins, enzymes, and immune traits. Only about 50 of these classical genetic markers exist, too few for a thorough analysis of human genetic history, says anthropological geneticist Joanna L. Mountain of Stanford University. Over the past decade, the scientific spotlight has shifted from classical markers to mitochondrial DNA.

This small part of the human genome is packaged outside the nuclei of cells in the energy-generating mitochondria. It looks particularly promising to researchers because it is passed along without the molecular reshuffling that occurs in nuclear DNA each generation. Because eggs, but not sperm, carry mitochondria, mitochondrial DNA is passed along only from mothers.

Mitochondrial DNA shows a great deal of individual variability, which has buttressed assertions that it can help to trace the evolutionary history of human females. Researchers have largely believed that mitochondrial DNA changes occur randomly and accumulate at a constant rate in isolated populations, making them suitable for dating ancient population splits.

But mitochondrial DNA may not be so predictable, according to some researchers. Sections of its sequence of nucleotides undergo surprisingly rapid changes, even within one or a few generations, argues Neil Howell of the University of Texas Medical Branch in Galveston. Mitochondrial DNA alterations may not tick away like hands on a reasonably accurate evolutionary clock, Howell maintains.

Some of these genetic-sequence variations have spread through populations with a speed suggesting that they somehow aid the survival of their bearers, he adds. If natural selection has reshaped the mitochondrial landscape over relatively short spans of time, it raises serious doubts about the accuracy of estimated ages for evolutionary trees and sizes of ancient populations.

Advocates of evolutionary branching, such as Mark Stoneking of the Max Planck Institute for Evolutionary Anthropology in Leipzig, Germany, say that feverish bursts of genetic change crop up only at certain mitochondrial "hot spots" that are not crucial to their findings.

"The best genetic evidence continues to point toward a recent African origin for modern humans," Stoneking asserts.

Yet even outside the mitochondrial realm, molecular evidence gets spun in different directions. A prime example concerns a study of nuclear DNA published in the September 1997 American Journal of Human Genetics.

Rosalind M. Harding of John Radcliffe Hospital in Oxford, England, and her colleagues examined a nucleotide sequence including the beta-globin gene, which contributes to immune functioning. Since nuclear DNA builds up variations at a considerably slower pace than its mitochondrial counterpart, the researchers were able to reconstruct an evolutionary tree with much older roots than those of mitochondrial trees.

Analyzing DNA samples from Africa, Asia, and Europe, Harding's group estimated that a common ancestor of modern beta-globin gene sequences originated in Africa around 800,000 years ago. Asian origins of this DNA region extend back more than 200,000 years, according to their analysis.

This pattern fits best with the multiregional evolution model, the scientists say. Modern humans had apparently spread through much of Asia by the time of what would have been mitochondrial Eve's debut. Differences in overall beta-globin diversity between Africa and Asia are modest at best, reflecting the unifying effect of consistent interbreeding, they conclude.

In contrast, Stoneking argues that Harding's data imply an initial spread of *H. sapiens* from Africa to Asia around 200,000 years ago, perhaps shortly after mitochondrial Eve made her mark in Africa. He contends that beta-globin sequences in Africa trace back to the time of *H. erectus*, a species that preceded *H. sapiens*.

A recent analysis of rapidly changing nuclear DNA segments in Chinese citizens lends support to Stoneking's argument (SN: 10/3/98, p. 212). It portrays East Asians as evolving from a single population in southeast Asia that had previously migrated out of Africa.

That study and most other genetic explorations suffer a fatal flaw, holds Alan R. Templeton, a geneticist at Washington University in St. Louis. Researchers typically run tree-building computer programs without first checking whether the genetic data conform

better to their underlying assumption—that a prehistoric split of Africans and non-Africans yielded separate breeding populations—or to the alternative possibility that recurrent, low levels of interbreeding have forged genetic ties among widespread human groups.

Genetic surveys and new statistical analyses of DNA trees, reported by Templeton in the November 1998 AMERICAN ANTHROPOLOGIST, indicate that human groups have always interbred to some extent. The most frequent genetic exchanges, predictably, have occurred among populations in closest proximity, he finds. If interbreeding had not occurred in this manner, prehistoric migrations would have yielded especially close genetic links between some far-flung groups.

Templeton has devised a statistical technique for picking out geographic patterns in the spread of genes throughout the branches of evolutionary trees. He says that his method distinguishes between the genetic influences of a sudden expansion of a population into new regions—as in the recent African-origins model—and those of sustained interbreeding that was most common in groups separated by short distances.

Templeton's reanalysis of data from other researchers on both mitochondrial DNA and the paternally inherited Y chromosome shows that genetic differences between populations are generally modest, but they are greatest in those groups that lived furthest from one another. So, for instance, East African pygmies and Melanesians (who live on islands near Australia) look far less alike genetically than either group compared with Europeans. Similarities in facial characteristics and skin tone between Africans and Melanesians probably represent common human adaptations to life in a tropical climate, Templeton says.

In his evolutionary scenario, separate human races with distinctive biological traits have never existed.

Local populations in a few regions might have died out within the past 100,000 years as interbreeding continued elsewhere, Templeton notes. This may explain mitochondrial DNA evidence for Neandertal extinction in Europe by around 30,000 years ago (SN: 7/19/97, p. 37). The fate of the Neandertals remains unsettled until additional prehistoric gene fragments are isolated and analyzed, the St. Louis researcher says.

A statistical analysis directed by Templeton and Michael F. Hammer of the University of Arizona in Tucson finds that modern Y-chromosome diversity probably arose through a number of prehistoric population movements from Africa to Asia, as well as from Asia back into Africa. Males may have moved over long distances throughout much of prehistory more often than females, Templeton suggests.

Other data, such as a mitochondrial DNA study directed by Mark T. Seielstad of the Harvard School of Public Health in Boston and published in the November 1998 NATURE GENETICS, suggest that females have more often moved over short distances than males. The tendency of men in hunter-gatherer groups to travel outside their native villages in search of brides, whom they then bring back home, may partly explain this finding.

Long- and short-distance movements among interbreeding groups facilitate the transfer of genes underlying variable biological traits, Templeton holds. Thus, different patterns of skeletal traits in creatures such as Neandertals do not necessarily banish them from the human species, in his view.

Many anthropologists assume, in contrast, that *H. sapiens* evolved a defining suite of skeletal features, even though no consensus exists on what they are. Absence of these features in creatures such as Neandertals leads to their designation as a separate species.

Templeton's views on human evolution spark heated debate. But reservations about the power of current DNA studies to describe human evolution are not uncommon.

Mountain, who views accumulated genetic evidence as moderately supportive of a recent African origin for humanity, still sees a pressing need for improved analyses of large DNA samples.

"Far too often, anthropological geneticists draw conclusions about human evolutionary history without testing hypotheses or exploring alternate models," Mountain remarks. "In some cases, this is because data are insufficient. In other cases, the immediate impression generated by the data blinds us to alternatives."

Hammer, who remains undecided on how modern humans evolved, suspects that investigators will increasingly experiment with statistical formulas for weighing the contributions of natural selection and other factors to DNA diversity.

"Over the next 10 years, more complex genetic models will emerge," Hammer says. "DNA research has not solved the mystery of human origins." □

*Letters continued from p. 83*

significantly over that of controls kept in 12 hours light–12 hours darkness (*Ann. N.Y. Acad. Sci.*, vol. 117, 88-104, 1964).

*Wolfgang Jöchle*
*Denville, N.J.*

**Since humans are** forever trying to beat the system, what about using a light-blocking mask that covers the eyes? The article's photograph implies that experimentation with masks is being done, but there was no mention of results. If the eyes are truly the primary photosensors affecting the melatonin cycle, it may be much easier to block the light at the eye rather than trying to prevent light, from its many modern-day sources, from entering a room.

*David Hattery*
*Washington, D.C.*

**In winter, when** the nights grow long,
My mind begins to quail and cower.
The only way to stave this off
Is burn the lights at every hour.

This helps a lot to ease the pain
Of what they're lately calling SAD.
Light gets me through the winter months;
But now you tell me that it's bad!

If winter lights cause cancerous growths,
I really don't know what to do.
Should I go wacko in the dark,
Or risk a fatal tumor or two?

I'll likely light the lamps as usual
To keep myself from out the dumps.
But I'll also daily probe my flesh
For any new suspicious lumps.

Thanks for nothing, SCIENCE NEWS.

*Matt Hinton*
*Trinidad, Calif.*

## Aid for brain deficits?

While the most recent findings on the growth of new brain cells by Fred H. Gage and Peter S. Eriksson lead to speculation about treatment for those with "strokes or who have neurodegenerative illnesses" ("Adult human brains add new cells," SN: 10/31/98, p. 276), this news may eventually also aid the palsied and the retarded/developmentally disabled.

I am led to wonder whether we may now look for a new mechanism with which to aid individuals with brain damage caused at or before birth, whether by trauma or disease or genetics. Could deficit cell areas of the brain be "repaired" or "added to" using this new combined knowledge?

Certainly, the need in the brain-damaged/deficit population is as significant as in the stroke and trauma population, and, perhaps, a true treatment may be near for both.

*Irwin Tyler*
*Spring Valley, N.Y.*

## Fair warning

In "Is natural pesticide too hard on people?" (SN: 11/7/98, p. 295), *B. cepacia* is proposed for use as natural biological protection for seeds and fruits. Concerns are raised because *B. cepacia* is a potent pathogen in patients with cystic fibrosis. *B. cepacia* is also a major cause of pneumonias in patients with chronic granulomatous disease. If levels of *B. cepacia* on seed, fruits, or cuttings are significantly increased over natural levels by design, then susceptible individuals who come in contact with these products will be at significantly greater risk of infection. Companies contemplating the widespread environmental use of such agents should not discount their liability to provide warnings to protect at-risk individuals.

*Harry Malech*
*National Institutes of Health*
*Bethesda, Md.*