AAAS☆93

An Array of Science From Mitochondrial Eve to EUVE

About 5000 scientists and science-watchers converged on Boston for the 159th Annual Meeting of the American Association for the Advancement of Science on 11-16 February. Last week, we reported on talks about pork-barrel science and the alleged ethical transgressions of Louis Pasteur. This week: topics ranging from human origins to the latest results in ultraviolet astronomy.

Mitochondrial Eve Refuses to Die

B. KALMBACH

Last rights. Milford Wolpoff declared the end of Eve, but new results presented at a symposium Wolpoff organized may keep her alive.

"It's over for Eve," proclaimed University of Michigan paleoanthropologist Milford Wolpoff at the beginning of a session he organized at the AAAS meeting last week on the origins of modern humans. Wolpoff didn't mean Adam's consort. He meant "mitochondrial Eve," brainchild of the late Allan Wilson of the University of California, Berkeley—the hypothesis that all modern humans can trace their maternal ancestry to a woman who lived in Africa 200,000 years ago. In fact, Wolpoff is an entrenched critic of Eve and has been giving her last rites ever since biologists admitted in *Science* a year ago (7 February 1992, p. 636 and 737) that there were serious flaws in the statistical evidence supporting the Eve hypothesis.

Contrary to Eve's backers, who think modern humans evolved relatively recently in Africa and fanned out across the world, Wolpoff defends the "regional continuity" notion, in which modern humans evolved gradually over a much longer period in many parts of the world. Now that some flaws have been showing up in the Eve data, Wolpoff organized the AAAS session to dance on her grave. But even as Wolpoff was getting ready for the funeral, Eve refused to die. In a last-minute addition to Wolpoff's AAAS program, one of the biologists who exposed flaws in the original mitochondrial Eve data analysis, Harvard University molecular anthropologist Maryellen Ruvolo, presented new data that support at least one aspect of the Eve hypothesis—the estimate of when Eve lived. While Ruvolo's data say nothing about Eve's whereabouts, her studies of a mitochondrial gene in a diverse group of modern humans indicate that these groups are very closely related and all evolved from a common ancestor quite recently.

In a paper titled "New Mitochondrial DNA Sequences: All About Eve?" Ruvolo presented calculations using a range of rates for the ticking of a "molecular clock" in the mitochondrial gene she studied. Molecular clocks are based on the idea that mutations occur at a steady rate, so differences in the same gene among various groups should provide an indication of how much time has passed since those groups shared a common ancestor. Using that premise, Ruvolo compared sequence data for the 684 base-pair cytochrome oxidase subunit II (*CO II*) gene in the mitochondria of pygmies and !Kung bushmen from Africa, a Taiwanese Asian, a Caucasian, chimpanzees, and gorillas. Although the sample was small, it represented the most genetically diverse humans other scientists had identified. Ruvolo found that the *CO II* gene differed little among the humans she studied and, as expected, there was a relatively large difference between humans and chimpanzees.

When Ruvolo calculated the date—the so-called coalescence time—at which these humans could trace their *CO II* gene to a common ancestor, she came up with an answer of either 126,000 years (with 95% confidence limits of 55,000 to 227,000 years) or 253,000 years (with limits of 110,000 to 455,000 years), depending on which estimate of the clock rate she chose. Although the ranges are large, the calculations would rule out a coalescence time of a million years or more, which would be required to fit the regional continuity theory. As a further check on the data, Ruvolo calculated the diversity between humans and chimps, and she came up with a figure 27 times the diversity within humans. She then used estimates of the time when the two species diverged (6 million to 10 million years ago) and derived a coalescence time for the human populations of between 222,000 and 370,000 years. Her conclusion: "On the basis of the new data, I don't see how you can get a very ancient date out of it."

Ruvolo's dates mirror those found by the authors of the Eve hypothesis, Wilson and his former graduate students Mark Stoneking and Linda Vigilant, now at Pennsylvania State University, and Rebecca Cann, now at the University of Hawaii. Using a different part of the mitochondrial genome, they had calculated that Eve had lived between 130,000 and 200,000 years ago. Their first study was criticized, however, for detecting the genetic variation with restriction analysis, which is less precise than actual nucleotide sequence data. Then they used sequence data from a rapidly evolving part of the mitochondria, which tends to accumulate more than one mutation at specific sites—making it difficult to detect all the variation. But now Ruvolo has arrived at similar dates by obtaining sequence data—and that from a more slowly evolving gene. "The implications are that they were correct on the original timing for Eve," says Ruvolo. "Modern humans are all still very closely related."

Wolpoff, however, wasn't swayed by Ruvolo's presentation at his own session. He dismissed the new dates saying, "I don't think molecular clocks work in this species (humans)." And he predicted that the debate about human ancestry will be settled by a study of fossils rather than molecules.

Among other anthropologists, however, the new data are likely to revive some support for replacement theories. Yet they won't resolve the thorny question of where modern humans first evolved. Ancestral trees constructed from molecular data from rapidly evolving regions are still unreliable and cannot determine whether the last common ancestor for modern humans was African or Asian (*Science*, 14 August 1992, p. 873). Stanford University geneticist Luigi Luca Cavalli-Sforza did, however, present data at another AAAS session that he has collected in collaboration with Yale University geneticists Kenneth and Judith Kidd showing more diversity in the nuclear DNA of Africans than other populations—a finding consistent with the Out-of-Africa hypothesis.

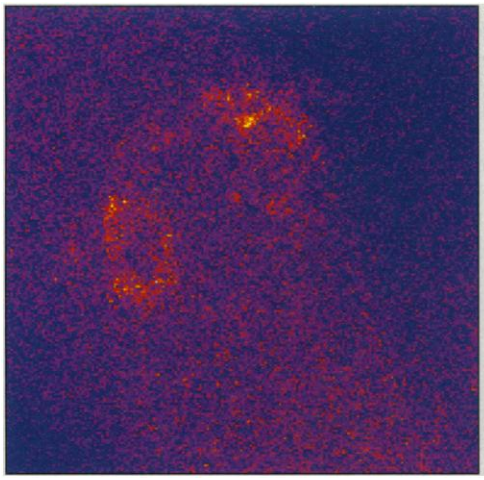
In the face of such uncertainty, many anthropologists have chosen to shelve the molecular data, for now, and have returned instead to discussing what the fossil record tells them about modern human origins. Indeed, even after Ruvolo presented her new data, most of the speakers stuck to a discussion of fossils. Wolpoff and his colleague at the University of Michigan, Rachel Caspari, for example, argued that some of the best candidates for a new species of "modern" humans from Africa exhibit a number of archaic features—casting in doubt claims that they were the progenitors of modern *Homo sapiens*.

But trying to settle the question of modern human origins on the basis of the fossil record is a frustrating exercise: "The fossil evidence is really scrappy. There just isn't enough of it," concludes A.G. "Kip" Thorne of the Australian National University, a co-organizer of the session. Like it or not, more new data have been arriving from the molecular studies than from the fossil record in recent years—and no ultimate solution to the problem of modern human origins will be able to ignore the molecular data—or the newly risen mitochondrial Eve.

–Ann Gibbons

Probing the Cosmos in Extreme Ultraviolet

"You haven't read about us in the papers because nothing has failed," joked astrophysicist Roger Malina of the University of California, Berkeley, as he presented the first results from the National Aeronautics and Space Administration's Extreme Ultraviolet Explorer (EUVE) satellite. But if the spacecraft's early glimpses of everything from flaring stars and supernova remnants to the interstellar medium and extragalactic objects are any indication, EUVE will be making a lot of news in the years to come.


EUVE image of the Vela supernova remnant.

VEDDER, ET. AL

Since its launch last June, the instrument has been conducting an all-sky survey of objects emitting extreme ultraviolet radiation—a task finished just the night before Malina's talk in a session on "Hot Results in High-Energy Astrophysics" at the AAAS meeting. Some astronomers had worried that EUVE's work might be redundant, since a British wide-field camera on the ROSAT spacecraft had already surveyed part of the extreme ultraviolet spectrum last year. But Malina reported that EUVE, which samples a much broader band and is more sensitive than ROSAT's camera, has already revealed hundreds of objects, many brand new, that deserve more attention. Furthermore, unlike the ROSAT instrument, EUVE can now shift to a nonsurvey mode, targeting specific sources and taking detailed spectroscopic measurements.

Among the sources EUVE pinpointed for more study are white dwarfs. These dense stars have long been known to shine brightly in the extreme ultraviolet, but EUVE's survey showed them to be unexpectedly diverse at that wavelength. "Hydrogen white dwarfs, which are featureless in the optical, turn out to have numerous features in the extreme ultraviolet. As we looked at more of them, they became more and more exotic," Malina says, explaining that their spectra show many peaks that will need explaining.

EUVE also took the first extreme ultraviolet snapshots of the moon and the Cygnus loop, a circular glow produced by the outrushing gaseous shell from an exploding supernova slamming into the interstellar medium. Pictures like these may provide new information on both supernovae and the distribution of the interstellar medium. And EUVE captured images of something quite unexpected: at least seven sources, so far, outside our galaxy. Astronomers had thought extreme ultraviolet radiation would mostly be unable to penetrate the interstellar medium, but EUVE apparently peers easily through gaps in the medium. "It's a delightful surprise that we can do extragalactic astronomy in the extreme ultraviolet," says Malina.

The spacecraft's sights will also be set on more familiar objects in the coming months: "cool" stars like our own sun, which emit extreme ultraviolet light from their atmospheres, or coronae. Astronomers are eager to see how closely these other stars match our extensive observations of the sun's corona. They hope to get a better understanding of stellar evolution by studying stars that appear older or younger than our own, and they're also eager to learn about the diversity of these cool stars, says Bernhard Haisch, deputy director at Berkeley's Center for EUV Astrophysics. While the optical surfaces of these stars all look identical, features of the extreme ultraviolet light from their coronae indicate they are radically different in ways that still need to be understood, he says.

As a result, EUVE investigators will be on the alert for flares—short-lived eruptions in the coronae of cool stars. Over the decades, astronomers have viewed flares on both our own sun and other stars in light ranging from the optical spectrum to x-rays. EUVE has already extended that picture to the extreme ultraviolet. One such serendipitous event happened in the middle of a 30,000-second exposure of a calibration star. "All of a sudden a flare took place. It lasted an hour," recalls Haisch, who says EUVE captured a beautiful record of a corona's spectrum before, during, and after an extreme ultraviolet flare. Now investigators are hoping for more such events. Says Malina, summing up EUVE's record so far: "It's kind of fun going to work and asking, 'What did we discover last night?' "

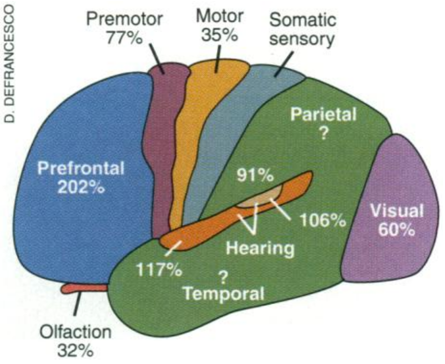
–John Travis

Empathy and Brain Evolution

What makes a human being different from a chimpanzee? Watch a few celebrated apes perform complex tasks in language studies, and it's hard to say what's so special about humans. But even the smartest apes appear to be incapable of doing at least one thing that humans can do: They cannot empathize with one another to the extent that they can project the effect their own actions might have on another's thinking or feelings in the distant future—an ability that forms the essence of moral reasoning. "We think differently from other species," says Terrence W. Deacon, a neurobiologist with appointments at Harvard Medical School and McLean Hospital in Boston. "We are capable of thinking of the abstract, of thinking of the impossible, the paradoxical—of asking, 'What will happen after I die?' "

At a session at the AAAS meeting on what it means to be human, Deacon presented his own bold theory about how the human brain evolved this unique capability to represent such complex symbols as other people's thoughts or actions—a capability he calls representational empathy. Unlike anthropological theories about how the brain expanded as a whole, Deacon's theory details specifically how the brain reorganized itself over 2 million years, expanding its ability to process language and symbolic representation at the expense of brain areas that are important for sight, smell, and vocalization.

His work started in the wet lab where Deacon dissected the brains of humans and other primates, looking for radical differences in structure. What he found was that the brains of humans and great apes have similar parts, although they differ in size and connectivity. He says there is much current evidence to suggest that entirely new structures



D. DEFRANCESCO

Reorganization. Sizes of regions of the human brain compared with equivalent regions of the brains of other primates scaled to match the human brain in total size.

and novel neuronal connections are not the basis for differences in species. Instead, he sees evidence of a "systematic reorganization," in which the human brain slowly recruited and modified areas and circuits once important for other functions so that they could be used to overcome difficulties imposed by symbolic learning.

The evidence for this reorganization lies mainly in the prefrontal cortex, which is twice as large in humans as in other primates, when adjusted for total brain size. Broca's area, which is important for producing and understanding speech, is included in this expanded region—and these areas are many times larger than would be expected in a typical primate brain. Deacon proposes that the prefrontal cortex inherited space and a vast array of circuits extending throughout the brain that once were important for vision, smell, and making specialized vocalizations—regions that seem to have shrunk over time.

That observation prompted him to ask, while he was a researcher at Harvard's Anthropology Department until last year, what "unusual demands" would have driven this reorganization? Here Deacon admits he's speculating, but he proposes in his forthcoming book *Symbolic Origins* that the ability to think symbolically arose about 2 million years ago, about the time of the birth of a species of human ancestor called *Homo habilis*. The increase of brain size in this species signals the beginning of brain reorganization in response to some unusual cognitive demands. This suggests to Deacon that *H. habilis* needed to find new ways to communicate symbolically with other early human ancestors. As they began to use stone tools to hunt game and to prepare meat, their social structure became more complex. They needed new ways to be able publically to negotiate long-term agreements with each other, and to enter into complex relationships, such as sexual exclusion and cooperative hunting.

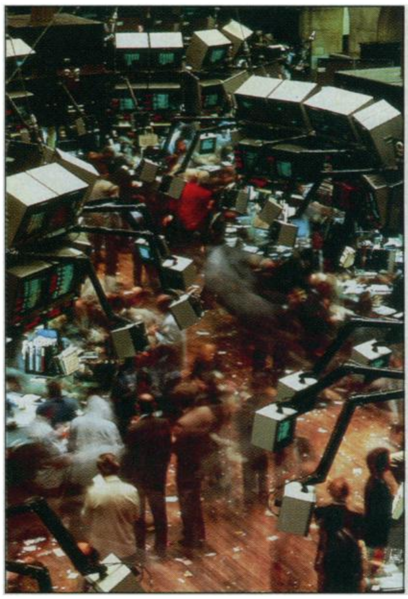
The difficult nature of such symbolic learning drove the evolution of the distinctly human brain, Deacon says. The result: Humans have a highly specialized brain that allows them to "represent to ourselves what goes on in other people's minds." And that, says Deacon, is "the basis of moral decisions. Human compassion as well as intentional cruelty evolved in parallel with language abilities."

–Ann Gibbons

Economics Meets Artificial Life

Move over Adam Smith. Ever since the 18th-century philosopher propounded his theory of free markets, economists have built up market models on the somewhat shaky assumption that buyers and sellers not only behave completely rationally but also assume that all other participants in a market are equally smart and rational. Now comes economist and computer wizard W. Brian Arthur of Stanford University and the Santa Fe Institute with a very different kind of model: a computer simulation of stock trading in which "dumb" agents "learn" when to buy and sell from patterns that emerge in stock prices, much the way live traders do.

Arthur, who described his model at a AAAS symposium on "artificial worlds," says it mirrors the behavior of real stock markets better than classical free-market models do. And, while the work of Arthur and his Santa Fe collaborators is far from widely understood, let alone accepted, in traditional economic circles, it is winning some recognition from mainstream economists like MIT Nobel laureate Robert Solow. He calls Arthur's model "more than just a curiosity."



A. LEVIN/PHOTO RESEARCHERS

Not quite rational. The Stock Exchange.

Traditional economics has relied on the assumption that a person's reasoning process in making an economic decision is deductive: A person uses all available information to make a rational decision about when to buy or sell a stock. But human beings with human failings act according to many motivations, which are often far from rational, Arthur points out. Otherwise, no trader would ever buy a stock—the trader would assume that anyone wishing to sell the stock at a given price must have a good reason to do so, and therefore, it would be a bad buy at that price. In fact, says Arthur, many decisions in life are more like entering an uncontrolled intersection at the same time as three drunk drivers: It is impossible to know rationally what to do, and the system is ill-defined. Just so with stock markets, and traders tend to respond to their "subjective beliefs about others' subjective beliefs." Such systems evolve constantly over time, and successful rules for behavior change too quickly to be of much use.

The key to Arthur's computer model is that the agents—the stock traders—learn not only from their own mistakes but from the rules that their competitors successfully apply, and the information is sometimes recombined into more complicated rules. This approach, which draws on the pioneering work of John Holland at the University of Michigan and others in the field of "artificial life" (*Science*, 21 August 1992, p. 1040), gives each unsuccessful agent a random chance to acquire more effective trading strategies. And successful agents are never safe from the potential effects of a "mutation" in the form of misleading information.

The result yields a good approximation of market behavior, says Arthur. At first, the agents' behavior starts out simple and slavishly rational, but "as more complex rules began to evolve, their behavior came closer and closer to what we observe in real markets," he told the symposium.

The method is not without flaws, as Arthur's collaborator Richard Palmer, a physicist at Duke, is quick to admit. Like all economic models, this one too is an "artificial system," he says. And MIT's Solow criticizes the model for being unrealistic in its assumptions about the way traders acquire information—"These agents [in Arthur's model] are not reading *The Wall Street Journal*," he says. Also, says Solow, real traders do indeed behave in a quite rational manner, "a heck of a lot more like what the textbook, infinitely rational person would do."

Nevertheless, Solow says that the whole field of economic modeling using machine learning is very young and deserves a chance to grow. Noting that models based on rational behavior "date back to Adam Smith," he says, "it is good to have some work going on from the other direction. I hope they someday meet in the middle."

–Steven Dickman

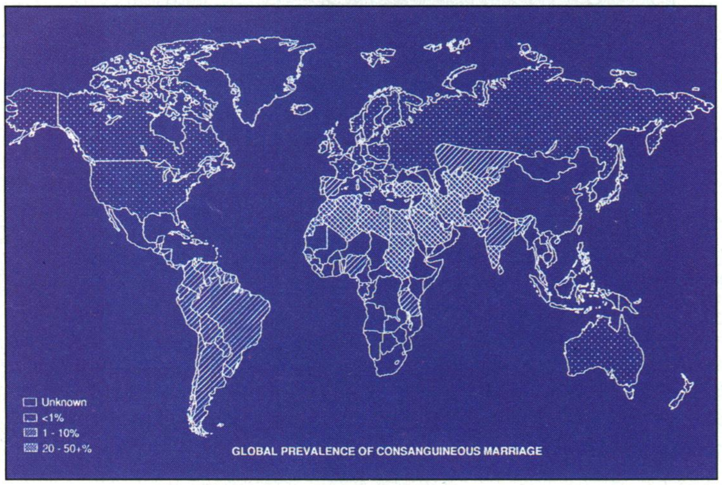
Steven Dickman is currently a Knight Science Journalism Fellow at MIT.

The Risks of Inbreeding

At the Ninth Annual Meeting of the AAAS in Providence, Rhode Island, in 1855, the Rev. Charles Brooks exhorted researchers to study the topic of human inbreeding. At stake, he said, is "the safety and elevation of society." At the time, fears that closely related couples would produce sick or mentally impaired children were so high that eight states soon passed laws making marriage between cousins a criminal offense, while another 30 states made it a civil offense.

Last week, 138 years after Brooks' challenge, a half-dozen geneticists reported back to the AAAS meeting. Surveys from around the world indicate that the children of these unions do have a higher incidence of genetic disease and are more likely to die before they reach adulthood. The reason: First cousins have one pair of grandparents in common, which means they have a greater chance of passing two identical forms of a gene to their child, making them more susceptible to diseases such as cystic fibrosis that are caused by recessive genes. But several researchers pointed out that the absolute level of risk is low—and today can often be dealt with more effectively by genetic counseling than by draconian laws.

Marrying one's cousin or close kin was probably the normal way of life for humans for thousands of years, when they lived in small, discrete tribes or villages, notes University of London geneticist Alan Holland Bittles. "We're all inbred to a certain extent," he says. In many parts of the world, the practice has never been abandoned: In regions of Asia and Africa, consanguineous marriages account for between 20% and 50% of all unions. And the practice is not declining in these areas, partly because there are many economic and social benefits to the families, says Bittles, who has studied the offspring of these marriages in India. Indeed, about 55% of marriages among Pakistanis in the UK are between first cousins.



By contrast, close-kin marriages are highly unusual in the United States and Europe. Only a few religious and ethnic communities—such as the Amish, Mormons, Hutterites, and recent immigrants from Asia and Africa—still practice close-kin marriage in the United States, and these unions have been on the decline; they now account for just 0.6% of all U.S. marriages. The practice also has become taboo in Japan, where until the 1960s, marriages between cousins accounted for up to 14.7% of all unions.

Yet, to avert a threat to public health, at least, current taboos may not be justified. In a study of data from postwar Japan, for example, University of Michigan population geneticist James Neel found only a 1.5% higher rate of mortality among children of first cousins than among the offspring of unrelated parents.

A more typical figure, however, may be that found by a review of 31 epidemiological studies around the world by Muin Khoury and colleagues at the U.S. Centers for Disease Control. They concluded that the offspring of first-cousin marriages were 1.41 times more likely to die before they reach adulthood. And in a new study of mortality among 400,000 Mormons in Utah over the past 100 years, University of Utah geneticist Lynn Jorde found that children whose parents were first cousins had a 22% chance of dying before they reached the age of 16, compared with a 13% risk for children of unrelated parents. (The absolute rates are high because the data include miscarriages and stillbirths, and because of the high incidence of child mortality at the beginning of the century.)

No one is minimizing the risk to these children. But most of the speakers at last week's session argued that laws banning close-kin marriages may be counterproductive. In Western nations, the goal should be to get related couples to undergo genetic screening rather than penalize them, said Bittles. The current laws, however, have the opposite effect: They discourage immigrants or others in close-kin marriages from seeking prenatal care. Concludes Bittles, "I feel legislation about first-cousin marriages is probably unneccessary, because the death rates don't warrant the intervention of heavy-handed legislation."

–Ann Gibbons

Producing Precocious Pests


VISUAL SYSTEMS

Forced maturity. The tobacco hornworm.

The metamorphosis of a sluggish caterpillar into a soaring butterfly is an almost magical process, stirring wonder and delight in both children and adults. Such insect transformations have also piqued the curiosity of researchers, who for decades have delved into the molecular signals that direct the transition. Much of their attention has focused on a substance called juvenile hormone, whose very presence in an insect prevents metamorphosis. When the time is right, the hormone disappears, and its absence turns on new genes that change the insect from an immature larva to its mature adult form. This crucial hormone was discovered in the early 1950s by noted entomologist Carroll Williams, a Harvard professor who died a few years ago.

At a AAAS session devoted to "The Boston Tradition of Insect Research," one of Williams' students, University of Washington zoologist Lynn Riddiford, announced a significant advance of her mentor's work: the cloning of a receptor for juvenile hormone. The identification of this protein may one day add new weapons to the arsenal of pesticide companies.

"This is most important for the caterpillar pests like the gypsy moths," says Riddiford, explaining that such insects, which include apple maggots and her research subject, the tobacco hornworm, do most of their damage as feeding larvae. Riddiford points out that if researchers can synthesize compounds that block the receptor, the juvenile maurauders would detect no hormone and metamorphose prematurely into less destructive adults. (Pesticide companies have already used chemical analogues of the hormone itself to freeze insects such as mosquitos and biting flies, which wreak havoc as adults, in their immature and less destructive stage. However, such treatments directed toward insects like the gypsy moth would only worsen the damage by preserving them in their voracious youth.)

Riddiford says the receptor protein, which lies in the nucleus of the hornworm cell, may hold a few surprises. No portion of it matches sequences common to DNA binding proteins. That's unusual, since steroid hormones generally exert their influence over DNA by directly attaching to it, says Riddiford. As a result, she suggests that the juvenile hormone receptor may belong to a new family of hormone receptors that alter gene expression more indirectly, perhaps by affecting chromatin structure or RNA synthesis.

–John Travis