that linguists dislike most, namely that the ancestors of all the Amerinds came in one wave. Overall, their more powerful method detected nine founding mtDNA sequences in native American peoples, and some of these sequences were only in Na-Dene speakers, Eskimos, and coastal Siberians, suggesting that those groups emerged from a common ancestral population, not from separate groups, as Wallace had proposed.

The team put this data together and proposed that the ancestors of the Amerinds came in the first wave from northeastern Siberia and carried all the variants, some of which were lost in northern Asians and Americans, perhaps due to climate. Later, the survivors rebounded, probably in Beringia, and gave rise to the Na-Dene and Eskimos. This scenario allows for either one or two migrations into North America, depending on whether the homeland of the surviving northerners was in North America or Siberia. Forster says: "We call it a re-expansion. It's a matter of taste whether you call it a separate migration."

The European group also explored an even more controversial issue, the timing of these migrations, by using the amount of genetic difference among populations as a molecular clock. The Amerind speakers show the most diversity, so the team concluded that they arrived in the first wave, 20,000 to 25,000 years ago. That predates the Clovis culture but matches dates from Wallace's group and from several new South American archaeological sites (*Science*, 19 April, p. 346). The re-expansion, they say, happened about 11,300 years ago—the time of the Clovis people.

In search of a homeland

If all of today's native Americans do go back to a single population in Asia, which one? The multiple-migration advocates put their founders in Siberia, as does the European team, because Siberians share some founding variants with Na-Dene speakers and Eskimos—and live close to the land bridge to the Americas. Merriwether and Kolman are skeptical, however, because all modern Siberians tested so far lack haplogroup B. In separate papers, Merriwether, and Kolman and her Smithsonian colleague Eldredge Bermingham have proposed that the founders may have been Mongolians, because they carry all four haplogroups.

Even on the number of migrations, there is no consensus. Satoshi Horai of the National Institute of Genetics in Mishima, Japan, for example, notes that his analyses of the genetic distance among native American peoples suggests that there are four groups that have been isolated for a relatively long period of time. He concludes that there were four separate migrations.

All this disagreement prompts Greenberg to simply ignore the new mtDNA data. He says: "Every time, it [mtDNA] seems to come to a different conclusion. I've just tended to set aside the mtDNA evidence. I'll wait until they get their act together."

Even some geneticists are reluctant to claim they have solved the problem of the peopling of the Americas. "I am worried that too much weight is being given to mitochondrial DNA," says Stanford University geneticist Luigi Luca Cavalli-Sforza. He notes that mtDNA reflects only the movements of women. Because women in some hunter-gatherer societies join their husbands' families and move more than men, their mtDNA may not reveal the migrations of the whole population. So Cavalli-Sforza and colleague Peter Underhill, as well as other teams, are studying markers on the paternally inherited Y chromosome. So far, their results don't rule out additional migrations.

Indeed, researchers warn that more data from several genetic lineages will be needed to provide a picture of the peopling of the Americas. However, that time may not be so far off. One of the other authors of the Greenberg hypothesis, University of Arizona geneticist Stephen Zegura, is taking the new studies seriously and has taken a sabbatical this year to try to sort out the findings: "I'm trying to decide if after 10 years, is the time right to do a new synthesis?" The answer from a new wave of young geneticists, at least, is a resounding yes.

–Ann Gibbons

ARCHAEOLOGY

Art Stirs Uproar Down Under

SYDNEY MORNING HERALD/REX FEATURES

Circling in on the dream time. Ancient dates for Australian rock art have sparked a furor among anthropologists.

It was almost the archaeological equivalent of finding life on Mars. Two weeks ago, what could be the biggest archaeological news in decades erupted from the northern Australian outback, with reports of an ancient site that puts humans on the continent between 116,000 and 176,000 years ago—up to three times as far back as most previous estimates. And the team of Australian researchers also found examples of rock art—small circular carvings—that they dated to about 60,000 years old, more than 20,000 years older than the most ancient known art of this kind.

Because most anthropologists believe that modern humans did not leave Africa until 100,000 years ago, these dates, if confirmed, would force a massive revision of human history. "If it could be demonstrated [that] people were in Australia more than 100,000 years ago, we would have to rethink everything we thought we knew about the later phases of human evolution," says Stanford University paleoanthropologist Richard Klein.

But that's a big if. The significance of the site hinges on its age, and many scientists are skeptical about the dating, which was done with a relatively new technique called thermoluminescence (TL). "Unbelievable," says archaeologist John Beaton of the University of California, Davis. "These dates are wildly out of line with everything else we know." Even archaeologist Rhys Jones of the Australian National University in Canberra, who last year made waves by dating two other Australian sites to 60,000 years with the same method (*Science*, 31 March 1995, p. 1908), warns that until more tests have been done, "we do not know how valid the present TL claims are."

The big news came out in a rather unorthodox fashion: A paper on the find was scheduled for the December issue of the British journal *Antiquity*. But editor Christopher Chippindale says someone at the Australian Museum in Sydney inadvertently leaked the story, and on 21 September the *Sydney Morning Herald* trumpeted the discovery of an "outback Stonehenge that will rewrite our history." *The New York Times* followed the next day, boldly asserting that the find held "signs of artists who predate *Homo sapiens*." The authors of the forthcoming paper—anthropologist Richard Fullagar of the Australian Museum, and Lesley Head and David Price of the School of Geosciences at the University of Wollongong in New South Wales—have been fielding a hail of phone calls, faxes, and e-mails ever since.

The paper describes a rocky site in the Kimberly area of northwestern Australia that is known to the local aborigines as Jinmium. There, Fullagar's team found buried artifacts, including pieces of ochre and tools made from carved rock, plus thousands of circles, all about 3 centimeters across, carved into boulders. The team dated the sediments with TL, which involves measuring electrons trapped in defects in quartz crystals; these electrons accumulate at a regular rate but are "bleached" out of the crystal by sunlight, so that the "clock" starts at zero when a sample

is buried. Researchers release the electrons by heating the sample, then measure the intensity of the brief glow produced to estimate the number of freed electrons.

The team found the artifacts in sediments they dated at between 116,000 and 176,000 years old. And, says co-author Head, a chunk of boulder bearing the circles lay in a stratum dated to between 58,000 and 75,000 years old. That would make the circles perhaps twice as old as the oldest known human art, the cave paintings at Chauvet in France.

All this has major implications for such issues as the definition of "modern" humans, because the ancient people must have boated to Australia from Indonesia—a feat that required technology and social organization, says Head. It also bears on how and where humans arose. Many researchers follow the "Out of Africa" theory, that modern humans arose in Africa, then spread across the globe sometime after 100,000 years ago, reaching Australia 40,000 to 60,000 years ago. Others, however, suggest that *Homo sapiens* evolved from precursors spread around the world, and the Jinmium dates add evidence for this "multiregional" hypothesis, says University of Michigan paleontologist Milford Wolpoff. "This kind of finding makes ultimate sense to me," he says.

But such conclusions depend on the dates, and TL dating is problematic because researchers can never be sure when the sample's "clock" started ticking. For example, a grain broken off from a long-buried chunk of sandstone might be mixed with the artifacts at the time they were buried. Because the sandstone's clock would already be running, it could make the artifacts seem much older than they are. Co-author Price defends the validity of his team's TL dates, noting that radiocarbon dates of charcoal fragments in the upper layers of the Jinmium site match the TL dates. But at the deepest levels, there are no controls such as bones or teeth that can be dated by other methods. "I can't imagine anyone calling this Australian Stonehenge or Australian anything at this stage," says archaeologist Henry Schwarcz of McMaster University in Ontario, Canada.

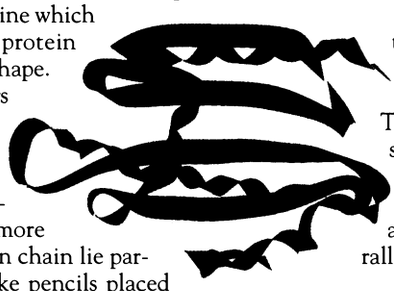
Still, earlier dates have been turning up for other Australian sites, notes anthropologist Alan Thorne of Australia National University. More data may come in soon, as Jones and Richard Roberts of La Trobe University in Melbourne are dating the Jinmium samples with a slightly different dating method, called optically stimulated luminescence (OSL). This method is similar to TL, but may be more reliable because the clock used is more likely to be reset to zero by even brief exposure to light, says Schwarcz. If the OSL dates confirm the TL ages, then the scientific debates will begin in earnest.

–Constance Holden

PROTEIN CHEMISTRY

Between the Sheets: Why Do Protein Strands Line Up?

The three-dimensional structures of proteins are as different as the sentences in a language. But just as different sentences share the same set of words, protein structure has a standard vocabulary: of helixes, U-turns, and so-called β sheets. To understand how protein chains fold up into their complex structures and mimic them to create new drugs and materials, researchers have to master that basic vocabulary. And that means learning how the properties of individual amino acids—the letters that spell out a protein—determine which structures form as a protein folds up into its final shape.

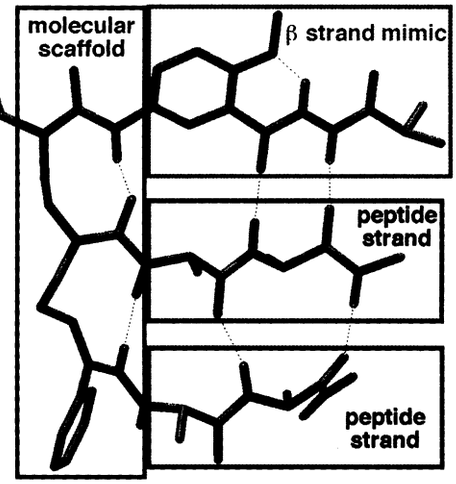


By now researchers know most of the rules governing the formation of helixes and U-turns. But β sheets—regions where two or more segments of the protein chain lie parallel to each other, like pencils placed side by side—have been more reluctant to give up their secrets. And so, in a growing subfield of protein chemistry, researchers are learning by doing: making their own small β sheets or disrupting natural ones in hopes of learning the key factors that hold them together.

One of the latest milestones in this effort came in late August at the American Chemical Society (ACS) meeting when researchers at the University of California, Irvine (UCI), reported designing a molecular scaffold that holds a trio of protein strands in a sheetlike arrangement—the largest artificial β sheet to date. By changing the chemical makeup of the strands to see whether the artificial sheet unravels, the UCI researchers hope to learn more of the principles of β sheet formation. Other researchers are taking a different approach toward reading the same rulebook: isolating the parts of natural proteins that fold into β sheets and systematically varying the amino acids at particular positions to see how the changes affect the fragment's sheet-forming ability. With researchers now beginning to reap the benefits of these efforts, "this field is really at the mountaintop right now," says Jeffrey Kelly, a chemist and β sheet expert at Texas A&M University in College Station.

To look at a β sheet's simple arrangement of parallel chains, you might not think it would hold many mysteries. But although the neighboring strands in a sheet sometimes lie adjacent to each other along the linear protein chain, simply connected by a sharp hairpin turn, more often they are from distant regions of the protein. They only become neighbors when the protein folds into its final structure and weak hydrogen bonds form between the strands, locking them together. As a result, few such sheets can simply be clipped out of a protein and studied separately. "That's what makes these things so hard to study," says James Nowick, who led the Irvine team.

But in a trio of studies over the last 2 years, Peter Kim and his colleagues at the Massachusetts Institute of Technology's Whitehead Institute analyzed one fragment of an immunoglobulin-binding protein known as G(GB1) that does naturally wrap itself into a β sheet.



Designer sheets. Parallel strands make up β sheets in the thiorodoxin protein *(top)* and a model compound *(above)*.

They genetically engineered bacteria to produce variants of the fragment in which one or more of the sheet-forming amino acids had been altered. They then looked at the structures of the resulting proteins to see whether the β sheets formed normally or not—and what amino acid properties were key to the difference. So far, they have learned that context is crucial: Amino acids such as valine and isoleucine, for example, seem to play a strong role in holding β sheets together when they are located in the middle