talking and exchanging DNA samples, if not collaborating. Thus, it was only logical that they should team up on this new venture.

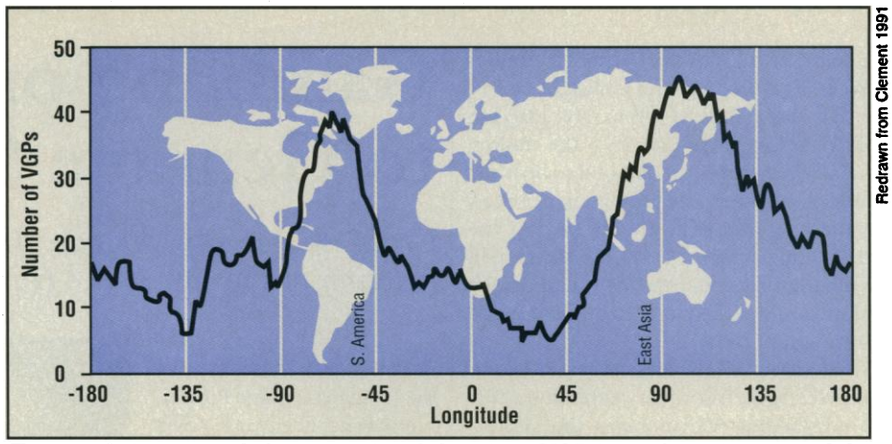
While the exact plan is still a matter of considerable debate (see box), the general idea is to collect blood and other tissue samples from 100 or so indigenous populations—in, for example, the Amazon, sub-Saharan Africa, and across southern Asia. "One hundred is a minimum," says Cavalli-Sforza, adding that the number could climb to 500, if money allowed. "Even at 100, you are leaving out some important populations." Within each group, the researchers would sample perhaps 100 individuals.

What they definitely don't envision is a planeload of Western geneticists descending on the jungle, collecting blood, and then disappearing. Rather, they hope to enlist the help of anthropologists, medical researchers, and local scientists who already have access to the more isolated groups. Already, says King, the group is thinking of what it can offer to the populations in return, such as medical supplies.

The bulk of the cost and the major technical obstacles will come from setting up the cell lines. The procedure itself is not complicated, he says, but the samples must be transported to a lab within a day or two—no small feat if they come from the upper reaches of the Amazon. The hope, he says, is to establish regional collection centers and train local workers in the technique, if need be. Eventually, all the cell lines would be collected in central repository, though the identify of each donor would be kept private.

Once the long-sought DNA is in hand, the group wants to determine genotypes of each individual for the same basic set of genes or DNA markers. This work might take several years and would probably be shared among numerous collaborators, says Cavalli-Sforza. After that, the anonymous DNA would be available to researchers around the world who wanted to use it, whether for investigating the population distribution of disease genes or for doing basic studies of evolution or human diversity.

Already, there are indications of the wealth of information harbored in the DNA of aboriginal peoples. Both Wilson and Cavalli-Sforza's data indicate that the prevailing view of race, which divides the world into blacks, whites, and so forth, is outmoded and mistaken, says Wilson. They and others have found that the genetic variation within a race is far greater than the variation between races. Says Berkeley colleague King: "The concept of race in America has a social meaning that does not correspond to its scientific meaning." She, like Wilson, predicts more surprises will emerge from their study of human variation. ■ LESLIE ROBERTS



Two roads to reversal. *Geomagnetic pole locations (VGPs) seen from sites around the globe cluster on two paths during a reversal some 730,000 years ago.*

A Core-Mantle Link?

Records of magnetic-field reversals point to a connection between the mantle and the underlying molten core

AT INTERVALS OF HUNDREDS OF THOUSANDS of years, Earth's magnetic field flip-flops, the north and south magnetic poles trading places. Geologists struggling to understand these reversals have concentrated on the churning liquid metal of the outer core, where the field is generated in the first place. They have paid little attention to the solid, rocky mantle encasing the core. Mantle and core, it seemed, were like ice floating on water—in contact but unlikely to influence each other.

Now researchers at a variety of institutions around the globe have stumbled on a hint that the mantle does leave its mark on magnetic reversals. They have found that as the poles wander from south to north or vice versa during successive reversals, they show a startling tendency to trace out the same paths across the surface of the planet. Something about the processes that generate or modulate the field must be persisting for millions of years, through reversal after reversal, the researchers realized. And that could only happen, they feel, with the help of the mantle, a far less mercurial layer of the deep interior than the core. Of course, the precise connection between mantle and core is far from clear, but if proven and understood it might shed light on the larger mystery of why the reversals happen in the first place.

The intriguing discovery of repetitive behavior during magnetic reversals emerged as paleomagneticians collected more and more geologic records that caught the field in the act of flipping. Ocean sediments and lava flows, accumulating layer by layer, capture snapshots of the field's orientation as they form. Most such records show the field in one of two orientations—either the present one, with magnetic field lines looping out of Earth's south geographic pole and into the north pole, or the reverse. But every few hundred thousand years or so, sediments or lavas record the 4000- to 8000-year period during which the field switches orientation. And these rarer specimens told scientists an interesting tale.

"We all started to see this startling pattern," says Bradford Clement of Florida International University (FIU). The presumption had been that there would be no consistency at all. The core churns too rapidly, researchers had thought, for any memory of a reversal to linger until the next one. During each reversal, the north magnetic pole as viewed from a given site should appear to follow a random path from one geographic pole to the other.

To Clement and colleagues it was an "astonishing thing" to find that the poles actually tend to follow one of two well-worn routes. One leads through North and South America; the other, less heavily traveled, path stretches across eastern Asia and Australia. Eric Tric of the Center for Studies in Weak Radioactivity in Gif-sur-Yvette, France, recently pointed out that fully two-thirds of 48 reversal records from the past 3 million years show the poles following one of these two paths. Despite its short memory, the core seems to recall where its magnetic poles should go during reversals hundreds of thousands or even millions of years apart.

The paleomagneticians suspect it is the mantle that reminds the core where the preferred pole paths are. In independent papers appearing this month, Clement of

FIU and Carlo Laj of the Center for Studies in Weak Radioactivity and colleagues point out that the mantle is the natural place to look for a long memory. Like the molten metal of the outer core, the solid rock of the mantle flows—but at centimeters per year, not the tens of kilometers per year of the core. If some irregularity were to develop in the mantle that could put its stamp on the field, it would persist long enough to guide reversal after reversal.

What aspect of the mantle could be responsible? Speculation has centered on several possibilities. Variations in the electromagnetic conductivity of the lower mantle—perhaps due to iron picked up from the core—could distort the field and channel reversing poles. Or the mantle might leave its mark by encouraging a persistent flow pattern in the core. Some workers think the base of the mantle is patterned with bulges and hollows, which could redirect core flow, the way mountains affect weather patterns. Others suggest that unusually hot and cold patches on the base of the mantle could shape core circulation, the way deserts or mountaintops affect atmospheric circulation.

If the mantle guided the reversals of the past few million years by influencing core flow, it may be doing so still. Laj points to flow patterns in the liquid metal at the top of the core, inferred by Jeremy Bloxham and Andrew Jackson of Harvard University from historical magnetic measurements. The flow seems to follow the same paths the reversals traced: It appears to be feeble beneath much of the Pacific Ocean but relatively strong along north-south paths beneath the Americas and East Asia.

In fact, Laj sees a good correlation between an existing feature of the lower mantle—its temperature, which other researchers have determined from the velocities of seismic waves—and the paths of past reversals. Two great lobes of unusually cold rock arc beneath the Americas and East Asia, forming a broken ring at a depth of 2300 kilometers, 600 kilometers above the core-mantle boundary. Some geophysicists interpret this ring of cold deep mantle as a huge pile of former ocean floor that has sunk into the deep mantle through the deep-ocean trenches that rim the Pacific.

If discarded ocean plate really does affect the magnetic field, the surface motions of plate tectonics are linked not just to the mantle but, through it, to the core itself. That would lend a remarkable unity to the layered Earth. ■ RICHARD A. KERR

ADDITIONAL READING

Bradford Clement, "Geographical distribution of transitional VGPs," *Earth Planet. Sci. Letts.* **104**, 48 (1991).

Carlo Laj *et al.*, "Geomagnetic reversal paths," *Nature* **351**, 447 (1991).

Gambling on a Shortcut to Genome Sequencing

Craig Venter says he can find all the human genes for a fraction of the cost of the Human Genome Project

ALMOST FROM THE START OF the Human Genome Project, a debate has been raging over whether to sequence the entire human genome, all 3 billion bases, or just the genes—a mere 2% or 3% of the genome, and by far the most interesting part. In England, Sydney Brenner convinced the Medical Research Council (MRC) to start with the expressed genes, or complementary DNAs. Brenner, who heads the MRC Molecular Genetics Unit in Cambridge, views sequencing the rest of the genome as "one of those problems we can and should leave to our successors."

NIH

Focusing on expressed genes. Craig Venter.

But the U.S. stance, from the outset, has been that the entire sequence is essential if we are to understand the blueprint of man. What's more, says James Watson, who directs the genome effort at the National Institutes of Health, existing tools for detecting cDNAs are so flawed that there is no chance of finding all of the genes without the full sequence. Lately, however, the U.S. stance has softened a bit, with both the Department of Energy and NIH venturing into cDNAs. Nonetheless, insists Watson, "cDNAs are not in any sense a replacement for genomic analysis. We feel that pretty strongly."

Now comes Craig Venter of the National Institute of Neurological Disorders and Stroke, who says that focusing on the expressed genes may be even more useful than expected (see p. 1651). It will provide much of the information being sought in the Human Genome Project—essentially, where and what the genes are—for a fraction of the cost, he claims. "It really moves the information from the genome project up by a decade or two." But if the reactions of his colleagues are any guide, the debate's not over.

Venter was convinced by the rapid progress being made in his ambitious new project to find and partially sequence every gene expressed in the human brain, thought to number 30,000. Venter, Mark Adams, and their colleagues started about a year ago, and so far they have partially sequenced, or "tagged," about 600 cDNAs, which are simply clones made from the messenger RNAs. Venter optimistically predicts he can wrap the whole thing up in a few years.

What persuaded Venter to try the cDNA approach was the enormous difficulty he and others were having in interpreting long stretches of DNA sequence. Last summer, hoping to turn up the Huntington's gene, Richard McCombie in Venter's group had sequenced a 60,000-base stretch from the region of chromosome 4 where it is thought to reside. Says Venter, "We found it is not trivial to find the genes, even if you have the sequence."

His new strategy—the "ultimate in simplicity"—offers a way around that problem, Venter says. It involves randomly selecting clones from cDNA "libraries," which theoretically contain all the genes that are switched on at a particular time in a particular tissue. Then the researchers sequence just a short stretch of each clone, about 400 to 500 bases, to create what Venter calls an "expressed sequence tag" or EST. The sequencing itself is trivial, says Venter, as it entails just one run on an automatic sequencing machine. The sequences of these ESTs are then stored in a database. Using that information, other researchers can then "recreate" that EST by using polymerase chain reaction techniques.

The ESTs contain enough information to enable investigators to search the databases for similar genes—the standard way to get a fix on what it is you have just found. The computer searches on the Venter group's first 600 clones turned up some intriguing similarities to known genes. But what is most exciting, says Venter, is that the clear majority of the expressed genes his group has identified have no match in the database. "They are new, totally unknown genes," says Venter. The ESTs also enable investigators to map the new clone to a particular chromosome, but the work is still slow and expensive, Venter says.

Venter calls his new effort "a bargain by