DNA Fingerprinting: Academy Reports

In its long-awaited report, the NAS crafts recommendations to shore up the scientific underpinnings of DNA fingerprinting and end the interminable courtroom debate

For several years now, leading scientists have waged heated courtroom battles over the reliability of forensic DNA fingerprinting—the powerful new technology that has been heralded as a tool of stunning precision, able to link the blood, semen, or hair left at the scene of a crime to a suspect's DNA. In case after case, the experts have argued over nearly everything about this new technology: the methods used to declare that two DNA samples match, the quality control practices of the labs that do the analyses, and, most recently, the statistical methods used to interpret a match.

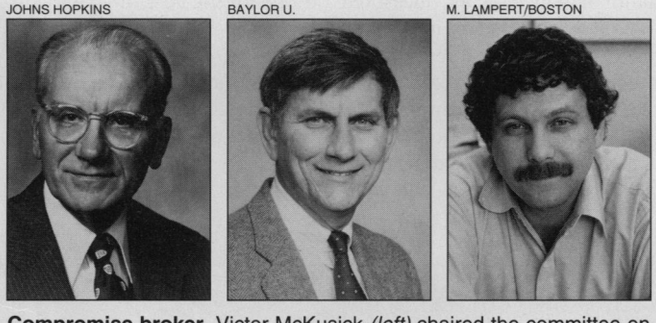
Countless dollars have been spent on expert witnesses, not to mention lawyers, in a series of pretrial admissibility hearings around the country. After weighing the competing claims of scientific experts, one court will find the procedures acceptable and the DNA evidence admissible, while the next court, often hearing from the same experts, will conclude just the opposite. And there has been no resolution in sight—at least not until now.

Even as these issues were being argued before the bench, the same battles were being fought, often with equal intensity, behind closed doors at the National Academy of Sciences (NAS), where a committee was created in 1989 to examine the whole range of technical and social issues surrounding forensic DNA typing. After much strife, a threatened minority opinion, and countless leaks of confidential drafts, the long-awaited report emerged this week, 7 months overdue. Described by NAS staff and committee members alike as one of the most contentious reports in recent years, the committee nevertheless achieved what at times seemed an impossible goal: a unanimous report.

And in perhaps its most significant achievement, the committee hammered out a compromise between the warring camps in the dispute over the statistical method to interpret a match—specifically, over the numbers so freely bandied around in court that the odds of two samples matching by chance are 1 in 5 million, or a trillion, or a quadrillion. In the report, the committee, chaired by Johns Hopkins geneticist Victor McKusick, offers a solution—a new and admittedly conservative way to calculate the odds—that it thinks could end the courtroom battles once and for all.

The committee also calls for sweeping changes to ensure that DNA evidence, because of its power and persuasiveness, is of the highest quality before it is admitted into court. The committee calls for vigorous quality assurance, with mandatory accreditation and proficiency testing, and says it should be overseen by scientists, not practitioners. It urges Congress to create an expert committee, again, largely composed of outside scientists, to vet new DNA technologies before they make it into court. And in a host of other recommendations, the committee nixes plans for a comprehensive national DNA profile databank as premature and affirms the privacy of genetic data.

What the committee does not recommend, as *The New York Times* mistakenly reported on 14 April, is that DNA fingerprinting be barred from the courtroom "unless a more scientific basis is established." The *Times* account, which came out 2 days before the report's scheduled release, prompted academy officials to call a hasty press conference on the same day to set the record straight about the report's conclusions. "I was very upset when I saw this article this morning," said chairman McKusick. "It seriously misrepresents our findings."



Compromise broker. Victor McKusick *(left)* chaired the committee on which Thomas Caskey *(middle)* and Eric Lander were at loggerheads.

Far and away the most contentious debate the committee encountered was on the statistics. At issue are just how accurate the estimated probabilities are—and how accurate they need to be. The question arises once a crime lab determines that two DNA samples match. This is done by examining the DNA at several sites where its sequence is known to vary. If all the sites match, it's "strong evidence" that both samples came from the same person, says the committee, but how strong? To figure that out, the lab calculates the frequency with which each sequence variation, or allele, occurs in the population to which the suspect belongs by examining, say, the Caucasian database. Then using what is known as the multiplication or product rule, the frequencies of the individual alleles are multiplied to calculate the frequency with which the complete pattern occurs in that population, often resulting in vanishingly small numbers.

But a number of leading population geneticists, including Richard Lewontin of Harvard and Daniel Hartl of Washington University, who fanned the flames with a recent article in *Science* (20 December 1991, pp. 1721, 1735, and 1745), say the numbers generated by this procedure are misleading and are based on misapprehensions of population genetics theory. They insist that populations contain subgroups in which the frequencies of the markers used in DNA fingerprinting vary dramatically from their frequencies in the population at large. And that, they say, means the likelihood of a match between samples may be grossly over- or under-estimated. Lewontin and Hartl further outraged those in the pragmatist camp by suggesting that the estimates shouldn't be used in court until populations are rigorously sampled to find out just what the marker frequencies are—an endeavor that could take 10 to 15 years.

The pragmatists, on the other hand, who include leading population geneticists like Ranajit Chakraborty of the University of Texas in Houston and Kenneth Kidd of Yale, along with FBI forensics experts, concede that population substructure may in fact exist, but they insist that current procedures are conservative enough to compensate for it. And a spate of recent studies, while not putting the nail in the coffin, show no sign of substructure for at least the markers now in use.

The NAS committee fell out roughly along those lines as well, with two strong-willed members holding down the extreme ends: Population geneticist Eric Lander of the Whitehead Institute took the cautious view, and molecular geneticist Thomas Caskey of Baylor, the pragmatic. At the outset, says

Philip Reilly, a lawyer and geneticist at the Shriver Center for Mental Retardation in Waltham, Massachusetts, the Lander camp held sway, and early drafts of the statistics chapter were very conservative. In fact, two committee members were so disgruntled that they leaked an early draft of the statistics chapter to FBI scientist Bruce Budowle, prompting outraged letters from his boss, John Hicks, director of the FBI's crime laboratory. Having Lander coordinate that chapter is like having "the fox guarding the hen house," Budowle complained to *Science*.

The final product, committee members agree, is a more moderate one that they all could live with. The evolution came not from a change in politics or external pressure as sometimes alleged, the members say, but simply from new data that emerged during their deliberations. In the final version, the committee does assume that population substructure exists, as the cautious camp argues, but they devised a "practical and sound" approach for accounting for it: using the multiplication rule, but in combination with what they call the "ceiling principle." This, they say, will ensure that the frequency estimates are biased in favor of the suspect.

It would work this way. First crime labs must establish the ceiling, or upper bound, frequency for each allele at each site in 15 to 20 genetically homogeneous populations, such as English, German, Russian, Vietnamese, and Puerto Rican. This would be done by collecting blood samples and establishing cell lines from 100 individuals in each population. When it comes time to calculate the odds of a match, the lab would use the highest frequency found in any of the populations, or 5%, whichever is higher. Collecting the samples should take about a year and cost about $1 million, says McKusick. In the interim, the group recommends a shortcut—using the highest frequency found in any of three major population groups in the United States, or 10%, whichever is higher.

The end result, says study director Oscar Zaborsky, is that the most "extravagant" probability estimates will be replaced with numbers in the range of 1 in several hundred thousand or a million. "It tones down the hype but will still be useful." Lander agrees: "It is sufficiently conservative, yet sufficiently usable. I don't think anyone would fight it."

In a number of far less contentious recommendations, the committee came out strongly in favor of mandatory accreditation of DNA typing labs and mandatory proficiency testing. The problem, the committee says, is that this new technology burst on the scene so rapidly that there are essentially no standards and no regulation—a disturbing prospect since the largest potential source of error lies in poor laboratory practice. The group urges Congress to adopt legislation requiring accreditation of all DNA typing labs, and recommends that the courts allow DNA evidence to be admitted only if the laboratory has been accredited. They delegate the task of setting up the program to the Department of Health and Human Services, in consultation with the Department of Justice—but not to Justice directly, as one bill before Congress now suggests.

Nearly everyone on both sides of the legal debate agrees that the current procedure for vetting new technologies—a string of interminable pretrial admissibility hearings—is not the way to go. To avoid these expensive courtroom fights in the future, the committee calls for the establishment of an ad hoc expert group, a National Committee on Forensic DNA Typing, whose primary job would be to evaluate new approaches. This committee should also oversee the collection of blood samples for the population studies, says the committee, and advise the courts on statistical questions as well. As they see it, the committee would be composed of molecular geneticists, population geneticists, ethicists, and lawyers, and would be housed in the National Institutes of Health or the National Institute of Standards and Technology, with support from the National Institute of Justice and the National Science Foundation.

The committee clearly hopes its new report will be the final word. And to McKusick, the fact that this disparate group was able to reach a consensus bodes well for the report's reception.

The committee's hard-earned compromise drew a tepid response from the FBI, the major practitioner of DNA typing and one of the report's sponsors. It's no secret that the FBI hated the November 1991 version that was leaked to them, which Budowle blasted as a "tainted document" that was skewed to the defense. But in another hastily called press conference on 14 April, Hicks said the bureau is "pleased with the report," although when pressed he wouldn't endorse it.

Nevertheless, the last-minute revisions of the report seem to have ameliorated most of the FBI's concerns. And that could be good news for everyone. Says committee member Reilly: "Tactically, it is unwise for them to oppose the report. It could cost them in court. If the FBI can live with it, this would close the door on much of the criticism from the defense side."

–Leslie Roberts

HUMAN GENOME

Why Watson Quit as Project Head

As predicted in last week's *Science*, James Watson has resigned as head of the genome effort at the National Institutes of Health (NIH). The resignation comes in the wake of a long-running feud with NIH director Bernadine Healy, punctuated by recent charges—and denials—of financial conflict of interest.

Watson resigned on 10 April, saying simply that, "Having accomplished this goal of launching the project, the time has come for me to step down." In a statement accepting his resignation, Healy replied: "Dr. Watson is an historic figure in the annals of molecular biology, and the National Institutes of Health has benefited from his leadership." Yet those carefully crafted words belie the tensions and animosity that led to Watson's departure. *Science* spoke with both Watson and Healy about the events leading up to the split. As will come as no surprise to their friends and colleagues, their versions are miles apart.

Rumors spread the first week in April that Healy had fired Watson over the alleged conflicts—his investments in several biotech firms including Amgen Inc. and DuPont-Merck Pharmaceuticals. Healy denies that, insisting that the two never discussed possible conflicts of interest until Watson resigned. But Watson, his friends, and his lawyer tell a different story. They maintain that Healy alleged conflict of interest to force Watson out because of his vehement criticism of her policies—specifically, NIH's attempt to seek patents on thousands of gene fragments (*Science*, 11 October 1991, p. 184). So while Healy's denial may be accurate, says Watson, she is splitting hairs: "She created conditions by which there was no way I could stay."

As Watson tells it, the patenting episode boded disaster right from the start. He was offended because Reid Adler, the director of technology transfer at NIH, filed the application—presumably with Healy's blessing—without bothering to inform him, even though it had major ramifications for the Genome Project. And Healy was clearly enraged when Watson began denouncing the plan as idiotic and destructive to the project, the biotech industry, and international relations. Faced with a groundswell of criticism here and abroad, Healy summoned Watson to her office last fall and told him to keep his criticisms "within the family." Since then, claims Watson, Craig Venter, the NIH researcher whose lab isolated the gene fragments, has become Healy's adviser on the Genome Project, while Healy made it very