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LETTERS

DNA Fingerprinting: The NRC Report

Peter Aldous's News & Comment article about the National Research Council (NRC) committee's report on DNA fingerprinting (*1*) (News & Comment, 5 Feb., p. 755) misconstrues the committee's goal. For scientific evidence to be legally admissible in court, it must satisfy the test that the methodology be "generally accepted in the scientific community," that is, that there is no significant controversy about the validity of the method. Early on, the NRC committee recognized that there was significant controversy brewing over DNA fingerprinting—a judgment abundantly confirmed by regular eruptions in *Science*. [Indeed, several state appellate and supreme courts have excluded DNA evidence citing the news and peer-reviewed pages of *Science* to prove the lack of "general acceptance" (see, for example, *2*).]

In order to ensure the admissibility of this important technology, the NRC committee sought to define common ground, namely, a standard of practice so conservative as to ensure that there would be no serious scientific argument that the evidence could be said to *overstate* the case against a defendant. We anticipated that some scientists would argue that the standard *understates* the evidence, but decided that (i) their arguments had merit but were not absolutely definitive (and the current round of articles adds little to the submissions these same authors made to the committee) and (ii) any loss of statistical power could be offset by testing one or two additional genetic loci.

Accordingly, it comes as no surprise to learn that the original proponents of a more liberal approach to population genetics now decry the committee's decision as "illogical" or "arbitrary." The committee prescribed an upper bound of 50:1 for the contribution of each genetic locus to the overall odds on the basis of quantitative estimates (of the effects of sample error and genetic drift) that indicated this would make adequate allowance for fluctuations among population subgroups. To be sure, all margins of safety involve some element of judgment, but this does not render them "illogical" or "arbitrary." In this case, the NRC committee simply concluded that the chosen upper bound sufficed to eliminate serious scientific objections to the population genetic statistics (whether based on theoretical or empirical grounds) while still allowing odds of up to 6,250,000:1 for a match at four genetic loci.

The NRC committee has clearly achieved its goal. DNA fingerprinting evidence prepared and presented in accordance with the NRC report is and should be legally admissible in all U.S. courts because it meets the test of "general acceptance" (notwithstanding that some would accept a looser standard). Even courts that cited previous controversies when they excluded DNA fingerprinting evidence have acknowledged that the NRC report now provides the basis for admissibility.

Critics are welcome to try to achieve "general acceptance" of a looser standard for DNA fingerprinting. However, this may be slow in coming, not least because, according to Aldous's article, the critics each prescribe a different solution. More important, a looser standard will not significantly increase the power of forensic DNA typing in courts (which is already sufficient to obtain convictions against guilty defendents), but it will likely provoke continued litigation that will hamper the use of this important and powerful criminalistic tool.

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1. Committee on DNA Technology in Forensic Science, *DNA Technology in Forensic Science* (National Academy Press, Washington, DC, 1992).
2. *California* v. *Barney*, 8 Cal. App. 4th 798 (1992).

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Directed Mutation

Any challenge to the conventional wisdoms of science must expect to face some opposition; most beliefs have been hard-won and they should not be discarded lightly. But the defense of orthodoxy by Richard E. Lenski and John E. Mittler (Articles, 8 Jan., p. 188) is surely too selective and partisan to be useful.

In 1988, my co-workers and I found that populations of bacteria undergoing selection for a particular phenotype seemed to accumulate the appropriate mutations without at the same time accumulating unselected mutations (*1*). Our paper provoked an outcry because, although there had been no test to see if cells have any special way of producing