ject. Since the legal system often turns to prestigious periodicals such as the *Journal* for guidance on technical matters, it is important that any confusion created by Lander's comments be clarified.

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0002-9297/91/4904-0023$02.00

Am. J. Hum. Genet. 49:892–893, 1991

A Response to Lander: The Courtroom Perspective

To the Editor:

As one of the prosecutors in the case of *United States v. Yee*, I read with great interest Lander's invited editorial entitled "Research on DNA Typing Catching up with Courtroom Application." As you may know, *United States v. Yee* involved what has been described as the most significant pretrial admissibility hearing on forensic DNA typing conducted to date. In *United States v. Yee*, the 12 expert witnesses included three population geneticists—Lander, Hartl, and Lewontin—named in the invited editorial; and the DNA evidence was still ruled admissible for consideration by the jury, despite the concerns raised by these witnesses.

My purpose in writing in response to the Lander editorial is not to rub anyone's face in the *Yee* decision. Nor is it to challenge or question the scientific assertions contained in the editorial, as I am obviously not qualified to do so. Instead, I am responding because the editorial does not address the issues of population substructure *in the context of the courtroom setting*, which is the only conceivably relevant context when the subject is forensic DNA typing. By ignoring the courtroom setting in his discussion of the population-substructure issue, Lander has made the substructure issue seem far more significant than it truly is in the debate over the validity of forensic DNA testing.

The typical courtroom setting which is ignored by Lander is this one: A suspect is arrested and charged with a violent crime and claims that the police have arrested the wrong person. Other than denying involvement, the suspect relies on the Fifth Amendment and says not another word to the police. A DNA test demonstrates a possible link between the suspect and biological evidence left at the crime scene. The jury is very much interested in this possible link (at a minimum, it means that the suspect cannot be excluded as a possible perpetrator), and they are in need of some way to assess the significance of the fact of a match. If we assume, arguendo, that Lander's (1991, p. 821) suggestion to study "ethnically distinct populations" has been fully implemented and that substructure has, in fact, been found, the question becomes this: What is the relevant subpopulation which should be used to estimate the frequencies and to convey to the jury whether the particular DNA pattern is common or rare? Is it the group to which the suspect belongs? That certainly is a possibility, but the prosecutor and the police have no idea what ethnic group or mix of groups the suspect belongs to, because the suspect is relying on his Fifth Amendment right not to talk. Do the police and prosecutor then simply guess the ethnicity of the suspect? Then again, why is the suspect's ethnic subgroup the relevant group in a case when the suspect is saying that he or she did not commit the crime and did not leave the biological evidence and that someone else did? Is it not the case that the subgroup which contains the true perpetrator—or which at least contains the class of persons who could have committed the crime—is the correct subgroup? If the correct subgroup is not the defendant's ethnic group but is the ethnic group which contains the class of potential perpetrators, how do we determine who the class of potential perpetrators is? And once we have accomplished that investigative miracle, how do we determine the ethnic makeup of the class of potential perpetrators?

The above questions are very real questions which occur in the real world of the courtroom, and they will not be answered by a flood of data on ethnically distinct subpopulations. Such data may answer questions of legitimate academic interest, but a jury's search for the truth will hardly be aided by such data, because the precise, relevant ethnic subgroup will rarely, if ever, be readily apparent. The jury needs to get a sense of whether a particular multilocus pattern is a common or rare event in the world and it gets this sense from estimates based on data bases differentiated solely on the basis of racial lines just as readily as it will ever get it from estimates based on data bases differentiated on the basis of some mythically relevant ethnic lines.

I do not belittle the importance of studying interethnic genetic variation in terms of VNTR genes. I do, however, belittle the effort to bootstrap from a perceived lack of study in this regard to a conclusion which the defense was unable to impress on the court in *United States v. Yee*—i.e., the conclusion that the fact of a match is irrelevant absent meaningful population data and that, since (because of possible substructure) the population data are not meaningful, DNA evidence is irrelevant. DNA evidence is highly relevant as it is currently being presented in our courts, and further studies of ethnic variation will neither diminish nor enhance its relevance to any meaningful extent.

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Am. J. Hum. Genet. 49:893–895, 1991

Comments on DNA-based Forensic Analysis

To the Editor:

I wish to respond to Eric Lander's (1991) invited editorial recently published in the AJHG *Journal*. I am concerned that this editorial does not contribute to solutions but, instead, confuses the issues.

In my opinion, there are four major scientific issues in application of DNA personal identification technology; they are (1) the scientific principles backing the DNA methods, (2) the criteria which determine match, mismatch, and inconclusive data with regard to RFLPs of forensic sample and suspect, (3) the "significance of the RFLP(s) match," and (4) quality control and assurance of data.

The questions related to issue 1 have been reviewed by the U.S. Congress OTA (1990, pp. 7–8), with the following excerpted conditions: "The Office of Technology Assessment (OTA) finds that forensic uses of DNA tests are both reliable and valid when properly performed and analyzed by skilled personnel." The National Academy of Sciences (NAS) will report its review shortly. The questions related to issue 2 have been studied and reported in the paper by Budowle et al. (1991). Each forensic laboratory is expected to establish, on the basis of laboratory performance of its protocols and staff, its standards for match. I find their decisions on match, mismatch, and inconclusive to be rational. The questions related to issue 3 have been considered in the OTA report, and the following summarizing conclusions have been made: That scientific principles of population genetics can be applied to forensic DNA analysis is not in question, but how best to apply which principles to RFLP analysis is under debate. Disagreement exists as to the extent to which such debate can or should be resolved (OTA 1990). The NAS will report its review shortly. The questions related to issue 4 will be reviewed in the NAS report and have already been published in the Federal Bureau of Investigation's TWGDAM and Association of Crime Laboratory Directors (ASCLAD) quality-assurance policy statements.

Lander argues that "Caucasian," "black," and "Hispanic" are not adequate as genetic classifications of population data bases. I would argue that they are operational genetic classifications which are readily understood in the courts. The possibility of population substructure and significant allelic variation has been proposed by Lewontin as a possible flaw in calculating significance of RFLP(s) match. Lewontin has always chosen outrider alleles to make this point. Lander's editorial implies that we lack significant subpopulation data to make an estimate of match significance. I disagree. I feel that it is possible to make an estimate of significance of RFLP(s) match by using available data bases. Let me illustrate the methods of that estimation.

1. One could ignore population genetics. Using a data base of individual RFLPs, one could argue to the courts that a given matching haplotype had or had