

# SCIENCE

# LETTERS

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## DNA Fingerprinting Report

In the News & Comment article “Geneticists attack NRC report as scientifically flawed” (5 Feb., p. 755), Peter Aldhous describes some of the criticisms being leveled at the National Research Council (NRC) report on the forensic use of DNA. The article ends with a quote from David Kaye that “nobody’s disputing that some number should be presented” when evidence of a matching profile is entered into court. Kaye is being overly optimistic. On 26 January 1993 District Court Judge Edward Lynch in Minnesota did indeed refuse to allow numbers to be presented (1).

Judge Lynch was told that one locus in each of two databases compiled by the Minnesota Bureau of Criminal Apprehension showed some evidence of departures from Hardy-Weinberg equilibrium. He was then misinformed that the NRC report would require the entire databases not to be used. The lack of logic in that chain of reasoning becomes clear when it is realized that it will always be possible to find a human locus out of Hardy-Weinberg equilibrium. This should not prevent use being made of all those loci that are in equilibrium. Judge Lynch’s decision follows from a lack of guidance in the NRC report as to the appropriate course of action when some disequilibrium is found, and this finding will be very common when as many as 20 databases are tested for equilibrium at each locus, as required by the report (multiple-test corrections are not called for, as the separate tests are not true replicates).

There is a simple solution. The profile frequency could be calculated in each database separately, using only the independent alleles. A conservative profile frequency estimate is then the maximum of the estimates from each database.

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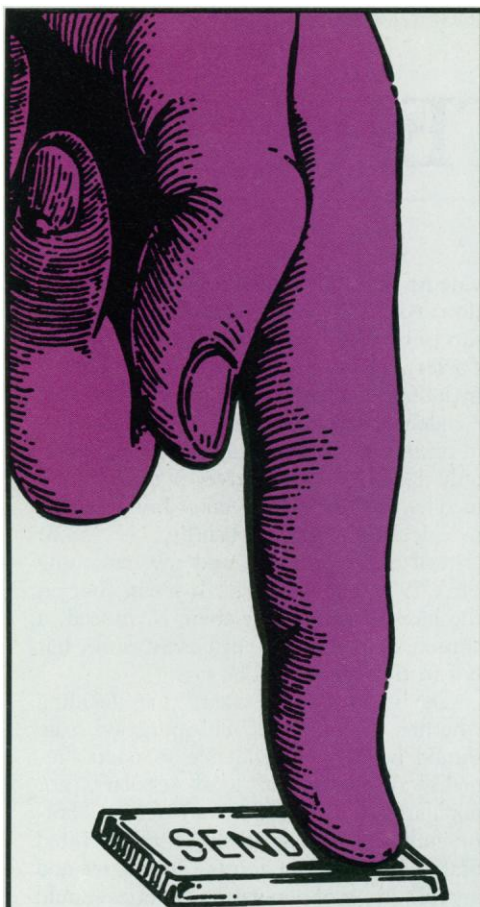
1. *State of Minnesota v. Robert Joseph Guevara*, Court File K9-92-1873, First Judicial District.

The critique that B. Devlin *et al.* (Policy Forum, 5 Feb., p. 748) aim at the NRC report on DNA typing (1) is itself open to some criticism. Devlin *et al.* assert a “consensus” favoring the multiplication rule for estimating genotype probability, but pro-

vide no supporting evidence or documentation. As it happens, an informal telephone survey by the population geneticist Charles Taylor (2) of 33 population geneticists, including four members of the National Academy of Sciences and 16 persons cited in textbooks of population genetics, found only 11 (33%) supportive of the method used by the Federal Bureau of Investigation to calculate match probability, 19 (58%) critical of the method, and the remaining three (9%) uncommitted. It seems that on the basis of this survey there is, indeed, a consensus in the sense of Devlin *et al.*, but not in the direction they say.

Devlin *et al.* also assert that deciding whether or not the multiplication rule should be used as evidence in court “remains the venue of legal scholars, not population geneticists or statisticians.” Fortunately for the citizens of the United States, four superior courts (3) disagree and say that issues of population genetics should be resolved by population geneticists. Finding no evidence of consensus among population geneticists, the justices have ruled that convictions based on faulty statistics should be set aside.

Scientifically, the critique of Devlin *et al.* is a rehash of old arguments and inadequate data discussed at length in previous issues of *Science* (4, 5). They attempt to refute the statement of one of us (R.C.L.) (6) that there is approximately as much genetic variation between ethnic groups as between major races by citing a number of authors who are characterized as having “failed to replicate his finding” or having reached “a conclusion very different from Lewontin’s,” but without providing any actual numbers. An examination of the works cited, however, leads to a different conclusion. Mitton (7) does not, in fact, use a measure of genetic variation and, in any event, gives no data on ethnic group differences. Nei and Roychoudhury (8) give no total values for the components, but these can be calculated from their paper by averaging. The resulting values are 0.03 and 0.02 for between-race and between-ethnic group distances. Smouse *et al.* (9) give values of 4.40 and 2.36 for between-race and between-ethnic group average distances. Latter (10) uses three different methods of estimating the variation between races and between ethnic groups, one of which is the same as Lewontin’s (6). Latter’s three sets of values are 0.104:0.056, 0.075:0.055, and 0.096:0.066. These values



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should be compared with Lewontin's values of 0.063:0.083 (6). We leave it to the reader to judge whether the differences represent biologically significant discrepancies. Averaging all of the estimates, after normalization of the values of Smouse *et al.* to percentages, yields 0.076:0.057, or a ratio of 1.3:1 of genetic variation among major races to genetic variation among ethnic groups. We reiterate the conclusion that there is approximately as much genetic variation among ethnic groups within major races as there is among the races.

Devlin *et al.* also say they are against additional research to obtain data relevant to population substructure for DNA-typing genes because they believe that new data will not resolve the population genetics debate. But new data have already been obtained (11) that categorically support our original conclusions (4), as well as those of the NRC report (1), and refute the arguments of Devlin *et al.* The data are from populations of ethnic Finns and Ethnic Italians as well as an ethnically heterogeneous Causasian population whose DNA was typed using several highly polymorphic markers (11, 12). The principal findings were as follows. (i) The ethnic groups often have significant differences in allele frequency distributions. (ii) Genetic differences between the ethnic groups could not be detected by conventional tests of Hardy-Weinberg equilibrium or linkage equilibrium—the tests are virtually useless for detecting substructure in human populations. (iii) When probabilities of DNA profiles were estimated using the product rule with frequencies from the “wrong” ethnic database (Italian database for Finns, Finnish database for Italians), 77% of the estimated probabilities were artificially small—34% by a factor of more than 10 and 4% by a factor of more than 100. (iv) When probabilities of DNA profiles were estimated using the product rule with frequencies from the mixed Caucasian database, 80% of the estimates were artificially small. Points (iii) and (iv) contradict the assertions that “even when there is substantial substructure, the multiplication rule still yields adequate approximations” and that “the methods used in court are already conservative.” On the contrary, the new data demonstrate that the methods currently used in court are not conservative—they are systematically prejudiced against the defendant—and no amount of argument will make them conservative.

As for the interim ceiling principle recommended by the NRC (1), we agree that the lower bound of 10% used for allele frequencies is arbitrary. Everyone agrees that it is conservative, and some believe

that it is too conservative. Whether or not it is excessively conservative is a matter that can be resolved empirically by ethnic group studies of the kind abjured by Devlin *et al.* In the Finnish and Italian data, the interim ceiling principle was not excessively conservative for genotype probabilities greater than  $5 \times 10^{-6}$ . Only additional data will reveal the general robustness and degree of conservatism of the interim ceiling principle. The call for “no new data” will only guarantee more contentiousness and controversy.

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10. B. D. H. Latter, *ibid.* **116**, 220 (1980).
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12. These data have been provided to the Federal Bureau of Investigation and to the Forensic Branch of the British Home Office for independent analysis.



### Extraterrestrial Intelligence

Ernst Mayr (Letters, 12 Mar., p. 1522) argues against the NASA search for extraterrestrial intelligence (SETI) on the basis that “only one of the approximately 50 billion species that have lived on Earth was able to generate civilizations. Among these approximately 20 civilizations, only one developed electronic technology.” The implication is that Earth history suggests that the evolution of intelligence and technology is rare, and so it would be fruitless to search. The quoted facts actually tell us something different and trivial: The first species to develop intelligent civilizations will discover that it is the only such species. Should it be surprised? Someone must be first, and being first says