

$4\sigma_1\sigma_2\rho_x$. As a second condition on matching we then used $|\delta_2 - \delta_1| < 4\tau$.
10. D. Bigbee, Federal Bureau of Investigation, personal communication.

Response: Since 1988, the FBI has analyzed blood samples from individuals of different population groups to establish a DNA database that is used to provide estimates of DNA profile frequencies for these groups. It is the intent of the FBI in the development of all its databases to use only samples from unrelated individuals. When duplicate samples or samples from identical twins are unintentionally included, it is proper to remove one of the matching profiles.

The FBI receives samples for its databases from different sources: Baylor University, Texas College of Osteopathic Medicine, Miami Red Cross, California Department of Justice, and elsewhere. However, the names of the individual donors are deleted before submission to the FBI to maintain the anonymity and privacy of the sample source. Once received by the FBI laboratory, the samples are given individual identification numbers. The quality of these records from this point on is not at issue; they are complete and correct. Accidental duplications that have occurred are not a consequence of the record-keeping of the FBI laboratory.

To ensure that no duplicate samples made it through the sample collection process, the FBI searched its database of samples from more than 2000 individuals with a computer matching program and found 25 matching sample sets. The FBI attempted to account for these duplicates by contacting the contributing laboratories. The Texas College of Osteopathic Medicine confirmed that 22 of the 25 matched pairs came from the same individuals. The Miami Red Cross could not confirm that the remaining three matched pairs came from the same individuals.

To address the possibility that the three matched pairs were in fact duplicates, the samples were typed by the FBI and also by Cellmark Diagnostics with additional loci. In this regard, Sullivan states that I "asked Cellmark Diagnostics . . . to examine the matching samples. Its probes also yielded unclear results. The Florida matches were then deleted from the databases, even though there was no explanation for their occurrence." This statement misrepresents evidence presented in *Minnesota v. Johnson* (1), in which Sullivan was the defense attorney.

The effort of the FBI laboratory to determine whether or not these matching samples from Florida were indeed duplicates was summarized in an affidavit submitted in *Minnesota v. Johnson*. It states (1),

additional probings with different probes were performed on these samples at the FBI. In

addition, these three duplicate pairs were sent to Cellmark Diagnostics so that additional probings using different probes and a different restriction enzyme could be performed; the profiles from Cellmark Diagnostics with respect to the duplicate pairs were consistent using their cocktail approach.

The three pairs in question exhibited variable number of tandem repeats (VNTR) profiles consistent with the hypothesis that each pair was derived from the same individual on the basis of at least seven VNTR loci typed by the FBI and an additional multilocus cocktail typed by Cellmark Diagnostics (1, p. 90). The FBI concludes that these three sample pairs are from the same individuals or from identical twins. This process was completed 6 to 8 months before the FBI sent its database to Risch and Devlin.

Sullivan also states that the removal of duplicates "is not an isolated practice. Budowle testified in *United States v. Yee* [2] that the FBI ran its match program over its South Carolina black database and found a large number of matches." He faults the FBI's record-keeping again and omits the fact that the Medical University of South Carolina (MUSC) has acknowledged that it accidentally forwarded a large number of duplicate African-American samples to the FBI. Because of the anonymity afforded the sample donors, MUSC could not confirm which of the samples were duplicates. This event motivated the FBI to develop a computer program to search the database for samples matching across all VNTR loci. The program first was tested on other database samples; it detected no matching samples, and none was expected. Thereafter, the South Carolina African-American database was searched, matched profiles across all loci were identified, and the duplicates were removed. By comparing the South Carolina African-American database with and without the duplicate samples, the FBI ensured that the two databases were statistically similar at each locus analyzed (3). Even so, a subsequent administrative decision was made to remove all of the South Carolina African-American samples from the African-American database.

Finally, Sullivan makes a puzzling reference to the Karitiana population study (4). Any reference to the Karitiana should be accompanied by the caveat that the Karitiana are an isolated, inbred kinship living in the Amazon basin of western Brazil. The members of the kinship are much more closely related than family members found in populations in the United States. There is no relevance of data about matching probabilities derived from the Karitiana to that of unrelated individuals in the United States.

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REFERENCES AND NOTES

1. *Minnesota v. Johnson*, S.I.P. No. 89-072014 (Minnesota District Court, Fourth Judicial District, 1991).
2. *United States v. Yee*, 129 Federal Rules Decisions 629 (Northern District of Ohio, 1990).
3. We used a chi-square test to determine homogeneity and found P values from 0.991 to 1.00 for D1S7, D2S44, D14S13, D16S85, and D17S79. As there was not statistical difference between the database with duplicates and with duplicates removed, there is no anticipated difference in the final estimate of the likelihood of occurrence of a DNA profile with either database.
4. J. R. Kidd, F. L. Black, M. Weiss, I. Balazs, K. K. Kidd, *Human Biol.* 63, 775 (1991).

Corrections and Clarifications

In the photograph on page 1142 accompanying the article "Chemical prospecting: Hope for vanishing ecosystems?" by Leslie Roberts (Research News, 22 May, p. 1142), Gerald Bills of Merck was on the right and Rodrigo Gamez of INBio was on the left.

In the News & Comment article by Richard Stone "Peer review catches congressional flak" (15 May, p. 959), Senator Robert C. Byrd (D-WV) and Representative William Natcher (D-KY) were incorrectly identified as having ordered a review of National Science Foundation (NSF) grants. The NSF grants were targeted by Byrd's Senate Appropriations Committee, as reported in Joseph Palca's article "Congress sends a message" (News & Comment, 29 May, p. 1274).

In Richard Stone's News article "Hard times in the promised land" (8 May, p. 728), the Russian city Novosibirsk, in Siberia, was incorrectly stated to be in Ukraine.

In the acknowledgements (note 25, p. 221) of the report "Centriole duplication in lysates of *Spisula solidissima* oocytes" by R. E. Palazzo et al. (10 Apr., p. 219), the American Cancer Society's grant to R.E.P. (JFRA 162121) was incorrectly stated to be from the American Chemical Society.

In Robert Pool's article "Bringing the computer revolution down to a personal level" ("Computing in Science" special section, 3 Apr., p. 55), the **Axiom** symbolic math program should have been listed as being available from the Numerical Algorithms Group in Downers Grove, Illinois.

In the news briefing "The world's most prolific scientists" (17 Jan., p. 283), Arnold L. Rheingold, a crystallographer at the University of Delaware, was inadvertently left off the list of the top 20 most prolific scientists. The Institute for Scientific Information has corrected its list and states that Rheingold published 391 articles and other scientific communications between 1981 and the end of 1990. He should have ranked 13th on the list.