Letters to the Editor

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DNA Typing in the Forensic Arena

To the Editor:

In his recently published article, "DNA Fingerprinting for Forensic Identification: Potential Effects on Data Interpretation of Subpopulation Heterogeneity and Band Number Variability," Cohen (1990) presented a compelling case for the exercise of caution in the statistical analysis of DNA "fingerprinting" data. In particular, he questioned the statistical validity of the breathtakingly small probabilities (10^{-8}–10^{-12}), reported by several DNA forensics laboratories, for the false identification of suspects in criminal cases, given a "match" between DNA band patterns identified as "suspect" and "evidence" on an autoradiogram. I would like to voice an additional concern—namely, that the reported probabilities do not take laboratory error into consideration as a source of false matches. This issue is particularly germane, since false match rates (due to laboratory error) in excess of one sample in 50 have been identified through blind proficiency testing of several DNA-typing laboratories (California Association of Crime Laboratory Directors DNA Committee 1988, 1990). In fact, a simple analysis (table 1) of the probability that an observed match is a false one leads to the conclusion that, if the laboratory error rate is much larger (as is usually the case) than the frequency of a given band pattern in the general population, the probability of obtaining a false match is *independent* of the population frequency, instead being given simply by the laboratory error rate. Thus, the prejudicial value of a reported "one-in-a-billion" probability of a false match far outweighs the probative value of the test itself.

The concern raised above is in no way intended to cast doubt on the utility of DNA typing in forensics; rather, addressing the problem of laboratory error through the development of laboratory policy should help to strengthen the use of DNA typing in the forensic arena. To this end, the following three measures should be implemented: (1) All laboratories should subject themselves to external, blinded proficiency studies on a regular basis and should publish or make available values for their error (false match/no match) rates. (2) Whenever possible, evidentiary samples should be split and sent, as independent samples to either (*a*) the same laboratory or (*b*) more than one laboratory. This procedure should effectively reduce the probability of a false match and should uncover laboratory errors. (3) Results of DNA typing should always be reported as the sum of the laboratory error rate and the estimated frequency of recurrent band patterns in the relevant population. Judges and juries must be told that the probability of a false match cannot be considered in the absence of knowledge of the laboratory error rate. Adherence to this third recommendation would also prevent untested laboratories from premature involvement in casework. Essential to the successful implementation of the above measures is the establishment of appropriate, independent proficiency-testing procedures, an important issue that is outside of the scope of the present communication.

Although the example presented above has considered only the case of a false match, the principle of in-

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Table 1

Overall Probability That Visual Match between DNA Band Patterns, Identified as "Suspect" and "Evidence" on Autoradiogram, Represents False Match

Probability	Suspect Did Not Contribute Evidentiary Material		Suspect Did Contribute Evidentiary Material (true match)
	False Match by Coincidental Pattern	False Match by Lab Error	
Anterior	Coincidental pattern in general population, P_R	Different band patterns, $1 - P_R$	Identical band patterns, 1
Conditional	No lab error, $\leqslant 1 - P_E$[a]	Lab error leading to false match, P_E	No lab error, $\leqslant 1 - P_E$
Joint	False match due to recurring patterns, $\leqslant P_R \times (1 - P_E)$	False match due to lab error, $P_E \times (1 - P_R)$	True match, $\leqslant 1 - P_E$
Posterior probability of false match: $\cong P_R + P_E \times q > P_R + P_E > P_E$, where $q \geqslant (1 - P_R)/(1 - P_E) > 1$[b]			

[a] Overall laboratory error rate will always be greater than the error rate (P_E) leading to false matches.
[b] For $P_E > P_R$. In general, the posterior probability is given by $(P_R + P_E \times q)/(1 + P_R + P_E \times q)$.

corporating laboratory error is equally important for instances of apparent "no-match." False no-matches could result in the inappropriate release of individuals responsible for serious crimes.

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Parental Origin of Chromosome 22 Alleles Lost in Meningioma

To the Editor:

It has been proposed that an important mechanism leading to the development of some embryonal malignancies involves parental imprinting, an epigenetic trait which is at least partly maintained in somatic cells. Support for this model is partly based on the demonstration of the loss of the maternally derived chromosome 11 in all six investigated cases of sporadic rhabdomyosarcoma (Scrable et al. 1989) and in 11 of 12 investigated cases of sporadic Wilms tumors (Reeve et al. 1984; Schroeder et al. 1987; Mannens et al. 1988; William et al. 1988). Similarly, loss of the maternally derived chromosome 13 was found in 12 of 13 studied cases of osteosarcoma (Toguchida et al. 1989). However, this asymmetry was not found in sporadic unilateral retinoblastoma, since the lost chromosome 13 was found to be of maternal origin in only four of 10 studied cases (Dryja et al. 1989; Zhu et al. 1989).

We have extended these studies to meningioma, a benign tumor of the nervous system. Loss of chromosome 22 is frequently observed in this tumor (Zang 1982; Dumanski et al. 1987; Seizinger et al. 1987), suggesting that loss of a tumor-suppressor gene is critical for development of these tumors.

Blood and the tumor DNA from 37 meningioma pa-