Comment

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1. GENERAL REMARKS

Let me congratulate Berry on a provocative and entertaining paper. The Bayesian perspective provides a rational framework for overcoming some of the inconsistencies of previous analyses. A particularly novel feature of Berry's approach is how the normal kernel estimates of the prior combine with the normal error distributions of the log band weights to give the simple formula (9) for the likelihood ratio R. I like the term "identity index" coined by Devlin, Risch and Roeder (1991) for the amended ratio (10). Having such straightforward formulas as (9) and (10) should promote the Bayesian cause in this forensic context. I agree with Berry that as a safeguard the kernel estimate should include the suspect. With this safeguard, a low value of his constant b seems reasonable. In my opinion, taking b as high as 5 distorts the fitted histograms too much. I also agree with Berry that band shifting should be correctable by regression against monomorphic probes of known band weights. This last issue is discussed at length in a recent paper by McNally, Baird, McElfresh, Eisenberg and Balazs (1990).

Berry does not dwell on possible departures from assumptions. There are two key independence assumptions. One, Hardy–Weinberg equilibrium, requires that the maternal and paternal bands of a person be independently and identically distributed at each genetic locus analyzed. (An allele is one of the finite number of possible qualitative variants at a genetic locus.) Because of band overlap, neither the number nor the population frequencies of the underlying alleles for the DNA fingerprinting loci are known. Despite these uncertainties, the concerns expressed by Lander (1989a) about violations of Hardy–Weinberg equilibrium have largely been laid to rest by Devlin, Risch and Roeder (1990). There is little a priori reason to expect significant departures since equilibrium is reached in a single generation in a well-mixed population.

The issue of linkage equilibrium is more vexing. This has to do with the independence of alleles, and consequently bands, between loci. If linkage disequilibrium holds, then knowing, say, a person's maternal allele at one locus tells us something about his maternal allele at a second locus. Even with perfect mixing of two ancestral populations, the departure from equilibrium is at most halved each generation. This optimal convergence rate holds for loci on different chromosomes. For closely spaced loci on the same chromosome, the convergence rate can be much slower. I am not inclined to go so far as Cohen (1990) in questioning the whole enterprise of DNA fingerprinting because of the potential lack of linkage equilibrium. In well-established racial groups, it should not be an issue. However, there is a clear need for further research to estimate the extent of linkage disequilibrium in typical American populations and to correct for it in the forensic calculations.

Berry tends to gloss over a few other complications. For instance, deciding the right reference population for the blood on Castro's watch more than just complicates the algebra. Presumably, one needs to define some kind of prior for weighting the various racial groups who might contribute such blood. Was Castro a gang member or habitual criminal? If so, then the evidence presented in the trial might sway the jury towards one prior rather than another. The same question arises in paternity calculations. Berry would probably agree that visual examination of the child might fail to establish with certainty the race of its father. Although these ambiguities can be captured in an appropriate Bayesian framework (Devlin, Risch and Roeder, 1991), I share with Geisser (1990) anxiety about the ability of judges and juries to adjust posteriors to priors. Nevertheless, these complications should not be allowed to obscure the strength of the Bayesian approach.

2. COMPARISONS WITH LESS POLYMORPHIC MARKERS

On a more fundamental biological level, I question why forensic laboratories are so enamored with the highly polymorphic VNTR loci. The large number of alleles present at such loci must be balanced against the uncertainties introduced by not being able to determine genotype qualitatively. For loci with fewer alleles, genotype is unambiguous and inferences are less subject to the doubts engendered by complicated modeling assumptions. For example, it is far easier to check Hardy–Weinberg and

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