A NEW APPROACH TO STATISTICAL REPORTING FOR FORENSIC DNA ANALYSIS

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The use of DNA analysis for forensic and paternity analysis has been a controversial subject for many years. The National Research Council's (NRC) first attempt to document this subject was in 1992. More recently (1996) the NRC published a new report that took into account many of the changes in the field. There remain, however some issues in the NRC report that are susceptible to laboratory misinterpretation, particularly those relating to statistical analysis of DNA profiling. While technology and methods of modern DNA analysis (sometimes called DNA fingerprinting) are well defined and reasonably consistent between laboratories, the statistical calculations and interpretations of the results are not. In our experience it is not uncommon for statistical results of DNA analysis to be presented in a manner that is at best difficult to understand or at worst, deceptive. It is not uncommon that the average juror is confused as to the significance of the product rule, the use and preparation of DNA databases and the significance of random match probabilities. It is from this prospective we suggest that (i) laboratories use as many loci as they can when analyzing DNA, (ii) laboratories should provide the statistical probabilities for each DNA locus used and the combined ratio for all of these loci and (iii) laboratories should report an "average" (relative) ratio for their DNA loci by taking the nth root of the combined ratio for all loci tested (the combined ratio being obtained from the product rule). This new value should then be reported as a percentage, representing the suspect's degree of match. We present numerical examples illustrating this approach using both RFLP and STR data from well-established sources. The ability to clearly and confidently interpret DNA analysis results from different laboratories is important for both the scientific and legal community.