

Lawyer's Guide to Forensic Statistics



Technical Bulletin 40-021

Setting the Standard for Quality DNA Identification

Before a forensic expert can conclude that DNA test results have the power to identify the source of an evidence sample, it must demonstrate that the DNA characteristics are variable among populations. While some people will attempt to circumvent this step, it is not scientifically justifiable to claim a match as proof of identity in the absence of statistics. When a DNA profile is relatively common, there is a more compelling argument that the suspect might not be linked to the crime scene. Similarly if the DNA profile is extremely rare, then the evidence is stronger that the suspect was a DNA donor to the crime scene sample.

When statistics are introduced in court, it is important to understand the exact meaning of what is being estimated. Quite often a jury may misinterpret precisely what is being represented, which may unjustly influence the value of the evidence collected and tested for DNA. Commonly, when dealing with probative evidence, we hear the terms Profile Frequency, Random Match Probabilities, Likelihood Ratios and Probability of Exclusion. They are all valid statistical treatments, but hopefully applied appropriately in different situations.

For evidence yielding full single source DNA profiles, laboratories will typically use *random match probabilities* which are based on genotype frequency estimates, while others will use a *likelihood ratio* under the primary hypothesis that the suspect is the source of the DNA profile versus the alternate hypothesis where an unrelated untested individuals from the general population was the DNA donor. The FBI uses a source attribution approach when random match probabilities are rare.

Crime scene samples that produce mixed DNA profiles from multiple individuals can be analyzed by *random match probabilities* when it is possible to confidently separate alleles from individual contributors. Complex mixtures that can not be separated into individual contributors can be analyzed using a *likelihood ratio* or *combined probability of exclusion*.

Random Match Probability

Random match probability is the chance of a random DNA profile match within a given population and is the reciprocal of the DNA profile frequency. A DNA profile frequency is estimated by determining the genotype frequency for each locus and then multiplying the frequency across all loci. Rare genotypes provide stronger evidence, and population databases sorted by race will yield somewhat different results, but it is important to understand that this is a representation of how rare a DNA profile is in a representative population.

Prosecutor's Fallacy

In the Prosecutor's Fallacy, the language and meaning of a random match probability is switched. For example, from a random match probability result of 1 in 10,000, a prosecutor might say there is only a 1 in 10,000 chance that a DNA profile came from somebody else, or there is only a 1 in 10,000 chance that the defendant is not guilty.



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Defense Attorney's Fallacy

In the Defense Attorney's Fallacy, the assumption is made that everyone else with the same genotype has an equal chance of committing the crime. Motive, access to the crime scene and legitimate alibis are all important considerations when putting the DNA evidence into perspective.

Correctly stated, the probability of selecting the observed DNA profile from a population of random unrelated individuals is 1 in 10,000.

Relatives

If the suspect and the true the person responsible for of the crime were related, especially as siblings, then their genotype frequencies are not independent and different calculations are required. The defense should always consider this possibility.

Likelihood Ratio

A likelihood ratio is a ratio of two probabilities of the same evidence under two mutually exclusive hypotheses, specifically the position of the prosecution and the position of the defense. It conveys the relative support for the weight of DNA evidence under the hypothesis that the defendant is the source of the DNA profile, versus an unrelated individual from the population at large.

While interpretation of the strength of the statistical value can be variable, and should ultimately be considered in context with all case circumstances, the table below summarizes published interpretative criteria for use as a guide.

Combined Likelihood Ratio	Value of Evidence in Support of Hypothesis
<1	Does Not Support
1	Neutral
1 to 10	Limited Support
10 to 100	Moderate support
100 to 1,000	Strong Support
1,000 and greater	Very Strong Support

Combined Probability of Exclusion

The combined probability of exclusion can be used to conservatively interpret complex DNA mixtures. This calculation provides an estimate of the portion of the population that has a genotype of at least one allele not observed in the DNA mixture. This is a conservative approach since all other alleles not observed are considered and an individual can be excluded if he has any allele at any locus that is not detected in the mixture.



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