

MATCHING ODDS FOR MITOCHONDRIAL AND Y-CHROMOSOMAL HAPLOYPES

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Mitochondrial and Y-chromosomal haplotypes offer special advantages to the forensic scientist for identifying criminals. For different reasons, each of them is sometimes detectable in a crime stain for which autosomal typing fails. But they also present special problems, including a simple mathematical one: When a rare haplotype is shared between suspect and crime scene, how strong is the evidence linking the two? The traditional methods of evaluating the strength of DNA evidence include fundamental misconceptions. Contrary to received wisdom, sample frequency is *not* a plausible estimate for population frequency – not, at least, for rare types. Moreover, the pertinent question is not even one of frequency despite what many of us (myself included) have long assumed, but of probability, and the distinction matters. For classical DNA evidence across multiple autosomal loci, the product rule ensures that the practical effect of these errors is likely to be nil. However for the correct evaluation of rare haplotype evidence, the traditional methods are not good enough. The institutionalized misconceptions that they embody are an unnecessary and serious obstacle to utilizing the power of a rare haplotype match. The right approach is conceptually simpler and gives much stronger conclusions as well. For example, the traditional “95% confidence interval from zero” approach for a new haplotype not only makes no sense, but also is tenfold too conservative.