Characterized not only give low match probabilities but also allow deconvolution not possible with single SNPs. Thus, microhaplotypes can detect and deconvolute mixtures in a sample, a very common problem encountered in crime scene samples.

Population genetics globally of over 62 microhaplotype loci selected to define multiple alleles has now been fully documented in over 2500 individuals from at least 54 different populations. All have multiple alleles (haplotype) and almost all have global average heterozygosities >0.5 (many over 0.6) and over 74% of individual heterozygosities are greater than the 0.5 maximum possible for any single SNP. Ongoing research on 19 selected microhaplotype comprised of 4 SNPs is yielding nearly 97% of heterozygosities >0.5 and a global mean of over 0.7.

These high heterozygosities make microhaplotypes a highly efficient type of genetic marker for typing by sequencing. For individual identification large numbers of microhaplotype loci can be multiplexed at affordable costs allowing high throughput power, much greater than even the expanded set of CODIS STR polymorphisms. The microhaplotypes have also been characterized not only to give low match probabilities but also allow ancestry inference. We have easily identified in HapMap and 1000 Genomes an additional several dozen such loci now being studied on our population samples. The phase-known data from a forensic sample will detect mixtures for these multiallelic loci allowing deconvolution not possible with single SNPs. Thus, microhaplotype loci constitute a statistically powerful new type of genetic marker ready for forensic applications using existing sequencing methods.

As the table shows, sequencing is the only method that allows all types of markers to be typed. As such, it is the logical method for a single SNP for use in forensic laboratories.

Crytic variation around Microhap048 (see figure)