

## **Analysis of DNA Forensic Markers Using High-Performance Mass Spectrometry**

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A DNA forensics platform based on PCR followed by fully automated high throughput electrospray ionization mass spectrometry (PCR/ESI-MS) has been developed. Forensic DNA markers are “weighed” with sufficient accuracy to provide base compositions (the number of A’s, G’s, C’s and T’s). Base compositions for multiple markers provide a DNA profile for an individual that can be referenced to existing forensics databases.

Assays for mitochondrial DNA (mtDNA) profiling, short tandem repeat (STR) analysis and Y-chromosomal STR (Y-STR) analysis have been developed to run on the fully-automated Ibis Biosciences ESI-MS platform. Mitochondrial profiling is not hindered by heteroplasmy, is capable of resolving mixtures, and mtDNA profiles may be compared to existing control region sequence databases or relevant sequence data may be compared to a MS-derived profile database. The PCR/ESI-MS system is capable of identifying and storing polymorphic STR and Y-STR alleles while maintaining backwards-compatibility with current STR databases. Because an intrinsic property of each amplification product (i.e., its mass) is measured, allelic ladders are unnecessary for STR analysis. The masses of the forward and reverse strands of each product directly identify the allele and also reveal polymorphisms relative to the nominal allele of the same length.

For autosomal STR loci, polymorphisms have been observed in 11 of 13 core CODIS loci, with six loci displaying polymorphisms in >20% of alleles observed in 863 samples (D13S317, D21S11, D3S1358, D5S818, D8S1179 and vWA). Moreover, instances of heterozygous loci displaying alleles of the same length (one or both alleles being polymorphic) have been observed in 9 of the 13 core CODIS loci, with five loci (D13S317, D3S1358, D5S818, D8S1179 and vWA) displaying frequencies of >5% of individuals being heterozygous with same-length alleles.