

**HIGH-RESOLUTION DNA MELTING CURVE ANALYSIS TO ESTABLISH STR
GENOTYPIC IDENTITY**

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The demand to perform forensic DNA analysis on greater numbers of evidentiary samples in violent crimes, and the expansion of DNA casework to include property and minor crimes, is driving the need for a screening method that can assess source attribution. One possible approach is to enlist high resolution melting curve analysis to identify a non-victim DNA profile during quantitation by qPCR, thus circumventing the need to take all samples through short tandem repeat (STR) amplification and capillary electrophoresis. Melt curve analysis was used to establish genetic identity of human biological sources using STR loci in post PCR amplification. The regions studied were the CSF1PO locus and the HUM THO1 locus. At these polymorphic sites, an individual's DNA length consists of integral number of tandem repeat units. An allele with longer number of repeat units will require a higher dissociation temperature whereas an allele with shorter number of repeat units will require a lower dissociation temperature. This results in a melt curve that can be used to identify the genotype of a biological specimen while discriminating it from non-identical genotype. Temperature modifier's such as MgCl₂, formamide, and betaine were used to investigate favorable conditions that generated discriminating melt curves. Melt curve analysis established identity in most allelic ranges. Identity was also established from various biological sources (blood, saliva, semen, etc.), substrate conditions (gasoline, oil, concrete, etc.), and degraded samples.