



B137 SWGDAM Validation of a 19 Locus Y-STR System for Forensic Casework

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After attending this presentation, attendees will be presented with a full SWGDAM developmental validation of two Y-STR multiplexes, and will understand the unique requirements of such systems.

This presentation will impact the forensic community by demonstrating that few Y-STR multiplexes have undergone a full SWGDAM validation. We intend to present the community with a complete set of experiments and discuss the differences between the newly developed systems and the current autosomal systems in use.

A SWGDAM developmental validation study was carried out on two Y-STR multiplex systems (MPI and MPII) that collectively permit the co-amplification of nineteen Y-STR markers including DYS393, DYS392, DYS391, DYS389I, DYS389II, Y-GATA-A7.2, DYS438, DYS385a and DYS385b (MPI); DYS425, DYS388, DYS390, DYS439, DYS434, DYS437, Y-GATA-C.4, Y-GATA-A7.1, Y-GATA-H.4, and DYS19 (MPII). Performance checks subsequent to PCR parameter optimization indicated that MPI and MPII were suitably reproducible, precise and accurate for forensic use. The sensitivity of the systems was such that a full 19-locus Y-STR profile was obtainable with 150-200 ng of male DNA, and some loci were detectable even with as little as 20-30 pg of input DNA. Primate specificity was demonstrated by the lack of cross reactivity with a variety of commonly encountered bacterial and animal species, with the single exception of a monomorphic canine product that was outside of the size range of human alleles from any of the nineteen loci. Unsurprisingly cross reactivity was observed with a number of male and female non-human primates. Environmentally compromised samples produced full or partial Y-STR profiles. For example, a semen stain exposed to the outdoor elements for six months still gave a 13-locus Y-STR profile. Although a limited number of female DNA artifacts were observed in mixed stains in which the male DNA comprises 1/300 of the total, the full 19-locus male profile was easily discernible. Even at a 1500-2000 fold dilution of male DNA with female DNA partial Y-STR profiles were obtained. Furthermore the potential utility of MPI and MPII for forensic casework is exemplified by their ability to dissect out the male haplotype in a variety of case type samples including, *inter alia*, post-coital vaginal swabs, admixed male and female bloodstains, the non-sperm fraction from a differentially extracted semen stain and to determine the number of male donors in mixed semen stains.

SWGDAM Validation, Y-STR Multiplex, MPI/MPII