NORMALIZATION OF DNA YIELD USING THE DNA IQ™ SYSTEM AND A QIAGEN M48 BIOROBOT

Sandra Haddad[1], Ph.D., Cristopher Cowan[2], Ph.D., Joanne B. Sgueglia[1], B.S.
[1]*Massachusetts State Police Forensic and Technology Center, DNA Unit, Maynard, MA*
[2]*Promega Corporation, Madison, WI*

Per SWGDAM guidelines, DNA extracted from "questioned" samples must be quantified prior to STR amplification. However, no such mandate exists for database and reference samples. Our goal was to develop a system whereby amplification of a single amount of extract from all single-source known samples would generate complete autosomal STR profiles. This process would eliminate the need to quantify the samples thus saving the lab time, effort, and money.

Using a Qiagen M48 BioRobot, the DNA IQ™ System from Promega, and a custom program written for the M48 by Promega, DNA yields from three samples types were tested: blood on FTA paper, buccal cells on saliva indicator paper, and buccal cells on cotton swabs. DNA yields from 2mm punches of saturated bloodstains on FTA paper were normalized to between 7.5 and 38 ng per sample while 4mm punches of buccal cells on saliva indicator paper were normalized to between 22 and 79 ng per sample. Non-saturated bloodstains yielded between 0.5 and 9 ng of DNA per sample. Autosomal STR amplification of 10 µL from each extract with the Identifiler® kit (Applied Biosystems) generated complete profiles from 30 of 38 samples using our standard parameters for capillary electrophoresis. Two of the 38 samples produced complete profiles when injection time was increased from 10 to 20 seconds. Complete profiles from five DNA samples extracted from the sub-optimal bloodstains were obtained when samples were concentrated and amplified.

DNA yields from buccal cells on cotton swabs ranged between 2.82 ng and 300 ng and three of the four samples produced complete profiles when 10 uL of extract was amplified.

Based on the results of this study, we expect that DNA normalization with the DNA IQ™ System and the Qiagen M48 BioRobot will allow us to eliminate the quantification step for the majority of our database and reference samples.