DETERMINING A STOP POINT AND OPTIMAL DNA TARGETING VALUES FOR DOWNSTREAM STR AND Y-STR AMPLIFICATION USING InnoQuant® HY QUANTITATION AND QUALITY ASSESSMENT SYSTEM

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Advancements in forensic quantitation systems have greatly improved the sensitivity and reliability of sample detection in past decades. The most recently available commercial kits employ the use of two autosomal targets of different sizes to determine the level of DNA degradation in a sample. This degradation value is known as the Degradation Index (DI), and is obtained by taking the ratio of the two target quantity values to determine the relative degradation of a sample. In addition to providing the DI, a male specific target on the Y chromosome also provides quantitation information for male DNA present in a sample. The InnoQuant® HY system, uses high copy number retrotransposable element as targets to increase the system's sensitivity as well as reproducibility.

The practical question becomes how to use results from these next-generation quantitation kits in the everyday laboratory workflow. Laboratories can now have additional information that may be used to more informatively target downstream typing systems, namely the long autosomal target. This study, utilized the InnoQuant® HY kit on semen samples had a two-fold goal:
To determine if one or more targets of the InnoQuant® HY kit may be used as a screening tool to reliably stop testing a forensic DNA sample after the quantitation step, and
To determine how degradation of a semen sample affects the quantitation values obtained from InnoQuant® H and what target quantification value is useful in order to obtain the most informative nuclear STR and Y-STR typing results.

Results indicate that the optimal target value to use for the downstream nuclear STR and Y-STR reaction depends on the degradation state of the sample. With pristine samples, any of the 3 InnoQuant® HY targets may be used to successfully obtain optimal nuclear STR and Y-STR profiles from the first attempt as the system has precision less than 11% variability when measuring within the standard curve for all 3 targets when comparing to NISTA SRM 2373. However, degraded samples yielded more successful STR results when the long autosomal quantitation value was used to target the nuclear and Y-STR reactions. Finally, a quantitation threshold value that may reliably be used as a stopping point was determined for AmpFLSTR® Yfiler® at 20pg and for Identifiler® Plus at 7pg based on the InnoQuant® HY system. This study demonstrates the utility of the InnoQuant® HY kit in selecting optimal quantitation values that will reliably yield the most informative nuclear and Y-STR profiles