## B58 Quantifiler® Trio or PowerQuant® System? Is One Kit Better at Predicting the Success of Short Tandem Repeat (STR) Typing of the Male Component of Sexual Assault Evidence?

*Danielle K. Gibbes, BS*, 7 N 8th Street, Apt 816, Richmond, VA 23219; Susan Greenspoon, PhD, Department of Forensic Science, 700 N 5th Street, Richmond, VA 23219; Sarah J. Seashols Williams, PhD, Virginia Commonwealth University, Dept of Forensic Science, PO Box 843079, Richmond, VA 23284-3079; and Bonnie Brown, PhD, 1000 W Cary Street, Richmond, VA 23284-2012*

After attending this presentation, attendees will better understand the relationship between the quantitation data for the male component of a complex mixture and the success of developing a meaningful male autosomal STR or Y-chromosomal Short Tandem Repeat (Y-STR) profile.

This presentation will impact the forensic science community by providing information about quantitation and prediction of STR genotyping success that can help streamline the DNA analysis process and decrease the sexual assault kit backlog.

The sexual assault kit backlog in forensic casework remains a prominent issue across the nation, despite additional funding from government programs such as the DNA Backlog Reduction Program.[1] The nationwide backlog problem has been attributed to factors including the timely submission of the sexual assault kits to the laboratories, the time required to analyze the complex samples in conjunction with the shortage of resources, shortage of qualified forensic scientists, and overall increased demand for forensic services.[2] A recent study, conducted in 2009, disclosed approximately 406,000 forensic biology requests estimated to be backlogged for DNA casework by the year's end nationwide.[3] DNA quantitation data using multi-target quantitation kits can help streamline the analysis process by identifying the total autosomal and male DNA concentrations, while also assessing the quality. Analysts can use this data to predict STR genotyping success, triage the samples for autosomal or Y-STR profiling or both, and determine if it is worthwhile to continue with DNA testing.

In this study, male and female buccal swabs were extracted organically and quantitated. A lower limit sensitivity study was conducted for both the Applied Biosystem® QuantifilerTrio® kit and the Promega® PowerQuant® System to determine the lower limit of DNA detection and percent Coefficient of Variation (CV). A dilution series was created ranging from 1ng to 0.0015ng for the male and female samples and run in triplicate with each quantitation kit. Next, a dilution male and female mixture series was prepared by increasing the female-to-male ratio of DNA template in a dilution series ranging from 1:1 to 163,840-fold while holding the male DNA template quantity constant at 0.010ng. The dilution mixtures were run in duplicate using both the QuantifilerTrio® kit and the PowerQuant® System and the performance differences were assessed.

When the sensitivity was assessed, the PowerQuant® and QuantifilerTrio® kits showed similar results with reproducible data. A low percent CV was observed down to 10pg of template DNA; thus, 10pg was the quantity of male DNA chosen to hold constant for the male:female ratio study. Dilution male:female mixtures were prepared in duplicate with each quantification kit. Using the quantitation data obtained for both kits, an average quantity value for each dilution was calculated for PowerQuant® and QuantifilerTrio® for both the autosomal data and the Y-chromosome data. There was little difference observed between the quantity averages for the autosomal data for each kit. Further statistical analysis will determine whether the difference is significant or not. Both kits were able to detect the male contributor when the female contributor was many thousand times greater in concentration. The data obtained thus far is promising; however, more work is necessary to establish which quantification kit is superior at detecting male DNA in an excess of female at extreme ratios.

Overall, this study will provide information to the forensic science community about using DNA quantitation to predict STR genotyping success to further streamline DNA analysis of sexual assault kits. Further work on this project will include analysis of degraded tissues from a variety of sources utilized to construct complex male:female mixtures. The ability to utilize the quantitation and degradation data in order to predict STR outcomes will be provided since all mixtures will be analyzed using the Promega® PowerPlex® Fusion and Applied Biosystem® Y Filer® STR kits.

**Reference(s):**

1. Nelson, M. Making Sense of DNA Backlogs, 2010 – Myths vs. Reality. National Institute of Justice. NCJ 232197. 2011: 1-10.
2. Peterson, J., Johnson, D., Herz, D., Graziano, L., Oehler, T. *Sexual Assault Kit Backlog Study.* U.S. Department of Justice. Document No. 238500. 2012: 1-120.
3. Durose, M.R., Walsh, K.A., and Burch, A.M. Census of Publicly Funded Forensic Crime Laboratories, 2009. *Bureau of Justice Statistics Bulletin.* 2012: 1-13.

**DNA Quantitation, Sexual Assault Kits, STR Genotyping**



*Presenting Author