E42 Post-Coital DNA Recovery in Minority Proxy Couples

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Learning Overview: After attending this presentation, attendees will have a better understanding of the challenge faced in the timing of post-coital collections in extended intervals.

Impact on the Forensic Science Community: Combining the previous post-coital study data with the minority post-coital study, using enhanced Y-chromosomal Short Tandem Repeat (Y-STR) methods, DNA detection is possible for up to nine days in 65%–70% of reproductive-aged participants. Additionally, this study discovered a 20% increase in allele detection when swabs were combined. The recommendation is consideration for triage of delayed post-coital samples by forensic laboratories.

Minorities are less likely to report rapes. The Post Coital DNA Recovery (PCDR) study (2009–2014) subjects were White (93%) where expanded collection times were not generalizable to minority populations. Aims: (1) What is the time period for collection of post-coital DNA in minority women using Y-STR laboratory methods? and (2) when compared to the former study sample, what are the physiological conditions, factors, or activities in minority couples influencing post-coital DNA recovery? The design includes mixed-methods duplication perfected in the first study, embracing descriptive and inferential techniques. Aim 1 analysis used in PCDR in Minority Proxy Couples (PCDR-M) data only. Aim 2 combined data from both PCDR and PCDR-M studies. Combined, DNA recovery, a binary outcome accounting for repeated methods in population regression analysis, used Generalized Estimating Equation (GEE) methods.

To answer the first aim with PCDR-M data, studies data combined to test association of minority to non-minority allele detection and found there is no association using standard methods (p=0.6768, 0.9015, 0.4687, 0.7537) or enhanced methods (p=0.3283, 0.4166 0.5981, 0.3304) across all times and locations, implying no allele difference between minority and non-minority populations. Fifty-three minority couples (N=106) completed the complex PCDR protocol. The laboratory accepted 39 PCDR-M kits, but rejected 16 for allele levels, 1 for duplicate, and others for PCDR protocol non-adherence. Of the 23 (59%) kits accepted for study analysis, 19 had full and expected allele levels for baseline and post-coitus allele levels (4-, 7- or 9-days post-coitus) and 4 had 1 timepoint removed, resulting in 130 samples possible for analysis (46 4-days, 44 7-days, and 40 9-days). Of the 130 samples, the standard Y Filer® Plus method revealed 64 (48%) had at least one allele, and 66 (52%) had no detectable alleles. The enhanced Y Filer® method revealed 98 (75%) had at least one allele. Standard testing revealed 48% allele detection, and enhanced testing revealed 75% allele detection, duplicating the results from the first PCDR study and providing homogeneity necessary for comparison of the two data sets in Aim 2. To answer the second aim, data from study kits in the first PCDR study were combined with the PCDR-M study data for analysis, revealing the two populations were homogenous and met the inclusion criteria. The combined kits (N=89) and potential 356 samples, 66 from PCDR and 23 from the PCDR-M, had full and expected allele levels for baseline and post-coitus allele levels (4-, 7-, or 9-days post-coitus). Standard methods revealed at least one allele detected at baseline (22.09%), 4-days (52.87%), 7-day (29.07%), and 9-day (33.33%). Conversely, standard methods revealed no alleles detected at baseline (77.91%), 4-days (47.13%), 7-day (70.93%), and 9-day (66.67%). Enhanced methods revealed at least one allele detected at baseline (63.64%%), 4-days (91.01%%), 7-day (78.41%), and 9-day (82.56%). Conversely, standard methods revealed no alleles detected at baseline (36.36%), 4-days (8.99%), 7-day (21.59%), and 9-day (17.44%).

The first PCDR study developed a validated *in vivo* study protocol and data model for establishing a valid scientific foundation for understanding extended interval post-coital DNA recovery and influencing variables of menses and hormone birth control use, which were duplicated with the PCDR-M study. Combined data also supports a single regional swabbing practice change—cervix and posterior fornix. Both study results validate collection from victims with expanded post-coital intervals, where laboratories use individual capacities and current science to determine which laboratory method is best suited for the submitted sample. The generalized findings to minority populations of victims increased the evidence for decisions made about DNA collection timing, recovery, and influences, with implications for improving laboratory capacities and algorithms for testing choices, minority victim engagement, and justice for the victim and accused alike.

Post-Coital DNA, Y-STR, Rape

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