Form	Deviation Request Form
Title	DRF_Procedure for Direct to DNA Workflow
Laboratory Location	Lab-wide
Discipline/Section	Forensic Biology
A. Requested deviation applies to:	Section 5.2.4.2
B. Requested deviation:	Change wording: Trace taping will be collected for underwear or the garment work as underwear for items collected within 48 hours from the time of offense. Exceptions are listed in the DNA_Trace form. Taping is not to be performed on items such as menstrual pads or diapers (those items should be transferred to Trace Evidence if analysis is required.) If only digital penetration is alleged to have occurred, a representative swabbing shall be collected from area(s) of interest from the underwear as guided by the details of the case. This swabbing will be processed as noted in 5.2.1.
C. Necessity for the deviation:	Change in Trace hair processing required wording change.
D: Technical Review and Authorization	
Technical Authorization	Yes - Authorized
Technical Authorizer	☐ DeHaan, Mackenzie
Duration	1 year / next procedure revision
E: Quality Assurance Authorization	
Acceptable within general QA guidelines and good laboratory practice?	Yes
Significant negative impact to Crime Laboratory Quality System?	No
QA Authorization	Yes - Authorized
QA Authorizer	☐ West, Jody
Effective Date:	7/15/2024

Version: 3.0
Created at 7/3/2024 9:51 AM by ☐ DeHaan, Mackenzie
Last modified at 7/3/2024 1:31 PM by ☐ West, Jody

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Procedure for Direct to DNA Work Flow

1.0 Purpose - This procedure specifies the method for processing a Sexual Assault Evidence Collection Kit (SAECK) and acceptable additional items through Forensic Biology case work analysis.

2.0 Scope - This procedure applies to those Forensic Scientists who have been released to do forensic casework in Forensic Biology. The procedure also applies to trainees.

3.0 Definitions - See Section Definition List

4.0 Equipment, Materials and Reagents - N/A.

5.0 Procedure

5.1 Background – Case scenarios of SAECKs are divided into two types that will guide the work flow determination (See 5.3). All SAECKs submitted for analysis must undergo DNA testing, however samples may be triaged for processing. If a consensual partner is reported up to 5 days prior to the incident, an elimination standard must be requested. SAECKs will be tested using a direct to DNA approach. Serology testing is not initially performed on direct to DNA items associated with sexual assault kits. Initial testing will include swabs contained within the SAECK as guided by the provided case related information, any relevant reference standards, and underwear and/or a condom if applicable. Supplemental testing of other evidence items may be requested if testing for the SAECK is negative; however, normally the results of the SAECK testing will be reported before any additional testing is commenced. The work flow charts are to be used as a general guide and may not be applicable for every sample in every case.

5.2 Sampling of Items

5.2.1 All swabs/samples collected within the SAECK will be tested based on applicable collection time frames. Testing will be performed using either using the Promega Casework Direct procedure (CW Direct) or the full extraction process using a direct to DNA manner. If samples are being processed using the full extraction process, then samples must be differentially extracted unless details of the case state that contact other than penile penetration occurred.

5.2.2 For CW Direct processing, see applicable procedure for sampling of swabs.

5.2.3 For full extraction processing:

5.2.3.1 If multiple swabs are collected from a single location, the swabs shall be tested by removing ½ of each swab collected (by type). If, due to sample type or other case information the scientist decides that more than ½ of each swab needs to be consumed, then the reason and the amount consumed shall be documented in the notes.

5.2.3.2 If a single swab is collected from a location, the swab shall be tested by removing the entirety of each swab (by type). If, due to the sample type or other case information, the scientist decides that less than the entirety of the swab is to be consumed in testing, then the reason and the amount consumed shall be documented in the notes.

5.2.4 Underwear contained inside or outside of SAECK: If up to two pair are present, collect a representative swabbing. If more than two pairs are present, either collect a representative swabbing or examine according to section procedure for semen analysis for clothing. Analysts may use case details in decision making process for the determination of the sampling method. A representative sample from the drainage area (or areas of interest identified) shall be analyzed from at least the pair most closely linked to the event.

5.2.4.1 Examine the underwear using an alternate light source (ALS) for areas of interest.

5.2.4.1.1 If areas of interest are noted, collect a representative swabbing. This swabbing will be processed as noted in **5.2.1.**

5.2.4.1.2 If no areas of interest are noted, a representative swabbing from the crotch area (or drainage area) shall be collected. This swabbing will be processed as noted in **5.2.1**.

5.2.4.2 Trace taping will be collected for underwear or the garment worn as underwear. Taping is not to be performed on items such as menstrual pads or diapers (those items should be transferred to Trace Evidence if analysis is required.) If only digital penetration is alleged to have occurred, a representative swabbing shall be collected from area(s) of interest from the underwear as guided by the details of the case. This swabbing will be processed as noted in **5.2.1**.

5.2.5 Condom contained inside or outside of SAECK

5.2.5.1 Two total swabbings shall be collected from a condom. One shall be collected from the inside of the condom, and one from the outside of the condom. These swabbings will be processed separately as noted in **5.2.1**.

5.2.6 Toilet paper, tampons, pads, or other similar items contained within the kit must be sampled for processing. Representative cuttings or swabbings shall be collected from the items(s). These cuttings/swabbings shall be extracted as noted in **5.2.1**.

5.2.7 The analyst should use the SWGDAM/NIJ recommended time frames for evidence collection in conjunction with the case information provided for decisions of which samples to process for testing. For the decision process for external swabs the analyst should take into account case details and type of sample for analysis.

Type of Assault	**Collection Time**
Vaginal	Up to 120 hours (5 days)
Anal	Up to 72 hours (3 days)
Oral	Up to 24 hours (1 day)
Bite marks/saliva on skin	Up to 96 hours (4 days)
Unknown	Collect respective samples within the time frames listed above

5.3 **Case Types** – as defined for the workflow for Direct to DNA processing of SAECK. All available case information shall be used in guiding the decision of case type. Analysts will use their best judgement when making decisions on Case Type. If this “best” sample does not produce meaningful results with autosomal DNA testing, it can be reasoned that extracts with less male DNA or a lower male:total DNA ratio will not produce meaningful autosomal results and therefore need not be analyzed.

5.4

5.4.1 Case Type 1 – Cases with a single assailant, female victim, no consensual partner.

5.4.1.1 One sample that meets the appropriate quantification metrics will be selected to move forward to STR testing. If more than one sample meets the appropriate quantification metrics, sample selection may be guided by the location from which the samples were collected and the case specific details.

Note: If the consent partner and alleged assailant are the same listed individual this may be treated as a Type I case – dependent on case details.

5.4.2 Case Type 2 –Cases with evidence of multiple assailants/donors.

5.4.2.1 At least one fraction from each item that meets the requirements for STR testing based on quantification results shall be taken forward (See Procedure for DNA Quantitation Using Quantifiler Trio). Analysts can make case specific decisions on whether to amplify both Fraction 1 and Fraction 2 from a sample, based on quantitation values, along with item and case details.

6.0 Limitations – Due to the nature of the cases worked by Forensic Biology, it is difficult to cover every possibility with a procedure. Exemptions may be made, in writing, by the Forensic Biology FSM or Supervisors on a case-by-case basis.

7.0 Safety – N/A

8.0 References

Forensic Biology Section Procedure for DNA Extraction using the EZ1 Advanced Biorobot.

Forensic Biology Section Casework Direct Procedure

Forensic Biology Section Procedure for DNA Extraction using the QIASymphony

Forensic Biology Section Procedure for DNA Quantitation Using Quantifiler Trio.

Forensic Biology Section Procedure for Semen and Sperm Analysis

National Best Practices for Sexual Assault Kits: A Multidisciplinary Approach (https://www.NIJ.gov)

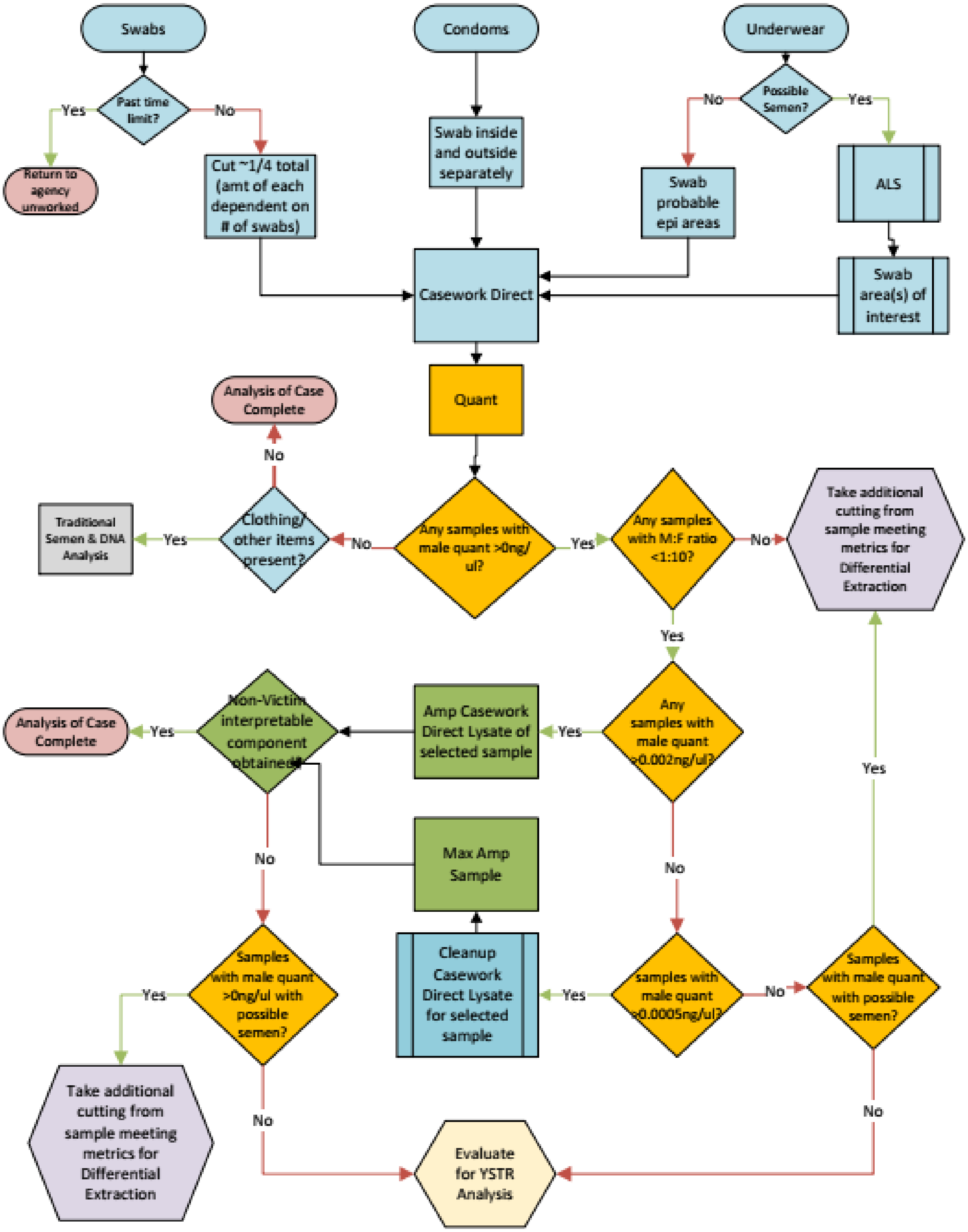
SWGDAM Recommendations for the Efficient DNA Processing of Sexual Assault Evidence Kits

9.0 Records - N/A

10.0 Attachments - N/A

Revision History		
Effective Date	Version Number	Reason
05/24/2024	6	5.1 – update wording; 5.2.4.1.3 – added trace taping; 5.3 – remove last sentence; 5.3.1.1 – clarify wording; 5.3.1.1.1 and 5.3.1.1.2 – delete; update work flow charts

Direct to DNA Workflow for SAECK: Case Type 1



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Direct to DNA Workflow for SAECK: Case Type 2