Case Management		
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Case Management

1 Guiding Principles and Scope

1.1 Case management is the process by which an analyst shepherds the evidence through the testing process. It is the responsibility of the analyst to ensure that evidence receives the necessary analysis, analytical results are evaluated promptly, any analytical problems resolved, the results interpreted, and the final report written within the time frame dictated by the target date.

2 Procedure

2.1 Most case management steps are done using the Laboratory Information Management System (LIMS); however, the "legacy" case management and documentation system in Forensic Biology, which utilizes various hard copy forms, is available for documenting the examination of evidence in exigent circumstances when the LIMS is unavailable for an extended period of time.

3 Production Team System

3.1 Many of the processes described in the following sections are handled by the Production Team staff and not necessarily the reporting analyst (RA). One goal of the Production Team system is to rapidly and efficiently extract, quantify, and amplify samples. Workflow and preparation of test batch samples is coordinated by the Production Teams.

3.2 Testing results are available to the RA through the LIMS interface.

3.3 It is the *responsibility of the test batch reviewer* to examine the samples and batch set-up information for completeness and accuracy of case numbers, sample identifiers, etc. Any discrepancies, inconsistencies, or omissions must be resolved before obtaining a witness and/or commencing testing.

3.4 It is the *responsibility of the witness* to examine the samples and batch set-up information for completeness and accuracy of case numbers, sample identifiers, etc. As above, resolve any issues prior to commencing testing.

4 Case Assignment

4.1 Case management begins as soon as evidence examination begins.

4.2 Cases are assigned based on priority and Evidence Received date. An initial priority level is assigned during the Sign-In process, but can be adjusted later.

4.2.1 **High Priority –** All parts of case that were promised (could just be semen Y/N, for example, or it could be a complete DNA report) are done ASAP, using overtime if necessary. Designating a case as **High Priority** requires a phone call from an NYPD high-level manager to a Forensic Biology (FB) manager or the Forensic Biology Customer Liaison, or a phone call from a DAO Bureau Chief-level to an FB manager or the Forensic Biology Customer Liaison. A "regular" ADA cannot make such a request. The High Priority request is accompanied by a Priority Request Form which will specify the date of completion of testing requested by the customer. If the status goes away later, the priority can be downgraded.

4.2.2 **Priority** – Started next, but the rest of the case gets processed as usual; this is the same as "expedite". The Priority request is accompanied by a Priority Request Form which will specify the date of completion of testing requested by the customer. All stranger rapes are in this category. Remember that "stranger rape" is NOT the same as "no suspect". A "stranger rape" is a "stranger rape" whether there is a named/arrested suspect or not.

4.2.3 **Routine** – Average, everyday, sort of case (excluding stranger rapes).

4.3 Review the case information (see Evidence Examination - General Guidelines section of the Evidence and Case Management Manual).

4.4 If this is additional evidence or an exemplar on a previously reported case, evaluate the earlier work.

4.4.1 It may be necessary to submit earlier DNA extracts for additional testing.

4.4.2 If an exemplar is submitted, type it in all DNA systems necessary for comparison.

4.5 Obtain the evidence from the evidence storage area and complete the chain of custody.

5 Initial analyses

5.1 Examine the evidence (see Evidence Exam procedure).

5.2 Test samples for KM, PSA, Amylase,or male DNA through Zygem lysis and/or DNA extraction as needed. Ensure that true exemplar samples and abandonment samples are submitted on the appropriate exemplar extraction batches and that evidence samples are submitted on the appropriate non-exemplar extraction batches.

5.3 The RA managing the case should ensure that their name is listed in LIMS as the RA.

5.4 Evidence examination notes and any serology or Zygem lysis results are reviewed by the RA for completeness and accuracy. Discrepancies or omissions need to be corrected by the analyst who performed the test. Check especially for correct FB number, swab description or stain description.

5.5 Extraction and quantitation results are reviewed by the RA for completeness and accuracy; any discrepancies or omissions need to be corrected by the analyst who performed the test. Check especially for correct FB number, swab description or stain description. The following information should be checked:

5.5.1 Does the extraction negative contain DNA?

5.5.2 If neat and dilution results were tested, do the results correlate with each other?

5.5.3 Is the DNA concentration too high?

5.5.4 Was there a problem with inhibition and/or background fluorescence preventing a determination of the DNA concentration? If so, the sample may need to be cleaned via microcon and re-quantified.

5.6 Re-quantitation needed due to any of the aforementioned reasons is generally taken care of in the Production Team System.

5.7 Microcon clean-up will be by the Production Team System.

6 DNA typing and case evaluation

6.1 Once acceptable quantitation results are available, the DNA samples requiring amplification will be processed.

6.1.1 In some instances, concordance of results may require additional amplification of samples. If this is the case, the sample(s) must be placed onto an amplification batch.

6.2 The RA reviews amplification and DNA typing results for completeness and accuracy; any discrepancies or omissions need to be corrected by the analyst who performed the test. Check especially for correct FB number, swab description or stain description. In addition, review all the electropherograms for your case.

6.2.1 Review the STR 3130xl Control Review report and the electropherograms to ensure that the positive control, amplification negative, and extraction negative (if applicable) gave the expected results. If not, the samples may need to be re-amplified or even re-extracted.

6.2.2 Did your samples amplify? If not, it may be necessary to re-amplify with more DNA extract or less DNA extract (if PCR inhibitors are suspected), or perform a microcon procedure.

6.2.3 In some situations, it may be necessary to start the DNA analysis over at the DNA extraction step or consider organic extraction.

6.2.4 Was a partial DNA profile detected in your sample? If so, it may be necessary to perform further testing.

6.2.5 Alternatively, it may be necessary to re-amplify with more DNA extract or less DNA extract (if PCR inhibitors are suspected), or perform a microcon procedure.

6.2.6 Was your sample over-amplified? If so, submit the sample for amplification again with less DNA extract or run at a dilution.

6.2.7 Were your samples properly edited? Evaluate any editing that was done on your samples; examine the electropherograms for artifacts, over-amplification, or other problems. If the sample was not edited properly, the STR analysis analyst or the reporting analyst may re-edit and reprint the electropherograms; make sure the new editing is added to the editing worksheet in LIMS and update the allele table.

6.2.8 Is there a mixture of DNA in your sample? If so, it may require additional work in a DNA system (the same one or a different one) to achieve concordance. Mixtures may also be amplified with more template DNA for better results.

6.2.9 Are there other samples that may require additional work to meet concordance? If so, identify those samples and start the appropriate steps (i.e., re-extraction or re-amplification).

6.2.10 Do the DNA results make sense in the context of the case and/or sample? If not, there may have been a sample mix-up at the aliquot, amplification, or DNA typing steps. Discuss with your supervisor.

6.3 Review the DNA typing results as soon as possible so that ample time remains to deal with any analytical problems.

6.3.1 Refer to the appropriate Interpretation manual (in the Forensic Biology Protocols for Forensic STR Analysis manual) to interpret the results of DNA typing.

6.4 Compare a single source or deconvoluted DNA profiles to the Lab Types Database within LDIS in order to detect possible exogenous DNA. Instructions for how to conduct searches of the database are found in the LAB TYPES DATABASE procedure in the Quality Assurance/Quality Control Manual.

6.4.1 If contamination is identified see the "Sample Contamination Policy" found in the GENERAL GUIDELINES FOR DNA CASEWORK procedure (in the Forensic Biology Protocols for Forensic STR Analysis manual).

6.5 Compare DNA results to the LINKAGE database and LDIS for potential matches (exact or partial). In addition, it may be necessary to compare DNA profiles within a case to other profiles in the case, and to any suspects submitted for that case, to identify partial matches. This may

require you to determine the DNA profile(s) present in a mixture, and may require consultation with a supervisor.

6.5.1 Only single-source profiles (clean or deduced) with ≥10 CODIS core loci should be compared for the purposes of discovering partial matches. Only such profiles are eligible for evaluation of any partial matches found. Such profiles shall not contain INC or Z at any of the ≥10 CODIS core loci being used for partial match evaluation.

6.5.2 To compare a profile to LDIS, perform a keyboard search. Only profiles that meet the necessary number of loci and statistical threshold for entry into LDIS should be searched in LDIS.

6.5.3 Before searching suspect exemplar profiles against Linkage and LDIS, ensure that there is not a Protective Order issued for that sample. Refer to the Protective Orders section of the Attorney Requests section of the Administrative Manual.

6.5.4 See the CODIS Manual for more detailed information regarding DNA matches.

6.5.5 Any potential case-to-case matches not identified in LINKAGE will be picked up by LDIS once the profile is entered there.

6.5.6 If a sample from your case matches a sample from a previous case, consult with your supervisor and follow the current local hit notification guidelines.

6.6 Not all samples require DNA analysis in all available DNA systems; in fact, the majority of samples require only STR DNA typing. Submission of samples for Y STR DNA typing is case dependent.

6.7 The DNA system chosen for additional testing may depend on the nature of the case.

6.7.1 Were the only DNA alleles detected in a sample containing male DNA those of the victim? If so, amplification using Y STR's may be needed.

6.7.2 Does it appear that there are multiple male donors? If so, amplification in Y-STR's may be needed.

6.7.3 Does the case involve a body identification of a male, and are there paternal relatives available for testing? If so, amplification using Y STR's may be needed.

6.7.4 Ensure that the laboratory concordance policy is satisfied.

6.8 Prepare a profile generation report or table of results, if applicable,

6.9 Prepare a Statistics sheet, if necessary. Enter all alleles that meet the allele calling criteria.

6.10 Prepare a DNA Profile Evaluation form, if necessary. Follow the guidelines listed for eligible profiles to determine how many (if any) alleles to enter at each locus.

6.11 Review the case file to ensure that all the necessary paperwork is present and is organized in a logical format.

6.12 Finalize the draft case report, approve, and submit for the required technical and administrative reviews. Submitting the report for approval is captured in LIMS.

6.12.1 The results are considered reviewed and authorized once the Reporting Analyst has documented their review of the case file and submitted the report for technical and administrative review.

7 Case Completion

7.1 A case is considered complete when the analytical work is done, the case report is written and passes technical and administrative reviews, and the case report is distributed to the requesting agency(s).

7.2 Evidence Return:

7.2.1 Within the LIMS, mark the individual vouchers of evidence for final return. The Evidence Unit will obtain the item(s) and prepare the item(s) for "pending release to the Property Clerk" using their normal procedures. With the exception of post-mortem items and exemplars, retained samples should no longer be indicated on the chain of custody.

8 Case Report Routing

8.1 Report distribution is usually done in conjunction with administrative review. For details see the Administrative Review procedure.

8.2 Most reports are distributed to the ECMS system of the NYPD. In addition to ECMS reports are distributed as follows:

8.2.1 Deaths: Reports are supplied to the OCME Records Department. Optional: The reports may also be supplied to the District Attorney's Office (to the assigned ADA) and/or NYPD units (to the assigned Detective).

8.2.2 Sexual Assaults and Suspect files for Sexual Assaults: Reports are supplied to the Bureau Chief of the appropriate Sex Crimes Bureau.

8.2.3 Miscellaneous and all other Suspect files: Reports are supplied to the District Attorney's Office (to the assigned ADA) and/or NYPD units (to the assigned Detective).

8.2.4 Property Crimes and Weapons case reports are supplied to the District Attorney's offices only if a suspect has been arrested.