
Procedure for Casework Report Writing

- 1.0 Purpose** – The purpose of this document is to provide casework report writing guidelines for autosomal DNA results when using the Identifiler® Plus amplification kit.
- 2.0 Scope** – This document applies to casework analysts and trainees in the Forensic Biology Section who are qualified to use the Identifiler® Plus amplification kit.
- 3.0 Definitions** - N/A (See Procedures for Statistical Calculations, GMID for Casework, and Casework DNA Interpretation.)
- 4.0 Equipment, Materials and Reagents** – N/A

5.0 Procedure

- 5.1 Introduction** - General reporting guidelines are provided throughout this procedure, and *most* reporting scenarios will fall within the provisions of this procedure. However, unique case circumstances may warrant the use of reporting language beyond those provided herein.

Wording used in reports may be modified with documented approval from the DNA Technical Leader. Approval shall be documented in writing. Forensic Scientists shall provide the DNA Technical Leader with the requested wording. The DNA Technical Leader shall then reply in writing with an approval or denial of the request. This correspondence shall be placed in the FA Case Record Object Repository.

The results statements shall reflect only work that is performed. Portions of the statements listed in the reporting guidelines may be omitted if not reflective of testing actually performed.

All inclusionary statements when compared to a reference sample shall be accompanied by the appropriate statistic (i.e., RMP or CPI/CPE). An exception to this requirement is when an assumed contributor is present in an intimate item (e.g., vaginal swab) or there is a written request from the investigating agency or the District Attorney's office.

5.2 General Principles

- 5.2.1** If a profile is determined to be partial (whether a single source, mixture, evidentiary or reference), the word partial shall be used to qualify the result. NOTE: comparisons between partial reference profiles and evidentiary profiles can be made only for the loci at which results exist in the partial reference profile.
- 5.2.2** If a differential extraction is performed, non-sperm and sperm fractions shall be used to qualify the results and both fractions shall be reported.
- 5.2.3** If a single source or single predominant profile (unknown) profile is obtained and a Y is present at Amelogenin, such profiles shall be qualified as male in the report.
- 5.2.4** If a Y is present at Amelogenin in a mixture and no inclusionary statement to a male reference standard has been made, the overall mixture shall be qualified as having a male contributor: *This mixture contains at least one male contributor.*

5.2.5 If multiple unknown profiles are present within a case, they may be qualified numerically. For example: first unknown (male), second unknown (male), etc.

5.2.6 For cases where evidence was analyzed prior to January 3, 2013 and a request is made to make additional comparisons, one of the following statements shall be added to the report:

“On January 3, 2013, the North Carolina State Crime Laboratory implemented new technologies for the analysis of DNA evidence in the Forensic Biology Section. Due to these changes in technology, comparisons to evidence analyzed before this date can be made only for those DNA profiles generated from the items listed below. For further information, please do not hesitate to contact the Forensic Scientist or the Forensic Scientist Manager of the Forensic Biology Section at the North Carolina State Crime Laboratory.”

“On January 3, 2013, the North Carolina State Crime Laboratory implemented new technologies for the analysis of DNA evidence in the Forensic Biology Section. Due to these changes in technology, comparisons to evidence analyzed before this date cannot be made. For further information, please do not hesitate to contact the Forensic Scientist or the Forensic Scientist Manager of the Forensic Biology Section at the North Carolina State Crime Laboratory.”

5.2.7 If DNA standards (to include alternate standards) are not suitable for comparison purposes (e.g., due to degradation, presence of a mixture, or if no DNA present), then the following statement shall be used in the report: “no DNA profile suitable for comparison purposes was obtained from ____ (Item ____); therefore, additional DNA standard(s) from ____ (name) need to be obtained and submitted.”

5.2.8 The Results of Examination and Conclusions section of each report shall contain a paragraph that details which items were extracted and specifies what methodology/technology was used. The report shall contain the following statement (or equivalent): “DNA extractions were performed on Item(s) _____, as well as on the known DNA standards from ____ (Item(s)). These extracts were then quantitated, amplified, and tested with the DNA genetic markers Amelogenin, CSF1PO, D13S317, D16S539, D18S51, D19S433, D21S11, D2S1338, D3S1358, D5S818, D7S820, D8S1179, FGA, TH01, TPOX, and vWA.”

5.2.9 The report section for disposition shall have the header changed to read “Disposition” and shall contain the following statement (or equivalent):

Note: DNA extracts (Container __) are being returned along with the items of evidence in this case. These extracts need to be kept frozen to avoid degradation.

5.3 Single Source Profiles

5.3.1 Matches and Exclusions: *A DNA profile was obtained from _____ (Item__) that matches the DNA profile obtained from _____ (Item__). The DNA profile(s) obtained from _____ (Item(s)__) is excluded as a contributor to this profile.*

- 5.3.2** An assumed contributor (i.e., victim or elimination reference standard profile) matches an intimate item: *The DNA profile obtained from ____ (Item __) is no different from that of the victim/subject (Item __) and the DNA profile obtained from ____ (Item __) is excluded as a contributor to this profile.*
- 5.3.3** Matches and Consistent With: If RMP is calculated at all core loci the word **MATCHES** shall be used. If RMP is calculated at fewer than all core loci, the phrase **IS CONSISTENT WITH** shall be used.

5.4 Mixtures

5.4.1 Mixtures with a Single Predominant Profile (Distinguishable)

5.4.1.1 Known Reference Sample(s) Included: *The DNA profile obtained from ____ (Item __) is consistent with a mixture of (# of contributors). The predominant DNA profile matches/is consistent with the DNA profile obtained from ____ (Item __). See 5.3.3 for use of “matches/consistent with.”*

5.4.1.2 Known Reference Sample(s) Excluded (i.e., unknown profile): *The DNA profile obtained from ____ (Item __) is consistent with a mixture of (# of contributors) containing a predominant DNA profile(s) from an unknown contributor.*

5.4.1.3 Contribution to Overall Mixture:

5.4.1.3.1 Cannot exclude from the mixture: *The DNA profile(s) obtained from ____ (Item(s) __) cannot be excluded as a contributor/as contributors to the mixture.*

5.4.1.3.2 Excluded from the mixture (including the predominant profile): *The DNA profile(s) obtained from ____ (Item __) is/are excluded as a contributor/as contributors to the mixture.*

5.4.2 Mixtures with Multiple Major Profile (Distinguishable):

5.4.2.1 Primary statement: *The DNA profile obtained from ____ (Item __) is consistent with a mixture of three contributors which contains a multiple major profile.*

5.4.2.2 Cannot exclude from the multiple major profile: *The DNA profile(s) obtained from ____ (Item __) cannot be excluded as a contributor/as contributors to the multiple major profile of this mixture.*

5.4.2.3 Excluded from the multiple major profile but not excluded from the minor component: *The DNA profile from ____ (Item __) is excluded as a contributor to the multiple major profile of the mixture. However, the DNA profile from ____ (Item __) cannot be excluded as a contributor to the minor component of the mixture.*

5.4.2.4 Excluded from the overall mixture: *The DNA profile(s) obtained from _____ (Item __) is/are excluded as a contributor/contributors to the mixture.*

5.4.3 Mixtures with No Predominance (Indistinguishable Mixture):

5.4.3.1 Primary statement: *The DNA profile obtained from ____ (Item__) is consistent with a mixture of (# of contributors).*

5.4.3.2 Cannot exclude from mixture: *The DNA profile(s) obtained from _____ (Item__) cannot be excluded as a contributor to/as contributors to the mixture.*

5.4.3.3 Excluded from the mixture: *The DNA profile(s) obtained from _____ (Item__) is/are excluded as a contributor to/are excluded as contributors to the mixture.*

5.5 Inconclusive Profiles/Component

5.5.1 For DNA profiles obtained from Items whose results are not suitable for comparison, the following statements shall be used:

5.5.1.1 If the profile has limited data: *The DNA profile obtained from ____ (Item __) is inconclusive due to insufficient quantity.*

5.5.1.2 If the profile is too complex: *The DNA profile obtained from ____ (Item __) is inconclusive due to insufficient quality.*

5.5.2 For minor component(s) of a mixture whose results are not suitable for comparison, the following statement shall be used: *The minor component of this mixture is inconclusive due to insufficient quality and/or quantity.*

5.6 No DNA Profile – When no alleles are detected above the analytical threshold: *No DNA profile was obtained from _____ (Item__).*

5.7 Additional Alleles – When additional alleles are present in an interpretable mixture that cannot be attributed to any of the known reference standards provided: *Additional DNA was present which cannot be accounted for by the standard(s) submitted.*

5.8 Presence of Male DNA Based Upon Quantitation Results

5.8.1 If the male Quantitation results indicate the presence of male DNA in a sample but the resulting STR profile is negative (either no profile is obtained or there is no indication of a male contributor), the Forensic Scientist shall report the following: *Based upon quantitation results, male DNA was detected on _____ (Item __); however, no male DNA profile was observed. This sample may be suitable for YSTR testing. If you need further information regarding this sample, please do not hesitate to contact the Forensic Scientist or the Forensic Biology Forensic Scientist Manager at the North Carolina State Crime Laboratory.*

Note: This statement only applies to evidence tested in sexual assault cases, and examination does not show a male profile.

5.9 CODIS Hit Notifications/Notification of CODIS Entry

5.9.1 Offender/Arrestee Hits: *Upon a (routine/one-time) search of the (FBI's National DNA Index System (NDIS)/ North Carolina state DNA database (SDIS)), a (high/moderate) stringency match occurred between the (mixture/partial) DNA profile obtained from _____(Item___) and the DNA profile contained within the (name of state/Federal) DNA Database identified as belonging to:*

*Name:
DOB:
SSN:
SID:
FBI:*

This information is to be used only as an investigational lead and supports probable cause to obtain a DNA standard from the above individual. Analysis in this case is not considered complete until a DNA standard has been obtained from this individual and submitted for comparison purposes. Please notify the NCSCCL if you determine that this individual is not a subject of your investigation (e.g., consensual sex partner or witness) so that this profile will no longer be routinely queried in the CODIS database.

If you need further information regarding this CODIS hit or need assistance in applying for or serving a search warrant in this case, please do not hesitate to contact (name of) Forensic Scientist or the State CODIS Administrator at 919-662-4500.

5.9.2 Forensic Hits: *Upon a (routine/one-time) search of the (FBI's National DNA Index System (NDIS)/ North Carolina state DNA database (SDIS)), a (high/moderate) stringency match occurred between the (mixture/partial) DNA profile obtained from _____(Item___) and the casework DNA profile contained within the (name of state/Federal) DNA Database with specimen ID# _____. The investigator's contact information is as follows:*

*Agency:
Name:
Telephone:
Email:
Case#:*

This information is to be used only as an investigational lead and suggests that these cases may be connected. If you need any further information regarding this CODIS hit, please do not hesitate to contact (name of Forensic Scientist) or the State CODIS Administrator at 919-662-4500.

5.9.3 One-time (keyboard) Searches: The following statement shall be used in addition to/in lieu of the auto-populated CODIS statements in FA in order to report out the results of a negative one-time search:

5.9.3.1 *The DNA profile obtained from _____ (Item ___) was queried against (name of state/Federal) DNA Database (SDIS/NDIS) and no high stringency matches were obtained. This profile will not be routinely searched in this database.*

5.9.4 Notification of CODIS Entry

5.9.4.1 If it is determined that a DNA profile generated by a vendor laboratory is eligible for search or entry into the CODIS database, the CODIS Administrator (or designee) shall notify the investigating agency.

5.9.4.1.1 *The DNA profile obtained from _____ (Item__; as provided by_____) will be routinely queried in the CODIS (Combined DNA Index System) Database.*

5.9.4.1.2 If it is determined that a DNA profile generated by a vendor laboratory is eligible for a one-time search, refer to 5.11.1 through 5.11.3.

5.9.4.2 If it is determined that a DNA profile generated by a vendor laboratory does not meet eligibility requirements for search or entry into the CODIS database, the CODIS Administrator (or designee) shall notify the investigating agency.

5.9.4.2.1 *The DNA profile obtained from _____ (Item__; as provided by_____) is not suitable for search or entry in the CODIS (Combined DNA Index System) Database.*

5.10 Comparisons Across Multiple Submissions – Unless necessary for clarification, repeated comparisons between items of evidence and reference standards already established in prior case records/submissions is not required. Once an individual's contribution or exclusion has been determined and reported, it need not be reiterated in subsequent case records/reports. Additionally, it need not be reiterated if no DNA profile or no interpretable profile was obtained previously.

5.11 Associations to Employees/Vendors/Batched Cases

5.11.1 Forensic Scientists shall follow the reporting guidelines already provided in this document and modify the positive association (i.e., match, consistent with, cannot be excluded) based upon the categories below.

5.11.2 Forensic Scientists shall report exclusions to known reference samples in the case. (Refer to **5.3** and **5.4**.)

5.11.2.1 DNA Forensic Scientist who worked the case: *...State Crime Laboratory Forensic Scientist (name) who performed the DNA analysis on this item of evidence...*

5.11.2.2 Forensic Scientist or Field Agent previously involved with the item: *...State Crime Laboratory Forensic Scientist/Agent _____. This scientist/agent performed the (type of testing: serology, latent print examination, etc.) on this item prior to DNA analysis...*

5.11.2.3 State Crime Laboratory Employee, Vendor or Visitor not involved with the item: *...State Crime Laboratory (employee, vendor, visitor) _____.*

This individual has been present in a Laboratory area within the Forensic Biology Section on at least one occasion...

5.11.2.4 Sample in a batched case: ...State Laboratory item number _____
which was analyzed along with items of evidence in this case...

5.12 Statistics

Note: Qualifiers such as partial, predominant, non-sperm fraction or sperm fraction shall be used as appropriate in the statistical statements. Refer to the Forensic Biology Section Procedure for Statistical Interpretations. If no statistical data is generated, the following statement shall be used: *No population frequency data were generated for the contribution of the DNA profile from _____ (Item) to this Item.*

5.12.1 Random Match Probability

5.12.1.1 When Random Match Probability statistics have been generated for a profile, the following statement shall be used: *The probability of randomly selecting an unrelated individual with a DNA profile that matches/is consistent with the DNA profile obtained from the _____ is approximately 1 in _____ in the N.C. Caucasian population, 1 in _____ in the N.C. Black population, 1 in _____ in the N.C. Hispanic population and 1 in _____ in the N.C. Lumbee Indian population.* If the statistics are generated for fewer than all core loci “consistent with” shall be used.

5.12.2 Combined Probability of Inclusion

5.12.2.1 If a known reference sample cannot be excluded from a mixture, the following statement shall be used: *The chance of randomly selecting an unrelated individual who would be expected to be included for the DNA mixture obtained from _____ (Item __) is approximately:*

N.C. Caucasian: 1 in _____
N.C. Black: 1 in _____
N.C. Hispanic: 1 in _____
N. C. Lumbee Indian: 1 in _____.

5.12.2.2 Note: If CPI/CPE is performed on a multiple major profile, the statement in 5.12.2.1 shall be modified to: *The chance of randomly selecting an unrelated individual who would be expected to be included for the multiple major profile obtained from _____ (Item __) is approximately:*

6.0 Limitations – N/A

7.0 Safety – N/A

8.0 References

Forensic Biology Section Procedure for Casework DNA Interpretation

Forensic Biology Section Procedure for Statistical Calculations

Forensic Biology Section Procedure for CODIS

9.0 Records – N/A

10.0 Attachments – N/A

Revision History		
Effective Date	Version Number	Reason
01/03/2013	1	Original Document
02/01/2013	2	Added 5.2.6 to add statement to report for cases with evidence worked prior to 01/03/2013
03/08/2013	3	Definitions – clarified CPE and CPI; 5.2.4 – clarified when statement is added to report; 5.4 - Note – reworded statement to read # contributors; 5.4.1.2 – changed “predominant profile” to “predominant DNA profile”
05/30/2013	4	5.2.6 – added option for situation where comparisons cannot be made
09/13/2013	5	3.0 – updated definition for reference standard; 5.1 – removed “victim” wording; 5.2.6, 5.3.2 – clarified wording; 5.10 – clarified note when statement would be used; 5.11 – clarified notification report wording; 5.11.3 - added wording for one-time searches
09/25/2013	6	Header – added issuing authority titles; 5.11.3 – clarified wording; 5.11.4 – added wording for Notification of CODIS entry
12/18/2013	7	5.1 – changed wording to generate pop clock in all RMP cases; 5.14.1.1 – combined 5.14.1.1 and 5.14.1.2 for RMP stats
04/18/2014	8	3.0 – removed definitions, added references; 5.1 – removed population clock (added to statistics procedure); 5.2.1 – removed predominant profile; 5.3.2 – removed; 5.5.2, 5.14 – clarified wording; 5.14.1.1 – added requirement for all population groups; 5.14.2.2 – reworded for clarity
08/29/2014	9	5.2.6 – removed phone number; 5.2.7 – added wording for standards not suitable for comparison purposes
02/27/2015	10	5.4.1.1 – added “DNA”; 5.4.1.2 – changed wording for consistency; 5.10 – reworded to make consistent throughout section reporting; 5.12 – clarified wording; 5.14.2.2 – changed word for consistency

12/28/2015	11	5.2.7 – clarified wording; 5.2.8 – added extraction wording; 5.2.9 – updated report header and disposition note wording; 5.3 – added wording for assumed contributor to profile; 5.4 – removed Note; 5.4.1 – clarified wording for inclusion or exclusion; 5.4.2 – clarified wording for multiple major; 5.5 – added inconclusive wording and removed un-interpretable wording; 5.9, 5.15.3 - removed limited wording; 5.12.1 - clarified Note; 5.13.1 – added wording to contact NCSCCL; 5.16.1.1 – removed world’s population reference; 8.0 – updated reference
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