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| <b>ATF-LS-FB18</b><br><b>Forensic Biology Report Wording: Reporting the Results of Forensic Biology Analysis</b> | Published Online:<br><b>March 2018</b> |
| Authority: Technical Leader  |  |
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## 1. Scope

The following guidelines outline the wording to be used when reporting the results of Forensic Biology analyses. These guidelines cannot encompass all possible circumstances encountered during casework analysis. Therefore, it is assumed that it may be necessary to deviate from the guidelines in certain circumstances.

## 2. References

2.1 Not applicable

## 3. Safety / Quality Assurance

- 3.1 Reports will undergo a technical review in accordance with ATF Laboratory Services PPG 5.9.4.
- 3.2 Reports will undergo an administrative review in accordance with ATF Laboratory Services PPG 5.9.4.

## 4. Equipment

4.1 Not applicable

## 5. Procedure

- 5.1 The general report format will comply with the relevant ATF Policy and Procedures for reporting of results.
- 5.2 If DNA analysis was performed, the first paragraph in the Results Section shall be stated as follows:
  - 5.2.1 DNA analysis performed at the Bureau of Alcohol, Tobacco, Firearms and Explosives Laboratory utilizes the Polymerase Chain Reaction and the *relevant amplification kit* to examine the following STR loci: *loci*. The methods used during analysis adhere to the Quality Assurance Standards for Forensic DNA Testing Laboratories.

- 5.3 Results shall be grouped by exhibit.
- 5.4 Results of serological examinations
  - 5.4.1 If an exhibit was examined for the presence of biological material but no suitable areas were found for testing:
    - 5.4.1.1 *No biological stains were observed on the item (Exhibit X).*
  - 5.4.2 If an item is not suitable for forensic biology examination:
    - 5.4.2.1 *The item (Exhibit X) is not suitable for forensic biology examination.*
  - 5.4.3 Results of testing for the presence of blood:
    - 5.4.3.1 *Blood was indicated on the item (Exhibit X). No confirmatory testing was performed.*
    - 5.4.3.2 *No blood was detected on the item (Exhibit X).*
    - 5.4.3.3 *Results for the examination of blood were inconclusive on the item (Exhibit X).*
- 5.5 Evidence sampling
  - 5.5.1 If the evidence is sampled in one or more areas for DNA analysis, the following statement will precede the results statement:
    - 5.5.1.1 *The following areas of the item were swabbed/sampled for DNA analysis:*
    - 5.5.1.2 *If all the DNA extracts are combined into a single DNA extract, the following statement shall be made:*
      - 5.5.1.2.1 These samples were combined into a single sample during DNA analysis (Exhibit X.Qcombo).
    - 5.5.1.3 *If a portion of the extracts are combined into a single DNA extract, the following statement shall be made:*
      - 5.5.1.3.1 The swabs/cuttings/etc. of the area 1 (Exhibit X.QX) and the swabs/cuttings/etc. of area 2 (Exhibit X.QY) were combined into a single sample during DNA analysis (Exhibit X.Qcombo).
- 5.6 If no DNA analysis was performed on the swabs/sampling of the exhibit, the following statement will be used:
  - 5.6.1 No DNA analysis was performed on the swabs/sampling of the *item* at this time.
  - 5.6.2 As per ATF Laboratory policy, the reason for not performing DNA analysis must be stated. For example, the request for examination was withdrawn.
- 5.7 Results for DNA examination
  - 5.7.1 For known reference samples (blood, buccal swabs, alternate knowns, etc.):
    - 5.7.1.1 *A male/female DNA profile was obtained from a cutting/sample/etc. of the item from John Doe (Exhibit X.QX).*
  - 5.7.2 If no DNA profile was obtained for an item:
    - 5.7.2.1 No DNA profile was obtained from *a swabbing/cutting/etc. of the item* (Exhibit X.QX).
  - 5.7.3 If limited data was obtained for an item:
    - 5.7.3.1 Due to limited results, the DNA profile obtained from *a swabbing/cutting/etc. of the item* (Exhibit X.QX) is not suitable for comparison purposes.

- 5.7.4 If a partial, single source profile was obtained for an item:
- 5.7.4.1 A partial *male/female* DNA profile was obtained from a *swabbing/cutting/etc.* of the item (Exhibit X.QX).
- 5.7.5 If a complete single source profile was obtained for an item:
- 5.7.5.1 A *male/female* DNA profile was obtained from a *swabbing/cutting/etc.* of the item (Exhibit X.QX).
- 5.7.6 If a partial or full single source profile was obtained from an item, the above statement shall be followed by a conclusion statement.
- 5.7.6.1 *Exclusion*
    - 5.7.6.1.1 If the known reference profile(s) is determined to be inconsistent with the unknown DNA profile and therefore the known reference is excluded as a possible contributor of the unknown biological material:
      - 5.7.6.1.1.1 This DNA profile is inconsistent with the DNA profile of *John Doe* (Exhibit Y.QX). Therefore, *John Doe* is excluded as the source of the biological material found on the *item*.
    - 5.7.6.2 *Inclusion*
      - 5.7.6.2.1 If the known reference profile is determined to be consistent with the unknown DNA profile and therefore the known reference is included as a possible contributor of the unknown biological material:
        - 5.7.6.2.1.1 This DNA profile is consistent with the known profile of *John Doe* (Exhibit Y.QX). Therefore, *John Doe* cannot be excluded as the source of the biological material found on the *item*.
        - 5.7.6.2.1.2 If a second reference profile is determined to be excluded, the following statement shall be added: *Bob Doe* (Exhibit Y.QX) is excluded as the source of the biological material found on the *item*.
- 5.7.7 If a partial mixed profile was obtained for an item:
- 5.7.7.1 A partial DNA profile consisting of a mixture of at least (*minimum # of contributors*) individuals was obtained from a *swabbing/cutting/etc.* of the *item* (Exhibit X.QX). NOTE: If an amelogenin Y peak is detected, then add the following: At least one of the contributors is a male.
- 5.7.8 If a complete mixed profile was obtained for an item:
- 5.7.8.1 A DNA profile consisting of a mixture of at least (*minimum # of contributors*) individuals was obtained from a *swabbing/cutting/etc.* of the *item* (Exhibit X.QX). NOTE: If an amelogenin Y peak is detected, then add the following: At least one of the contributors is a male.

5.7.9 If no conclusions regarding inclusion or exclusion can be drawn due to the complexity or low level nature of the mixture, the following statement will be used:

5.7.9.1 *Due to the complex nature of this mixed DNA profile, this DNA profile is not suitable for comparison purposes.*

5.7.10 If a partial or complete mixed profile that is suitable for comparison for which a major and minor component cannot be determined was obtained from an item, the initial results statement shall be followed by a conclusion statement:

5.7.10.1 *Exclusion*

5.7.10.1.1 If it is determined that the known reference profile(s) is not a possible contributor to the unknown DNA mixed profile:

5.7.10.1.1.1 The DNA profile of *John Doe* (Exhibit X.QX) is not consistent with being a contributor to this mixture. Therefore, *John Doe* is excluded as a possible contributor to the biological material found on the *item*.

5.7.10.2 *Inclusion*

5.7.10.2.1 If it is determined that the known reference profile(s) is a possible contributor to the unknown DNA mixed profile:

5.7.10.2.1.1 The DNA profile of *John Doe* (Exhibit X.QX) is consistent with being a contributor to this mixture. Therefore, *John Doe* cannot be excluded as a possible contributor to the biological material found on the *item*.

5.7.11 If a partial or complete mixed profile that is suitable for comparison for which a major and minor component can be determined was obtained from an item, the initial statement above shall be followed by a conclusion statement.

5.7.11.1 *Exclusion*

5.7.11.1.1 If it is determined that the known reference profile(s) is not a possible contributor to the unknown DNA mixed profile (both the major and minor components):

5.7.11.1.1.1 The DNA profile of *John Doe* (Exhibit X.QX) is not consistent with being a contributor to this mixture. Therefore, *John Doe* is excluded as a possible contributor to the biological material found on the *item*.

5.7.11.2 *Inclusion*

5.7.11.2.1 If it is determined that the known reference profile(s) is a possible contributor to the major component of the unknown DNA mixed profile(s):

5.7.11.2.1.1 The major component of this mixture is consistent with the DNA profile of *John Doe* (Exhibit X.QX). Therefore, *John Doe* cannot be excluded as the source of the major component of the biological material found on the *item*.

OR

5.7.11.2.1.2 The DNA profile of *John Doe* (Exhibit X.QX) is consistent with being a contributor to the minor component of this mixture. Therefore, *John Doe* cannot be excluded as a possible contributor to the minor component of the biological material found on the *item*.

5.8 Alternatively, the results and conclusions can be reported in a table format.

5.9 If a known reference is included as a possible contributor to a single source profile or mixed profile and the result is probative, a statistical result shall be reported.

5.9.1 A Random Match Probability calculation shall be reported if the unknown profile is a single source or is a major component of a distinguishable mixture:

5.9.1.1 *Assuming a single contributor, the probability of randomly selecting an unrelated individual with a DNA profile consistent with the DNA profile obtained from a swabbing/cutting/etc. of the item (Exhibit X.QX) is listed below for the following populations:*

1 in X (*billion, trillion, etc.*) US Caucasians

1 in X (*billion, trillion, etc.*) US African Americans

1 in X (*billion, trillion, etc.*) US Southwest Hispanics

OR

5.9.1.2 *Assuming the major component is a single contributor, the probability of randomly selecting an unrelated individual with a DNA profile consistent with the major component of the DNA profile obtained from a swabbing/cutting/etc. of the item (Exhibit X.QX) is listed below for the following populations:*

1 in X (*billion, trillion, etc.*) US Caucasians

1 in X (*billion, trillion, etc.*) US African Americans

1 in X (*billion, trillion, etc.*) US Southwest Hispanics

5.9.2 A Random Match Probability calculation shall be reported if the unknown profile is a mixture with indistinguishable major and minor components or a mixture with a distinguishable major and minor component for which the minor component is probative:

5.9.2.1 *Assuming N number of contributors, the probability of randomly selecting an unrelated individual who could be included as a contributor to the mixture obtained from a swabbing/cutting/etc. of the item (Exhibit X.QX) is listed below for the following populations:*

1 in X (*billion, trillion, etc.*) US Caucasians

1 in X (*billion, trillion, etc.*) US African Americans

1 in X (*billion, trillion, etc.*) US Southwest Hispanics

OR

5.9.2.2 *Assuming N number of contributors, the probability of randomly selecting an unrelated individual who could be included as a contributor to the minor component of the mixture obtained from a swabbing/cutting/etc. of the item (Exhibit X.QX) is listed below for the following populations:*

1 in X (*billion, trillion, etc.*) US Caucasians

1 in X (*billion, trillion, etc.*) US African Americans

1 in X (*billion, trillion, etc.*) US Southwest Hispanics

5.9.3 When stating the statistical results for a partial profile (single source or a mixture), any loci not used for the calculation due to inconclusive results shall be listed. Alternatively, the loci used for the calculation may be listed.

5.9.3.1 *The following loci were not used in the statistical calculation because the loci did not meet the required interpretation criteria: Locus A, Locus B, Locus C, etc.*

OR

5.9.3.2 *The following loci were used in the statistical calculation: Locus A, Locus B, Locus C, etc. The remaining loci did not meet the required interpretation criteria.*

5.9.4 The disposition of all DNA extracts shall be noted in the Disposition of Evidence section of the report.

5.9.4.1 *DNA Extracts Retained: The following DNA extracts will be retained by ATF Laboratory: Exhibits 1.Q1, 2.Q1, etc.*

5.9.4.2 *DNA Extracts Consumed in Analysis: The following DNA extracts were consumed in analysis: Exhibits 1.Q1, 2.Q1, etc.*

5.9.5 If any potential biological evidence is remaining on an exhibit, the following statement shall be made at the end of the report

5.9.5.1 *Note: Exhibit X may potentially contain biological evidence subject to specific storage and preservation requirements. Please reference ATF O 3400.1D and the ATF Property Taken into Bureau Custody Manual to review the storage and preservation requirements of this evidence for the purposes of possible future DNA analysis.*

## 5.10 CODIS Eligibility

### 5.10.1 NDIS Eligible

5.10.1.1 *At least 10 of core 13 loci (at least one locus meeting the requirements for statistical analysis) and meets other eligibility criteria (i.e. directly associated with crime).*

5.10.1.1.1 The DNA profile obtained from a *swabbing/cutting/etc.* of the item (Exhibit X.QX) will be entered into the Combined DNA Index System (CODIS) and searched at the national level.

### 5.10.2 SDIS Eligible

5.10.2.1 *At least 8 of core 13 loci (at least one locus meeting the requirements for statistical analysis) and meets other eligibility criteria (i.e. directly associated with crime).*

5.10.2.1.1 The DNA profile obtained from a *swabbing/cutting/etc.* of the item (Exhibit X.QX) will be entered into the Combined DNA Index System (CODIS). Due to the profile's limited nature, it can only be searched against DNA profiles generated by the ATF and other federal law enforcement agencies.

### 5.10.3 LDIS Eligible

5.10.3.1 *At least 6 of the 15 loci, at least one locus meeting the requirements for statistical analysis, meets other eligibility criteria (i.e. directly associated with crime)*

5.10.3.1.1 The DNA profile obtained from a *swabbing/cutting/etc.* of the item (Exhibit X.QX) will be entered into the Combined DNA Index System (CODIS). Due to the profile's limited nature, it can only be searched against other ATF-generated DNA profiles.

- 5.10.4 For PGI only, non-PGI, etc.
  - 5.10.4.1 *Low-level samples going into the PGI*
    - 5.10.4.1.1 Due to limited results, the DNA profile obtained from a *swabbing/cutting/etc.* of the *item* (Exhibit X.QX) cannot be entered into the Combined DNA Index System (CODIS).
- 5.10.5 Mixture violating 4x4 rule
  - 5.10.5.1 Due to the nature of this mixture, the mixture DNA profile obtained from a *swabbing/cutting/etc.* of the *item* (Exhibit X.QX) cannot be entered into the Combined DNA Index System (CODIS).
- 5.10.6 If waiting for a reference before making determination regarding uploading / association with crime / entry into LDIS / etc.
  - 5.10.6.1 At this time, the DNA profile obtained from a *swabbing/cutting/etc.* of the *item* (Exhibit X.QX) cannot be entered into the Combined DNA Index System (CODIS).
- 5.10.7 Unable to determine if “directly associated with a crime”.
  - 5.10.7.1 Due to the nature of the evidence, the DNA profile obtained from a *swabbing/cutting/etc.* of the *item* (Exhibit X.QX) cannot be entered into the Combined DNA Index System (CODIS) at this time.
- 5.10.8 Solved forensic profile (matches submitted suspect, for example).
  - 5.10.8.1 *Use appropriate CODIS eligibility verbiage from above.*
- 5.11 Evidentiary Profiles Associated with Contamination or Failed Controls

- 5.11.1 For evidentiary samples associated with contamination or failed controls where it is reasonable to assume that the integrity of the DNA analysis was not affected, the results shall be reported as described above.
  - 5.11.2 For evidentiary samples associated with contamination or failed controls where it is reasonable to assume that the integrity of the DNA analysis may have been affected, the results shall be reported as described above. In addition, a note shall be made in the report briefly describing the issue and stating the results should be interpreted with caution.
  - 5.11.3 For single source evidentiary samples demonstrating the presence of a staff member or a known contaminant, a note shall be made in the report describing the issue.
  - 5.11.4 For mixed DNA evidentiary profiles demonstrating the presence of a staff member or known contaminant, a note shall be made in the report describing the issue. The LR may be calculated conditioning on the presence of the staff member or known contaminant based on the analyst's discretion and with DNA Technical Leader Approval.
- 5.12 Comparisons to reference DNA profiles from another Laboratory
- 5.12.1 If a reference DNA profile generated by another laboratory was used for comparison to an ATF-generated evidentiary profile, a note shall be made in the report describing the source of the reference DNA profile.
    - 5.12.1.1 *Example: "The DNA profiles obtained from the evidence in this case were compared to DNA profiles identified as coming from Jonathan Doe (SERI Exhibit 2A) and Christopher Doe (SERI Exhibit 4) analyzed and reported by the Serological Research Institute, SERI (see SERI report dated May 5, 2014, signed by Thomas Brown). SERI was accredited by the American Society of Crime Laboratory Directors/Laboratory Accreditation Board (ASCLD/LAB) at the time the analysis was conducted."*
- 5.13 Reporting multiple consistent profiles from the same exhibit
- 5.13.1 If multiple DNA profiles are obtained from the same exhibit, but each has a different statistical weight, the group of profiles may be reported together using the lowest statistical weight to describe the entire group.
    - 5.13.1.1 *Example: "Assuming a single contributor, the probability of randomly selecting an unrelated individual with a DNA profile consistent with the DNA profiles obtained from the swabbings/cuttings/etc. of the item (Exhibit X.QX) is listed below for the following populations:*
      - At least 1 in X (billion, trillion, etc.) US Caucasians
      - At least 1 in X (billion, trillion, etc.) US African Americans
      - At least 1 in X (billion, trillion, etc.) US Southwest Hispanics