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Reporting DNA Conclusions

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Foreword

This standard defines the required components for reporting human autosomal STR and haplotype DNA interpretations and conclusions.

This document was revised, prepared, and finalized as a standard by the DNA Consensus Body of the AAFS Standards Board. The draft of this standard was developed by the Biology/DNA Biological Data Interpretation and Reporting Subcommittee of the Organization of Scientific Area Committees (OSAC) for Forensic Science.

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Keywords: *human DNA, autosomal STR, haplotype, mitochondrial, Y-STR, interpretation, conclusions, statistics, report, protocol, inclusion, exclusion, inconclusive*

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Reporting DNA Conclusions

1 Scope

This standard contains the reporting requirements for human autosomal STR and haplotype DNA conclusions for results obtained from evidentiary samples in forensic casework and does not apply to paternity or any other biological relatedness conclusions. This standard only addresses the requirements for providing DNA conclusions in the report.

2 Normative References

There are no normative references. Annex A (Bibliography) contains informative references.

3 Terms and Definitions

For purposes of this document, the following definitions apply.

3.1
assumed/conditioned contributor
An individual whose DNA on an evidentiary sample is reasonably expected or whose DNA data are used in the interpretation of evidentiary data.

3.2
comparative statement
A qualitative conclusion of any comparison performed to assess the degree of similarity or difference between DNA data (e.g., inclusion or exclusion).

3.3
conclusion
conclusionary statement
A reasoned deduction based on the results or a comparison. Conclusionary statements may have multiple elements: interpretive, comparative, and/or statistical statements.

3.4
evidentiary data
Data generated from an evidentiary sample and not from a reference sample.

3.5
evidentiary sample
Biological sample recovered from a crime scene or collected from persons or objects associated with a crime.

3.6
exclusion
exclusionary conclusion
A conclusion that eliminates an individual as a contributor of DNA obtained from an evidentiary sample based on the comparison of DNA data.

3.7
inclusion
inclusionary conclusion
A conclusion for which an individual is a potential contributor of DNA (i.e., cannot be excluded) obtained from an evidentiary sample based on the comparison of DNA data; a statement of inclusion does not confirm that an individual is a source of the DNA.

3.8
inconclusive
A determination that no conclusion (i.e., inclusion or exclusion) can be drawn from the comparison of reference data to evidentiary data. This could also result from statistical analyses that fail to provide sufficient support for an inclusion or exclusion.

3.9
interpretive statement
A qualitative description of the DNA data (e.g., partial data, mixture data).

3.10
probative
Possessing the potential to provide information that may be valuable to an investigation.

3.11
reference data
Data generated from a reference sample.

3.12
reference sample
Biological material obtained from a known individual and collected for purposes of comparison to evidentiary samples.

3.13
statistical statement
A quantitative statement that provides a measure of support for the comparison performed (e.g., random match probability, likelihood ratio).

3.14
uninformative
A scenario where the laboratory has concluded that the data do not support or refute a proposition as defined by the laboratory and based on validation studies.

3.15
unsuitable for comparison
Data that cannot be used for comparisons for reasons including, but not limited to, poor or limited data quality, mixture complexity, or a failure to meet quality assurance requirements.

4 Requirements

4.1 The laboratory shall have a protocol for reporting conclusions. Statistical evaluation shall be conducted and reported based on a documented laboratory protocol. The protocols shall be based on, developed from, and supported by internal validation studies.

NOTE See ANSI/ASB Standard 018, ANSI/ASB Standard 020 and ANSI/ASB Standard 040 for additional information (Bibliography).

4.1.1 The laboratory shall define when inclusions are considered probative and therefore when statistical evaluations are required. An example of a probative statement of inclusion that requires a statistical statement would be the inclusion of a person of interest to DNA data developed from a stain on the complainant's clothing.

4.1.2 A statistical statement shall be provided for any probative inclusion irrespective of the number of alleles detected or the quantitative value.

4.1.3 The laboratory shall define when inclusions are not considered probative and therefore when statistical evaluations are not required. The inclusion of an individual on her own clothing or the habitual driver's DNA on a vehicle steering wheel are examples of a statement of inclusion that may not be considered probative and may not require a statistical statement.

4.2 A conclusion shall be stated for each evidentiary sample tested.

4.2.1 All evidentiary samples tested shall have an interpretive, comparative, and/or statistical conclusionary statement in the report, as applicable. Laboratories should provide definitions or other explanations in the body of, as a footnote to, or in an appendix to the report, for clarification of scientific terms, technical terms or other discipline-specific terminology used in the report. This is important when the terminology used may be confusing or misleading to end users (e.g., statement that the use of the term "sperm fraction" is a technical description based on the methodology used and does not confirm the presence of sperm) or when the definition of terms may vary between laboratories (e.g., "match" or "consistent with").

NOTE 1 Interpretive statements that may be provided include, but are not limited to, any conclusion regarding: the biological sex of the contributor(s); the lack of sufficient DNA for further testing; the quality of the DNA data obtained; the suitability of the data for comparison; or the resolution of a mixture into contributor components.

NOTE 2 If the same conclusion applies to multiple items tested, they may be combined into one statement or paragraph.

4.2.2 If an evidentiary sample is used as an alternate reference sample, then its usage shall be clearly stated in the report. For example, when a known reference sample is not available from an individual, it may be possible to use an evidentiary sample as an alternative (or presumed) reference sample (e.g., blood on clothing at a stab wound; oral swab from a sexual assault kit).

4.3 Reported DNA conclusions shall be clearly stated and shall contain the information in 4.3.1 through 4.3.9.

4.3.1 Any assumptions of number, or minimum number, of contributors.

4.3.2 Any assumed/conditioned contributor(s) used in the interpretation of the data. The report shall also state when an assumption used is based on information provided by a source external to the laboratory and identify the source of the information used.

NOTE Examples of possible scenarios where a contributor to a DNA mixture may be assumed/conditioned include the individual whose body was swabbed for the collection of possible deposited biological fluids (e.g., samples labelled as a vaginal swab, breast swab, bitemark swab, oral swab, penile swab), consensual sexual partner, individuals known to have worn, touched or handled an item (e.g., clothing, bedding, steering wheel of car), or contamination events having a known source (e.g., staff involved in evidence handling, collection or testing), and other included person(s) of interest. Other case scenarios may involve the evaluation of data by assuming/conditioning the analysis on other profile(s) and may be performed as needed.

4.3.3 Any statements of inclusion with associated statistical statements in support of the probative inclusions.

4.3.4 The limitations of lineage testing for haplotype testing inclusions shall be disclosed in the report.

NOTE Haplotype testing is limited in that two specimens that exhibit the same haplotype may have originated from either a common individual source, from individuals with a close paternal (Y-STR) or maternal (mitochondrial) lineage, or unrelated individuals. Attribution of the haplotype typing results to a single individual, to the exclusion of relatives in the paternal or maternal lineage, is generally not possible.

4.3.5 Any limitation or restriction on the number of loci used. Only those loci present in both the evidentiary and reference data shall be used in interpretation and statistical calculations.

NOTE Due to the nature of some evidence (e.g., degraded, mixed DNA, tested with a legacy kit), it is common for the data from an evidentiary sample to be limited as compared to the data from known reference samples. Alternatively, situations may arise when the data from the reference sample is more limited (e.g., bone, tested with a legacy kit). This includes any scenario where the evidentiary and reference data are connected via intermediary data (e.g., the comparison of two profiles via an intermediary profile that shares loci with both the evidentiary and reference data).

4.3.6 Any statements of exclusion that result from comparisons to reference samples.

NOTE Laboratories may define situations where statements of exclusion may be unnecessary, such as in scenarios where additional comparisons will not be performed. These situations may include: when no DNA data foreign to an assumed contributor are obtained from an item, or when single source DNA data have been associated to an individual. The laboratory is not precluded from providing exclusion statements in these situations.

4.3.7 The reason(s) any DNA data, or minor components of mixed data, were deemed uninterpretable.

4.3.8 The reason(s) no definitive conclusion(s) can be reached (e.g., inconclusive, unsuitable for comparison, or uninformative).

4.3.9 Statement(s) regarding the termination of analysis of an evidentiary sample, including the reason the termination occurred (e.g., insufficient amount of DNA detected).

4.4 Reference samples that give expected results do not require a conclusion statement; however, reference samples that produce unexpected results (e.g., partial data, mixture) or no results shall have an interpretive statement included in the report.

4.5 A statement shall be included in the report regarding whether DNA data will be entered, or will not be entered, into a searchable database for the purpose of generating investigative leads (e.g., CODIS).

4.6 A statement shall be included indicating that the report does not contain all of the documentation associated with the work performed.

NOTE In order to understand and evaluate all the work performed a review of the case record is required.

Annex A
(informative)

Bibliography

The following bibliography is not intended to be an all-inclusive list, review, or endorsement of literature on this topic. The goal of the bibliography is to provide examples of publications addressed in the standard.

1] ANSI/ASB Standard 018, *Standard for Validation of Probabilistic Genotyping Systems, First Edition,* 2020.[a]

2] ANSI/ASB Standard 020, *Standard for Validation Studies of DNA Mixtures, and Development and Verification of a Laboratory's Mixture Interpretation Protocol, First Edition*, 2018.[b]

3] ANSI/ASB Standard 040, *Standard for Forensic DNA Interpretation and Comparison Protocols*, First Edition, 2019.[c]

4] ASTM E620-18, *Standard Practice for Reporting Opinions of Scientific or Technical Experts.*[d]

5] FBI, *Quality Assurance Standards for Forensic DNA Testing Laboratories*, 2020.[e]

6] ISO/IEC 17025:2017, G*eneral requirements for the competence of testing and calibration laboratories*.[f]

7] Department of Justice, National Commission for Forensic Science (2015) Views of the Commission - Documentation, Case Record and Report Contents.[g]

8] Department of Justice, National Commission for Forensic Science (2016) Recommendation to the Attorney General - Documentation, Case Record, and Report Contents.[h]

9] SWGDAM. *Interpretation Guidelines for Autosomal STR Typing by Forensic DNA Testing Laboratories*.[i]

[a] Available from: https://www.aafs.org/asb-standard/standard-validation-probabilistic-genotyping-systems
[b] Available from: https://www.aafs.org/asb-standard/standard-validation-studies-dna-mixtures-and-development-and-verification-laboratorys
[c] Available from: https://www.aafs.org/asb-standard/standard-forensic-dna-interpretation-and-comparison-protocols
[d] Available from: https://www.techstreet.com/standards/astm-e620-18?product_id=2012164
[e] Available from: https://www.swgdam.org/_files/ugd/4344b0_d73afdd0007c4ed6a0e7e2ffbd6c4eb8.pdf
[f] Available from: https://www.iso.org/standard/66912.html
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10] SWGDAM. *Interpretation Guidelines for Y-Chromosome STR Typing by Forensic DNA Laboratories*.[i]

11] SWGDAM. *Scientific Working Group on DNA Analysis Methods Interpretation Guidelines for Mitochondrial DNA Analysis by Forensic DNA Testing Laboratories*.[i]

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