

ASB Standard 139, First Edition
2020

Reporting DNA Conclusions



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ASB Approved Xxxxxx 2020

ANSI Approved Xxxxxxx 2020



Academy Standards Board
410 North 21st Street
Colorado Springs, CO 80904

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Foreword

This standard defines the required components for reporting 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: *DNA, autosomal STR, haplotype, mitochondrial, Y-STR, interpretation, conclusions, statistics, report, protocol, inclusion, exclusion, inconclusive*

Table of Contents

1	Scope.....
2	Normative References
3	Terms and Definitions
4	Requirements
	Annex A (informative) Bibliography

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Reporting DNA Conclusions

1 Scope

This standard contains the reporting requirements for 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 contributor

An individual whose DNA on an evidentiary sample is reasonably expected or whose DNA data are used (i.e., conditioned upon) in the interpretation of evidentiary data.

3.2

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.

3.3

evidentiary data

Data generated from an evidentiary sample. These data may be compared to data from reference sample(s) in an attempt to identify the possible source of the evidentiary sample.

3.4

evidentiary sample

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

3.5

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.

3.6

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.

**3.7
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 (e.g., an uninformative likelihood ratio).

**3.8
interpretive statement**

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

**3.9
probative**

Possessing the potential to provide details that are valuable to an investigation.

**3.10
reference data**

Data generated from a reference sample for purposes of comparison to data from other biological samples.

**3.11
reference sample**

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

**3.12
statistical statement**

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

**3.13
uninformative**

A scenario where the laboratory has concluded that the data do not support or refute a proposition.

**3.14
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.

4.1.1 The laboratory shall define when inclusions are considered probative and therefore 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 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.

NOTE 1 Interpretive statements that may be provided include, but are not limited to, any conclusion regarding: the gender 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 contributor(s) used in the interpretation of the data.

Examples of possible scenarios where a contributor to a DNA mixture may be assumed include the individual whose body was swabbed for the collection of possible deposited biological fluids (e.g., vaginal swab, breast swab, bite mark 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). Other case scenarios may involve the evaluation of data by conditioning (i.e., assuming) 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 any individual within the same 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. 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).

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 interpretable.

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) 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).

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] SWGDAM. *Interpretation Guidelines for Autosomal STR Typing by Forensic DNA Testing Laboratories.*^a
- 2] SWGDAM. *Interpretation Guidelines for Y-Chromosome STR Typing by Forensic DNA Laboratories.*^a

^a Available at www.swgdam.org.

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