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Standard for Training in Forensic Autosomal Short Tandem Repeat (STR) Data and Y-STR Data Interpretation and Comparison

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Foreword

This standard defines the minimum requirements to be met in a forensic DNA analyst training program for autosomal STR data and Y-STR data interpretation and comparison. The aim is to provide framework for quality training that will result in consistency in the forensic DNA community.

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 Biological Data Interpretation and Reporting Subcommittee of the Organization of Scientific Area Committees (OSAC) for Forensic Science.

The American Academy of Forensic Sciences established the Academy Standards Board (ASB) in 2015 with a vision of safeguarding Justice, Integrity and Fairness through Consensus Based American National Standards. To that end, the ASB develops consensus based forensic standards within a framework accredited by the American National Standards Institute (ANSI), and provides training to support those standards. ASB values integrity, scientific rigor, openness, due process, collaboration, excellence, diversity and inclusion. ASB is dedicated to developing and making freely accessible the highest quality documentary forensic science consensus Standards, Guidelines, Best Practices, and Technical Reports in a wide range of forensic science disciplines as a service to forensic practitioners and the legal system.

Questions, comments, and suggestions for the improvement of this document can be sent to AAFS-ASB Secretariat, asb@aafs.org or 401 N 21st Street, Colorado Springs, CO 80904.

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ASB procedures are publicly available, free of cost, at www.aafs.org/academy-standards-board.

Keywords: *training, interpretation, mixture deconvolution, comparison, DNA standard, autosomal STR, Y-STR*

Table of Contents *(to be finalized prior to publication)*

Standard for Training in Forensic Autosomal Short Tandem Repeat (STR) Data and Y-STR Data Interpretation and Comparison

1 Scope

This standard defines the minimum requirements to be met in a forensic DNA analyst training program for autosomal and Y-STR data interpretation and comparison. This standard excludes training for DNA sequencing.

2 Normative References

The following reference is indispensable for the application of the standard. For dated references, only the edition cited applies. For undated references, the latest edition of the referenced document (including any amendments) applies.

ANSI/ASB Standard 022*, Standard for Forensic DNA Analysis Training Programs,* First Edition, 2019[a]*.*

3 Terms and Definitions

For purposes of this document, the following definitions apply.

3.1
analytical threshold
The minimum height requirement at and above which detected peaks on a STR DNA profile electropherogram can be reliably distinguished from instrument background noise; peaks above this threshold are generally not considered noise and are either artifacts or true alleles.

3.2
degradation
The fragmenting, or breakdown, of DNA by chemical, or physical means.

3.3
drop-in
Allelic peak(s) in an electropherogram that are not reproducible across multiple independent amplification events.

3.4
drop-out
Failure of an otherwise amplifiable allele to produce a signal above analytical threshold because the allele was not present or was not present in sufficient quantity in the aliquot that underwent PCR amplification.

[a] Available from: www.aafs.org/academy-standards-board.

3.5
inclusion
A conclusion for which an individual cannot be excluded as a potential contributor of DNA obtained from an evidentiary item based on the comparison of known and questioned DNA profiles (or multiple questioned DNA profiles to each other); a statement of inclusion does not confirm that an individual is a source of the DNA.

3.6
inconclusive
A statement provided as the conclusion when testing results are insufficient or lacking in quality and/or quantity, as defined by the laboratory, for comparison purposes; the data are inadequate to draw any meaningful conclusions.

3.7
inhibition
The act of interfering with or preventing the synthesis of DNA during the amplification process of the polymerase chain reaction (PCR).

3.8
match
When used in a DNA testing report, a match refers to genetic profiles that show the same types at all loci tested in common; a match statement does not confirm that an individual is the source of the DNA.

3.9
mixture
DNA typing results originating from two or more individuals.

3.10
mutation
A change in DNA sequence; an alteration or change of an allele at a particular locus resulting in genetic inconsistency between a biological or cellular parent and offspring.

3.11
peak height ratio
The relative ratio of two peaks at a given locus in a diploid heterozygous single-source sample.

3.12
single source
DNA typing results originating from one individual.

3.13
stochastic threshold
The peak height value in a DNA profile above which it is reasonable to assume that, at a given locus, allelic drop-out of a sister allele in a heterozygous pair has not occurred in a single source DNA sample.

3.14
stutter
An artifact of polymerase chain reaction (PCR) amplification typically observed one or more repeat units smaller or larger than a short tandem repeat (STR) allele in a DNA profile, may result from strand slippage during PCR amplification. A stutter peak is generally of lower relative fluorescence units (RFU) than the allele peak.

3.15
tri-allelic pattern
The detection of three alleles in one individual at a particular short tandem repeat (STR) locus.

4 Requirements

4.1 General

Based upon the laboratory procedures, some of the requirements in this section may be omitted from the training program.

4.2 Knowledge-based Training

4.2.1 At a minimum, the knowledge-based portion of the training program shall require review of the following:

a) the laboratory's protocols for forensic autosomal and Y-STR data interpretation;

b) the laboratory's applicable validation studies;

c) literature used to support validation;

d) literature used to support the laboratory's interpretation protocol;

e) applicable literature as assigned by the trainer.

4.2.2 The knowledge-based training component of the laboratory's training program shall provide the trainee with a basic understanding of the steps for forensic autosomal and Y-STR data interpretation. The training shall provide instruction on the interpretation parameters used by the laboratory, how the parameters were determined by the laboratory and any limitations of the laboratories validation studies (such as mixtures with number of contributors above what the laboratory considered during validation). The training shall also address documentation requirements of decisions made during the interpretation process. It is critical the training includes manual interpretation and comparison even when software tools may be used. The training shall include, at minimum, the following topics, in 4.2.2.1 through 4.2.2.3.

4.2.2.1 Quality control indicators:

a) positive controls;

b) negative controls;

c) internal lane standards;

d) primer peak;

e) allelic ladder.

4.2.2.2 Data suitable for interpretation and/or comparison:

a) factors in data interpretation:

1) peak height thresholds:

i) analytical threshold,

ii) stochastic threshold;

2) artifacts:

i) drop-in/drop-out,

ii) stutter (forward and backward),

iii) spike,

iv) pull-up,

v) other [e.g., (-A), dye blobs];

3) peak height ratios;

4) PCR inhibition;

5) DNA degradation;

6) preferential and differential amplification;

7) other considerations (e.g., mutations, tri-allelic patterns, microvariants).

b) requirements for single source data interpretation;

c) requirements for mixture data interpretation including mixture sample types and number of contributors;

d) limitations of mixture interpretation (e.g., if the laboratory is validated to interpret four person mixtures, the trainee needs to be trained on four-person mixture interpretation and understand why the laboratory does not interpret mixtures with more than four contributors. See 4.2.1-b.);

1) mixture assumptions:

i) determination of number of contributors,

ii) appropriate conditioning/assumption of expected (known) individuals,

iii) estimating the ratio of contributors in mixtures,

iv) biological relatives in mixtures;

2) mixture considerations:

i) stutter including how stutter can mask or elevate a minor component in a mixture,

ii) allelic drop-in/drop-out,

iii) allele sharing in mixtures on apparent contributor ratios,

iv) inhibition and degradation,

v) tri-allelic patterns, mutations, etc.;

vi) data too limited, or too complex.

3) mixture deconvolution:

i) major component(s),

ii) minor component(s),

iii) foreign component(s);

4) probabilistic genotyping (if utilized by the laboratory):

i) scientific principle of probabilistic model,

ii) hypothesis development,

iii) statistical methodology,

iv) limitations of software;

e) Comparison of evidentiary data to reference data (as applicable):

i) match,

ii) consistent,

iii) inclusion/cannot be excluded,

iv) exclusion,

v) inconclusive.

4.2.2.3 Data unsuitable for interpretation and comparison:

a) Data too limited.

b) Data too complex.

4.3 Practical Training

4.3.1 The practical component of the laboratory's training program shall provide the trainee with sufficient practical instruction for the trainee to obtain the skills for forensic autosomal and Y-STR data interpretation protocol(s) used by the laboratory to include, at minimum all components in 4.12.

4.3.2 The protocol(s) shall be observed by the trainee at least once.

NOTE This can be done by direct observations and supplemental case file review until the protocols are clearly understood.

4.3.3 Practical exercises shall be representative of the range, type, and complexity of routine casework or database samples processed by the laboratory that include using the laboratory's own data.

4.3.4 The number and quality of samples interpreted by the trainee shall include manual and automated methods, as applicable, and shall be appropriate to demonstrate the ability to follow the laboratory's forensic autosomal and Y-STR data interpretation protocol(s) and to produce reliable and accurate results.

4.4 Competency Component

4.4.1 General

The competency component of the laboratory's training program shall demonstrate knowledge based and practical competency in the application of forensic autosomal and Y-STR data interpretation protocol(s) as used by the laboratory. The format of the test(s) shall meet section 4.3 of ANSI/ASB Std 022.

4.4.2 Knowledge-based Competency

The trainee shall successfully complete a knowledge-based test covering the critical information obtained during the training of forensic autosomal and Y-STR data interpretation protocol(s). The format of the test(s) shall be at the discretion of the DNA technical leader or comparable authority. The test(s) shall cover, at a minimum, the topics outlined under 4.12.

4.4.3 Practical Competency

The trainee shall successfully complete a practical competency test covering each of the forensic autosomal and Y-STR data interpretation protocol(s) for which he or she will be independently authorized. All types of samples for which the trainee will be authorized to interpret shall be included in the practical competency test.

5 Conformance

In order to demonstrate conformance with this standard, the laboratory shall meet Section 5 of the ANSI/ASB Std 022.

Annex A
(informative)

Bibliography

The following information provides a list of the literature resources that may assist the DNA technical leader in defining the breadth and scope of the materials to be reviewed by the trainee. This list is not meant to be all-inclusive.

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