Deadline of Submission of Comments: 10-Jul-23

Document Number: ANSI/ASB Std 078

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

#	Section	Type of Comment (E-Editorial, T-Technical)	Current Document Wording	Comments	Proposed Resolution	Final Resolution
	Forward	E	The aim is to provide a framework for quality training that will result in consistency in the forensic DNA community.	changed for consistency across training documents	The aim is to provide a framework for quality training resulting in consistency within a laboratory and in the forensic DNA community.	Accept
49	General	T		The standard seems a little backward looking.	Provide more guidance on probabilsitic thinking instead of (or at very alongside) emphasizing categorical conclusions.	Reject. The CB adjuciated this comment in round 01 and voted to approve the previous resolution.
16	keywords	E	training, interpretation, mixture deconvolution, comparison, DNA standard, autosomal STR, Y-STR	remove mixture interpretation	It isn't a focus of this training document, maybe for a mixture standard, but not for a training document broadly on interpretation	Reject. Comment too vague. The CB cannot make assumptions about what wording the commenter would like to propose.
33	1	T		The standard does not discuss how to present the interpretations in legal proceedings and does not address any other legal training for analysts. This limitation should be noted in the statement of scope. The scope should also note that legal training documents have been added to the bibliography. We recommend adding LTG legal training guidance doc, found at https://sites.google.com/nist.gov/osac/osac-units/legal-task-group?authuser=0, to the bibliography. Unfortunately, none of the DNA training docs include any specifics about legal training, even Std 022. The subcommittee should take this opportunity to correct that with this doc	Note in the scope that the standard does not discuss how to present the interpretations in legal proceedings. However, a guidance document regarding legal training is referenced in the bibliography.	Reject. A similar comment was adjudicated in round 01 and the CB voted to approve the following resolution: presentation in legal proceedings in out of scope for this standard. Standard 154, : Standard for Training on Testimony for Forensic Biology
18	3.3	T	~~Allelic peak~~Peak(s) in an electropherogram that are not reproducible across multiple independent amplification events.	This definition is incorrect in that it fails to distinguish several phenomena that are conceptually distinct (sporadic contamination of 1 or 2 alleles that are not reproducible; artifacts of the PCR or CE process; an allele from a true contributor to a sample pre-extract which only shows up say in 1 of 3 amplifications because it is a low level profile and the allele has dropped out of the other two amps. The edit removing "allelic" only confounds this problem. It really seems like a hard phenomenon to define. A possible suggestion: "Presence of one or two spurious alleles only in a profile; these alleles are not reproducible across multiple independent amplifications; also theory of same to explain 1-2 alleles not belonging to known contributor in a profile " Maybe include a cite to DNA Commission.	Drop in definition is inconsistent with the scientific literature. From Draft NIST Mixture Foundation Review: " 385 Allele drop-in: allele peak(s) in an electropherogram (EPG) that are not reproducible across multiple 386 independent amplification events; also, a hypothesis/postulate for the observation of one or more 387 allelic peaks in an electropherogram that are inconsistent with the assumed/known contributor(s) to a 388 sample"; Michael D. Coble & Jo-Anne Bright, *Probabilistic genotyping software: An overview*, FSI Int'l Genetics Vol. 38 (2019) "Drop-in is the presence of low amounts of DNA within a profile that are not inherent to the DNA extract.". DNA Commisison of ISFG, *Recommendations on the evaluation of STR typing results that may include drop-out and/or drop-in using probabilistic methods* (2012): ". In this context, we distinguish between drop-in and contamination. The latter term specifically describes more than two or more alleles that come from a single individual. Conversely, drop-in alleles come from different individuals. The distinction is important,because the assumption of independence enables the use of the product rule to multiply drop-in probabilities, whereas this is novalid if the events are dependent." At 681.	Reject, the suggested definition is specific to probabilistic genotyping and the WG feels it is not the most appropriate definition for this training document. The definition used in standard 078 is based on that from 2010 Fundamentals book by John Butler.
22	3.4	E		above analytical	above the analytical	Accept.
34	3.5	T		"Inclusion is defined as "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." OSAC has asked that "conclusion" not be used in standards.	Define "inclusion" as "A determination that a specific individual cannot be excluded as a source of some or all of the DNA in a sample."	Reject. This section was not part of the redline, therefor not open for comment in this round.

35	3.6	E		"Inconclusive" is defined as "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." The phrase "testing results are insufficient" is unclear. Insufficient in what respect other than quality or quantity?	Define "inconclusive" as "a determination that the samples or the test results are inadequate to draw any meaningful conclusions." (Of course, OSAC has decreed that the word "conclusions" cannot be used in standards, but it seems different in kind and appropriate here.)	Reject. This section was not part of the redline, therefor not open for comment in this round.
36	3.8	E		The section defines "match" implicitly rather than explicity, as "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." Why the restriction to reports? Does the word have a different meaning in testimony?	Define "match" as "The condition in which two genetic profiles show the same types at all loci tested in common."	Reject with modification. "match" has been deleted from the document and the terms.
21	3.8 & 4.2.2.2	T	use of word match	I thought the community was moving away from the word "match"--though the definition in 3.8 appropriately malkes clear that a match does not equate to "is the source of"		Accept with modification. Comment vague with no proposed resolution. "match" has been deleted from the document and the terms.
37	3.9	T		"Mixture" is defined as "DNA typing results originating from two or more individuals." However, a mixture is a state of the world--a combination of DNA molecules from more than one individual in the same sample. A low-level mixture may not produce results that would let an analyst recognize it as a mixture, but it is mixture nevertheless.	Define "mixture" as "A combination of DNA from two or more individuals in the same sample; a mixture with low level components may not be recognized as such based on the detected results"	Reject. This section was not part of the redline, therefor not open for comment in this round.
38	3.10	E		"Mutation" is defined as "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." The phrase "genetic inconstency" is obscure. What makes the mutated allele "inconsistent"? How can there be an alterationn that is not a change? How can there be a change other than a change in in the sequence? Deletions, insertions, and substitutions all change the sequence of base-pairs within an STR allele.	Define "mutation" as "a change in the sequence of base-pairs in a genome. Mutations can consist of insertions, deletions, or substitutions of base pairs."	Reject. This section was not part of the redline, therefor not open for comment in this round.
39	3.11	T		"Data produced when the emitted fluorescence from the PCR products being measured saturates the detector in an electropherogram". This is confusingly worded, sounds like the electropherogram has a detector	Change to: "Data produced when the emitted fluorescence from the PCR products being measured saturates the detector in an electrophoretic device" (or, in a capillary electrophoresis instrument, or genetic analyzer...)	Accept with modification, it was corrected to read "Data produced when the emitted fluorescence from the PCR products being measured saturates the detector; may result in flat-topped peaks in an electropherogram for STR alleles and pull-up peaks in one or more color channels corresponding to the off-scale peak." This definition was obtained from NIST STRbase.
50	3.11	E	Data produced when the emitted fluorescence from the PCR products being measured saturates the detector in an electropherogram; may result in flat-topped peaks for STR alleles and pull-up peaks in one or more color channels corresponding to the off-scale peak.	Data produced when the emitted fluorescence from the PCR products being measured saturates the detector during capillary electrophoresis ~~in an electropherogram~~, may present on the electropherogram as a ~~result in~~ flat-topped peak for an STR allele and pull-up peak(s) in one or more color channels corresponding to the off-scale peak.	provide clarity in the definition (e.g., the detector is not in the electropherogram); generally results in a single flat-topped peak per allele (changed to singular)	Accept with modification, it was corrected to read "Data produced when the emitted fluorescence from the PCR products being measured saturates the detector; may result in flat-topped peaks in an electropherogram for STR alleles and pull-up peaks in one or more color channels corresponding to the off-scale peak." This definition was obtained from NIST STRbase.
6	3.11	E	may result in flat-topped peaks for STR alleles and pull-up peaks in one or more color channels corresponding to the off-scale peak	may result in flat-topped peaks for STR alleles and pull-up peaks in one or more color channels that is the same size of the STR allele peak	removing the ending takes a portion of the term out of the definition, adding additional wording clarifies where to expect the pull-up peak	Accept with modification, it was corrected to read "Data produced when the emitted fluorescence from the PCR products being measured saturates the detector; may result in flat-topped peaks in an electropherogram for STR alleles and pull-up peaks in one or more color channels corresponding to the off-scale peak." This definition was obtained from NIST STRbase.
7	3.11	T	Data produced when the emitted fluorescence from the PCR products being measured saturates the detector in an electropherogram	Unsure	I do not feel like this definition captures all the reasons for off-scale data, such as bacterial contamination which can produce a peak and it isn't on scale	Reject with modification. Comment too vague. The CB cannot make assumptions about what wording the commenter would like to propose. Definition was revised based on other comments.

1	3.12	T		I haven't seen any forensic biology laboratories calculating PHR using way 1. The second calculation method is the most common (i.e. shortest peak/tallest peak * 100%) and should be listed as number 1.	Consider switching ways 1) and 2).	Accept
23	3.12	E		divided by the taller peak.	divided by the taller peak height.	Accept
40	3.12	T		"Peak height ratio" is defined as "The relative ratio of two peaks at a given locus in a diploid heterozygous single-source sample." The ratio is a simple ratio, not a relative ratio (which would be a ratio of ratios).	Define "peak height ratio" as "The ratio of the heights of two peaks at a given locus in an electropherogram". (please not that our recommended definition is more concordant with textbook definitions (e.g. Butler, Fundamentals)	Reject with modification. The CB adjuciated this comment in round 01 and voted to approve the previous resolution. Separate modifications were made based on comments #1 and #23
41	3.13	T		Preferential amplification. This includes a definition of preferential amplification *within* a locus; why is there no definition of amplification efficiency between loci, i.e. locus specific amplification efficiency, a concept used in PGS	Add locus specific amp efficiency, as well as other prob gen concepts that are missing from this document	Reject, the community accepted definition is specific to within a locus. Imbalance across loci resulting in a sloping profile is usually caused by degradation. Under standard 4.2.2.2, a) 9), "other considerations (...imbalance observed between loci)" was added.
10	3.13	T	A situation where one allele of a heterozygous pair at a locus is amplified by PCR with greater efficiency than the other allele	Unsure	This definition does not account for preferential amplification of smaller loci versus larger loci.	Reject, the community accepted definition is specific to within a locus. Imbalance across loci resulting in a sloping profile is usually caused by degradation. Under standard 4.2.2.2, a) 9), "other considerations (...imbalance observed between loci)" was added.
42	3.15	E		"Stochastic threshold" is defined as "The peak height value in a DNA electrophoretic 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" It's nonsensical to say a stochastic threshold is a peak height value in a profile. If you develop no profile from a sample, the stochastic threshold still exists (there would be no alleles above the analytical or stochastic threshold).	Change to "The stochastic threshold is a peak height value, measured in RFUs, above which it is reasonable to assume... "	Accept with modification, "commonly measured in RFUs" added to definition
24	3.16	E		doesn't make sense	clarify	Reject. Comment too vague. The CB cannot make assumptions about what wording the commenter would like to propose.
9	3.17	T	The detection of three alleles in one individual at a particular short tandem repeat (STR) locus	The detection of three alleles in one individual at a particular **autosomal** short tandem repeat (STR) locus	to be very clear in where trialleles occur since this is an autosomal and Y-STR document	Reject with modification. This definition was not part of the redline, therefor not open for comment in this round. For simplicity an editorial modification was made: the written out "short tandem repeat" was deleted and "STR" remains.
43	3.18	T		"Variant allele. A non-standard form of an allele due to a point mutation, an insertion or a deletion relative to other commonly seen alleles." Confusingly written, b/c insertions and deletions are types of point mutation. Also, to the extent a point mutation is commonly considered an insertion, deletion or substitution of a single nucleotide, and mutations that result in variant alleles could plausibly come from deletion or insertion from a small number, but nore than one nucleotide, is the "point mutation" part necessary?	Cut "point mutation" and just say "A non-standard form of an allele due to insertion or deletion of nucleotide base(s) relative to commonly seen alleles"	Reject with modification. a point mutation is not the same as an insertion or deletion. Modification made based on comment #8
8	3.18	T	A non-standard form of an allele due to a point mutation, an insertion or a deletion relative to other commonly seen alleles	A form of an allele not represented on the allelic ladder due to a point mutation, an insertion or a deletion relative to other commonly seen alleles.	the term 'non-standard' would mean that there are standard alleles, where this varies between allelic ladders which varies between previously identified variants.	Accept with modification. Definition changed to "A form of an allele due to an insertion or a deletion relative to other commonly seen alleles."
44	4.1	E		"The laboratory's training program shall include all requirements applicable to the work conducted by the laboratory and by the individual in training."	Insert "to be" before "by the individual in training" (presumably the scope of what that person does before they are fully trained is limited)	Reject, this wording is consistent across all the training documents
11	4.2.1c	E	literature used to support validation	literature used to support validation studies and reporting	I feel like this is vague, does it refer to the literature used to conduct the validation and write the report, the literature referenced in the report? More similar to how 4.2.1d is worded	Reject. This section was not part of the redline, therefor not open for comment in this round.
12	4.2.1e	E	applicable literature as assigned by the trainer.	applicable literature as assigned by the trainer;	change period to semicolon	Accept.
25	4.2.2	E		(such as mixtures with number of	(such as mixtures with numbers of	Accept
51	4.2.2	E	last line: ...in 4.2.2.1 through 4.2.2.3	4.2.2.1 through 4.2.2.2	there is no section 4.2.2.3	Accept. Revised to 4.2.2.2.
2	4.2.2.1	T		The internal PCR control (IPC) may be considered a positive control, but it's important to classify it separately, especially since it may differ from kit to kit.	Add "internal PCR controls" to the list.	Reject. This section was not part of the redline, therefor not open for comment in this round.

3	4.2.2.2	T		"[A]llele sharing" may be more suitable under 4.2.2.2(d)	Remove 4.2.2.2(a)(7) and put it under 4.2.2.2(d)	Accept, became 4.2.2.2 d) ii)
26	4.2.2.2	E		punctuation within lists not consistent	make consistent	Accept. ASB Staff will clean fix.
13	4.2.2.2	E	Consistency in semicolons, commas, and periods are needed throughout			Accept. ASB Staff will clean up punctuation.
45	4.2.2.2	T		"Data suitable for interpretation and/or comparison" … "(a) factors in data interpretation" … "(8) data too limited and/or too complex" This section is confusingly structured. It shouldn't be titled "Data suitable for interpretation" if one of the concepts included is "data is too limited and/or complex". Also, "data too limited and/or complex" feels tacked on at the end. Shouldn't it precede all of the stuff on interpretation, since it involves data deemed unsuitable for interpretation/comparison?	EITHER add a section before this section called "Data unsuitable for interpretation and comparison", with subsections for "data too limited" and "data too complex" (with sub-subsections on what makes profiles too limited or complex), OR change the title of this section to "Data suitability for interpretation and/or comparison" and lead off with data suitability determination, before getting into interpretation issues	Accept, 4.2.2.2 changed to "Data suitability..."
19	4.2.2.2(a)(2)	T	2) artifacts (i) drop out/drop in	Make Drop-out and drop-in theiir own number under (a) factors in DNA intepretation (i.e. make drop out and drop in number 2); remove them from artifacts	drop out and drop in are not artifacts	Accept. Moved to it's own item
52	4.2.2.2 a) 2) i)	T	drop-in/drop-out	delete "drop out" here and move below as a separate number still under 4.2.2.2 a)	drop out is NOT an artifact	Accept. Moved to it's own item
53	4.2.2.2 d)	E	;;	delete extra ; at the end	two ;;	Accept. ASB Staff will clean up punctuation.
4	4.2.2.2(d)	E		There's an extra semicolon.	Remove extra semicolon.	Accept. ASB Staff will clean up punctuation.
5	4.2.2.2(d)(iii)	T		This is also known as "mixture ratios" or "mixture proportions". It would be useful to define mixture ratio or proportion and provide calculation methods (similar to how peak height ratio was define).	Specify the term "mixture ratio" or "mixture proportion" and define it with suggested calculations.	Reject. This section was not part of the redline, therefor not open for comment in this round.
46	4.3.1	E		"At a minimum, the practical portion of the training program shall include the observation of a trained analyst performing the processes at least once or until clearly understood 4.3.2 with exercises representative of the range, type, and complexity…" Confusingly redlined, is this whole sentence supposef to be in 4.3.2?	Move the part of the sentence in 4.3.1 to 4.3.2	Accept with modification, revised paragraph based on multiple comments
54	4.3.1	E	The laboratory's training program shall provide…to obtain the skills for forensic…STR data interpretation and comparison protocols(s) used by the laboratory	The laboratory's training program shall provide…to obtain the skills for *the use of the laboratory's* forensic…STR data interpretation and comparison protocols(s) ~~used by the laboratory~~	words missing	Accept with modification, revised paragraph based on multiple comments
55	4.3.2	E	...at least once or until clearly understood with exercises...	...at least once or until clearly understood, with exercises...	added comma for better ease of reading	
20	4.3.2	E	4.3.2 ~~Practical~~ with exercises shall berepresentative of the range, type, and complexity of routine casework or database samples processed by the laboratory.	double check to ensure it is a sentence--maybe reinsert Practical and delete "with"	may just be the redline aking the flow look confusing but doesn't seem to be a sentence	
27	4.3.2	E		4.3.2 not needed	delete "4.3.2" as it does nt appear to be a new item in the list, and renumber	Reject, CB feels the numbering is necessary for clarity
47	4.3.3	T		"At a minimum, the practical portion of the training program shall include hands-on exercises representative of the range, type, and complexity of routine casework…" Needs some guidance as to what this means, ala other OSAC docs	Add a parenthetical "(e.g. considering number of contributors, template input, allele sharing, degradation)"	Reject, consistent with language in QAS, training topics are detailed in 4.2
56	4.3.3	E	...samples processed by the laboratory that include using the laboratory's own data	samples processed by the laboratory using current testing methods.	unclear what is meant by "laboratory's own data" and how that differs from "samples processed by the labortory" so advise deleting that language. Also not in 4.3.2.	Accept
28	4.4.2	E		the quality controls steps	the quality control steps	Accept (4.4.2 c) extra "s" deleted
14	4.4.2b	E	the function of the reagent controls used in forensic autosomal and Y-STR data interpretation and comparison	the purpose and function of the controls used in forensic autosomal and Y-STR data interpretation and comparison	function is the way an object accomplishes its purpose, the purpose is the intended or ultimate goal of an object - both should be captured in the competency test; remove the word reagent since that is not defined, this generalizes all controls that may be interpreted	Accept
15	4.4.2c	E	the quality controls steps	the quality control steps	remove plural form of 'controls'	Accept (4.4.2 c) extra "s" deleted
17	4.4.2 & 4.4.3	E		ISO/IEC 17025 requires a laboratory define what "successfully complete" means. A lot of labs miss this.	"The trainee shall successfully complete (as defined by the laboratory's policy) a…" OR Add a "NOTE The laboratory must define how they determine what "successfully complete" means.	Accept with modification (as defined by the laboratory's policy) added to 4.4.2 and 4.4.3. sentence structure edited for consistency across all training documents.

32	4.4.3	E		For the following language "a) properly and accurately execute forensic autosomal and Y-STR data interpretation and comparison protocol(s)", the difference between properly and accurately is unclear/not defined/	either define the difference or delete the word properly	Accept "Properly" removed from 4.4.3 a)
57	4.4.3	E	…for which the trainee will be authorized to interpret shall be included...	…for which the trainee will be authorized to interpret *and compare* shall be included...	the comparison aspect of the training is missing from this statement	Accept "and compare" added to 4.4.3
58	4.4.3 c)	E	…and software used in the laboratory for forensic…interpretation and comparison protocol(s);	*properly and accurately* operate relevant equipment, instrumentation, and software ~~used~~ as stated in the laboratory *protocol(s)* for forensic…interpretation and comparison ~~protocol(s)~~;	working awkward and confusing, and align with a) ; also, what's the difference between equipment and instrumentation - just keep equipment or instruments?	Accept with modification "accurately" and "as stated in the laboratory's protocol for "added to 4.4.3 c) Instruments are used for measuring, equipment is a tool with a specific purpose, not always used for measuring. Both words are necessary to cover all operations in the laboratory.
59	Annex A 6)	E	Butler, John	Butler, J	correction	Accept
60	Annex A 7)	E	Dror, et al.	Dror, I., et al.	correction	Accept
61	Annex A general	E	formating/spacing needs correcting		inconsistent spacing	Accept. ASB Staff will clean up layout.
48	Bibliography	T		The bibliography seems dated and scattered (other than the OSAC standards and Butler's textbook (2015), there is nothing on this list post 2011. I.e. it predates the rise of complex DNA interpretation (and lessons learned). It's particularly problematic given this training is intended to cover PGS. The readings associated with each topic in the body of the standard should be identified in the pertinent sections. That would greatly assist anyone seeking to create a training program.	Eliminate the bibliography and provide a list of recommended readings (classic or modern) on each required topic within the each topic section or subsection. Whether or not the bibliography is kept, add references related to PGS. Include more recent literature re: mixture interpretation challenges . Include reference to LTG guidance on legal training (found at found at https://sites.google.com/nist.gov/osac/osac-units/legal-task-group?authuser=0).	Reject with modification, recommended LTG reference is not publicly available. ASB 018 referenced as 1) in bibliography
29	ref 3]	E		vol.1	vol. 1	Accept
30	ref list	E		inconsistent use of et al.	make consistent (e.g. if three or more authors in the list)	Accept - ASB staff to clean up formatting
31	ref 9]	E		article title is capitalised	make sentence case	Accept - ASB staff to clean up formatting