

**Deadline of Submission of Comments: 18-Jul-25**  
**Document Number: ASB Std 039**  
**Document Title: Standard for Internal Validation of Human Short Tandem Repeat Profiling on Capillary Electrophoresis Platforms**

Comment #	Text Line # (s)	Document Section	Type of Comment E-Editorial T-Technical	Current Document Wording	Proposed Revision	Revision Justification	For Working Group and Consensus Body use only, not to be completed by commenter.
							Final Resolution
1		2	E	...the latest edition of the referenced document (including any amendments applies).	...the latest edition of the referenced document (including any amendments) applies.	the added closed parenthesis was placed in the wrong position	Accept
2		2	E	First Edition, 2020	delete "First Edition" and "2020"	this document is up for its 5 year review; this version will soon be out of date	Reject; the first edition is what our document is based upon and we don't know what changes may be made therefore it is important to keep the information
3		3	E		make definitions consistent between 129 and 039 and check for consistency of spellings, hyphens, etc. throughout both documents	make definitions consistent between 129 and 039 and check for consistency of spellings, hyphens, etc. throughout both documents	Accept
4		3.1	E	The minimum height requirement at and above which detected peaks on a STR DNA profile...	Replace 'on' with 'in'	Other locations in the document (Section 3.4.3.13) have 'in' when talking about peaks in an electropherogram. Change to make it consistent throughout the document.	Accept
5		3.4	T	Allele peak(s) in an electropherogram that are not reproducible across multiple independent amplification events.	Allele peak(s) in an electropherogram that are caused by random DNA found in the environment that are introduced during sample collection or testing of the sample and are not reproducible across multiple independent amplification events.	Add what drop in is caused by.	Reject, definition focuses on the outcome not the reason and random DNA introduced is not the only reason for drop-in
6		3.5	T	Failure of an otherwise amplifiable allele to produce a signal above analytical threshold because the allele was not present in sufficient quantity in the aliquot that underwent PCR amplification.	Failure of an otherwise amplifiable allele to produce a signal above analytical threshold because the allele was not present due to a mutation or due to insufficient quantity in the aliquot that underwent PCR amplification.	Drop out is also caused by mutations.	Reject, if there is a mutation in the primer binding site it is not amplifiable
7		3.13	T	3.13 stochastic threshold The peak height value in a DNA electrophoretic profile above which the results of validation studies show that it is statistically justified 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;; due to the possibility of shared alleles in mixed samples, the presence of allele peaks above the stochastic threshold is no guarantee that allele dropout/drop-out did not occur in mixed DNA sample profiles.	"It is reasonable to assume, based on validation studies,...."	Reasonableness determination be based on empirical data from validation study	Accept; this has been changed multiple times between document revisions and the working group believes inclusion of the validation study adds clarity
8		4.1.1 (now 4.1.2)	E	The laboratory shall conduct an STR genotyping concordance study.	Replace 'an' with 'a'	Other locations in the document (Section 3.1) have 'a STR..'. Change it to make it consistent throughout the document.	Accept with modification; changing to "an" and making consistent throughout the document. An is gramatically correct. Change will be made in BPR 129 as well.
9		4.1.1 (now 4.1.2)	E	concordance study seems out of place being listed first	move concordance study standard to the end of the STD or move the concordance study in the BPR to the front to match the order of studies	match order between STD and BPR	Accept; will change the BPR to match the Std
10		4.1.7 (now 4.1.8)	T	The laboratory shall conduct studies utilizing mixed DNA samples having a range of DNA ratios, DNA template input quantities, and numbers of contributors with varied degrees of allele sharing expected to be interpreted by the testing laboratory.	add wording that requires testing of actual relatives..."Validation shall include testing of mixtures comprised of related individuals" or "The laboratory shall conduct a study with mixtures comprised of related individuals and where non-contributing individuals are compared to mixtures which contain a relative"	Casework samples include mixtures of relatives and samples where the true contributor to the mixture is related to a noncontributing POI/suspect	Accept with modification; added additional clarity on the relationships to be included;"... and degrees of allele sharing (including mixtures of first-degree biological relationships i.e., parent and child; siblings)...."
11			Ballot Comment	Minor suggestion for standard 4.1.7 NOTE: put ASB standards in numerical order of 18, 20, and 40.			Reject with modification; The order is consistent with the description that preceded, "respectively" added to the end of the note for clarification.
12		4.1.10 (now 4.1.11)	E	"assessment"	evaluation	consider using the word "evaluation" instead of "assessment"; assessment is used in an audit setting and may be causing confusion for that reason	Accept
13		Bibliography	E	Standards 018, 020, 038, 040	delete "First Edition" and year from all standards listed	these documents are currently undergoing the 5 year review; these versions will be out of date and irrelevant before the 5year anniversary of this document (Note: keep the year for the companion BPR)	Accept

14		Bibliography	E		Add 1) NIST DNA Mixture Interpretation Foundational Review; 2) User's Manuals and developmental validation publication(s) for kits, instruments and software; 3) NIST Forensic DNA and Human Factors; 4) OSAC DNA Testing Process Map; NIST STRbase website	updated information	Accept with modification; item 2 was not added as it would be difficult to be all inclusive, but was listed as an example in section 4.1.
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