31-May-21
ASB Standard 140, Standard for Training in Forensic Human Mitochondrial DNA Analysis, Interpretation, Comparison, Statistical Evaluation, and Reporting

#	Section	Type of Comment	Comments	Proposed Resolution	Final Resolution
8	4.2.1	E	The explicit addition of limitations in this section is a good change to this standard. However, I think the content and wording could be improved to ensure that the context for limitations is not misintepreted. As it reads now, with the parenthetical expression, a reader could associate limitations only with the "technical procedures for generating a mitochondrial DNA sequence," as I did initially. The parenthetical expression essentially seems to be a definition for mtDNA analysis that was probably felt to be needed since the scope or context for the term analysis is not completely clear. Based on its common usage analysis could refer to the whole process of assessing and reporting on mtDNA evidence or, as I believe is intended here, to a particular aspect of the whole process. Instead of including a definition for just one of the actions covered in this standard, I think it would be better to add definitions for each of the actions in section 3 with the rest of the terminology. Most, if not all, of the other action terms also would benefit from specific definitions since the words used to designate them each also have common usages that may not exactly correspond to what is meant here, just like the term analysis.	evaluation, so drawing those lines clearly will pay off with improved understanding and communication by all. The laboratory's training program shall provide the trainee with an understanding of the fundamental principles and limitations of forensic human mtDNA analysis-(technical procedures for generating a mitochondrial DNA sequence), interpretation, comparison, statistical evaluation, and reporting, including the laboratory's own mtDNA protocols.	Reject 1st recommendation: adding recommended terms to section 3 is not necessary. Reject with modification 2nd recommendation: The section was updated for clarity.
1	4.2.3 b-2	Т	Outdated, transmission from mtDNA sperm has not been an area of controversy for well over a decade, if not much longer.	Consider removing this, since matrnal inheritance of mtDNA is not questioned in the courts these days.	Reject: Understanding sperm's role in the transition of mtDNA is critical fundamental knowledge. This comment is not on the redlined portions of this document and it is not open for comment.
2	4.2.3 c1-5	Т	Heteroplasmy detection and therefore rates and prevalence may not be the same for Sanger and Massively Parallel Sequencing (MPS)/ Next Generation Sequencing (NGS).	Consider combining c3-5 into one less-specific requirment to compare effect of detection of heteroplasmy from different sequencing technologies & their effect on forensic mtDNA analysis	Reject: These are important topics and this comment is not on the redlined portions of this document and it is not open for comment.
3	4.2.3 d-3	Т	Sequence alignment has moved from a strictly rules-based method to a method that places considerably more weight on phylogenetic alignments.	Consider adding knowledge of known phylogentic alignments/known patterns of polymorphisms.	Reject: These are important topics and this comment is not on the redlined portions of this document and it is not open for comment.
4	4.2.3 f-4	Т	The terms 'root cause analysis' and 'corrective actions' may mean very different things to different laboratories. For instance, in my lab our protocols address the course of action if mtDNA contamination is detected. There is no root cause analysis or corrective action undertaken, as those actions are more for when systemic and serious issues occur in my laboratory.	Consider using other softer, but equivalent terms to the spirit of the requirement, like "'mitigation procedures' when contamination occurs".	Reject: This topic is under the knowledge based portion of the training program and therefore content is customized to the laboratory.
9	4.2.3 f) 5)	E/T	I notice that throughout the rest of this standard the training topics covered, in addition to data generation, always include the same four expressed as "interpretation, comparison, statistical evaluation, and reporting." In this section statistical evaluation has been left out. It seems to me it would be better to list it here as done elsewhere. If statistical evaluation was omitted deliberately for some reason, however, then a brief note to explain why it does not apply in this section would be useful.	Add "statistical evaluation" to the list of topics in 4.2.3 f) 5) to match the other listings of these topics throughout the standard.	Accept
5	4.2.3-h-3	Т	Size of the databases being used in haplotype markers are an important factor in the resulting statistics.	Consider adding 'composition and size of the mtDNA sequence databases'	Reject: These are important topics and this comment is not on the redlined portions of this document and it is not open for comment.

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6	4.2.3 i-2	Т	There is no use of a population correction factor in mtDNA analysis. By extension no match probability or confidence interval that incorporates such are used in the mtDNA community. This may be used in some laboratories for YSTR analsyis, but not for mtDNA analysis. Profiles probabilities using a confidence interval is the community-wide agreed upon statistic and is considered very conservative. A liklihood ratio can be calculated from the profile probability, if a laboratory wishes to do so.	Consider removing altogether.	Reject: This comment is not on the redlined portions of this document and it is not open for comment.
7	4.2.3 i-4-ii	Т	See above, match probabilities are not a viable alternative for mtDNA.	Consider removing altogether.	Reject: This comment is not on the redlined portions of this document and it is not open for comment.