Response to STG, LTG on Wildlife Forensics:
ANSI/ASB 029, Report Writing in Wildlife Forensics: Morphology and Genetics

The following is an explanation of why taxonomic classifications in wildlife forensics do not require statistical support in the same way that declarations of a “match” in human DNA or in pattern disciplines such toolmark analysis do.

In wildlife forensics, an examiner identifies a sample as belonging to a particular taxonomic level (e.g. species) by looking up the set of characteristics that define that taxonomic level and determining whether the sample has those characteristics. New species are continually being identified, based on additional characteristics that scientists find, including both morphological features (e.g. a pink snout) and sequencing (e.g. a particular mtDNA haplotype). This process involves *validation* in the sense that scientists ensure through research that new taxonomic level definitions are based on characteristics that are new, distinguishable, and identifiable in a repeatable, reliable manner.

But the discipline does not require population variability studies to determine whether a sample belongs to a particular taxonomic level. That is because taxonomic definitions are based on invariant characters that are diagnostic for the taxon. Particular species may exhibit great variability, but variable characters are not included in the species definition. Thus, unlike disciplines seeking to attribute a particular sample to a particular source based on the rarity of shared features, in wildlife forensics, *any sample exhibiting the diagnostic characteristics associated with a taxonomic level belongs to that level BY DEFINITION*. For example, a sample that an examiner identifies as having all the diagnostic characteristics of the species *Alligator mississippiensis*, is, by definition, a member of that species, because taxonomists have defined that species to include all animals that have those characteristics.

Thus, the only source of error in an examiner’s determination that a sample belongs to a taxonomic level (e.g. species) is the examiner’s identification of the characteristics the sample has. Once the examiner correctly identifies the characteristics, and the characteristics that define the taxonomic level (e.g. the characteristics that define the genus *Alligator*, or the species *Alligator mississippiensis*), any sample with those defining characteristics is a member of that level *by definition.* If a sample is only partial or damaged or degraded, an examiner might only be able to classify the sample as belonging to a higher taxonomic level (e.g. as a member of the genus *Alligator*, but not any particular species of *Alligator*). *Note that species identification only identifies a sample as having the defining characteristics of a particular taxonomic level. It does not involve the individual identification of a member within the taxonomic group*.

Of course, like in other disciplines, examiners might commit errors in determining the characteristics a sample has (either morphological or sequencing). An estimate of such an error rate could be determined, like in other disciplines, through performance studies. As in other disciplines, this error rate would vary depending on the examiner’s experience, training, skill level, and judgment, and whether the examiner’s determination is subject to verification. We do not read this standard as speaking to performance studies; the standard merely explains why statistical statements are not appropriate for species identification made based on the documentation of definitional characters.

OSAC Registry Request Comment Adjudication Template

Document Title	ANSI/ASB 029, 2019, Report Writing in Wildlife Forensics: Morphology and Genetics
Requesting Subcommittee	Wildlife

Subcommittee Chair

Name:	Kim Frazier
Affiliation:	WGFD
Email:	
Phone:	

Subcommittee Technical Contact

Name:	
Affiliation	
Email:	
Phone:	

Beginning Comment Period Date	4/7/20	
End Comment Period Date	5/7/20	
Comment Adjudication Meeting Dates	7/9/20	10/5/20
# of Members Present	18	4

Note: This template is intended for use by all subcommittees considering a new document for addition into OSAC Registry

#	Person	Assigned To	Attached File
1	William Guthrie		None
2	David H Kaye		None

Comment/Proposals	Response	Status
I do not think ANSI/ASB 029, Report Writing in Wildlife Forensics: Morphology and Genetics, 2019, should be added to the OSAC Registry as is. Overall I think this standard and those from the same series that also are receiving comments at this time will be helpful to the field. However, I think it is critical that in the presentation of numerical results based on measured data in forensic science standards that both indications of the uncertainty of each result and discussion of the assumptions underlying the analysis of the data be given. This is not done in either Example Report B.1 in the second paragraph of the Nuclear DNA Analysis section or in results table of Example Report B.3. I urge the developers of this standard to address this issue prior to its addition to the Registry so that this standard will set the best example possible for laboratories and other stakeholders in forensics who look to OSAC for the highest level of scientific rigor in forensic science.	Previously considered-Please see attached	
The OSAC Legal Resources Task Group (LRTG) discussed ANSI/ASB Standard 029, First Edition 2019 (Report Writing in Wildlife Forensics: Morphology and Genetics) and saw no major legal concerns that should keep it from being on the OSAC Registry. For future reference by the subcommittee, Andrea Roth and David Kaye offer these observations: Section 3.7.7 contains this note: "Statistical support is not necessary when determining minimum number of individuals using either morphology or sequencing or when determining exclusions. When conducting species identification using morphology or sequencing, statistical support is not appropriate." Why is statistical support for an inference or classification "not appropriate"? OSAC should be working toward standards with methods that have statistical support. (One could say that statistical calculations are not necessary when it has been established that certain sequences or morphological features are known to be species-specific. Of course, such knowledge itself requires statistical support.) Annex B.1. The two propositions and the likelihood ratio required in 3.7.6(b) do not appear in the report. Annex B.2. There is no statement about uncertainty or limitations in the report. Submitted 5/7/2020 by David H. Kaye, Chair, LRTG	Previously considered- Please see attached	

Resolution	Disposition	Resolution Date and Vote Outcome	Company Name
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No response needed

Interest Category	Submission Date	Group Name	Document Name

Revision Number	Document Description	History