

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 as 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.