

OSAC Biology Scientific Area Committee Intent/Clarification Update September 2, 2020

Intent of [ANSI/ASB Standard 040 Standard for Forensic DNA Interpretation and Comparison Protocols](#)
Requirement 4.3

Requirement 4.3 from ANSI/ASB Standard 040 as proposed by the [Organization of Scientific Area Committees \(OSAC\) for Forensic Science's Biology Scientific Area Committee](#) is intended to ensure that evidentiary data are interpreted prior to performing comparisons. The standard defines interpretation as *the process of evaluating DNA data for purposes including, but not limited to, defining assumptions related to mixtures and single source profiles, distinguishing between alleles and artifacts, assessing the possibility of degradation, inhibition, and stochastic effects, and determining whether the data are suitable for comparison* (Definition 3.4). See below for clarification.

Alleles versus artifacts in any samples are to be determined prior to comparison. Reference profiles will not be used during interpretation of evidence sample data to determine if a peak in the evidence sample is, or is not, an artifact.

For evidence samples with a reasonably expected contributor (assumed donor), the reference profile of the assumed contributor may be used as part of the evidentiary profile deconvolution process as long as the assumption (and assumed contributor profile) are documented in the case record (See Requirement 4.3.3). If changes are needed to the interpretation based on comparisons of reference profile(s) to the evidence sample, Requirement 4.4.2 may be consulted.

Samples that qualify per laboratory protocol for the use of an assumed contributor, in general, require the following steps to be performed and documented prior to comparison to assumed contributor reference profiles:

1. Data interpretation (as defined above) completed
2. Determination of whether data are suitable for interpretation and comparison
3. Determination of assumptions that MAY be used per laboratory protocol (such as number of contributors, presence of an assumed contributor, etc.)

For samples where no contributors may be reasonably assumed, a reference profile will not be used to determine if low-level data (i.e., in the stochastic range) is suitable for comparison. Additionally, if using binary methods, acceptable contributor genotypes must be resolved prior to comparison to reference profiles. If changes are needed to the interpretation based on comparisons of reference profile(s), Requirement 4.4.2 may be consulted.

The use of one fraction of a differential extraction to assist in the interpretation of the data from the other fraction of the same sample is appropriate and does not involve the use of a reference profile.

Note: This standard does not conflict with the 2017 SWGDAM Interpretation Guidelines for Autosomal STR Typing by Forensic DNA Laboratories.