SWGDAM Guidelines for the Use of Probabilistic Genotyping with Autosomal STR Typing Results

TrueAllele® Casework System Compliance

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Introduction

This document describes Cybergenetics TrueAllele® Casework system compliance with the 2025 Scientific Working Group on DNA Analysis Methods (SWGDAM) guidelines for the use of probabilistic genotyping with autosomal STR typing results.

The SWGDAM guidelines are downloadable from:
https://www.swgdam.org/_files/ugd/4344b0_8fabde7c6aac46e4825d2468aa6763cc.pdf

Cybergenetics Standard Operating Protocol (SOP) [1] for its TrueAllele® Casework Process is downloadable from:
https://www.cybgen.com/reliability/Procedure.pdf

Relevant TrueAllele articles cited by SWGDAM are listed in the References [2, 4, 5, 6].

Compliance

The numbers given in parentheses refer to sections within the SWGDAM document that provide additional details.

The laboratory must establish and apply standard operating procedures that specify the following:

I. *(1.1) Appropriate analytical controls.*

   Not applicable. Cybergenetics receives electronic data and analytical controls generated by DNA laboratories that follow their own SOPs.

II. *(1.2; 1.6; 3.2; 3.3) Criteria for the suitability of DNA typing results for comparisons and/or probabilistic genotyping.*

Cybergenetics SOP contains suitability criteria for comparisons (sections 5.3, 5.4, 5.5, 5.7, 6, 7.3, 7.4, 7.5, 12).

III. *(1.3; 1.4) Procedures for interpreting the results and using probabilistic genotyping when multiple amplifications of a DNA sample or multiple capillary electrophoresis injections of an amplified sample are obtained.*

Cybergenetics SOP describes such procedures for interpreting replicated experiments (sections 4.2, 5.4, 7.3, 12.2).

IV. *(1.5; 2.1) Procedures for assigning the number of contributors to the DNA typing results, if such is required by the probabilistic genotyping software, that do not consider any person of interest (POI). The procedures for assigning the number of contributors may use any reasonably assumed contributor(s), if applicable.*

Cybergenetics SOP describes such procedures for addressing the number of contributors (sections 4.2, 5.4, 12.2, 12.3, 12.4).

V. *(1.7) Any manual determination of exclusion in lieu of probabilistic genotyping.*

Not applicable.

VI. *(2.1; 2.2; 2.3; 2.4) Procedures for the formulation of propositions used in calculating likelihood ratios and conditioning an interpretation on the genotype of an assumed contributor.*

Peer-reviewed articles [2] and conference papers [3] explain TrueAllele likelihood ratio formulation. Cybergenetics SOP describes genotype conditioning procedures (sections 5.4, 12.2).

VII. *(2.5) Procedures complying with National DNA Index System Procedures for any CODIS-eligible DNA typing results that are produced using probabilistic genotyping software.*

Cybergenetics SOP describes moderate match estimates used for NDIS procedures (sections 7.5, 7.6).

VIII. *(3) Review of the probabilistic genotyping output relative to the DNA analyst's expectations for those results.*

Please see Cybergenetics SOP for TrueAllele output review (sections 5, 5.4, 5.7, 6.1, 6.2, 12.1, 12.2, 12.3, 12.4, 12.5).

References

1. Cybergenetics. "TrueAllele® Casework Process: Standard Operating Procedures." June 2025.

2. Perlin MW, Legler MM, Spencer CE, Smith JL, Allan WP, Belrose JL, Duceman BW. Validating TrueAllele® DNA mixture interpretation. *J Forensic Sci.* 2011;56(6):1430-1447.

3. Perlin MW. Explaining the likelihood ratio in DNA mixture interpretation. *Promega's Twenty First International Symposium on Human Identification*, 2010; San Antonio, TX.

4. Perlin MW. Efficient construction of match strength distributions for uncertain multi-locus genotypes. *Heliyon*, 4(10):e00824, 2018.

5. Bauer DW, Butt N, Hornyak JM, Perlin MW. Validating TrueAllele® interpretation of DNA mixtures containing up to ten unknown contributors. *J Forensic Sci*, 2020; 65(2):380-398.

6. Greenspoon SA, Schiermeier-Wood L, Jenkins BA. Establishing the limits of TrueAllele® Casework: a validation study. *J Forensic Sci.* 2015;60(5):1263-1276.