

Standard for Training in Forensic DNA Amplification Methods for Capillary Electrophoresis Sequencing

Biological Methods Subcommittee Biology/DNA Scientific Area Committee Organization of Scientific Area Committees (OSAC) for Forensic Science





OSAC Proposed Standard

Standard for Training in Forensic DNA Amplification Methods for Capillary Electrophoresis Sequencing

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Foreword

This standard defines the minimum requirements that shall be met in a forensic DNA analyst training program for DNA amplification for capillary electrophoresis (CE) sequencing methods. The aim is to provide a framework for quality training that will result in consistency in the forensic DNA community.

This standard was revised, prepared and finalized as a standard by the DNA Consensus Body of the AAFS Standards Board (ASB). The initial draft document was developed by the Biological Methods Subcommittee of the Organization of Scientific Area Committees. All hyperlinks and web addresses shown in this document are current as of the publication date of this standard.

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	able of Contents	
1	Scope	.1
2	Normative References	.1
3	Terms and Definitions	.1
4	Requirements	. 2
	4.1 Knowledge-based training	.2
	4.2 Practical training	.5
	4.3 Competency testing	. 5
5 Conformance		.6
Aı	nnex A	.7



1 Scope

This standard provides the requirements of a forensic DNA laboratory's training program to ensure proper training in the approved methods of DNA amplification for capillary electrophoresis (CE) sequencing used within the trainee's forensic DNA laboratory.

2 Normative References

ASB Standard 022 - Standard for Forensic DNA Analysis Training Programs¹

3 Terms and Definitions

For the purpose of this document the following definitions apply:

3.1

Control region

A presumed non-coding portion of the mitochondrial DNA molecule analyzed through DNA sequencing, which may be used to determine an individual's mitochondrial haplotype or for taxonomic discrimination. The control region often contains hypervariable regions (in humans: HV1 and HV2) that differ in sequence among non-maternally related individuals. The control region encompasses the D-loop region in humans and other species.

3.2

Chloroplast DNA (cpDNA)

A circular DNA molecule, approximately 120-190kbp, which is located in the chloroplasts of plants. The DNA is maternally inherited and contains genes involved in the photosynthetic pathway.

3.3

Degradation

The fragmenting, or breakdown, of DNA or protein (e.g. loss of enzymatic-activity) by chemical, physical, or biological means; a common occurrence when biological samples containing DNA encounter warm moist environments or excessive UV light.

3.4

dNTPs

Abbreviation for deoxynucleotide tri-phosphates; used in PCR as building blocks to construct new DNA strands.

3.5

Hypervariable region

A segment of DNA that often contains polymorphisms and thus is useful for differentiating taxa or unrelated individuals.

3.6

Hypervariable region 1 (HV1)

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A section of the human mtDNA control region spanning nucleotide positions 16024-16365, that often differs among non-maternally related individuals.

3.7

Hypervariable region 2 (HV2)

A section of the human mtDNA control region spanning nucleotide positions 73-340, that often differs among non-maternally related individuals.

3.8

Inhibitor

As related to the polymerase chain reaction (PCR), any substance that interferes with or prevents the synthesis of DNA during the amplification process.

3.9

Mitochondrial DNA (mtDNA)

An often small (~16,500 bp in humans), circular DNA molecule located in eukaryotic mitochondria that is typically maternally inherited; the resistance to degradation and presence of multiple copies of mtDNA in each cell make it useful with samples originating from limited or damaged biological material.

3.10

Polymerase chain reaction (PCR)

An enzymatic process by which a specific region of DNA is replicated during repetitive cycles that consist of the following: denaturation of the template; annealing of primers to complementary sequences at an empirically determined temperature; and extension of the bound primers by a DNA polymerase. The goal of the PCR process is to generate many copies (termed products or amplicons) of a specific region of DNA for further analysis.

3.11

PCR product quantification

An analytical procedure to determine the amount of amplicon obtained after DNA amplification.

3.12

Primer

A short polynucleotide chain, usually 18-30 bases long, which targets a specific region of the template DNA and allows a DNA polymerase to initiate synthesis of a complementary strand; two primers are required for amplification of a particular section of DNA. The primers are complementary to opposite strands and are designed to bracket the region of interest for amplification. Polymerization is initiated at the 3' end of the primer and extends in a 5' to 3' manner.

4 Requirements

4.1 Knowledge-based training component

The laboratory's training program shall provide the trainee with an understanding of the fundamental principles of the theory behind DNA amplification for CE sequencing, the function of



the amplification reagents and other components used in the method, the limitations of amplification, and the laboratory's own DNA amplification guidelines.

- 4.1.1. At a minimum, the knowledge-based portion of the training program shall require review of the following:
 - a) The laboratory's protocols for DNA amplification for CE sequencing
 - b) The laboratory's applicable validation studies
 - c) Literature used to support validation
 - d) Applicable literature as assigned by the trainer (e.g., see references in Annex A)
- 4.1.2 At a minimum, the knowledge-based portion of the training program shall cover the following topics:

NOTE: Knowledge of historical methods is intended to provide an educated perspective. In-depth understanding of these methods may not be required for successful training.

- a) Principles of PCR-based DNA amplification methods for CE sequencing
 - i. Reaction components
 - a. dNTPs
 - b. Primers
 - c. Buffer
 - d. Polymerase
 - e. MgCl₂
 - f. PCR enhancers (if applicable, e.g. bovine serum albumin)
 - ii. Primer design
 - iii. Amplification parameters
 - iv. PCR inhibitors
 - v. DNA degradation
- b) Primer selection for specific target regions of DNA amplification (as applicable to the laboratory)
 - i. Mitochondrial DNA
 - a. Control region



- b. Portions of control region
- c. Whole genome
- ii. Chloroplast DNA
 - a. Coding regions
 - b. Transgenic spacer regions
- iii. Nuclear/genomic DNA
 - a. Coding regions
 - b. Non-coding regions
- iv. Primer binding site mutations
- v. Quality and source of DNA
- c) Contamination control and prevention
 - i. Use of personal protective equipment
 - ii. Ultraviolet cross-linking of consumables and utensils
 - iii. Decontamination of work surfaces (e.g. sodium hypochlorite, UV light)
 - iv. Workflow set-up
- d) Quality controls used for DNA amplification
- e) Purification of amplification product
- f) Post-amplification quantification
 - i. Evaluation of the controls
 - ii. Determination of DNA concentration
- g) Instrumentation and reagents
 - i. Thermal cycling instruments and parameters
 - ii. Software parameters associated with instruments
 - iii. Maintenance and calibration
 - iv. Storage of amplification reagents
- h) Troubleshooting



- i. Amplification and post-amplification quantification failure
- ii. Instrument failure and recovery

4.2 Practical training

The laboratory's training program shall provide the trainee with sufficient practical instruction for the trainee to obtain the skills for performing the DNA amplification for CE sequencing protocols used by the laboratory.

- 4.2.1 At a minimum, the practical portion of the training program shall include the observation of the processes at least once and until clearly understood. These include:
 - a) DNA amplification for CE sequencing methods to be utilized by the trainee
 - b) Documentation of the process
- 4.2.2 At a minimum, the practical portion of the training program shall include exercises representative of the range, type, and complexity of routine casework and/or database samples processed by the laboratory. These include:
 - a) DNA amplification for CE sequencing methods to be utilized by the trainee
 - b) Documentation of the process
 - c) NOTE: The number and quality of samples processed by the trainee shall be appropriate to demonstrate the ability to follow the laboratory's DNA amplification for CE sequencing protocol(s) and to produce reliable and accurate results.

4.3 Competency testing

The laboratory's training program shall include knowledge-based and practical competency testing in the application of amplification of DNA for CE sequencing methods. The format of the test(s) shall meet Section 4.3 of the ASB Standard 022.

4.3.1 Knowledge-based competency

The trainee shall successfully complete a knowledge-based test covering the critical information obtained during the training of DNA amplification for CE sequencing methods. The test(s) shall cover, at a minimum:

- a) The theoretical and scientific bases of DNA amplification for CE sequencing
- b) The function of the reagents and other components used for DNA amplification for CE sequencing
- c) The quality control steps pertaining to DNA amplification for CE sequencing



d) The laboratory's analytical procedures pertaining to DNA amplification for CE sequencing methods

4.3.2 Practical competency

The trainee shall successfully complete a practical test covering each of the DNA amplification for CE sequencing protocol(s) for which he or she will be independently authorized. The trainee shall be able to satisfactorily perform the following, as applicable:

- a) Properly and accurately execute the analytical procedures related to DNA amplification for CE sequencing
- b) Apply the laboratory's analytical procedures to a set of samples representing the range of DNA quality and quantity expected to be encountered in the laboratory
- b) Operate relevant equipment and instrumentation used in the laboratory
- c) Document work performed in accordance with laboratory procedures

5 Conformance

In order to demonstrate conformance with this standard, the laboratory shall meet Section 5 of the ASB Standard 022.



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> Annex A (informative)

Bibliography

The following information provides a list of the literature resources that may assist the DNA technical leader in defining the breadth and scope of the materials to be reviewed by the trainee. This list is not meant to be all inclusive. The laboratory shall develop a list tailored to its specific needs. Updated references shall be added to the laboratory's list as new methods or technologies are incorporated into the laboratory's protocols.

- 1) Anderson S, Bankier AT, Barrell G, de Bruijn MH, Coulson AR, Drouin J et al. Sequence and organization of the human mitochondrial genome. Nature 1981;290(5806):457 65.
- 2) Andrews R.M., Kubacka,I., Chinnery,P.F., Lightowlers,R.N., Turnbull,D.M. and Howell,N. Reanalysis and revision of the Cambridge reference sequence for human mitochondrial DNA Nat. Genet. 23 (2), 147 (1999)
- 3) Berger, C., and Parson, W. (2009). Mini-midi-mito: Adapting the amplification and sequencing strategy of mtDNA to the degradation state of crime scene samples. Forensic Science International: Genetics, 3, 96-103.
- 4) Butler, J. M. (2012) Advanced Topics in Forensic DNA Typing: Methodology. Academic Press, chapter 14, 405-456.
- 5) CBOL Plant Working Group. A DNA barcode for land plants. Proceedings of the National Academy of Sciences Aug 2009, 106 (31) 12794-12797; DOI:10.1073/pnas.0905845106
- 6) Dormontt, E., Boner, M., Braun, B., Breulmann, G., Degen, B., Espinoza, E., Lowe, A. (2015). Forensic timber identification: it's time to integrate disciplines to combat illegal logging. *Biological Conservation*, *191*, 790-798.
- 7) Eckert, K.A., and Kunkel, T.A. (1990). High fidelity DNA synthesis by the *Thermus aquaticus* DNA polymerase. Nucleic Acids Research, 18, 3739-3744.
- 8) Eckert, K.A. and Kunkel, T.A. (1991). DNA polymerase fidelity and the polymerase chain reaction. Genome Research, 1, 17-24.
- 9) Edson, S.M., et al. (2004). Naming the dead confronting the realities of rapid identification of degraded skeletal remains. Forensic Science Review, 16, 63-90.
- 10) Eichmann, C. and Parson, W. (2008). "Mitominis" Multiplex PCR analysis of reduced size amplicons for compound sequence analysis of the entire mtDNA control region in highly degraded samples. International Journal of Legal Medicine, 122, 385-388.



- 11) Ewart KM, Frankham GJ, McEwing R, Webster LMI, Ciavaglia SA, Linacre AMT, The DT, Ovouthan K, Johnson RN. An internationally standardized species identification test for use on suspected seized rhinoceros horn in the illegal wildlife trade. Forensic Sci Int Genet. 2018 Jan;32:33-39.
- 12) Ferri, G., Alù, M., Corradini, B. et al. Forensic botany: species identification of botanical trace evidence using a multigene barcoding approach. Int J Legal Med (2009) 123: 395.
- 13) Folmer, O, Black, M, Hoeh, W, Lutz, and Vrijenhoek, R. 1994. DNA primers for amplification of mitochondrial cytochrome c oxidase subunit I from diverse metazoan invertebrates. Molecular Marine Biology and Biotechnology. 3(5): 294-299.
- 14) Gabriel, M. N., et al. (2001). Improved mtDNA sequence analysis of forensic remains using a "mini-primer set" amplification strategy. Journal of Forensic Sciences, 46, 247-253.
- 15) Irwin, J. A., et al. (2007). Development and expansion of high-quality control region databases to improve forensic mtDNA evidence interpretation. Forensic Science International: Genetics, 1, 154-157.
- 16) Jesmok EM, JM Hopkins and DR Foran 2016 Next-Generation Sequencing of the Bacterial 16S rRNA Gene for Forensic Soil Comparison: A Feasibility Study. Journal of Forensic Sciences 61, 607–617
- 17) Kanthaswamy, S Review: domestic animal forensic genetics biological evidence, genetic markers, analytical approaches and challenges. Animal Genetics 2015 46, 473-484
- 18) Kocher, TD, Thomas, WK, Meyer, A, Edwards, SV, Pääbo, S, Villablanca, FX, and Wilson, AC. 1989. Dynamics of mitochondrial DNA evolution in animals: amplification and sequencing with conserved primers. PNAS. 86(16): 6196-6200.
- 19) Lopez, JV, Yuhki, N, Masuda, R, Modi, W, O?Brien, SJ. 1994. Numt, a recent transfer and tandem amplification of mitochondrial DNA to the nuclear genome of the domestic cat. J Mol Evol 1994 Nov;39(5):544
- 20) Palumbi, S, Kewalo, M, Romano, S, McMillan, WO, Stice, L, Grabowski, G. 2002. Simple Fool's Guide to PCR, Version 2.0. University of Hawaii.
- 21) Quaak, F.C.A., de Graaf, ML.M., Weterings, R. et al. Microbial population analysis improves the evidential value of faecal traces in forensic investigations. Int J Legal Med (2017) 131: 45.
- 22) Roca, AL, Georgiadis, N, O;Brien, SJ. Cyto-nuclear genomic dissociation and the African elephant species question. Quat Int. 2007 Jul; 169-170: 4-16.
- 23) Sorenson, MD, Ast, JC, Dimcheff, ,Yuri, T, Mindell, DP. 1999. Primers for a PCR-Based Approach to Mitochondrial Genome Sequencing in Birds and Other Vertebrates. Mol. Phyl. Evol. 12(2): 105-114.



- 24) Wesselink, Monique et al. Species identification of botanical trace evidence using molecular markers. Forensic Science International: Genetics Supplement Series, Volume 1, Issue 1, 630 -632
- 25) Wilson, M.R. et al. (1995). Extraction, PCR amplification and sequencing of mitochondrial DNA from human hair shafts. Biotechniques, 18, 662-669.
- 26) Young, Jennifer M. et al. Forensic soil DNA analysis using high-throughput sequencing: A comparison of four molecular markers. Forensic Science International: Genetics , Volume 13 , 176 184
- 27) Yu, M., Jiao, L. C., Guo, J., Wiedenhoeft, A. C., He, T., Jiang, X. M. and Yin, Y. F. 2017. DNA barcoding of vouchered xylarium wood specimens of nine endangered Dalbergia species. Planta, 246, 1165-1176.