

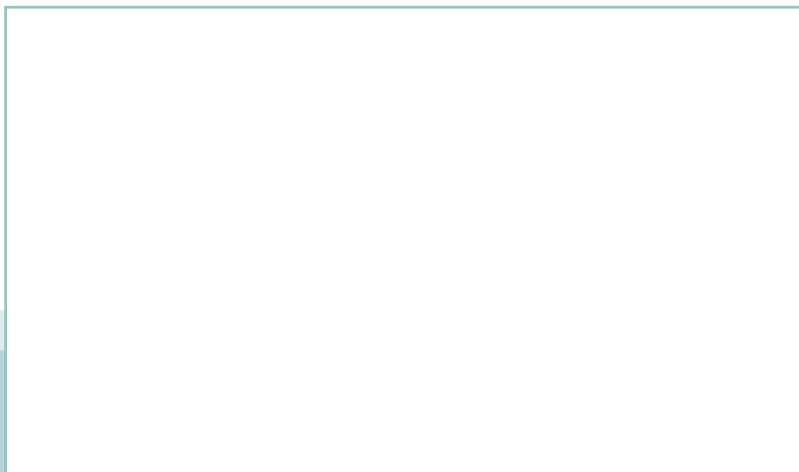
Teknisk specifikation

SIS-CEN/TS 17303:2019

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Livsmedel – DNA-streckkodning av fisk och fiskprodukter med användning av definierade mitokondriella gensegment av cytokrom b- och cytokrom c-oxidas I

Foodstuffs – DNA barcoding of fish and fish products using defined mitochondrial cytochrome b and cytochrome c oxidase I gene segments



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TECHNICAL SPECIFICATION
SPÉCIFICATION TECHNIQUE
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CEN/TS 17303

March 2019

ICS 67.120.30

English Version

**Foodstuffs - DNA barcoding of fish and fish products using
defined mitochondrial cytochrome b and cytochrome c
oxidase I gene segments**

Produits alimentaires - Codes-barres d'ADN de
poissons et de produits à base de poissons à l'aide de
segments de gènes mitochondriaux du cytochrome b et
cytochrome c oxydase I

Lebensmittel - DNA-Barcoding von Fisch und
Fischprodukten anhand definierter mitochondrialer
Cytochrom-b- und Cytochrom-c-Oxidase-I-
Genabschnitte

This Technical Specification (CEN/TS) was approved by CEN on 14 January 2019 for provisional application.

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European foreword

This document (CEN/TS 17303:2019) has been prepared by Technical Committee CEN/TC 275 “Food analysis - Horizontal methods”, the secretariat of which is held by DIN.

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Introduction

Food safety is a key aspect in terms of consumer protection. In the last three decades, globalization has taken place in the trade of food. Fish trade channels are becoming steadily longer and more complicated so that sophisticated traceability tools are needed to ensure food safety. Correct food labelling is a prerequisite to ensure safe fish products and fair trade as well as to minimize illegal, unreported and unregulated (IUU) fishing. In particular, the fact that fish is increasingly being processed in export countries makes the identification of species by morphological characteristics impossible.

The development of harmonized and standardized protocols for the authentication of fish products is necessary to establish reliable methods for the detection of potential food fraud.

1 Scope

This document describes a procedure for the identification of single fish and fish fillets to the level of genus or species.

The identification of fish species is carried out by PCR amplification of either a segment of the mitochondrial cytochrome b gene (*cytb*) [1] or the cytochrome c oxidase I gene (*cox1*, *syn COI*) [2], [3] or both, followed by sequencing of the PCR products and subsequent sequence comparison with entries in databases [4], [5]. The methodology allows the identification of a large number of commercially important fish species.

The decision whether the *cytb* or *cox1* gene segment or both are used for fish identification depends on the declared fish species, the applicability of the PCR method for the fish species and the availability of comparative sequences in the public databases.

This method has been successfully validated on raw fish fillets, however, laboratory experience is available that it can also be applied to processed, e.g. cold smoked, hot smoked, salted, frozen, cooked, fried, deep-fried samples.

This document is usually unsuitable for the analysis of highly processed foods, e.g. tins of fish, with highly degraded DNA where the fragment lengths are not sufficient for amplification of the targets. Furthermore, it is not applicable for complex fish products containing mixtures of two or more fish species.

2 Normative references

The following documents are referred to in the text in such a way that some or all of their content constitutes requirements of this document. For dated references, only the edition cited applies. For undated references, the latest edition of the referenced document (including any amendments) applies.

EN ISO 24276, *Foodstuffs — Methods of analysis for the detection of genetically modified organisms and derived products — General requirements and definitions (ISO 24276)*

ISO 16577, *Molecular biomarker analysis — Terms and definitions*

3 Terms and definitions

For the purposes of this document, the terms and definitions given in ISO 16577 and the following apply.

ISO and IEC maintain terminological databases for use in standardization at the following addresses:

- IEC Electropedia: available at <http://www.electropedia.org/>
- ISO Online browsing platform: available at <http://www.iso.org/obp>

3.1 alignment

process or result of matching up the nucleotide residues of two or more biological sequences to achieve maximal levels of identity

[SOURCE: BLAST Glossary]

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3.2

BLAST

(The Basic Local Alignment Search Tool) [4]

sequence comparison algorithm optimized for speed used to search sequence databases for optimal local alignments to a query

Note 1 to entry: It directly approximates alignments that optimize a measure of local similarity, the maximum signal pair (MSP) score or high scoring signal pair (HSP) score.

3.3

BOLD

(Barcode of Life Data Systems) [5]

informatics workbench aiding the acquisition, storage, analysis, and publication of DNA barcode records

Note 1 to entry: By assembling molecular, morphological, and distributional data, it bridges a traditional bioinformatics chasm. BOLD is freely available to any researcher with interests in DNA barcoding. By providing specialized services, it aids the assembly of records that meet the standards needed to gain BARCODE designation in the global sequence databases. Because of its web-based delivery and flexible data security model, it is also well positioned to support projects that involve broad research alliances.

[SOURCE: BOLDSYSTEMS About Us]

3.4

FASTA format

text-based format for representing either nucleotide sequences or amino acid sequences, which begins with a single-line description, followed by lines of sequence data

Note 1 to entry: The description line (define) is distinguished from the sequence data by a greater-than (“>”) symbol at the beginning.

[SOURCE: BLAST topics, modified]

EXAMPLE An example sequence in FASTA format is shown below:

```
> Sample_04_cytb
ATGGCCAGCCTCCGAAAACTCATCCCCTTCTAAAGATTGCTAATGATGCATTAGTAGACCTTCCTGCCCCCTCTAACCTCT
CAACATTATGAACTTCGGGTCTCTCCTAGGCCTCTGCTTAGCCGCCAAATCTTAACAGGACTATTTCTAGCGATACATT
ATACCGCAAACGTGAGATAGCTTTCTCATCCGTCGTACACATCTGCCGCGACGTAAATTACGGATGACTAATCCGCAACA
TACACGCCAACGGCGCTTCTTTCTTCTTCATCTGCCTCTACCTACACATTGCACGAGGCCTATATTACGGCTCCTACTTATT
CATAGAGACCTGAAACATTGGAGTTGTAATAATGACCGCCTTCGTAGGCTACGTCCTCCCT
```

3.5

FishBase

global biodiversity online platform on finfishes providing a wide range of information on all species currently known in the world

3.6

GenBank

comprehensive public database of e. g. genetic sequences [6]

Note 1 to entry: GenBank is part of the [International Nucleotide Sequence Database Collaboration](#), which comprises the DNA DataBank of Japan (DDBJ), the European Nucleotide Archive (ENA), and GenBank at National Center for Biotechnology Information (NCBI). These three organizations exchange data on a daily basis.

3.7

identity

extent to which two (nucleotide or amino acid) sequences have the same residues at the same positions in an alignment, often expressed as a percentage

[Source: BLAST Glossary]

Note 1 to entry: In the database BOLD, the term similarity is used instead of identity.

3.8

introgressed DNA

DNA sequence (allele) from one taxonomic entity (species) incorporated in the gene pool of another, divergent entity (species)

Note 1 to entry: Introgression has usually happened via hybridization and backcrossing of individuals belonging to different species.

3.9

NCBI (National Center for Biotechnology Information)

institution which houses molecular biology databases (e.g. GenBank) and provides the BLAST suite

3.10

nucleotide collection (nr/nt)

non-redundant database consisting of GenBank sequences, in which identical sequences have been merged into one entry

3.11

query

sequence (or other type of search term) to which all of the entries in a data base are to be compared

[SOURCE: BLAST Glossary].

3.12

query coverage

percentage of query covered by alignment to the data base sequence

[SOURCE: BLAST help]

4 Principle

DNA is extracted from fish and fish products applying a suitable method. Segments of approximately 460 base pairs of the *cytb* gene and/or approximately 650 base pairs of the *cox1* gene are amplified by PCR. In the further course, the nucleotide sequence of the PCR product is determined by a suitable DNA sequencing method (e.g. Sanger sequencing). The sequence is evaluated by comparison to sequence entries in databases, thus allowing the assignment to a fish species or genus according to the degree of identity with stored sequences.

5 Reagents and materials

5.1 General

During the analysis, unless otherwise stated, use only reagents of recognized molecular biology grade and distilled or demineralized water or water of equivalent purity, according to EN ISO 24276. Regarding laboratory organization, see EN ISO 24276.