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Microbiology of the food chain — Polymerase chain reaction (PCR) for the detection and quantification of microorganisms — General requirements and definitions

Microbiologie de la chaîne alimentaire — Réaction de polymérisation en chaîne (PCR) pour la recherche et la quantification de micro-organismes — Exigences générales et définitions

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Foreword

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The procedures used to develop this document and those intended for its further maintenance are described in the ISO/IEC Directives, Part 1. In particular, the different approval criteria needed for the different types of ISO document should be noted. This document was drafted in accordance with the editorial rules of the ISO/IEC Directives, Part 2 (see www.iso.org/directives).

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This document was prepared by Technical Committee TC 34, Food products, Subcommittee SC 9, Microbiology, in collaboration with the European Committee for Standardization (CEN) Technical Committee CEN/TC 463, Microbiology of the food chain, in accordance with the Agreement on technical cooperation between ISO and CEN (Vienna Agreement).

This second edition cancels and replaces ISO 22174:2005, ISO 20837:2006, ISO 20838:2006 and ISO 22119:2011, which have been technically revised. At 2024 https://standards.itch.ai/catalog/standards/iso/09061f1c-a5d9-4f72-b7eb-4e27bc123320/iso-22174-2024

The main changes are as follows:

- inclusion of requirements for the implementation of digital PCR;
- inclusion of requirements for laboratory flows monitoring including environmental monitoring for PCR;
- extension of <u>12.2.2</u> control reaction with descriptions of the different controls;
- change of 12.3 to include quantitative evaluation;
- inclusion of <u>Clause 14</u> on validation and verification.

Any feedback or questions on this document should be directed to the user's national standards body. A complete listing of these bodies can be found at www.iso.org/members.html.

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Microbiology of the food chain — Polymerase chain reaction (PCR) for the detection and quantification of microorganisms — General requirements and definitions

1 Scope

This document specifies the general requirements for the *in vitro* amplification of nucleic acid sequences (DNA or RNA).

This document is applicable to the testing for microorganisms and viruses from the food chain using the polymerase chain reaction (PCR). This document, or parts of it, is applicable to other fields of PCR diagnostics based on a case-by-case evaluation.

The minimum requirements laid down in this document are intended to ensure that comparable and reproducible results are obtained in different laboratories.

This document has been established for microorganisms from the food chain and is applicable to:

- products intended for human consumption;
- products for feeding animals;
- environmental samples in the area of food and feed production and handling;
- samples from the primary production stage.

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.

ISO 6887 (all parts), Microbiology of the food chain — Preparation of test samples, initial suspension and decimal dilutions for microbiological examination

ISO 7218, Microbiology of the food chain — General requirements and guidance for microbiological examinations

ISO 20836, Microbiology of the food chain — Polymerase chain reaction (PCR) for the detection of microorganisms — Thermal performance testing of thermal cyclers

3 Terms and definitions

For the purposes of this document, the following terms and definitions apply.

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

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

3.1 General terms

3.1.1

laboratory sample

sample as prepared for sending to the laboratory and intended for inspection or testing

[SOURCE: ISO 7002:1986, A.19]

3.1.2

test sample

sample prepared from the *laboratory sample* (3.1.1) according to the procedure specified in the method of test and from which *test portions* (3.1.3) are taken

3.1.3

test portion

measured (volume or mass) representative sample taken from the *laboratory sample* (3.1.1)

[SOURCE: ISO 6887-1:2017, 3.5, modified — "for use in the preparation of the initial suspension" and Note 1 to entry deleted.]

3.1.4

reference material

material, sufficiently homogeneous and stable with respect to one or more specified properties, which has been established to be fit for its intended use in a measurement process

Note 1 to entry: Reference material producers fulfilling the requirements of ISO 17034 are considered to be competent.

[SOURCE: ISO Guide 30:2015, 2.1.1, modified — Notes to entry deleted and a new Note 1 to entry added.]

3.1.5

matrix

all the components of the sample

[SOURCE: ISO 16140-1:2016, 2.38, modified — "(product)" deleted in the term.]

3.1.6

deoxyribonucleic acid

DNA s://standards.iteh.

polymer of deoxyribonucleotides occurring in a double-stranded (dsDNA) or single-stranded (ssDNA) form

3.1.7

deoxyribonuclease

DNase

enzyme which degrades deoxyribonucleic acid (DNA) (3.1.6)

3.1.8

amplicon

deoxyribonucleic acid (DNA) (3.1.6) amplified by polymerase chain reaction (PCR) (3.1.17)

3.1.9

ribonucleic acid

RNA

polymer of ribonucleotides occurring in a double-stranded or single-stranded form

3.1.10

ribonuclease

RNase

enzyme which degrades ribonucleic acid (RNA) (3.1.9)

3.1.11

nucleic acid

polymer of deoxyribonucleotides or ribonucleotides

3.1.12

target nucleic acid sequence

nucleic acid sequence selected for amplification

3.1.13

endogenous sequence

nucleic acid sequence naturally present in the tested *matrix* (3.1.5)

3.1.14

exogenous sequence

nucleic acid sequence naturally absent in the tested *matrix* (3.1.5)

3.1.15

detection of polymerase chain reaction product

detection of amplicon

process which signals the presence of an *amplicon* (3.1.8)

3.1.16

confirmation of polymerase chain reaction product

confirmation of amplicon

process which demonstrates that the *amplicon* (3.1.8) originates from the *target nucleic acid sequence* (3.1.12)

3.1.17

polymerase chain reaction

PCR

enzymatic procedure that allows in vitro amplification of deoxyribonucleic acid (DNA) (3.1.6)

3.1.18

endpoint polymerase chain reaction

endpoint PCR

procedure using PCR amplification followed by separate detection of *amplicons* (3.1.8) after the completion of the PCR

3.1.19

real-time polymerase chain reaction

real-time PCR ds.iteh.ai/catalog/standards/iso/090

procedure which combines PCR amplification with the detection and/or quantification of specific *amplicons* (3.1.8) during the amplification process

3.1.20

multiplex polymerase chain reaction

multiplex PCR

PCR (3.1.17) allowing the detection of multiple targets simultaneously within a single reaction tube, where more primer pairs (and probes) are used within one *master mix* (3.4.4)

3.2 Terms related to the extraction and purification of DNA/RNA

3.2.1

nucleic acid extraction

sample treatment for the release of *nucleic acids* (3.1.11)

3.2.2

nucleic acid purification

method to reduce the amount of polymerase chain reaction (PCR) (3.1.17) inhibitors in the eluate

3.3 Terms related to reverse transcription of RNA to DNA

3.3.1

reverse transcriptase

enzyme which catalyses the *reverse transcription* ($\underline{3.3.2}$) of *ribonucleic acid* (*RNA*) ($\underline{3.1.9}$) to a complementary single-stranded deoxyribonucleic acid (cDNA)

3.3.2

reverse transcription

RT

synthesis of complementary single-stranded deoxyribonucleic acid (cDNA) from a ribonucleic acid (RNA) template using a *reverse transcriptase* (3.3.1)

3.3.3

reverse transcription-polymerase chain reaction

RT-PCR

method consisting of two reactions, a *reverse transcription (RT)* (3.3.2) of *ribonucleic acid (RNA)* (3.1.9) to single-stranded complementary deoxyribonucleic acid (cDNA), followed by a PCR (3.1.17)

Note 1 to entry: One-step RT-PCR is performed in a single tube.

Note 2 to entry: Two-step RT-PCR can either be performed sequentially in a single tube or in two different tubes.

3.4 Terms related to DNA amplification by PCR/RT-PCR

3.4.1

deoxyribonucleic acid polymerase

DNA polymerase

thermostable enzyme which catalyses *DNA* (3.1.6) synthesis

Note 1 to entry: DNA polymerase can also cleave a hybridized nucleic acid molecule using its 5'-3'-exonuclease activity. It is dependent on the type of enzyme and can be present in, for example, Taq-, Tth- and Tfl-polymerase.

3.4.2

$deoxyribonucleoside\ triphosphate$

dNTP

solution containing deoxyadenosine triphosphate (dATP), deoxycytidine triphosphate (dCTP), deoxyguanosine triphosphate (dGTP), deoxythymidine triphosphate (dTTP) and/or deoxyuridine triphosphate (dUTP)

3.4.3

thermal cycler

automatic device that performs defined heating and cooling cycles usable for *polymerase chain reaction* (PCR) (3.1.17) or *real-time PCR* (3.1.19) or *digital PCR* (3.7.1)

Note 1 to entry: The thermal cycler can be a block-based or (individual) reaction-chamber-based thermal cycler.

[SOURCE: ISO 20836:2021, 3.2.1, modified — "or digital PCR" added.]

3.4.4

master mix

mixture of reagents needed for nucleic acid amplification except for the target nucleic acid sequence (3.1.12)

[SOURCE: ISO 17822:2020, 3.27, modified — "nucleic acid sequence" replaced "DNA and the controls".]

3.4.5

primer

oligonucleotide of defined length and sequence complementary to a segment of the *target nucleic acid sequence* (3.1.12), used to signal the starting point for deoxyribonucleic acid (DNA) polymerase to extend the new DNA strand

3.4.6

fluorescent probe

oligonucleotide of defined sequence coupled with one or more fluorescent molecules

Note 1 to entry: Any system emitting a fluorescence signal after specific hybridization to the *target nucleic acid sequence* (3.1.12) which can be detected by the specific equipment can be used as a fluorescent probe.

3.4.7

background fluorescence

background

intrinsic level of fluorescence resulting from the reagents, consumables and instruments used

3.4.8

molecular beacon

fluorescent probe consisting of three different parts: a central part complementary to the *target nucleic acid* sequence (3.1.12), plus a 5'-part and a 3'-part which are complementary, and where the reporter is attached to one arm of the molecule, while the end of the other arm carries the quencher

3.4.9

hybridization probe

system of two fluorescent probes coupled with one fluorescent molecule each, where one molecule serves as fluorescence resonance energy transfer (FRET) donor and the other serves as FRET acceptor

3.4.10

hydrolysis probe

fluorescent probe coupled with a fluorophore and quencher which are sterically separated by the 5'-3'-exonuclease activity of the enzyme during the amplification process

3.4.11

denaturation

process which results in the separation of the double-stranded nucleic acid into single-stranded nucleic acids

3.4.12

hybridization

specific binding of complementary nucleic acid sequences under suitable reaction conditions

3.4.13

annealing

pairing of complementary single strands of nucleic acids to form a double-stranded molecule

3.4.14

hot-start polymerase chain reaction

hot-start PCR

activation of thermostable deoxyribonucleic acid (DNA) polymerase by an initial heating step to avoid non-specific amplification

3.5 Terms related to controls

3.5.1

negative process control

target free sample which is run through all stages of the analytical process

Note 1 to entry: The process can include sample preparation, enrichment, nucleic acid extraction and target amplification.

3.5.2

positive process control

sample, spiked with a microorganism, treated in the same way as the *test samples* (3.1.2) to monitor the entire process of the polymerase-chain-reaction-based method