

ISO/~~CD~~-DTS 20224-11:2023(E)

ISO-/TC_34/SC_16/~~WG-8~~

Secretariat: ANSI

Date: 2023-10-05

Molecular biomarker analysis — Detection of animal-derived materials in foodstuffs and feedstuffs by real-time PCR — Part 11: Pigeon DNA detection method

—Analyse de biomarqueurs moléculaires — Détection de matériaux d'origine animale dans les denrées alimentaires et les aliments pour animaux par PCR en temps réel — Partie 11: Méthode de détection de l'ADN de pigeon

~~CD~~ stage

Warning for WDs and CDs

This document is not an ISO International Standard. It is distributed for review and comment. It is subject to change without notice and may not be referred to as an International Standard.

Recipients of this draft are invited to submit, with their comments, notification of any relevant patent rights of which they are aware and to provide supporting documentation.

ISO/DTS 20224-11

<https://standards.iteh.ai/catalog/standards/sist/74930bb2-404f-4c81-9855-0ce571087a68/iso-dts-20224-11>

iTeh Standards
(<https://standards.itih.ai>)
Document Preview

[ISO/DTS 20224-11](#)

<https://standards.itih.ai/catalog/standards/sist/74930bb2-404f-4c81-9855-0ce571087a68/iso-dts-20224-11>

ISO/~~TS~~ DTS 20224-11:2023(E)

© ISO 2023

All rights reserved. Unless otherwise specified, or required in the context of its implementation, no part of this publication may be reproduced or utilized otherwise in any form or by any means, electronic or mechanical, including photocopying, or posting on the internet or an intranet, without prior written permission. Permission can be requested from either ISO at the address below or ISO's member body in the country of the requester.

ISO Copyright Office

CP 401 • CH-1214 Vernier, Geneva

Phone: + 41 22 749 01 11

Email: copyright@iso.org

Email: copyright@iso.org

Website: www.iso.org www.iso.org

Published in Switzerland.

iTeh Standards (<https://standards.iteh.ai>) Document Preview

ISO/DTS 20224-11

<https://standards.iteh.ai/catalog/standards/sist/74930bb2-404f-4c81-9855-0ce571087a68/iso-dts-20224-11>

Contents

Foreword.....vi

Introduction.....vii

1 Scope.....1

2 Normative references.....1

3 Terms and definitions.....1

4 Scientific basis.....1

5 Reagents and materials.....2

5.1 General.....2

5.2 PCR reagents.....2

6 Apparatus.....3

6.1 Real-time thermocycler instrument.....3

7 Procedure.....3

7.1 Preparation of the test portion/sample.....3

7.2 Preparation of DNA extracts.....3

7.3 PCR setup.....3

7.4 Temperature-time programme.....4

8 Accept/reject criteria.....5

8.1 General.....5

8.2 Identification.....5

9 Validation status and performance criteria.....5

9.1 General.....5

9.2 Robustness.....6

9.3 Reproducibility.....6

9.4 Sensitivity.....7

9.5 Specificity.....10

10 Test report.....13

Annex A (informative) BlastN +2.12.0 results for query of GenBank RefSeq genome (refseq_genomes) and whole genome shotgun contigs (wgs).....14

Annex B (informative) Members of the Columbidae family and its family tree established with available public genomic sequences.....17

Bibliography.....23

Foreword.....vi

Introduction.....vii

1 Scope.....1

2 Normative references.....1

3 Terms and definitions.....1

4	Scientific basis	1
5	Reagents and materials	2
5.1	General	2
5.2	PCR reagents	2
5.2.1	PCR master mix	2
5.2.2	Oligonucleotides	2
	Table 1 — Oligonucleotides	2
6	Apparatus	3
6.1	Real-time thermocycler instrument	3
7	Procedure	3
7.1	Preparation of the test portion/sample	3
7.2	Preparation of DNA extracts	3
7.3	PCR setup	3
7.3.1	Reaction mixes	3
	Table 2 — Reaction setup for the amplification	4
7.3.2	PCR controls	4
7.3.3	Real-time PCR thermocycler plate set-up	4
7.4	Temperature-time programme	4
	Table 3 — Temperature-time programme	4
8	Accept/reject criteria	5
8.1	General	5
8.2	Identification	5
9	Validation status and performance criteria	5
9.1	General	5
9.2	Robustness	6
9.3	Reproducibility	6
	Table 4 — Results of the collaborative trial	7
9.4	Sensitivity	7
	Figure 1 — Map of the multi-target DNA plasmid	9
	Figure 2 — Complete sequence of nucleotides (nt) and annotation of the insertion in plasmid pUC57	9
	Table 5 — Collaborative trial results for the limit of detection (LOD_{95%})	10
	Table 6 — Collaborative trial results for the probability of detection (POD)	10
9.5	Specificity	10
	Table 7 — Specificity of the target pigeon genomic sequence detection method	11
10	Test report	13
	Annex A (informative) BlastN +2.12.0 results for query of GenBank RefSeq genome (refseq genomes) and whole-genome shotgun contigs (wgs)	14
A.1	Query	15
A.2	Descriptions	15

<u>Table A.1 — Descriptions.....</u>	<u>15</u>
<u>A.3 — Alignments.....</u>	<u>15</u>
<u>Annex B (informative) — Members of the <i>Columbidae</i> family and its family tree established with available public genomic sequences</u>	<u>17</u>
<u>B.1 — Members of the <i>Columbidae</i> family.....</u>	<u>18</u>
<u>Table B.1 — Member of the <i>Columbidae</i> family.....</u>	<u>18</u>
<u>B.2 — The family tree of the <i>Columbidae</i> established with available public genomic sequences.....</u>	<u>29</u>
<u>Figure B.1 — The family tree of <i>Columbidae</i> with public genomic sequences.....</u>	<u>30</u>
<u>Bibliography</u>	<u>31</u>

iTeh Standards
(<https://standards.itih.ai>)
Document Preview

ISO/DTS 20224-11

<https://standards.itih.ai/catalog/standards/sist/74930bb2-404f-4c81-9855-0ce571087a68/iso-dts-20224-11>

✦

© ISO 2022 – All rights reserved

© ISO 2023 – All rights reserved

Foreword

ISO (the International Organization for Standardization) is a worldwide federation of national standards bodies (ISO member bodies). The work of preparing International Standards is normally carried out through ISO technical committees. Each member body interested in a subject for which a technical committee has been established has the right to be represented on that committee. International organizations, governmental and non-governmental, in liaison with ISO, also take part in the work. ISO collaborates closely with the International Electrotechnical Commission (IEC) on all matters of electrotechnical standardization.

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 documents 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).

Attention is drawn to the possibility that some of the elements of this document may be involved in the subject of a patent right. ISO takes no position concerning the evidence, validity or applicability of any claimed patent rights in respect thereof. As of the date of publication of this document, ISO had not received notice of (a) patent(s) which may be required to implement this document. However, implementers are cautioned that this may not represent the latest information, which may be obtained from the patent database available at www.iso.org/patents. ISO shall not be held responsible for identifying any or all such patent rights. Details of any patent rights identified during the development of the document will be in the Introduction and/or on the ISO list of patent declarations received (see www.iso.org/patents).

Any trade name used in this document is information given for the convenience of users and does not constitute an endorsement.

For an explanation of the voluntary nature of standards, the meaning of ISO specific terms and expressions related to conformity assessment, as well as information about ISO's adherence to the World Trade Organization (WTO) principles in the Technical Barriers to Trade (TBT), see www.iso.org/iso/foreword.html.

This document was prepared by Technical Committee ISO/TC 34, *Food products*, Subcommittee SC 16, *Horizontal methods for molecular biomarker analysis*.

A list of all parts in the ISO 20224 series can be found on the ISO website.

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.

Introduction

Fraudulent adulteration of meat in food and feed threatens both public safety and commerce. Adulteration can affect those adhering to ethnological dietary rules, economic development and social stability. This document provides a real-time polymerase chain reaction (real-time PCR) analytical method for the identification of meat animal species from nucleic acid present in the ingredients of food and feed.

Animal-derived biological materials in food and feed are detected and identified in the laboratory with the following successive (or simultaneous) steps: preparation of the test portion/sample, nucleic acid extraction and purification, PCR amplification and interpretation of results. This document provides guidance for PCR amplification and interpretation of results, specific to rock pigeon (*Columba livia*) DNA detection.

The ISO 2024 series consists of technical specifications that describe specific applications. New species DNA detection methods established in the future will be added as independent parts.

iTeh Standards (<https://standards.iteh.ai>) Document Preview

ISO/DTS 20224-11

<https://standards.iteh.ai/catalog/standards/sist/74930bb2-404f-4c81-9855-0ce571087a68/iso-dts-20224-11>

Molecular biomarker analysis — Detection of animal-derived materials in foodstuffs and feedstuffs by real-time PCR — Part 11: Pigeon DNA detection method

1 Scope

This document specifies a real-time polymerase chain reaction (real-time PCR) method for the qualitative detection of pigeon-specific DNA derived from food and feed. The method can be applied to distinguish rock pigeon (*Columba livia*) from other domestic poultry meats (e. g. goose, duck, quail, pheasant). It requires the extraction of an adequate amount of PCR amplifiable DNA from the relevant matrix.

The target sequence is a partial fragment of *Columba livia* breed Danish Tumbler unplaced genomic scaffold, Cliv_1.0 scaffold114 (i.e. GenBank accession number NW_004973337.1) which is present as a single copy per haploid genome. The provided PCR assay for this target has an absolute limit of detection of five copies per reaction, with ≥ 95 % confidence at this concentration (LOD₉₅ %).

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 16577, *Molecular biomarker analysis* — Vocabulary for molecular biomarker analytical methods in agriculture and food production

ISO 20813, *Molecular biomarker analysis* — Methods of analysis for the detection and identification of animal species in foods and food products (nucleic acid-based methods) — General requirements and definitions

ISO 21571, *Foodstuffs* — Methods of analysis for the detection of genetically modified organisms and derived products — Nucleic acid extraction

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

3 Terms and definitions

For the purposes of this document, the terms and definitions given in ISO 16577 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 <http://www.electropedia.org/>

4 Scientific basis

DNA is extracted from the test portion by applying a suitable method (see ISO 21571:2005, A.1). The DNA analysis consists of two parts:

ISO/DTS 20224-11:2023(E)

- verification of the quality and amplifiability of the extracted DNA using a PCR assay specific for eukaryotes (i.e. 18S rRNA gene) or mammals and poultry (i.e. myostatin gene);
- detection of the pigeon species-specific DNA sequence of the single-copy *Columba livia* unplaced genomic scaffold sequence (i.e. GenBank accession number NW_004973337.1) in a real-time PCR.

NOTE The copy number of the eukaryotic ribosomal 18S RNA (18S rRNA) gene in a cell varies from several hundred to several thousand, while the specific target sequence in the pigeon genome and myostatin gene in mammals and poultry genome are single copy. The copy number of the specific target sequence in the pigeon genome was confirmed by bioinformatics analysis at the whole genome scale (see Annex A) and digital PCR for absolute quantification.

5 Reagents and materials

5.1 General

For this document, only reagents and water of recognized analytical grade, appropriate for molecular biology, shall be used. Unless stated otherwise, solutions should be prepared by dissolving the corresponding reagents in water followed by autoclave sterilization. For all operations in which gloves are used, gloves shall be powder free. The use of aerosol protected pipette tips (protection against cross-contamination) is recommended.

5.2 PCR reagents

5.2.1 ~~5.2.1~~ PCR master mix.

In general, real-time PCR master mix contains thermostable DNA polymerase, dNTPs, MgCl₂, KCl, and buffer as a dilutable concentrated mixture, that is ready to use.

5.2.2 ~~5.2.2~~ Oligonucleotides.

The quality of the oligonucleotides shall be sufficient for their use as primers and probes. See Table 1.

Table 1 — Oligonucleotides

Name	DNA sequence of the oligonucleotide	Final concentration in PCR
Specific sequence in <i>Columba livia</i> unplaced genomic scaffold sequence (i.e. GenBank accession number NW_004973337.1) ^a		
Pigeon-113bp-F	5'- GCAGTTGTTTAGTCTCCTGTAAC -3'	400 nmol/l
Pigeon-113bp-R	5'- GGGCTAACATCAAGACGCAAAG -3'	400 nmol/l
Pigeon-113bp-P	5'- [FAM]- CGGACTCCTAAGAGCACTTCTCAGCCTGG -[TAMRA] ^b -3'	200 nmol/l
^a PCR product = 3 716 744 - GCAGTTGTTT AGTCTCCTG TAACACGGAC TCCTAAGAGC ACTTCTCAGC CTGGCTTTGT TTTCGTCACA CTGTGTATCT GAACGCCGT TCTTTGCGTC TTGATGTTAG CCC - 3 716 856 - NW_004973337.1		
^b _FAM: 6-carboxyfluorescein, TAMRA: 6-carboxytetramethylrhodamine.		

Pigeon-113bp-F is base pairs 3 716 744 – 3 716 767, Pigeon-113bp-R is base pairs 3 716 835 – 3 716 856 and Pigeon-113bp-P is 3 716 769 – 3 716 797 of NW_004973337.1, pigeon unplaced genomic scaffold

sequence. Equivalent reporter dyes and/or quencher dyes can be used if they yield the same or better results.

6 Apparatus

Requirements concerning apparatus and materials shall follow ISO 20813. In addition to the usual laboratory equipment, the following equipment is required.

6.1 ~~6.1~~ Real-time thermocycler instrument.

A device that amplifies DNA *in vitro* and performs the temperature-time cycles is needed for PCR. Additionally, the device shall be capable of exciting fluorescence molecules at specific wavelengths and detecting sufficient emitted fluorescent light of the fluorophore used to perform TaqMan format assays.

7 Procedure

7.1 Preparation of the test portion/sample

The test sample used for DNA extraction shall be representative of the laboratory sample and homogeneous, e.g. by grinding or homogenizing the laboratory sample to a fine mixture. Test portion/sample preparation shall follow the general requirements and specific methods described in ISO 21571 and ISO 20813.

7.2 Preparation of DNA extracts

The extraction/purification and quantification of DNA from the test portion shall follow the general requirements and methods provided in ISO 21571. DNA extraction methods described in ISO 21571: 2005, Annex A, are recommended.

7.3 PCR setup

7.3.1 Reaction mixes

The method is for a total volume of 25 µl per PCR. The reaction setup is given in Table 2. Reagents shall be completely thawed at room temperature. Each reagent shall be carefully mixed and briefly centrifuged immediately before pipetting. A PCR reagent mixture is prepared to contain all components except for the sample DNA. The required total amount of the PCR reagent mixture prepared depends on the number of reactions to be performed, including at least one additional reaction as a pipetting reserve. The number of sample and control replicates shall follow ISO 20813. Set up the PCR tests as follows:

- a) mix the PCR reagent mixture, centrifuge briefly and pipette 20 µl into each reaction vial;
- b) add 5 µl of each sample DNA or positive DNA target control or extraction blank control or water to the respective reaction vials;
- c) mix and centrifuge briefly.