



JRC VALIDATED METHODS, REFERENCE METHODS AND MEASUREMENTS REPORT

# Event-specific Method for the Quantification of Maize Event DP51291 Using Real-time PCR

*Validation Report*

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2024



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## Abstract

In line with its mandate (1) the European Union Reference Laboratory for GM Food and Feed (EURL GMFF), in collaboration with the European Network of GMO Laboratories (ENGL), validated an event-specific real-time polymerase chain reaction (qPCR) method for detecting and quantifying maize event DP51291 (unique identifier DP-Ø51291-2). The validation study was conducted according to the EURL GMFF validation procedure [<http://gmo-crl.jrc.ec.europa.eu/guidancedocs.htm>] and the relevant internationally accepted guidelines (2-6).

In accordance with current EU legislation (1), Corteva Agriscience Belgium B.V. (on behalf of Corteva Agrisciences LLC) provided the detection method and the positive and negative control samples (genomic DNA from seeds of DP51291 maize as positive control DNA, and genomic DNA from seeds of conventional maize as negative control DNA). The EURL GMFF verified the method performance data provided by the applicant, where necessary experimentally, prepared the validation samples (calibration samples and blind samples at different GM percentage [copies GM/total maize haploid genome copies]), organised an international collaborative study and analysed the results.

The EURL GMFF in-house verification and the collaborative study confirmed that the method meets the method performance requirements as established by the EURL GMFF and the ENGL, in line with the provisions of Annex III-3.C.2 to Regulation (EU) No 503/2013 (5), and it fulfils the analytical requirements of Regulation (EU) No 619/2011 (6). This validation report is published at <https://gmo-crl.jrc.ec.europa.eu/method-validations>.

## Quality assurance

The EURL GMFF is ISO/IEC 17025:2017 accredited [certificate number: BELAC 268 TEST (Flexible Scope for determination of Genetically Modified content in % (m/m) and % (cp/cp) in food and feed by DNA extraction, DNA identification and Real-time PCR and for determination of Genetically Modified content in % (cp/cp) in food and feed by DNA extraction and digital PCR)].

The original version of the document containing evidence of internal checks and authorisation for publication is archived within the EURL GMFF quality system.

# Event-specific Method for the Quantification of Maize DP51291 Using Real-time PCR

## Validation Report

10 April 2024

European Union Reference Laboratory for GM Food and Feed

### 1 Introduction

In line with Regulation (EC) No 1829/2003 (1), Corteva Agriscience Belgium B.V. (on behalf of Corteva Agrisciences LLC) provided the EURL GMFF with an event-specific method for detection and quantification of maize event DP51291 (unique identifier DP-Ø51291-2) together with genomic DNA as positive and negative control samples.

The dossier was found complete (step 1 of the EURL GMFF validation procedure) and the scientific dossier assessment (step 2) concluded that the reported method performance characteristics, assessed against the ENGL method acceptance criteria (7), allowed moving the method forward to step 3 of the procedure (experimental testing), where the EURL GMFF verified the purity of the control samples provided and conducted an in-house testing of samples and method.

The positive and negative control DNA, submitted in accordance with Art 5(3)(j) and Article 17(3)(j) of Regulation (EC) No 1829/2003, were found of good quality.

Step 3 was completed with the conclusion that the method could be submitted to the collaborative study (step 4). This study confirmed that the method is well suited for quantifying genomic DNA of GM maize DP51291, appropriately extracted from food or feed, down to a GM content level of 0.1% m/m.

The preparation of the report (step 5) was aligned with the timeline communicated by EFSA for its risk assessment.

### 2 Dossier reception and acceptance (step 1)

Corteva Agriscience Belgium B.V. (on behalf of Corteva Agrisciences LLC) submitted the identification and quantification method, data demonstrating its adequate performance when applied to genomic DNA extracted from maize DP51291 GM event and from non GM maize, and the corresponding positive and negative control DNA samples.

The dossier was found to be complete and was thus moved to step 2.

### 3 Scientific assessment and bioinformatics analysis (step 2)

Documentation and data supplied by the applicant were evaluated by the EURL GMFF for compliance with the ENGL method acceptance criteria.

The specificity of the event-specific method was verified by the applicant and confirmed by the EURL GMFF by means of bioinformatics analysis, on the basis of the sequence data provided by the applicant.

### 3.1 Specificity assessment conducted by the applicant

The specificity of the event-specific method was assessed by the applicant in triplicate real-time PCR reactions, according to the method described in Annex 1 (Tables 1, 2, 3, 4 and 5), using at least 50 ng genomic DNA extracted from 10%:

maize DP51291, DAS1131, DP910521, DP915635, DP202216, DP56113, DP23211, T25, TC1507, NK603, MIR162, MIR604, MON 810, 3272, 98140, 59122, 5307, MON88017, MON89034, MON863, GA21, Bt11, Bt176, MON87427, MON87460, DAS-40278-9, DP4114, VCO-01981-5, MON87403, MON87411, MZHGOJG, MZIR098;

soybean DAS-44406-6, A2704-12, A5547-127, CV127, DAS-81419-2, MON87705, MON87751, FG72, MON87769, 356043, 305423, GTS40-3-2, MON87701, DAS-68416-4, MON89788, MON87708, SYHTOH2, GMB151;

cotton LLCotton25, GHB614, MON 531, MON15985, MON1445, 281-24-236 x 3006-210-23, GHB119, T304-40, MON88913, MON88701, DAS-81910-7, COT102, GHB811;

oilseed rape Rf3, GT73/RT73, MON88302, Rf1, Ms1, T45, Rf2, Ms8, Topas19/2, 73496, Ms11;

potato EH92-527-1, AM04-1020, AV43-6-G7, PH05-026-0048;

rice LLRICE62 (5% GM);

sugar beet (15% GM) H7-1;

and conventional maize, conventional soybean, conventional cotton, conventional oilseed rape, conventional potato, conventional rice, conventional sugar beet, conventional wheat. According to the method developer, the DP51291 method did not react with any sample except the positive control.

In addition, the applicant performed an *in-silico* specificity analysis by using the amplicon sequence as a query for BLASTN 2.13.0+ algorithm search against public sequence of National Center for Biotechnology Information (NCBI) and Patent Genbank databases. No sequence showed alignment of both forward and reverse primers or with the full length of the probe, besides relevant similarity hits to GHB811 patents.

A previously validated maize-specific PCR method ([https://gmo-crl.jrc.ec.europa.eu/summaries/2012-08-15\\_EURL-VL-10-10%20VM\\_JRC76621.pdf](https://gmo-crl.jrc.ec.europa.eu/summaries/2012-08-15_EURL-VL-10-10%20VM_JRC76621.pdf)), which amplifies a 79 base pair (bp) fragment of the HMG Protein A (*hmg*) of *Zea mays*, was used as a reference method.

### 3.2 Specificity assessment conducted by the EURL GMFF

The detection method spans the 3' insert-to-plant junction in maize DP51291. The forward primer "DP-051291-2\_for" binds to the insert. The reverse primer "DP-051291-2\_rev" binding site was found in the maize (*Zea mays*) genomic border adjacent to the insertion. The probe "DP-051291-2\_probe FAM:MGB" binds to the junction between the insert and the 3' genomic region of *Zea mays*.

The amplicon size is expected to be 80 bp, consistent to what reported by the applicant. The sequence of the amplicon was analysed by BLAST (NCBI) against local copies of the "nt" and "patents" databases, and no significant similarity was found with any other published sequence. In addition, the primers were tested against the sequences of the other GMO events present in the Central Core Sequence Information System (CCSIS) of the JRC, as well as the whole genomes of more than 80 plants (including *Brassica rapa*, *Glycine*

*max*, *Oryza sativa*, *Solanum lycopersicum* and *Zea mays*) using the e-PCR prediction tool (NCBI); a potential amplicon was identified in the GM event NS-B50027-4 (EURL-VL-04/19, oilseed rape, chromosome 5): the forward primer DP-051291-2\_for was found to produce an amplicon of 100 nt (with the DP-051291-2\_probe partially annealing to this amplicon, with 15 out of 21 nt). In this context, an experimental testing was carried out, showing no interference with the current detection method (data not shown). In addition, a perfect match of the amplicon and of the primers was identified with the sequence deposited for DP51291.

### 3.3 Verification of the ENGL acceptance parameters

The applicant prepared the calibration curve from a DNA solution (S1) of 10% maize event DP51291 genomic DNA (expressed as copy number ratio) which was serially diluted (1:6) in TE 0.1x to obtain samples S2 and S3, while S3 was diluted (1:8) to obtain S4. The parameters (slope,  $R^2$  coefficient) of eight runs of the calibration curve are reported as provided by the applicant (Table 1).

Table 1. Summary of the slope and  $R^2$  values obtained by the applicant

Run	DP51291		<i>hmg</i>	
	Slope	$R^2$	Slope	$R^2$
1	-3.44	0.999	-3.38	1.000
2	-3.45	1.000	-3.37	1.000
3	-3.40	1.000	-3.41	1.000
4	-3.29	0.998	-3.34	0.999
5	-3.37	1.000	-3.29	0.999
6	-3.42	1.000	-3.37	0.999
7	-3.39	1.000	-3.45	0.999
8	-3.34	1.000	-3.31	0.999
Mean	-3.39	1.000	-3.37	0.999

According to the ENGL method acceptance criteria, the average value of the slope of the standard curve shall range from -3.1 to -3.6 and the  $R^2$  coefficient shall be  $\geq 0.98$ .

Table 1 indicates that the slope and  $R^2$  coefficient of the standard curves for the GM (DP51291) and the maize-specific HMG Protein A (*hmg*) target, as established by the applicant, were within the ENGL acceptance criteria.

Precision and trueness of the method were established by the applicant and sixteen values for each of four GM levels (expressed as copy number ratio) were provided. Table 2A reports precision and trueness values for the four GM-levels as provided by the applicant. Both parameters were within the ENGL acceptance criteria (trueness  $\pm 25\%$ ,  $RSD_r \leq 25\%$  across the entire dynamic range).



Table 2A. Mean %, precision and trueness values (\*) provided by the applicant estimated

Expected GM % **	Test results			
	5.0	0.9	0.09	0.042
Measured mean GM %	5.13	0.871	0.092	0.038
Precision (RSD <sub>r</sub> %)	5.8	9.4	10.5	11.6
Trueness (bias %)	2.6	-3.2	2.2	-9.5

\* Numbers are not rounded but are presented as reported by the applicant

\*\* Expressed as copy number ratio

The method met the ENGL acceptance criteria for trueness and precision at the lowest GM level [i.e. 0.042% (expressed as copy number ratio)], which contains 50 copies of DP51291 in 325 ng of total DNA per reaction. The GM content of this sample is in line with the requirements for testing the Limit of Quantification (LOQ, below or equal to 0.09% or 50 copies).

The absolute limit of detection (LOD<sub>abs</sub>) of the DP51291 event-specific and the maize reference real-time PCR methods was assessed by the applicant in 60 PCR replicates. The LOD<sub>abs</sub> was found to be below 10 haploid genome copies for DP51291 event-specific method and below 20 haploid genome copies for *hmg* reference method. The relative LOD (LOD<sub>rel</sub>) of the combined method was assessed by the applicant in 60 PCR replicates and it was found to be at least 0.0084% (related to copies GM/total haploid genome copies in 325 ng of total maize DNA per reaction. The LOD<sub>abs</sub> and LOD<sub>rel</sub> are in line with the ENGL acceptance criteria (below 0.045% or 25 copies with a level of confidence of 95%).

The robustness of the method was assessed in sixteen combinations of the following variations to the method: exact/ $\pm$ 10% enzyme mix concentration, exact/ $\pm$ 30% primer concentration, exact/ $\pm$ 30% probe concentration, exact/ $\pm$ 1  $\mu$ L Master Mix volume,  $\pm$ 1 °C in annealing temperature. The RSD<sub>r</sub> and the trueness calculated for each combination of variations on a sample at the LOQ level (0.042%) did not exceed 30%, thus meeting the ENGL acceptance criteria.

Precision and trueness of the method were tested in a transferability study: mean values from triplicates for each of three GM levels (expressed as copies GM/total haploid genome copies) were provided. Table 2B reports precision and trueness values for the three GM-levels as provided by a laboratory different from the method developer. Both parameters were within the ENGL acceptance criteria (trueness  $\leq$  25%, RSD<sub>r</sub>  $\leq$  25% across the entire dynamic range).

Table 2B. Mean %, precision and trueness values obtained in the transferability study of the applicant

Laboratory	Test Results								
	Laboratory 2 (QS5 *)			Laboratory 3 (LC480 II)			Laboratory 3 (QS5 *)		
Expected GM %	0.9	0.09	0.042	0.9	0.09	0.042	0.9	0.09	0.042
Measured mean GM %	0.995	0.100	0.046	0.960	0.098	0.044	0.910	0.091	0.043
Precision (RSD <sub>r</sub> %)	6.4	12.7	6.1	5.9	5.8	3.2	1.5	10.1	6.5
Trueness (bias %)	10.6	11.1	9.5	6.7	8.9	4.8	1.1	1.1	2.4

\* QuantStudio 5

### 3.4 DNA extraction

Genomic DNA was isolated from ground maize seeds, using a cetyltrimethylammonium bromide (CTAB)-based DNA extraction protocol previously submitted for detection of maize event DP4114 that has already been validated in-house by the EURL GMFF. The protocol for DNA extraction and a report on testing are published at <https://gmo-crl.jrc.ec.europa.eu/summaries/EURL-VL-02-14-XP.pdf>. According to the data submitted by the applicant, the protocol for DNA extraction generated DNA of suitable quantity and quality for PCR-based applications when applied to ground seeds from the maize event DP51291.

In agreement with the ENGL position, endorsing the modularity principle (see also Annex III to Regulation (EU) No 503/2013), and given the similarity in the matrix, the EURL GMFF considers the above mentioned DNA extraction protocol applicable in the context of the validation of the method for maize event DP51291.

Annex III to Reg. (EU) No 503/2013 (5) requires the applicant to discuss the validity and limitations of the detection methods in the various types of foods and feeds (matrices) that are expected to be placed on the market. To this regard the applicant stated that *“the foundation to detect the presence of transgenes in seed, food and feed matrices is primarily based on the quality of genomic DNA template that is utilized. Pure DNA extractions such as the cetyltrimethyl ammonium bromide (CTAB) method or the Wizard (Promega) method are suitable for the isolation of pure genomic DNA from a wide variety of cereal-based matrices (1, 2, 3). Exceptionally pure DNA, applicable for molecular biology procedures, such as Polymerase Chain Reaction (PCR) amplification, is imperative to provide adequate source template suitable for use for a wide variety of agricultural products, including maize grain and derived matrices supporting food and feed products. The processing of maize grain involves varying degrees of mechanical, enzymatic, solvent, heat, acid, pressure treatment, or combinations of these steps (4, 5, 6, 7, 8, 9, 10). These steps influence the quality and intactness of DNA contained in the final processed maize products (1, 11, 12, 13) which may result in significant degradation of high molecular weight DNA and failure to PCR amplify products greater than a few 100 base pairs (11, 12). Random DNA fragmentation is known to lead to variability in quantifying DNA by qPCR (14), thus affecting the ability to accurately quantify the presence of a GM event and taxon-specific target in processed fractions. Moreover, the DNA extraction procedure necessary for some of these processed matrices may need additional rounds of processing to clean-up the DNA, to eliminate PCR inhibitors in order to achieve quality genomic DNA suitable for PCR testing (15, 16). These extraction methods are widely used for plant-based materials, are economical and can be easily scaled (17). The DP51291 maize detection method has been developed and was*

<sup>1</sup> Nguyen T, et al. (2009) Comparison of DNA extraction efficiencies using various methods for the detection of genetically modified organisms (GMOs). *International Food Research Journal*, 16: 21-30

<sup>2</sup> Sönmezoglu ÖA, et al. (2015) Determination of Genetically Modified Corn and Soy in Processed Food Products. *Journal of Applied Biology and Biotechnology*, Vol. 3 (03): 032-037

<sup>3</sup> Stefanova P, et al. (2013) A Modified CTAB Method for DNA Extraction from Soybean and Meat Products. *Biotechnology and Biotechnological Equipment*, 27:3: 3803-3810

<sup>4</sup> Alexander RJ (1987). Corn dry milling: processes, products, and applications. *Corn: Chemistry and Technology*, Chapter 11, 351-375.

<sup>5</sup> May JB (1987). Wet milling: process and products. *Corn: Chemistry and Technology*, Chapter 12, 377-397.

<sup>6</sup> Gwirtz JA, et al. (2014) Processing maize flour and corn meal food products. *Annals of the New York Academy of Sciences* 1312: 66-75.

<sup>7</sup> Khalsa N (1994) Methods for making tortilla chips and tortilla chips produced thereby. US Patent 5298274 A

<sup>8</sup> Pollak LM et al. (1995). Corn as a food source in the United States: Part I. Historical and current perspectives. *Cereal Foods World*, 40, 1-6.

<sup>9</sup> Watson SA (1988). Corn marketing, processing and utilisation. In: *Corn and corn improvement - Agronomy Monograph*. GF Sprague, JW Dudley. American Society of Agronomy, Crop Science Society of America and Soil Science Society of America, Madison, Wisconsin, 881-940.

<sup>10</sup> White PJ et al. (1995). Corn as a food source in the United States: Part II. Processes, products, composition, and nutritive values. *Cereal Foods World*, 40, 756-762

<sup>11</sup> Bauer T, et al. (2003). The effect of processing parameters on DNA degradation in food. *European Food Research and Technology*, 217, 338-343

<sup>12</sup> Murray SR, et al. (2007). Use of quantitative realtime PCR to estimate maize endogenous DNA degradation after cooking and extrusion or in food products. *Journal of Agricultural and Food Chemistry*, 55, 2231-2239.

<sup>13</sup> Terry C, et al. (2002) Detection of Genetically Modified Crops and Their Derivatives: Critical Steps in Sample Preparation and Extraction. *Journal of AOAC International*, 85:3: 768-774

<sup>14</sup> Sedlackova T, et al. (2013). Fragmentation of DNA affects the accuracy of the DNA quantitation by the commonly used methods. *Biological Procedures Online*, 15, 1-9.

<sup>15</sup> Demeke T et al. (2010). Influence of DNA extraction methods, PCR inhibitors and quantification methods on real-time PCR assay of biotechnology-derived traits. *Analytical and Bioanalytical Chemistry*, 396, 1977-1990.

<sup>16</sup> Peano C, et al. (2004). Qualitative and quantitative evaluation of the genomic DNA extracted from GMO and Non-GMO foodstuffs with four different extraction methods. *Journal of Agricultural and Food Chemistry*, 52, 6962-6968.

<sup>17</sup> Smith DS, et al. (2005) Comparison of Several Methods for the Extraction of DNA from Potatoes and Potato-Derived Products. *Journal of Agricultural and Food Chemistry*, 53: 9848-9859

*pre-validated on maize seed and tissues. The DP51291 maize detection method can, in principle, be applied to any sample from which sufficient quantities of maize DNA, free of PCR inhibitors, can be purified. This DNA extraction method will be specifically applicable to the certified reference materials that have been produced for quality control and calibration of the detection method.”*

Whenever DNA is extracted from more complex and difficult matrices, a thorough control of the quality of the DNA is recommended in order to ensure that it has the required quality for subsequent PCR analysis.

## 4 Materials and method

### 4.1 Samples

The following positive and negative control samples were provided by the applicant to the EURL GMFF in accordance to Regulation (EC) No 1829/2003 Art 2.11 <sup>(18)</sup>:

- genomic DNA extracted by the applicant from hemizygous maize seeds harbouring the DP51291 event, and
- genomic DNA extracted by the applicant from conventional maize seeds genetically similar to those harbouring the DP51291 event.

### 4.2 Method for the PCR analysis

The PCR method provided by the applicant is an event-specific, quantitative, real-time TaqMan<sup>®</sup> PCR procedure for the determination of the relative content of GM event DP51291 DNA to total maize DNA. The procedure is a simplex system, in which a maize specific method targeting the endogenous gene of HMG Protein A (*hmg*), and the GM target method for DP51291 are performed in separate wells. The validated method protocol is published by the EURL GMFF at <https://gmo-crl.jrc.ec.europa.eu/method-validations> and can be found in Annex 1 to this report.

For the detection of GM event DP51291, an 80 bp fragment of the region spanning the 3' insert-to-plant junction in maize DP51291 is amplified using specific primers. PCR products are measured during each cycle (real-time) by means of a target-specific oligonucleotide probe labelled with FAM (6-carboxyfluorescein) as reporter dye at its 5' end and MGBNFQ<sup>™</sup> (Minor Groove Binding Non-Fluorescent Quencher) as non-fluorescent quencher dye at its 3' end.

For the relative quantification of GM event DP51291, a maize taxon-specific method amplifies a 79 bp fragment of an maize HMG Protein A (*hmg*) endogenous gene, using *hmg* gene-specific primers and a *hmg* gene-specific probe labelled with FAM (6-carboxyfluorescein) as reporter dye at its 5' end and BHQ-1 (Black Hole Quencher<sup>®</sup> 1) as non-fluorescent quencher dye at its 3' end.

Standard curves are generated for both the DP51291 and the *hmg* by plotting the C<sub>q</sub> values measured for the calibration points against the logarithm of the DNA copy numbers and by fitting a regression line into these data. Thereafter, the standard curves are used to estimate the copy numbers in the test sample DNA by interpolation from the standard curves.

For the relative quantification of event DP51291 DNA in a test sample, the DP51291 copy number is divided by the copy number of the maize haploid genome and multiplied by 100 to obtain the percentage value (GM % = DP51291/ maize haploid genome x 100).

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<sup>18</sup> Control sample defined as the GMO or its genetic material (positive sample) and the parental organism or its genetic material that has been used for the purpose of the genetic modification (negative sample).

The absolute copy numbers of the calibration curve samples are calculated by dividing the sample DNA mass (nanograms) by the published average 1C value for the maize genome (2.73 pg) (8). The copy number values used in the quantification, the GMO contents of the calibration samples, and the total DNA quantity used in the PCR reactions are listed in Table 3.

*Note: Numerical values presented in the following tables were rounded keeping two digits for values  $\leq 1$ , one digit for values between 1 and 10 and no digit for values  $\geq 10$ , unless otherwise reported. The calculations in the MS Excel files however were done over not rounded data. This approach might create small inconsistencies in the numerical values reported in the tables but it allows a higher precision in the final results.*

Table 3. Copy number values of the standard curve samples

Sample code	S1	S2	S3	S4
Total amount of maize DNA in the reaction (ng)*	325	54	9	1.1
Target taxon haploid genome copies	119048	19841	3307	413
Target DP51291 copies	11905	1984	331	41

\* Total nanograms are rounded to the integral value

### 4.3 EURL GMFF experimental testing (step 3)

#### 4.3.1 Determination of the zygosity ratio in the positive control sample

The EURL GMFF experimentally verified the zygosity ratio (GM-target to reference target ratio) in the positive control sample to assess the method performance at 0.1% GM level -expressed as mass fraction of GM material- in relation to the provisions of Regulation (EU) No 619/2011 (6).

The copy number of the DP51291 and of the *hmg* targets in the positive control sample were determined by digital PCR (dPCR) performed on the Bio Rad QX200 Droplet Reader.

Reaction mixes were prepared in order to test the zygosity in eighteen replicates to a final volume of 22  $\mu\text{L}$  and contained 1X ddPCR Super Mix no dUTP (Bio Rad, Cat. number 64469973), primers and probes at concentrations indicated in the corresponding validated method (DP-Ø51291-2 Forward Primer and DP-Ø51291-2 Reverse Primer at 600 nM each, DP-Ø51291-2 Probe at 120 nM; *hmg* primer 1 and 2 at 300 nM each, *hmg* probe at 180 nM), and 1  $\mu\text{L}$  of DNA at a concentration of 65 ng/ $\mu\text{L}$ .

Reaction mixes were loaded into a semi skirt 96-well plate. 'No template controls' were included. After sealing with a sealing aluminium foil using the PX1™ PCR Plate Sealer, the plate was briefly centrifuged (1 min at 1000 rpm) and placed on Bio Rad Automated Droplet Generator (AutoDG).

The instrument added the Automated Droplet Generation oil for Probes (Bio Rad, Cat. number 1864110), generated the droplets in a final volume of 40  $\mu\text{L}$  of the emulsion containing droplets. The AutoDG then transferred all the emulsions into a new semi skirt 96-well plate. The new plate was sealed with a sealing foil

with the PX1™ PCR Plate Sealer and run in a Bio Rad C1000 TouchThermal Cycler. The thermal cycling conditions in a final volume of 40 µL is described below.

Box 1: Thermal cycling conditions in a final volume of 40 µL.

Step	Temperature (°C)	Time (mm:ss)	Ramp rate	Number of cycles
Polymerase activation	95	10:00	2°C/sec	1
DNA denaturation	94	00:30		40
Annealing/extension	60	01:00		1
Enzyme deactivation	98	10:00		1
Hold	4	infinite		1

The sealed 96-well plate was then placed in the QX200 Droplet Reader to determine through cytofluorimetry the fraction of fluorescent PCR-positive droplets with respect of the total number of droplets in the original sample by selecting the proper fluorescent dye used. Data analysis and copy number calculations were performed using the Bio-Rad QX200 Droplet Reader Analysis software (QuantaSoft version 1.7.4).

Calculations of means and variances were carried out according to the procedure outlined for random variables in the Annex 4 of the ENGL guidance document 'Verification of analytical methods for GMO testing when implementing interlaboratory validated methods - Version 2' (9).

#### 4.3.2 In-house verification of the method performance against ENGL method acceptance criteria

The method performance characteristics were verified by quantifying on a copy number basis five blind test samples distributed over a range of GM levels (5.0% - 0.039%, see Table 4). The blind test samples were prepared by the EURL GMFF from the genomic DNA provided by the applicant (see 4.1 for details) by mixing DP51291 maize DNA and non-GM maize DNA.

Table 4. DP51291 blinded samples GM % contents

DP51291 GM % GM copy number/maize haploid genome copy number x 100
5.0
2.0
0.90
0.09
0.039

The calibration sample S1 was prepared from the genomic DNA provided by the applicant by mixing the appropriate amount of DP51291 DNA with control non-GM maize DNA to obtain a 10% (in copy number ratio related to haploid genome copies) GM sample. Calibration samples S2-S3 were prepared by 6-fold serial dilutions from the S1 sample and sample S4 by an 8-fold serial dilution from the S3 sample (see Table 3).

The experiments were performed on an ABI 7500, a QuantStudio 7 Flex System and a Roche LC480 II real-time platform under repeatability conditions and followed the protocol provided by the applicant.

Test samples from GM level 5.0%, to 0.039%, were tested in two real-time PCR runs with two replicates for each GM-level on each plate (total of four replicates per GM-level). The test sample with GM level 0.039% (in copy number ratio, equal to 0.10% mass ratio), containing 46 copies of DP51291 in 325 ng of total DNA per reaction, was tested in 15 replicates in an additional run for each platform. Average values of the slope and of the  $R^2$  coefficient of the standard curves and method trueness and precision over the dynamic range were evaluated against the ENGL method acceptance criteria. On Roche LC480 II platform the method was run at 45 cycles as described in the validated method published at <https://gmo-crl.jrc.ec.europa.eu/method-validations> and in Annex 1 below, and analysed with the second derivative maximum method.

#### 4.4 International collaborative study (step 4)

The international collaborative trial involved twelve randomly selected laboratories, all being “national reference laboratories, assisting the EURL GMFF for testing and validation of methods for detection”, as listed in annex to Regulation (EC) No 120/2014 (10) who had expressed their interest in participation. The study was carried out in accordance with the following internationally accepted guidelines:

- The IUPAC “Protocol for the design, conduct and interpretation of method-performance studies.” (Horwitz, 1995) (2)
- 5725-1: 2023 “Accuracy (trueness and precision) of measurement methods and results. General principles and definitions.” (3)
- 5725-2: 2019. “Accuracy (trueness and precision) of measurement methods and results — Basic method for the determination of repeatability and reproducibility of a standard measurement method” (4)

The objective of the international collaborative study was to verify in experienced laboratories the trueness and precision of the PCR analytical method provided by the applicant and verified in-house by the EURL GMFF.

#### 4.4.1 List of participating laboratories

The twelve laboratories participating in DP51291 international collaborative study were randomly selected from twenty-five national reference laboratories (NRL) that offered to participate.

Clear guidance was given to the selected laboratories for strictly following the validation protocol that was provided to them. The participating laboratories are listed in Table 5.

Table 5. Laboratories participating in the validation of the detection method for maize event DP51291

Laboratory	Country
Swedish Food Agency, Science Department	SE
Center for Agricultural Technology Augustenberg	DE
State Institute of Chemical and Veterinarian Analysis - Freiburg	DE
Plant Health Laboratory	FR
Voivodeship Sanitary and Epidemiological Station in Rzeszów	PL
Hellenic Agricultural Organisation, Dimitra	GR
LUFA Speyer	DE
Walloon Agricultural Research Centre	BE
Independent Authority of Public Revenue (IAPR)	GR
BioGEVES - Groupement d'Intérêt Public - Groupe d'Etude et de contrôle des Variétés	FR
Service commun des laboratoires du ministère de l'économie et des finances	FR
Sciensano	BE

#### 4.4.2 Real-time PCR equipment used in the study

Laboratories involved in the collaborative study used the following real-time PCR equipment: four laboratories used QuantStudio 5, two used CFX96, two ABI 7500, one QuantStudio 3, one QuantStudio 7Flex, one Roche LC480 II and one PCRmax ECO48.

This variability of equipment, with its known potential influence on PCR results, reflects the real-life situation in the control laboratories and provides additional assurance that the method is robust and usable under real conditions.



#### 4.4.3 Materials used in the international collaborative study

For the validation of the quantitative event-specific method, calibration samples (of known GMO content) and blind test samples (of undisclosed GM content = blind samples) were provided by the EURL GMFF to the participating laboratories (for test samples preparation see 4.3.2).

The twelve NRLs participating in the validation study received the following materials:

- ✓ Four calibration samples with known concentrations of GM-event (175 µL of DNA solution each) labelled from S1 to S4 (Table 3).
- ✓ Twenty blinded test DNA samples (87.5 µL of DNA solution, each at 65 ng/µL) labelled from U1 to U20, representing five GM levels, each in four replicates (Table 4)
- ✓ Reaction reagents:
  - TaqMan® Universal PCR Master Mix (no UNG) (2x), one vial: 8 mL
  - Distilled sterile water, one vial: 4 mL
- ✓ Primers and probes (1 tube each) as follows:
  - hmg* taxon-specific
    - *hmg* primer1 (10 µM): 240 µL
    - *hmg* primer2 (10 µM): 240 µL
    - *hmg* probe (10 µM): 144 µL
  - DP51291
    - DP-Ø51291-2 Forward Primer (10 µM): 480 µL
    - DP-Ø51291-2 Reverse Primer (10 µM): 480 µL
    - DP-Ø51291-2 Probe (10 µM): 100 µL

#### 4.4.4 Design of the collaborative study

Participating laboratories received a detailed validation protocol that included the exact design of the PCR plates, ensuring that on each PCR plate the samples were analysed for the DP51291 event-specific target and for the *hmg* taxon-specific target. In total, two plates were run by each participating laboratory.

The laboratories prepared the PCR master-mixes for the maize event DP51291 and *hmg* in accordance with the description provided in the validation protocol. Calibration and test samples were loaded on the PCR plates as per pre-determined plate layout.

The amplification reaction followed the cycling program specified in the protocol. Participants determined the GM % in the test samples according to the instructions and also reported the raw data to the EURL GMFF on an Excel sheet that was designed, validated and distributed by the EURL GMFF. All data are stored by the EURL GMFF on a dedicated and protected server.

The EURL GMFF analysed the data against the parameters and the limits set by the ENGL, i.e. trueness, precision, amplification efficiency and linearity.

#### 4.4.5 Deviations reported from the protocol

Ten laboratories reported no deviations from the validation protocol. One laboratory reported repeating the test with one plate, due to contamination; one laboratory reported using 48 wells instead of 96, due to the type of PCR system available.

## 5 Results

### 5.1 EURL GMFF experimental testing

#### 5.1.1 Zygoty ratio in the positive control sample

The results of the digital PCR analysis conducted by the EURL GMFF on the DP51291 and *hmg* targets to determine the zygoty ratio in the positive control samples are shown in Table 6. For reference, the zygoty ratio reported by the applicant was 0.42; their measured value was 0.38, which was not considered significantly different from the expected ratio of 0.42.

Table 6. Zygoty ratio of the DP51291 and *hmg* targets in the positive control sample.

Mean ratio (DP51291/ <i>hmg</i> )	0.38
Standard deviation	0.01
RSD <sub>r</sub> (%)	2.6
Standard error of the mean	0.002
Upper 95% CI of the mean	0.38
Lower 95% CI of the mean	0.37

The mean ratio (DP51291/*hmg*) equals 0.38, as expected for a maize control sample, hemizygous for the GM-locus, with a GM parental contribution of male origin and assuming single-copy endogenous gene target. Therefore, the measured mean ratio is not significantly different from the expected ratio, for an alpha = 0.05.

Hence, both 0.039% GM and 0.038% GM in haploid genome copy numbers corresponds to 0.1% in mass fraction of GM DNA.

#### Box 2: Note on reporting of analytical results

The zygoty ratio herein reported is valid for the positive control sample DNA in the context of the present validation study. It is used to assess the method performance at 0.1% GM level -expressed as mass fraction of GM material- in relation to the provisions of Regulation (EU) No 619/2011.

When analytical results of official laboratories are primarily expressed as ratio of GM- DNA copy numbers, they shall be translated into mass fraction results by means of the specific conversion factor published in the document “Conversion factors (CF) for certified references materials (CRM)” (<https://gmo-crl.jrc.ec.europa.eu/guidancedocs.htm>).

#### 5.1.2 In-house verification of method performance against ENGL method acceptance criteria

Test samples with GM levels from 5.0% to 0.09% (expressed in copy number) were tested in two real-time PCR runs with two replicates for each GM-level on each plate (total of four replicates per GM-level). The sample at 0.039% GM-level (copy number, corresponding to 0.1% mass fraction) was tested for its precision in quantification in 15 replicates in separate runs.

Tests were conducted on ABI 7500, a Q7 (QuantStudio 7 Flex System) and a Roche LC480 II for robustness.

The standard curve parameters and the results of efficiency, linearity, trueness and precision obtained in the three real-time PCR runs with the test samples are shown in Tables 7A, 7B, 8, 9 and 10.

According to the ENGL method acceptance criteria, the average value of the slope of the standard curve shall range from -3.1 to -3.6 and the  $R^2$  coefficient shall be  $\geq 0.98$ . Table 7A and 7B document that the slopes of the standard curves and the  $R^2$  coefficients were within the limits established by the ENGL. The EURL GMFF in-house results confirm the data provided by the applicant.

Table 7A. Standard curve parameters of the real-time PCR tests, carried out on ABI 7500, Q7 and Roche LC480 II to quantify GM-levels in the range 5.0% to 0.09% in four replicates each. Slope and  $R^2$  coefficient values were rounded to two digits.

	DP51291			hmg		
	Slope	PCR efficiency (*)	$R^2$	Slope	PCR efficiency (*)	$R^2$
Run A	-3.33	100	1.00	-3.37	98	1.00
Run B	-3.31	101	1.00	-3.36	98	1.00
Run C	-3.46	95	1.00	-3.37	98	1.00
Run D	-3.31	101	1.00	-3.38	98	1.00
Run E	-3.36	99	1.00	-3.37	98	1.00
Run F	-3.42	96	1.00	-3.38	98	1.00

\* PCR efficiency (%) is calculated using the formula  $\text{Efficiency} = (10^{(-1/\text{slope})} - 1) \times 100$

Runs A-B were carried out on QS7; runs C-D were carried out on ABI 7500; runs E and F were carried out on Roche LC480 II.

Table 7B. Standard curve parameters of the real-time PCR tests, carried out on ABI 7500, Q7, and Roche LC480 II to quantify the GM-level 0.039% (copy number, equal to 0.1% in mass fraction) in 15 replicates. Slope and  $R^2$  coefficient values were rounded to two digits.

	DP51291			hmg		
	Slope	PCR efficiency (*)	$R^2$	Slope	PCR efficiency (*)	$R^2$
Run G	-3.46	95	1.00	-3.39	97	1.00
Run H	-3.32	100	1.00	-3.39	97	1.00
Run I	-3.39	97	1.00	-3.42	96	1.00

\* PCR efficiency (%) is calculated using the formula  $\text{Efficiency} = (10^{(-1/\text{slope})} - 1) \times 100$

Run G was carried out on QS7; run H was carried out on ABI 7500; run I was carried out on Roche LC480 II.

According to the ENGL method acceptance criteria the method trueness (measured as bias in% of the target GM level) should be within  $\pm 25\%$  of the accepted reference value over the entire dynamic range and the precision, expressed as  $\text{RSD}_r\%$  (relative standard deviation of repeatability), should be  $\leq 25\%$ , also over the entire dynamic range.

Tables 8, 9 and 10 show that trueness and precision of quantification were within the limits established by the ENGL for the PCR machines used.

Table 8. Values of trueness and precision as established by the EURL GMFF in its in-house verification using a QS7. GM % in copy/copy haploid genomes.

Target GM-levels %	Measured GM-level %	Bias % of the target GM-level	Precision (RSD <sub>r</sub> %)
5.0	4.9	-1.9	2.4
2.0	2.0	-1.8	2.1
0.90	0.86	-4.2	5.1
0.09	0.08	-15	6.8
0.039	0.04	0.21	17

Table 9. Values of trueness and precision as established by the EURL GMFF in its in-house verification using an ABI 7500. GM % in copy/copy haploid genomes.

Target GM-levels %	Measured GM-level %	Bias % of the target GM-level	Precision (RSD <sub>r</sub> %)
5.0	4.7	-6.1	4.1
2.0	1.9	-7.2	4.2
0.90	0.82	-9.1	3.0
0.09	0.08	-6.5	8.9
0.039	0.033	-15	17

Table 10. Values of trueness and precision as established by the EURL GMFF in its in-house verification using a Roche LC480 II. GM % in copy/copy haploid genomes.

Target GM-levels %	Measured GM-level %	Bias % of the target GM-level	Precision (RSD <sub>r</sub> %)
5.0	4.9	-2.1	0.99
2.0	1.8	-11	2.5
0.90	0.82	-9.4	1.3
0.09	0.08	-8.3	6.4
0.039	0.038	-2.7	25

## 5.2 Results of the international collaborative study

### 5.2.1 PCR efficiency and linearity

The PCR efficiency (%) and R<sup>2</sup> values (expressing the linearity of the regression) for the standard curve, reported by participating laboratories are displayed in Table 11. The PCR efficiency (%) was calculated from the standard curve slopes using the formula:

$$\text{Efficiency (\%)} = \left( 10^{\frac{-1}{\text{slope}}} - 1 \right) \times 100$$

Table 11 indicates that the efficiency of amplification for DP51291 ranges from 95% to 119% and the linearity from 0.98 to 1.00; the amplification efficiency for the maize-specific target ranges from 95% to 106% and the linearity from 0.99 to 1.00. The mean PCR efficiency was 100% for DP51291 and 99% for *hmg*. The average R<sup>2</sup> of the methods was 1.00 for both DP51291 and *hmg*. With the exception of PL06 laboratory (highlighted in Table 11), both PCR efficiency and linearity values were within the ENGL acceptance criteria. These results confirm the appropriate performance characteristics of the methods tested in terms of efficiency and linearity.

Table 11. Values of slope, PCR efficiency and R<sup>2</sup> obtained during the international collaborative trial. Slope and R<sup>2</sup> coefficient values were rounded to two digits.

Lab	Plate	DP51291			<i>hmg</i>		
		Slope	PCR Efficiency (%)	R <sup>2</sup>	Slope	PCR Efficiency (%)	R <sup>2</sup>
1	A	-3.36	98	1.00	-3.38	97	1.00
	B	-3.36	98	1.00	-3.39	97	1.00
2	A	-3.41	97	1.00	-3.34	99	1.00
	B	-3.36	99	1.00	-3.39	97	1.00
3	A	-3.18	106	0.99	-3.34	99	1.00
	B	-3.34	99	1.00	-3.36	98	1.00
4	A	-3.42	96	1.00	-3.41	97	1.00
	B	-3.38	98	0.99	-3.37	98	1.00
5	A	-3.44	95	1.00	-3.42	96	1.00
	B	-3.37	98	1.00	-3.35	99	1.00
6	A	-3.15	108	0.99	-3.25	103	0.99
	B	-2.94 *	119 *	0.98	-3.19	106	1.00
7	A	-3.42	96	1.00	-3.38	97	1.00
	B	-3.29	101	0.99	-3.36	99	1.00
8	A	-3.30	101	1.00	-3.38	98	1.00
	B	-3.29	101	1.00	-3.33	100	1.00
9	A	-3.38	98	1.00	-3.44	95	1.00
	B	-3.45	95	1.00	-3.40	97	1.00
10	A	-3.38	98	1.00	-3.38	98	1.00
	B	-3.38	97	1.00	-3.36	99	1.00
11	A	-3.35	99	1.00	-3.30	101	1.00
	B	-3.14	108	1.00	-3.26	103	1.00
12	A	-3.42	96	0.99	-3.31	101	1.00
	B	-3.35	99	1.00	-3.31	101	1.00
	Mean	-3.33	100	1.00	-3.35	99	1.00

\* Outside of ENGL acceptance criteria (-3.1 ≥ slope ≥ -3.6, corresponding to amplification efficiencies of 110% to 90%).

## 5.2.2 GMO quantification

Table 12 reports the values of quantification for the four replicates of each GM level as reported by each of the twelve participating laboratories.

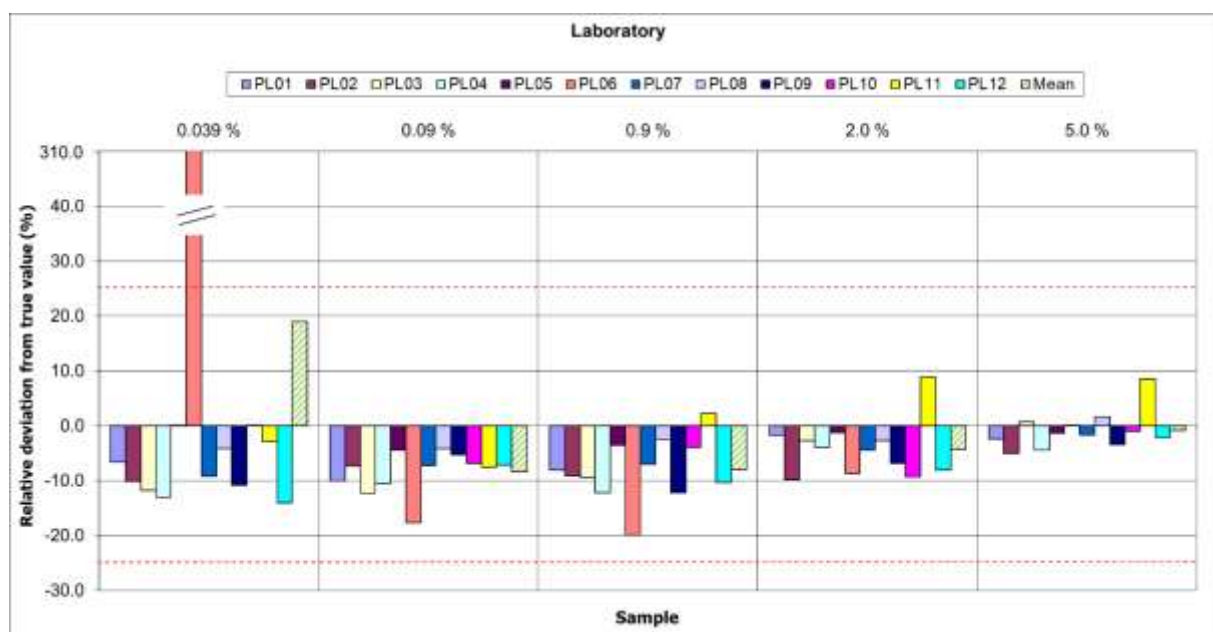
Table 12. GM % values determined by laboratories for test samples (Cochran outliers are highlighted in bold).

LAB	GMO content (%) (*)																			
	5.0				2.0				0.90				0.09				0.039			
	REP 1	REP 2	REP 3	REP 4	REP 1	REP 2	REP 3	REP 4	REP 1	REP 2	REP 3	REP 4	REP 1	REP 2	REP 3	REP 4	REP 1	REP 2	REP 3	REP 4
1	5.0	4.7	5.2	4.6	1.9	1.9	2.1	2.0	0.84	0.77	0.82	0.88	0.08	0.07	0.09	0.09	0.04	0.04	0.03	0.03
2	5.0	4.6	4.7	4.7	1.9	1.8	1.8	1.8	0.84	0.82	0.81	0.80	0.09	0.09	0.08	0.08	0.03	0.04	0.04	0.04
3	5.0	4.9	5.1	5.2	2.0	2.0	1.9	1.9	0.84	0.83	0.82	0.77	0.09	0.08	0.08	0.07	0.04	0.04	0.04	0.03
4	4.8	4.3	4.9	5.1	1.8	1.8	2.2	2.0	0.84	0.66	0.88	0.78	0.08	0.07	0.08	0.09	0.03	0.04	0.04	0.03
5	5.0	4.8	5.0	4.9	2.0	1.9	2.0	2.0	0.81	0.84	0.97	0.86	0.08	0.08	0.10	0.09	0.04	0.03	0.03	0.05
6	4.4	4.4	4.8	6.4	1.6	1.5	1.9	2.4	0.54	0.78	0.73	0.83	0.14	0.04	0.06	0.06	0.04	0.46	0.11	0.03
7	5.0	4.9	4.9	4.8	1.9	1.9	2.0	1.9	0.83	0.81	0.85	0.85	0.08	0.08	0.09	0.09	0.04	0.03	0.04	0.03
8	5.2	5.0	5.1	5.1	2.0	2.0	1.9	1.9	0.84	0.84	0.83	1.00	0.08	0.08	0.10	0.08	0.05	0.03	0.03	0.04
9	4.3	4.8	5.0	5.2	1.9	1.7	2.0	1.8	0.77	0.76	0.82	0.81	0.10	0.08	0.08	0.09	0.03	0.04	0.03	0.04
10	4.8	4.9	4.9	5.2	2.0	1.4	1.9	2.0	0.85	0.89	0.86	0.86	0.09	0.08	0.08	0.08	0.04	0.04	0.05	0.03
11	5.1	5.4	5.6	5.6	2.1	2.1	2.2	2.3	0.83	0.93	0.92	1.00	0.07	0.07	0.09	0.10	0.05	0.04	0.03	0.04
12	5.1	5.0	4.8	4.6	1.9	1.8	2.0	1.8	0.77	0.78	0.82	0.86	0.08	0.08	0.09	0.09	0.04	0.03	0.03	0.03

\* GMO % = (GMO copy number/maize haploid genome copy number) x 100

A graphical representation of the data reported in Table 12 is provided in Figure 1 that shows the relative deviation from the true value for each GM level tested by the participating laboratory. The coloured bars represent the deviation of the GM level measured in % of the true GM level; the green-stripes bar on the right represents the mean relative deviation over all data before eliminating outliers for each GM level.

Figure 1. Relative deviation (%) from the true value of GM level (\*).



\* For PL05 and PL10 at level 0.039%, and PL06 at 5.0%, very small relative deviations from the true values were observed and therefore the corresponding histogram does not show up in Figure 1. PL = participating laboratory. Red dotted lines indicate  $\pm 25\%$  relative deviation.

Overall, most laboratories' mean relative deviations from the true values were within a maximum of  $\pm 25\%$ . At GM-level 5.0%, 2.0%, 0.90% and 0.09% all laboratories were within the limit; at GM-level 0.039% eleven laboratories were within the limit. One laboratory overestimated GM-level 0.039% by more than 25% (*i.e.* 310%, showing a clear outlier). Interestingly, a trend for underestimation was observed in all laboratories but two.



### 5.2.3 Method performance requirements

Among the performance requirements established by ENGL and adopted by the EURL GMFF (<https://gmo-crl.jrc.ec.europa.eu/guidance-documents>), repeatability and reproducibility are to be assessed through an international collaborative trial. Table 13 illustrates the estimation of repeatability and reproducibility at the various GM levels tested during the study (see Table 5 for a list of the participant laboratories).

According to the ENGL method performance requirements the relative reproducibility standard deviation ( $RSD_R$ ), that describes the inter-laboratory variation, should be below 35% at the target concentration and over the majority of the dynamic range, while it should be below 50% at the lower end of the dynamic range.

As it can be observed in Table 13, the method satisfies this requirement at all GM levels tested. Indeed, the highest value of  $RSD_R$  % is 15% at the 0.039% GM level, thus within the acceptance criterion.

Table 13. Summary of validation results for the DP51291 method, expressed as GM copy numbers in relation to target taxon haloid genome copy numbers.

	Test Sample Expected GMO %				
	5.0	2.0	0.90	0.09	0.039
Laboratories having returned valid results	12	12	12	12	12
Samples per laboratory	4	4	4	4	4
Number of outliers	1	2	0	1	1
Reason for exclusion (*)	C**	C**, C	-	C**	C**
Mean value	5.0	1.9	0.83	0.08	0.04
Relative repeatability standard deviation, $RSD_r$ (%)	4.5	4.7	7.6	9.8	15
Repeatability standard deviation	0.01	0.01	0.06	0.09	0.22
Relative reproducibility standard deviation, $RSD_R$ (%)	5.4	6.7	9.1	9.8	15
Reproducibility standard deviation	0.27	0.13	0.08	0.01	0.01
Bias (***) (absolute value)	-0.05	-0.07	-0.07	-0.007	-0.003
Bias (%)	-0.97	-3.3	-8.0	-7.5	-7.5

\* C= Cochran's test; DG=Double Grubbs' test; identification and removal of outliers through these tests, according to ISO 5725-2.

\*\* All four Cochran outliers originate from a single laboratory.

\*\*\* Bias is estimated according to ISO 5725 data analysis protocol.

Table 13 also documents the relative repeatability standard deviation ( $RSD_r$ ) estimated for each GM level. In order to accept methods for collaborative study, the EURL GMFF and ENGL require that the  $RSD_r$  value indicated by the applicant and confirmed by the EURL GMFF through in-house experiments, is below 25% (see ENGL document "Definition of Minimum Performance Requirements for Analytical Methods of GMO Testing" <http://gmo-crl.jrc.ec.europa.eu/guidancedocs.htm>). As it can be observed from the values reported, the repeatability standard deviation is below 25% at all GM levels, with the highest value of 15% at the 0.039% GM level.

The trueness of the method is estimated using the measures of the method bias for each GM level. According to ENGL method performance requirements, trueness should be  $\pm 25\%$  across the entire dynamic range. The method satisfies this requirement across the dynamic range tested, with the highest value of bias (%) of -8.0% at the 0.90% GM level.

## 6 Compliance of the method for detection and quantification of event DP51291 with the requirements of Regulation (EU) No 619/2011

To verify the compliance of the method under validation with the requirements of Regulation (EU) No 619/2011, the following steps were carried out and their outcome is summarised in Table 14:

- at step 2 of the validation process (scientific assessment of the dossier), the EURL GMFF acknowledged that the  $RSD_r$  value at the 0.042% level shown by the applicant's dossier (expressed as copy number ratio and corresponding to 0.10% in mass fraction) was 11.6%, based on sixteen replicates (Table 2A), and between 3.2% and 6.5% based on triplicates in the transferability study (Table 2B), hence below the maximum value of 25% required by the ENGL. The EURL GMFF therefore concluded that it could accept the applicant's data on method performance;

- at step 3 of the validation process (experimental testing of samples and methods), the EURL GMFF determined the  $RSD_r$  % value at the level of 0.1% in mass fraction of GM-material (corresponding to 0.039% expressed in terms of copy number ratio to haploid genome copy numbers). The experiments were carried out under repeatability conditions on fifteen replicates. The  $RSD_r$  resulted to range between 17% and 25% (Table 8, 9 and 10) depending on the qPCR platform applied, hence also below 25%;

- the collaborative study (step 4 of the validation process) established that over the twelve participating laboratories at the level of 0.1% related to mass fraction of GM-material the  $RSD_r$  of the method was 15%, therefore also below 25% and well in line with the previous data.

The outcome of the different steps is summarised in Table 14.

Table 14. Precision of the event-specific method for quantitative detection of DP51291 at or around 0.1% level related to mass fractions of GM material.

Source	$RSD_r$ %	GM %
Applicant's method optimisation	11.6%	0.042%*
Applicant's transferability study	3.2 – 6.5%	0.042%*
EURL GMFF tests	17 - 25%	0.1%
Collaborative study	15%	0.1%

\* expressed as copy number ratio

Based on the results of the EURL GMFF in-house verification and of the international collaborative study, it is concluded that the method  $RSD_r$  % is lower than 25% at the level of 0.1% related to mass fraction of GM material, hence the method meets the requirement laid down in Regulation (EU) No 619/2011.

## 7 Conclusion

The method provided by the applicant has been validated in accordance to the EURL GMFF validation process, respecting all requirements of the relevant EU legislation and international standards for method validation.

This validation study confirmed that the method is applicable to the control samples provided by the applicant (see paragraph 4.1), in accordance with the requirements of Annex I-3.C.2 to Commission Regulation (EU) No 503/2013 and (EU) No 619/2011 and meets all method performance requirements established by the ENGL and the EURL GMFF. The method is therefore valid to be used for regulatory purposes, including the quantification of low level presence of 0.1% (m/m) of the GM event. It can be assumed that it is applicable to any appropriately extracted maize genomic DNA.

In any case the user of the method is advised to verify the quality of the extracted genomic DNA in order to ensure that it is suitable for the subsequent PCR analysis. This is particularly relevant for more complex matrices of samples from food and feed products.

The validated method is described in detail as “Validated Method” at <https://gmo-crl.jrc.ec.europa.eu/method-validations> and in Annex 1.

## 8 References

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## List of abbreviations and definitions

EURL GMFF	European Union Reference Laboratory for GM Food and Feed
PCR	Polymerase chain reaction
RT-PCR	Real-time PCR
dPCR	digital Polymerase chain reaction
ENGL	European Network of GMO Laboratories
LOD	Limit of Detection
LOQ	Limit of Quantification

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# Annex 1. Event-specific Method for the Quantification of Maize DP51291 by Real-time PCR

## **Validated Method**

Method development:

Corteva Agriscience Belgium B.V. (on behalf of Corteva Agrisciences LLC)

## 1. General information and summary of the methodology

This protocol describes an event-specific real-time quantitative TaqMan® PCR (polymerase chain reaction) procedure for the determination of the relative content of maize event DP51291 DNA to total maize DNA in a sample.

Template DNA extracted by means of suitable methods should be tested for quality and quantity prior to use in PCR. Tests for the presence of PCR inhibitors (e.g. monitor run of diluted series, use of DNA spikes) are also recommended to ensure suitability of the extracted DNA.

For the detection of GM event DP51291, an 80 bp fragment of the region spanning the 3' insert-to-plant junction in maize DP51291 is amplified using specific primers. PCR products are measured during each cycle (real-time) by means of a target-specific oligonucleotide probe labelled with FAM (6-carboxyfluorescein) as reporter dye at its 5' end and MGBNFQ™ (Minor Groove Binding Non-Fluorescent Quencher) as non-fluorescent quencher dye at its 3' end.

For the relative quantification of GM event DP51291, a maize taxon-specific method amplifies a 79 bp fragment of a maize HMG Protein A (*hmg*) endogenous gene (Accession number, GeneBank: AJ131373), using *hmg* gene-specific primers and a *hmg* gene-specific probe labelled with FAM (6-carboxyfluorescein) as reporter dye at its 5' end and BHQ-1 (Black Hole Quencher® 1) as non-fluorescent quencher dye at its 3' end.

The measured fluorescence signal passes a threshold value after a certain number of cycles. This threshold cycle is called the “Cq” value. For quantification of the amount of DP51291 DNA in a test sample, Cq values for DP51291 and *hmg* are determined for the sample. Standard curves are then used to estimate the relative amount of DP51291 DNA to total maize DNA.

## 2. Validation and performance characteristics

### 2.1 General

The method was optimised for suitable DNA extracted from genetically modified and conventional maize seeds and grain. Precision and trueness of the method were tested through an international collaborative ring trial using DNA samples at different GM contents.

### 2.2 Collaborative trial

The method was validated in an international collaborative study by the European Union Reference Laboratory for GM Food and Feed (EURL GMFF). The study was undertaken with twelve participating laboratories in November 2023.

A detailed validation report can be found at <https://gmo-crl.jrc.ec.europa.eu/method-validations>.

### 2.3 Limit of detection (LOD)

According to the method developer, the relative LOD of the method is at least 0.0084% (related to copies GM/total haploid genome copies/mass fraction of GM material) in 325 ng of total suitable maize DNA. The relative LOD was not assessed in the collaborative study.

## 2.4 Limit of quantification (LOQ)

According to the method developer, the relative LOQ of the method is at least 0.042% (related to copies GM/total haploid genome copies/mass fraction of GM material) in 325 ng of total suitable maize DNA. The lowest relative GM content of the target sequence included in the collaborative trial was 0.1% (mass fraction of GM-material).

## 2.5 Molecular specificity

The method exploits a unique DNA sequence in the region spanning the 3' insert-to-plant junction in maize DP51291 and is therefore event-specific for the event DP51291. This was confirmed in the validation study.

## 3. Procedure

### 3.1 General instructions and precautions

- The procedures require experience of working under sterile conditions.
- Laboratory organisation, e.g. “forward flow direction” during PCR-setup, should follow international guidelines, e.g. ISO 24276:2006.
- PCR reagents should be stored and handled in a separate room where no nucleic acids (with exception of PCR primers or probes) or DNA degrading or modifying enzymes have been handled previously. All handling of PCR reagents and controls requires dedicated equipment, especially pipettes.
- All the equipment should be sterilised prior to use and any residue of DNA should have been removed. All material used (e.g. vials, containers, pipette tips, etc.) must be suitable for PCR and molecular biology applications. They must be DNase-free, DNA-free, sterile and unable to adsorb protein or DNA.
- Filter pipette tips protected against aerosol should be used.
- Powder-free gloves should be used and changed regularly
- Laboratory benches and equipment should be cleaned periodically, with 10% sodium hypochlorite solution (bleach).
- Pipettes should be checked regularly for precision and calibrated, if necessary.
- All handling steps, unless specified otherwise, should be carried out at room temperature.
- In order to avoid repeated freeze/thaw cycles aliquots should be prepared.

### 3.2 Real-time PCR for quantitative analysis of maize event DP51291

#### 3.2.1 General

The real-time PCR set-up for the taxon (*hmg*) and the GMO (event DP51291) target sequences are carried out in separate vials. Multiplex qPCR (using differential fluorescent labels for the probes) has not been tested or validated by the EURL GMFF.

The method is developed for a total volume of 25 µL per reaction mixture for the GM (event DP51291) and the taxon (*hmg*) targets with the reagents as listed in Table 2 and Table 3.

### 3.2.2 Calibration

The calibration curves have to be established on at least five samples. The first point of the calibration curve (S1) should be established for a sample containing 10% maize DP51291 DNA in a total of 325 ng of maize DNA (corresponding to 119048 maize haploid genome copies with one haploid genome assumed to correspond to 2.73 pg of maize genomic DNA) (1). Standards S2 to S4 are to be prepared by serial dilutions (dilution factor 6 for samples S2-S3 and dilution factor 8 for standard S4) according to Table 1 below.

Table 1. Copy number values of the standard curve samples

Sample code	S1	S2	S3	S4
Total amount of maize DNA in reaction (ng) (*)	325	54	9.1	1.1
Maize haploid genome copies	119048	19841	3307	413
DP51291 copies	11905	1984	331	41

\* Total nanograms are rounded to the integral value

A calibration curve is to be produced by plotting the C<sub>q</sub> values against the logarithm of the target copy number for the calibration points. This can be done by means of spreadsheet software, e.g. Microsoft Excel, or directly by options available with the software.

The copy number measured for each unknown sample DNA is obtained by interpolation from the standard curves.

### 3.2.3 Real-time PCR set-up

1. Thaw, mix and centrifuge the components needed for the run. Keep thawed reagents on ice.
2. In two tubes on ice, add the components in the order mentioned below (except DNA) to prepare the reaction mixes for DP51291 (Table 2) and *hmg* (Table 3). Please note that additional volume is included in the total to cover pipetting variability due to the viscosity of the solution.

Table 2. Amplification reaction mixture in the final volume/concentration per reaction well for DP51291.

Component	Final concentration	µL/reaction
TaqMan® Universal PCR Master Mix (no UNG) (2x)	1x	12.5
DP-Ø51291-2 Forward Primer (10 µM)	600 nM	1.5
DP-Ø51291-2 Reverse Primer (10 µM)	600 nM	1.5
DP-Ø51291-2 Probe (*) (10 µM)	120 nM	0.30
Nuclease free water	-	4.2
DNA	-	5.0
Total reaction volume:		25 µL

\*TaqMan® probe labelled with 6-FAM at its 5'-end and MGBNFQ™ at its 3'-end

Table 3. Amplification reaction mixture in the final volume/concentration per reaction well for maize *hmg*.

Component	Final concentration	µL/reaction
TaqMan® Universal PCR Master Mix (no UNG) (2x)	1x	12.5
<i>hmg</i> primer1 (10 µM)	300 nM	0.75
<i>hmg</i> primer2 (10 µM)	300 nM	0.75
<i>hmg</i> probe (10 µM) (*) (10 µM)	180 nM	0.45
Nuclease free water	-	5.55
DNA	-	5.0
Total reaction volume:		25 µL

\*TaqMan® probe is labelled with 6-FAM at its 5'-end and BHQ1 at its 3'-end

3. Mix well and centrifuge briefly.
4. Prepare two 0.5 mL reaction tubes (one for DP51291 and one for *hmg*) for each DNA sample to be tested (standard curve samples, unknown samples and control samples).
5. Add into each reaction tube the amount of reaction mix for 3.5 PCR repetitions (70 µL for DP51291 and 70 µL for *hmg*). Add to each tube the correct amount of DNA for 3.5 PCR repetitions (17.5 µL DNA). The volume for the additional 0.5 repetition will ensure adequate volume when loading the samples. Vortex each tube for approx. 10 seconds. This step is mandatory to reduce to a minimum the variability among the repetitions of each sample.
6. Spin down the tubes. Aliquot 25 µL for DP51291 and for *hmg* in each well.
7. Place an optical cover on the reaction plate and briefly centrifuge the plate.

8. Place the reaction plate in the real-time PCR apparatus (possibly apply a compression pad, depending on the model), according to the manufacturer's instructions and your Standard Operating Procedures and start the run.
9. Select FAM as reporter dye for DP51291 and for *hmg*. Define MGBNFQ as non-fluorescent quencher dye for DP51291 and BHQ1 for *hmg*. Select ROX as the passive reference dye. Enter the correct reaction volume (25 µL).
10. Run the PCR with the cycling program described in Table 4. Users who plan to use the second derivative maximum analysis method (an option e.g. on Roche LC480 instruments) are advised to program 45 cycles instead of 40, in order to be able to quantify down to Cq 40.

Table 4. Cycling program for DP51291 / *hmg*.

Step	Stage	T (°C)	Time (s)	Acquisition	Cycles	
1	Initial denaturation	95	600	No	1	
2	Amplification	Denaturation	95	15	No	40 (**)
		Annealing & Extension	60	60	Yes	

\* UNG: Uracil-N-glycosylase

\*\* see comment above for users of second derivative maximum analysis method

### 3.3 Data analysis

After the real-time PCR, analyse the run following the procedure below:

After the real-time PCR, analyse the run following the procedure below:

- a) Set the threshold following the automatic or the manual mode. In the manual mode display the amplification curves of the event-specific target in logarithmic mode. Locate the threshold line in the area where the amplification profiles are parallel (exponential phase of PCR) and where there is no "fork effect" between repetitions of the same sample. Press the "update" button to ensure changes affect Cq values (only needed for some analysis software). Switch to the linear view mode by clicking on the Y axis of the amplification plot and check that the threshold previously set falls within the exponential phase of the curves.
- b) Set the baseline following the automatic or the manual mode. In the manual mode: determine the cycle number at which the threshold line crosses the first amplification curve and set the baseline three cycles before that value (e.g. earliest Cq = 25, set the baseline crossing at Cq = 25 - 3 = 22).
- c) Save the settings.
- d) Repeat the procedure described in a), b) and c) on the amplification plots of the taxon specific method.
- e) Save the settings and export all the data for further calculations.

### 3.4 Calculation of results

After having defined a threshold value within the logarithmic phase of amplification as described above, the instrument's software calculates the C<sub>q</sub> values for each reaction.

The standard curves are generated both for *hmg* and DP51291 by plotting the C<sub>q</sub> values measured for the calibration points against the logarithm of the DNA copy numbers and by fitting a linear regression line into these data.

Thereafter, the standard curves are used to estimate the DNA copy number in the unknown samples.

To obtain the percentage value of event DP51291 DNA in the unknown sample, the DP51291 copy number is divided by the copy number of the maize endogenous gene *hmg* and multiplied by 100 (GM% = DP51291 / *hmg* x 100).

## 4. Equipment and Materials

### 4.1 Equipment

- Real-time PCR instrument for plastic reaction vessels (glass capillaries are not recommended for the described buffer composition) and appropriate analysis software
- 96-well reaction plates
- Optical caps/adhesion covers
- Microcentrifuge
- Micropipettes
- Standard bench top centrifuge with rotor or standard microfuge fit for 0.5 mL reaction tubes, centrifuge for 96-Well reaction plates
- Vortex
- Racks for reaction tubes, also cooled
- 0.5, 1.5 mL and 5 or 15 mL DNase free reaction tubes

### 4.2 Reagents

- TaqMan<sup>®</sup> Universal PCR Master Mix (no UNG). Applied Biosystems Part No 4324020.

### 4.3 Primers and Probes

Table 5. Primers and probes for the DP51291 and *hmg* methods

	DP51291	<b>DNA Sequence (5' to 3')</b>	Length (nt)
Forward primer	DP-Ø51291-2 Forward Primer	CGC AAT GTG TTA TTA AGT TGT CTA AGC	27
Reverse primer	DP-Ø51291-2 Reverse Primer	CAC GGT TAG CTG TAC CAA ATG C	22
Probe	DP-Ø51291-2 Probe	6-FAM-TTT GTT TAC ACC ACA TAC ACG-MGBNFQ™	21
	<i>hmg</i>	<b>DNA Sequence (5' to 3')</b>	Length (nt)
Forward primer	<i>hmg</i> primer1	TTG GAC TAG AAA TCT CGT GCT GA	23
Reverse primer	<i>hmg</i> primer2	GCT ACA TAG GGA GCC TTG TCC T	22
Probe	<i>hmg</i> probe	6-FAM-CAA TCC ACA CAA ACG CAC GCG TA-BHQ1™	23

FAM: 6-carboxyfluorescein; MGBNFQ: Minor Groove Binding Non-Fluorescent Quencher; BHQ1: Black Hole Quencher.

### 5. References

1. Plant DNA C-values Database. Royal Botanic Gardens, Kew, <https://cvalues.science.kew.org/>



## List of abbreviations and definitions

EURL GMFF	European Union Reference Laboratory for GM Food and Feed
PCR	Polymerase chain reaction
RT-PCR	Real-time PCR
ENGL	European Network of GMO Laboratories
LOD	Limit of Detection
LOQ	Limit of Quantification

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