

# JRC VALIDATED METHODS, REFERENCE METHODS AND MEASUREMENTS REPORT

## Event-specific Method for the Quantification of Maize Line MON 88017 Using Real-time PCR

*Validation Report, Validated Method and DNA Extraction  
Corrected version 2*



European Union Reference Laboratory for  
Genetically Modified Food and Feed

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The corrections made in the new version are:

*In Report on the Validation of a DNA Extraction Method for Maize Seeds and Grains*

At Page 6

**5. PEG Precipitation Buffer (20% w/v) (store at room temperature)**

Changed to

**5. PEG Precipitation Buffer (20% w/v) (store at room temperature)**

- 20% w/v PEG (MW 8000)

- 2.5 M NaCl

#### Note:

Since 01/12/2009 the term "Community Reference Laboratory (CRL)" is changed into "European Union Reference Laboratory (EURL)".

Since 01/03/2009 to 31/06/2016 the JRC-unit that hosts the EURL GMFF is named "Unit for Molecular Biology and Genomics" instead of "Biotechnology and GMO Unit".

Since 01/07/2016 the JRC-unit that hosts the EURL GMFF is named "Food and feed compliance"



# Event-specific Method for the Quantification of Maize Line MON 88017 Using Real-time PCR

## Validation Report

13 October 2008

Corrected version 1 - 30/03/2010 (see page 2)

**Joint Research Centre  
Institute for Health and Consumer Protection  
Unit for Molecular Biology and Genomics**

### Executive Summary

The JRC as European Union Reference Laboratory for GM Food and Feed (EURL-GMFF), established by Regulation (EC) No 1829/2003, in collaboration with the European Network of GMO Laboratories (ENGL), has carried out a collaborative study to assess the performance of a quantitative event-specific method to detect and quantify the MON 88017 transformation event in maize DNA (unique identifier MON-88Ø17-3). The collaborative trial was conducted according to internationally accepted guidelines <sup>(1, 2)</sup>.

In accordance with Regulation (EC) No 1829/2003 of 22 September 2003 on genetically modified food and feed and with Regulation (EC) No 641/2004 of 6 April 2004 on detailed rules for the implementation of Regulation (EC) No 1829/2003, Monsanto provided the detection method and the samples (maize seeds containing the transformation event and conventional maize seeds). The JRC prepared the validation samples (calibration samples and blind samples at unknown GM percentage [DNA/DNA]). The collaborative trial involved twelve laboratories from nine European countries.

The results of the international collaborative trial met the ENGL performance requirements. The method is therefore considered applicable to the control samples provided, in accordance with the requirements of Annex I-2.C.2 to Commission Regulation (EC) No 641/2004.

The results of the collaborative study are made publicly available at <http://gmo-crl.jrc.ec.europa.eu>.

Correction from the previous version:

**Corrected version 1 - 30/03/2010**

**Page 8 §5 :**

*For the specific detection of maize event MON 88017 DNA, a 94-bp fragment ....*  
changed by

*For the specific detection of maize event MON 88017 DNA, a 95-bp fragment .....*

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## Report on Steps 1-3 of the Validation Process

Monsanto submitted the detection method and control samples for maize event MON 88017 (unique identifier MON-88Ø17-3) under Article 5 and 17 of Regulation (EC) No 1829/2003 of the European Parliament and of the Council "on genetically modified food and feed".

The European Union Reference Laboratory for GM Food and Feed (EURL-GMFF), following reception of the documentation and material, including control samples, (step 1 of the validation process) carried out the scientific assessment of documentation and data (step 2) in accordance with Commission Regulation (EC) No 641/2004 "on detailed rules for the implementation of Regulation (EC) No 1829/2003 of the European Parliament and of the Council as regards the application for the authorisation of new genetically modified food and feed, the notification of existing products and adventitious or technically unavoidable presence of genetically modified material which has benefited from a favourable risk evaluation" and according to its operational procedures ("Description of the EURL-GMFF Validation Process", <http://gmo-crl.jrc.ec.europa.eu/guidancedocs.htm>).

The scientific assessment focused on the method performance characteristics assessed against the method acceptance criteria set out by the European Network of GMO Laboratories and listed in the "Definition of Minimum Performance Requirements for Analytical Methods of GMO Testing" (<http://gmo-crl.jrc.ec.europa.eu/guidancedocs.htm>) (see Annex 1 for a summary of method acceptance criteria and method performance requirements). During step 2, three scientific assessments were performed and requests of complementary information addressed to the applicant. Upon reception of complementary information, the scientific evaluation of the detection method for event MON 88017 was positively concluded in March 2006.

Between February 2007 and June 2007, the EURL-GMFF verified experimentally the method characteristics (step 3, experimental testing of samples and methods) by quantifying five blind GM levels within the range 0.09%-8% on a genome copy number basis. The experiments were performed under repeatability conditions and demonstrated that the PCR efficiency, linearity, trueness and precision of the quantifications were within the limits established by the ENGL. The DNA extraction module of the method was tested on samples of food and feed.

A Technical Report summarising the results of tests carried out by the EURL-GMFF (step 3) is available on request.

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## 1. Introduction

Monsanto submitted the detection method and control samples for maize event MON 88017 (unique identifier MON-88Ø17-3) under Article 5 and 17 of Regulation (EC) No 1829/2003 of the European Parliament and of the Council "on genetically modified food and feed".

The Joint Research Centre (JRC, Molecular Biology and Genomics Unit of the Institute for Health and Consumer Protection) as European Union Reference Laboratory for GM Food and Feed (see Commission Regulation EC (No) 1829/2003) organised the international collaborative study for the method of detection and quantification of MON 88017 maize. The study involved twelve laboratories from nine European countries, as listed in Annex II ("National reference laboratories assisting the EURL-GMFF for testing and validation of methods for detection") of Commission Regulation (EC) No 1981/2006 of 22 December 2006.

Upon reception of method, samples and related data (step 1), the JRC carried out the assessment of the documentation (step 2) and the in-house evaluation of the method (step 3) according to the requirements of Commission Regulation (EC) No 641/2004 and following its operational procedures.

The internal experimental evaluation of the method was carried out between February 2007 and June 2007.

Following the evaluation of the data and the results of the in-house laboratory tests, the international collaborative study was organised (step 4) and took place in July 2007.

A method for DNA extraction from maize seeds, submitted by the applicant, was evaluated by the EURL-GMFF; laboratory testing of the method was carried out between February and October 2007 in order to confirm its performance characteristics. The protocol for DNA extraction and a report on method testing is available at <http://gmo-crl.jrc.ec.europa.eu>.

The operational procedure of the collaborative study included the following module:

- ✓ Quantitative real-time PCR (Polymerase Chain Reaction). The methodology is an event-specific real-time quantitative TaqMan<sup>®</sup> PCR procedure for the determination of the relative content of event MON 88017 DNA to total maize DNA. The procedure is a simplex system, in which a maize *hmg* (*high mobility group*) endogenous assay (reference gene) and the target assay (MON 88017) are performed in separate wells.

The international collaborative study was carried out in accordance with the following internationally accepted guidelines:

- ✓ ISO 5725 (1994).
- ✓ The IUPAC "Protocol for the design, conduct and interpretation of method-performance studies" (Horwitz, 1995).

## 2. Selection of participating laboratories

As part of the international collaborative study the method was tested in twelve laboratories to determine its performance.

On 11<sup>th</sup> July 2007 the EURL-GMFF invited all National Reference Laboratories nominated under Commission Regulation (EC) No 1981/2006 of 22 December 2006 and listed in Annex II ("National reference laboratories assisting the EURL-GMFF for testing and validation of methods for detection") of that Regulation to express the availability to participate in the validation study of the quantitative real-time PCR method for the detection and quantification of maize GM event MON 88017.

Twenty-seven laboratories expressed in writing their willingness to participate, two declined the invitation, while forty-three did not answer. The EURL-GMFF performed a random selection of twelve laboratories out of those that responded positively to the invitation, making use of a validated software application.

Clear guidance was given to the selected laboratories with regards to the standard operational procedures to follow for the execution of the protocol. The participating laboratories are listed in Table 1.

Table 1. Laboratories participating in the validation of the detection method for maize MON 88017.

Laboratory	Country
Agricultural Institute of Slovenia	SI
Austrian Agency for Health and Food Safety, Competence Centre Biochemistry	AT
Central Agricultural Office, Directorate Food and Feed Safety, Central Feed Investigation Laboratory - National Reference Laboratory	HU
Crop Research Institute - Reference Laboratory for GMO Detection and DNA fingerprinting	CZ
Federal Institute for Risk Assessment	DE
National Food Administration	SE
National Institute of Engineer, Technology and Innovation - Food Industry Laboratory	PT
National Laboratory of Plant Protection	FR
Saxon State Institute for Agriculture, Department for Agricultural Analysis	DE
State Institute of Chemical and Veterinarian Analysis	DE
State Laboratory for examination of Food, Drugs and Epizootics of Berlin	DE
The Food and Consumer Product Safety Authority	NL



### 3. Materials

For the validation of the quantitative event-specific method, genomic DNA was extracted from samples consisting of:

- i) seeds of maize harbouring the MON 88017 event (Line DKC51-43, Lot number GLP-0409-15525-S) and;
- ii) seeds of conventional maize (Line EXP258, lot number GLP-0409-15528-S)

Samples were provided by the applicant in accordance to the provisions of Regulation (EC) No 1829/2003, Art 2.11 [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)].

Samples containing mixtures of 100% MON 88017 maize and non-GM maize genomic DNA at different GMO concentrations were prepared by the EURL-GMFF, using the control samples provided, in a constant amount of total maize DNA.

Participants received the following materials:

- ✓ Five calibration samples (150 µL of DNA solution each) for the preparation of the standard curve, labelled from S1-1605 to S5-1605.
- ✓ Twenty unknown DNA samples (80 µL of DNA solution each), labelled from U1-1605 to U20-1605.
- ✓ Reaction reagents:
 

<input type="checkbox"/> Universal PCR Master Mix 2X, 2 vials:		5 mL each vial
<input type="checkbox"/> TaqMan buffer A (10X):		800 µL
<input type="checkbox"/> MgCl <sub>2</sub> (25 mM):		2100 µL
<input type="checkbox"/> dNTP mix (10 mM each):		160 µL
<input type="checkbox"/> AmpliTaq Gold® polymerase (5 U/µL):		80 µL
<input type="checkbox"/> Sterile distilled water:		9 mL
- ✓ Primers and probes (1 tube each) as follows:
 

<i>hmg reference system</i>		
<input type="checkbox"/> <i>hmg</i> primer forward	(10 µM):	240 µL
<input type="checkbox"/> <i>hmg</i> primer reverse	(10 µM):	240 µL
<input type="checkbox"/> <i>hmg</i> TaqMan® probe	(5 µM):	260 µL
 <i>MON 88017 system</i>		
<input type="checkbox"/> MON88017 primer forward	(10 µM):	240 µL
<input type="checkbox"/> MON88017 primer reverse	(10 µM):	240 µL
<input type="checkbox"/> MON88017 TaqMan® probe	(5 µM):	160 µL

## 4. Experimental design

Twenty unknown samples, representing five GM levels, were used in the validation study (Table 2). On each PCR plate, the samples were analysed with the MON 88017 specific system and with the *hmg* specific system. In total, two plates were run per participating laboratory and four replicates for each GM level were analysed. PCR analysis was performed in triplicate for all samples. Participating laboratories carried out the determination of the GM% according to the instructions provided in the protocol and using the electronic tool provided (Excel spreadsheet).

Table 2. MON 88017 GM contents

MON 88017 GM% (GM copy number/maize genome copy number x 100)
0.09
0.50
0.90
5.00
8.00

## 5. Method

### *Description of operational steps followed*

For the specific detection of event MON 88017 DNA, a 95-bp fragment of the integration region of the construct inserted into the plant genome (3' insert-to-plant junction) is amplified using two specific primers. PCR products are measured at each cycle (real-time) by means of a target-specific oligonucleotide probe labelled with FAM dye and TAMRA as quencher dye.

For the relative quantification of event MON 88017 DNA, a maize-specific reference system amplifies a 79-bp fragment of the maize endogenous gene *hmg* (*high mobility group*), using a two *hmg* gene-specific primers and a *hmg* gene-specific probe labelled with FAM and TAMRA.

Standard curves are generated for both the MON 88017 and the *hmg* specific systems by plotting the Ct 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 unknown sample DNA by interpolation from the standard curves.

For relative quantification of event MON 88017 DNA in a test sample, the MON 88017 copy number is divided by the copy number of the maize reference gene (*hmg*) and multiplied by 100 to obtain the percentage value (GM% = MON 88017 / *hmg* x 100).

The calibration sample S1 was prepared by mixing the appropriate amount of MON 88017 DNA in control non-GM maize DNA to obtain a 10% GM MON 88017 in a total of 200 ng maize DNA.

Samples S2 and S3 were prepared by fourfold serial dilution from the S1 sample and samples S4 and S5 were prepared by threefold serial dilution from the S3 sample.

The absolute copy numbers of the calibration curve samples are determined by dividing the sample DNA weight (nanograms) by the published average 1C value for maize genome (2.725 pg)<sup>(3)</sup>. The copy number values used in the quantification, the GM contents of the calibration samples and total DNA quantity used in PCR are provided in Table 3 (% GM calculated considering the 1C value for maize genome as 2.725 pg)<sup>(3)</sup>.

Table 3. % GM values of the standard curve samples.

Sample code	S1	S2	S3	S4	S5
Total amount of DNA in reaction (ng / 4 µL)	200	50	12.5	4.2	1.4
Maize genome copies	73394	18349	4587	1529	510
MON 88017 maize copies	7339	1835	459	153	51

## 6. Deviations reported

Nine laboratories reported no deviations from the protocol.

One laboratory entered a PCR reaction volume of 30 µL instead of 50 µL.

One laboratory used MicroAmp® Reaction Tubes with cap; the same laboratory, using an iCycler (Biorad), replaced the the signal of ROX, the passive reference, by the well factors obtained from an experimental plate.

One laboratory did not set the ramping rate to 1°C / second.

## 7. Summary of results

### *PCR efficiency and linearity*

The values of the slopes [from which the PCR efficiency is calculated using the formula  $(((10^{-1/\text{slope}})-1) \times 100)$  of the reference curve and of the  $R^2$  (expressing the linearity of the regression) reported by participating laboratories for the MON 88017 system and the *hmg* reference system are summarised in Table 4.

Table 4. Values of reference curve slope, PCR efficiency and linearity ( $R^2$ )

LAB	MON 88017			<i>hmg</i>		
	Slope	PCR Efficiency (%)	Linearity ( $R^2$ )	Slope	PCR Efficiency (%)	Linearity ( $R^2$ )
1	-3.60	89	0.99	-3.34	99	0.98
	-3.67	87	0.97	-3.24	104	0.99
2	-3.30	101	1.00	-3.21	105	0.99
	-3.42	96	0.98	-3.06	112	1.00
3	-3.61	89	0.98	-3.09	111	1.00
	-3.17	107	0.99	-3.01	115	0.99
4	-3.02	114	0.98	-2.86	124	0.97
	-3.47	94	0.99	-3.13	109	1.00
5	-3.74	85	0.99	-3.27	102	0.99
	-3.72	86	0.99	-3.20	105	0.99
6	-3.43	96	0.99	-3.04	113	0.99
	-3.38	98	1.00	-3.04	113	0.99
7	-3.54	92	0.98	-3.72	86	1.00
	-4.35	70	0.92	-4.00	78	1.00
8	-3.53	92	1.00	-3.20	105	1.00
	-3.43	96	0.99	-3.17	107	0.99
9	-3.57	91	0.99	-3.13	109	0.99
	-3.31	101	1.00	-3.05	113	0.99
10	-3.43	96	1.00	-3.12	109	0.99
	-3.63	89	0.99	-3.14	108	0.99
11	-3.53	92	0.98	-3.17	107	0.99
	-3.21	105	0.99	-3.13	109	0.99
12	-3.40	97	0.98	-3.10	110	1.00
	-3.69	87	0.99	-3.16	107	1.00
Mean	-3.51	94	0.99	-3.19	107	0.99

The mean PCR efficiency was 107% for the *hmg* reference system and 94% for the MON 88017 system. The linearity of the method was on average 0.99 for both systems. Data reported confirm the appropriate performance characteristics of the method tested in terms of efficiency and linearity.

**GMO quantification**

Table 5 shows the mean values of the four replicates for each GM level as provided by all laboratories. Each mean value is the average of three PCR repetitions.

Table 5. GM% mean values determined by laboratories for unknown samples.

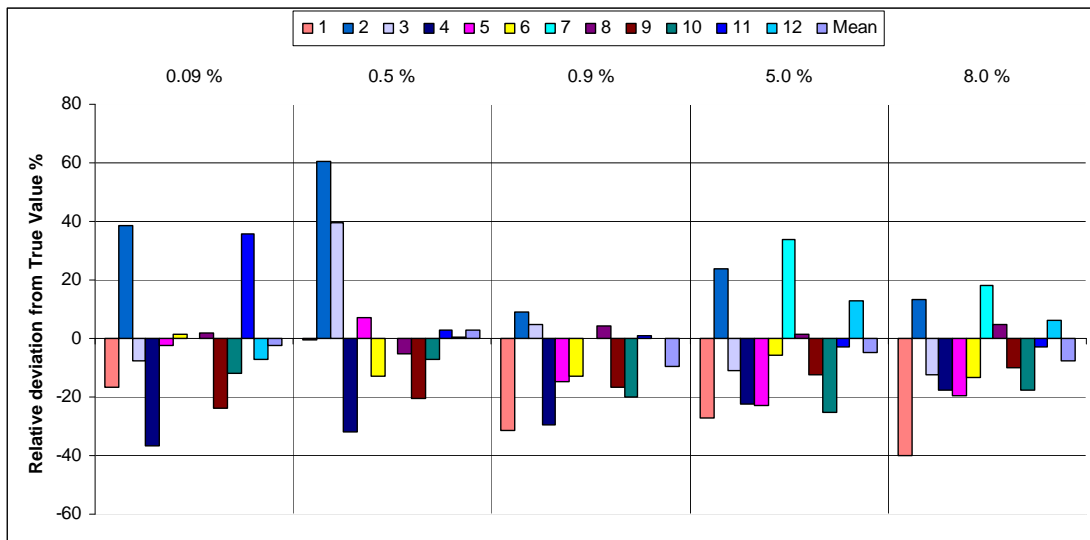
LAB	Sample GMO content (GM% = GM copy number/maize genome copy number x 100)																			
	0.09				0.5				0.9				5.0				8.0			
	REP 1	REP 2	REP 3	REP 4	REP 1	REP 2	REP 3	REP 4	REP 1	REP 2	REP 3	REP 4	REP 1	REP 2	REP 3	REP 4	REP 1	REP 2	REP 3	REP 4
1	0.09	0.09	0.09	0.03	0.44	0.57	0.38	0.59	0.48	0.84	0.56	0.59	2.84	3.70	2.81	5.27	7.55	2.44	5.05	4.09
2	0.15	0.17	0.09	0.08	0.76	0.83	0.83	0.80	1.14	1.17	0.70	0.92	5.24	5.74	7.34	6.44	11.47	6.50	9.96	8.35
3	0.07	0.11	0.09	0.07	0.68	0.63	0.81	0.67	1.32	1.08	0.64	0.73	3.61	4.13	6.26	3.81	6.78	7.85	6.39	7.06
4	0.07	0.07	0.03	0.06	0.38	0.27	0.43	0.27	0.75	0.64	0.60	0.55	3.39	3.78	2.64	5.72	7.11	5.91	5.42	7.95
5	0.11	0.08	0.08	0.08	0.52	0.57	0.48	0.57	0.93	0.85	0.55	0.73	3.13	3.25	4.72	4.33	7.30	5.64	6.98	5.81
6	0.07	0.08	0.10	0.12	0.42	0.40	0.49	0.43	0.87	0.63	0.91	0.73	5.04	5.30	4.14	4.35	6.34	6.86	7.12	7.36
7	0.37	0.13	0.12	0.11	1.35	0.72	1.04	0.67	1.28	2.29	0.94	1.32	7.07	6.70	6.70	6.28	9.15	6.38	9.58	12.69
8	0.08	0.09	0.08	0.11	0.42	0.56	0.41	0.51	0.88	1.07	0.88	0.93	4.98	4.68	5.57	5.07	8.05	9.03	8.12	8.29
9	0.03	0.07	0.10	0.08	0.33	0.43	0.33	0.49	0.79	0.69	0.71	0.81	4.73	4.26	4.36	4.19	7.47	7.61	7.28	6.50
10	0.11	0.09	0.06	0.06	0.48	0.46	0.46	0.46	0.79	0.83	0.65	0.61	3.34	3.13	4.46	4.02	8.15	5.30	6.94	6.00
11	0.14	0.12	0.11	0.11	0.41	0.61	0.59	0.45	0.93	0.89	0.79	1.03	4.53	5.25	4.58	5.10	8.05	8.45	7.67	6.98
12	0.09	0.10	0.06	0.07	0.54	0.42	0.47	0.57	0.84	0.95	0.98	0.82	4.85	4.34	5.26	8.11	9.24	8.27	8.43	8.02

In Figure 1 the relative deviation from the true value for each GM level tested is shown for each laboratory. The coloured bars represent the relative GM quantification obtained by the participating laboratories; the purple represents the overall mean for each GM level.

As observed in Figure 1, the relative deviations from the true values are slightly negative for GM levels of 0.09%, 0.9, 5% and 8%, and in general very limited or close to zero. More specifically, two laboratories over-estimated significantly the true value at the 0.09% and 0.5% GM levels, while one laboratory under-estimated the true value significantly at the 0.09% and 8.0% GM levels. Other laboratories showed a negative bias around the accepted limit (25%) at various GM levels.

Overall, the bias % was below 10% at all GM levels tested, indicating a very satisfactory trueness of the method.

Figure 1. Relative deviation (%) from the true value of MON 88017 for all laboratories



## 8. Method performance requirements

Among the performance criteria established by the ENGL and adopted by the EURL-GMFF (<http://gmo-crl.jrc.ec.europa.eu/guidancedocs.htm>, see also Annex 1), repeatability and reproducibility are assessed through an international collaborative trial, carried out with the support of twelve European laboratories (see Table 1). Table 6 illustrates the estimation of repeatability and reproducibility at various GM levels, according to the range of GM percentages tested during the collaborative trial.

The relative reproducibility standard deviation ( $RSD_R$ ), that describes the inter-laboratory variation, should be below 33% 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 6, the method satisfies this requirement at all GM levels tested, with the highest value of  $RSD_R$  (%) equal to 33% at the 0.09% GM level.

Table 6 also reports the relative repeatability standard deviation ( $RSD_r$ ), as estimated for each GM level. In order to accept methods for collaborative study evaluation, the EURL-GMFF requires that the  $RSD_r$  value is below 25%, as indicated by the ENGL (Definition of Minimum Performance Requirements for Analytical Methods of GMO Testing" (<http://gmo-crl.jrc.ec.europa.eu/guidancedocs.htm>)).

Table 6. Summary of MON 88017 validation results.

Unknown sample GM%	Expected value (GM0 %)				
	0.09	0.50	0.90	5.00	8.00
Laboratories having returned results	12	12	12	12	12
Samples per laboratory	4	4	4	4	4
Number of outliers	1	1	1	0	0
Reason for exclusion	1 C. test	1 C. test	1 C. test	-	-
Mean value	<b>0.09</b>	<b>0.51</b>	<b>0.81</b>	<b>4.76</b>	<b>7.39</b>
Relative repeatability standard deviation, RSD <sub>r</sub> (%)	28	13	19	19	18
Repeatability standard deviation	0.02	0.07	0.15	0.91	1.32
Relative reproducibility standard deviation, RSD <sub>R</sub> (%)	33	28	23	27	23
Reproducibility standard deviation	0.03	0.14	0.19	1.26	1.74
Bias (absolute value)	0.00	0.01	-0.09	-0.24	-0.61
Bias (%)	-2.6	2.9	-9.6	-4.8	-7.6

C = Cochran's test; identification and removal of outliers through Cochran and Grubbs tests, according to ISO 5725-2. Bias is estimated according to ISO 5725 data analysis protocol.

As can be observed from the values reported in Table 6, the method showed a relative repeatability standard deviation below 25% from 0.5% to 8%, with a minor deviation at the lowest GM level (i.e. 0.09%), for which the RSD<sub>r</sub> value is 28%.

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. In this case the method fully satisfies this requirement across the entire dynamic range tested; in fact, the highest value of bias (%) is -10%% at the 0.9% level, well within the acceptance criterion.

## 9. Conclusions

The overall method performance has been evaluated with respect to the method acceptance criteria and method performance requirements recommended by the ENGL (as detailed under <http://gmo-crl.jrc.ec.europa.eu/guidancedocs.htm>). The method acceptance criteria were reported by the applicant and used to evaluate the method prior to the international collaborative study (see Annex 1 for a summary of method acceptance criteria and method performance requirements).

The results obtained during the collaborative study indicate that the analytical module of the method submitted by the applicant complies with ENGL performance criteria, with a minor deviation of the RSD<sub>r</sub> value at 0.09% (28%).

The method is therefore applicable to the control samples provided (see paragraph 3 "Materials"), in accordance with the requirements of Annex I-2.C.2 to Commission Regulation (EC) No 641/2004.

## 10. Quality assurance

The EURL-GMFF carries out all operations according to ISO 9001:2000 (certificate number: CH-32232) and ISO 17025:2005 (certificate number: DAC-PL-0459-06-00) [DNA extraction, qualitative and quantitative PCR in the area of Biology (DNA extraction and PCR method validation for the detection and identification of GMOs in food and feed materials)]

## 11. References

1. Horwitz W., 1995. Protocol for the design, conduct and interpretation of method performance studies. *Pure and Appl. Chem.* 67: 331-343.
2. International Standard (ISO) 5725. 1994. Accuracy (trueness and precision) of measurement methods and results. International Organization for Standardization, Genève, Switzerland.
3. Arumuganathan K., Earle ED., 1991. Nuclear DNA content of some important plant species. *Plant Molecular Biology Reporter* 9: 208-218.



## 12. Annex 1: method acceptance criteria and method performance requirements as set by the European Network of GMO Laboratories (ENGL)

Method Acceptance Criteria should be fulfilled at the moment of submission of a method (Phase 1: acceptance for the collaborative study).

Method Performance Requirements should be fulfilled in a collaborative study in order to consider the method as fit for its purpose (Phase 2: evaluation of the collaborative study results).

### **Method Acceptance Criteria**

#### ***Applicability***

Definition: the description of analytes, matrices, and concentrations to which a method can be applied.

Acceptance Criterion: the applicability statement should provide information on the scope of the method and include data for the indices listed below for the product/s for which the application is submitted. The description should also include warnings to known interferences by other analytes, or inapplicability to certain matrices and situations.

#### ***Practicability***

Definition: the ease of operations, the feasibility and efficiency of implementation, the associated unitary costs (e.g. Euro/sample) of the method.

Acceptance Criterion: the practicability statement should provide indication on the required equipment for the application of the method with regards to the analysis *per se* and the sample preparation. An indication of costs, timing, practical difficulties and any other factor that could be of importance for the operators should be indicated.

#### ***Specificity***

Definition: property of a method to respond exclusively to the characteristic or analyte of interest.

Acceptance Criterion: the method should be event-specific and be functional only with the GMO or GM based product for which it was developed. This should be demonstrated by empirical results from testing the method with non-target transgenic events and non-transgenic material. This testing should include closely related events and cases where the limit of the detection is tested.

#### ***Dynamic Range***

Definition: the range of concentrations over which the method performs in a linear manner with an acceptable level of accuracy and precision.

Acceptance Criterion: the dynamic range of the method should include the 1/10 and at least 5 times the target concentration. Target concentration is intended as the threshold relevant for legislative

requirements. The acceptable level of accuracy and precision are described below. The range of the standard curve(s) should allow testing of blind samples throughout the entire dynamic range, including the lower (10%) and upper (500%) end.

### ***Accuracy***

Definition: the closeness of agreement between a test result and the accepted reference value.

Acceptance Criterion: the accuracy should be within  $\pm 25\%$  of the accepted reference value over the whole dynamic range.

### ***Amplification Efficiency***

Definition: the rate of amplification that leads to a theoretical slope of  $-3.32$  with an efficiency of 100% in each cycle. The efficiency of the reaction can be calculated by the following equation: Efficiency =  $[10^{(1/\text{slope})} - 1]$

Acceptance Criterion: the average value of the slope of the standard curve should be in the range of  $(-3.1 \geq \text{slope} \geq -3.6)$

### ***R<sup>2</sup> Coefficient***

Definition: the R<sup>2</sup> coefficient is the correlation coefficient of a standard curve obtained by linear regression analysis.

Acceptance Criterion: the average value of R<sup>2</sup> should be  $\geq 0.98$ .

### ***Repeatability Standard Deviation (RSD<sub>r</sub>)***

Definition: the standard deviation of test results obtained under repeatability conditions. Repeatability conditions are conditions where test results are obtained with the same method, on identical test items, in the same laboratory, by the same operator, using the same equipment within short intervals of time.

Acceptance Criterion: the relative repeatability standard deviation should be below 25% over the whole dynamic range of the method.

*Note:* estimates of repeatability submitted by the applicant should be obtained on a sufficient number of test results, at least 15, as indicated in ISO 5725-3 (1994).

### ***Limit of Quantitation (LOQ)***

Definition: the limit of quantitation is the lowest amount or concentration of analyte in a sample that can be reliably quantified with an acceptable level of precision and accuracy.

Acceptance Criterion: LOQ should be less than 1/10<sup>th</sup> of the value of the target concentration with an RSD<sub>r</sub>  $\leq 25\%$ . Target concentration should be intended as the threshold relevant for legislative requirements. The acceptable level of accuracy and precision are described below.

### ***Limit of Detection (LOD)***

Definition: the limit of detection is the lowest amount or concentration of analyte in a sample, which can be reliably detected, but not necessarily quantified, as demonstrated by single laboratory validation.

Acceptance Criterion: LOD should be less than  $1/20^{\text{th}}$  of the target concentration. Experimentally, quantitative methods should detect the presence of the analyte at least 95% of the time at the LOD, ensuring  $\leq 5\%$  false negative results. Target concentration should be intended as the threshold relevant for legislative requirements.

### ***Robustness***

Definition: the robustness of a method is a measure of its capacity to remain unaffected by small, but deliberate deviations from the experimental conditions described in the procedure.

Acceptance Criterion: the response of an assay with respect to these small variations should not deviate more than  $\pm 30\%$ . Examples of factors that a robustness test could address are: use of different instrument type, operator, brand of reagents, concentration of reagents, and temperature of reaction.

## **Method Performance Requirements**

### ***Dynamic Range***

Definition: in the collaborative trial the dynamic range is the range of concentrations over which the reproducibility and the trueness of the method are evaluated with respect to the requirements specified below.

Acceptance Criterion: the dynamic range of the method should include the  $1/10$  and at least five times the target concentration. Target concentration should be intended as the threshold relevant for legislative requirements.

### ***Reproducibility Standard Deviation ( $RSD_R$ )***

Definition: the standard deviation of test results obtained under reproducibility conditions. Reproducibility conditions are conditions where test results are obtained with the same method, on identical test items, in different laboratories, with different operators, using different equipment. Reproducibility standard deviation describes the inter-laboratory variation.

Acceptance Criterion: the relative reproducibility standard deviation should be below 35% at the target concentration and over the entire dynamic range. An  $RSD_R < 50\%$  is acceptable for concentrations below 0.2%.

### ***Trueness***

Definition: the closeness of agreement between the average value obtained from a large series of test results and an accepted reference value. The measure of trueness is usually expressed in terms of bias.

Acceptance Criterion: the trueness should be within  $\pm 25\%$  of the accepted reference value over the whole dynamic range.



# **Event-specific Method for the Quantification of Maize Line MON 88017 Using Real-time PCR**

## **Validated Method**

**13 October 2008**

Corrected version 1 - 30/03/2010 (see page 2)

**Joint Research Centre  
Institute for Health and Consumer Protection  
Molecular Biology and Genomics Unit**

### **Method development:**

Monsanto Company

### **Collaborative trial:**

Community Reference Laboratory for GM Food and Feed (CRL-GMFF)  
Molecular Biology and Genomics Unit

Correction from the previous version:

**Corrected version 1 - 30/03/2010**

**Page 4 §1 :**

...

*For the specific detection of maize event MON 88017 DNA, a 94-bp fragment ....  
(located at the 5' flanking DNA region)*

changed by

...

*For the specific detection of maize event MON 88017 DNA, a 95-bp fragment .....  
(located at the 3' flanking DNA region)*

**Address of contact laboratory:**

European Commission, Joint Research Centre

Institute for Health and Consumer Protection (IHCP)

Molecular Biology and Genomics Unit – Community Reference Laboratory for GM Food and Feed

Via Fermi 2749, 21027 Ispra (VA) - Italy

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## 1. General information and summary of the method

This protocol describes an event-specific real-time quantitative TaqMan<sup>®</sup> PCR procedure for the determination of the relative content of event MON 88017 DNA to total maize DNA in a sample.

The PCR assay was optimised for use in real-time PCR instruments for plastic reaction vessels.

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

For the specific detection of maize event MON 88017 DNA, a 95-bp fragment of the integration region of the construct inserted into the plant genome (located at the 3' flanking DNA region) is amplified using two specific primers. PCR products are measured at each cycle (real-time) by means of a target-specific oligonucleotide probe labelled with the fluorescent dye 6-FAM as a reporter at its 5' end and with TAMRA as a quencher dye at its 3' end. The 5' nuclease activity of the Taq DNA polymerase results in the specific cleavage of the probe, leading to increased fluorescence, which is then monitored.

For the relative quantification of maize event MON 88017 DNA, a maize-specific reference system amplifies a 79-bp fragment of the maize endogenous *hmg* gene (*high mobility group*), using two specific primers and a *hmg* gene-specific probe labelled with 6-FAM and TAMRA as described above.

The measured fluorescence signal passes a threshold value after a certain number of cycles. This threshold cycle is called the "Ct" value. For quantification of the amount of event MON 88017 DNA in a test sample, MON 88017 and *hmg* Ct values are determined for the sample. Standard curves are then used to estimate the relative amount of maize event MON 88017 DNA to total maize DNA.

## 2. Validation status and performance characteristics

### 2.1 General

The method was optimised for suitable DNA extracted from maize seeds and grains containing mixtures of genetically modified and conventional maize.

The reproducibility and trueness of the method were tested through an international collaborative ring trial using DNA samples at different GMO contents (%).

## 2.2 Collaborative trial

The method was validated in an international collaborative study by the Joint Research Centre (JRC) of the European Commission. The study was undertaken with twelve laboratories in July 2007.

Each participant received twenty blind samples containing MON 88017 genomic DNA at five GM contents, ranging from 0.09% to 8.0%.

Each test sample was analysed by PCR in three repetitions. The study was designed as a blind quadruplicate collaborative trial; each laboratory received each level of GM MON 88017 in four unknown samples. Four replicates of each GM level were analysed on the same PCR plate.

A detailed validation report can be found at <http://gmo-crl.jrc.ec.europa.eu/statusofdoss.htm>

## 2.3 Limit of detection (LOD)

According to the data provided by the applicant, the relative LOD of the method is at least 0.045% in 200 ng of total maize DNA. The relative LOD was not assessed in collaborative study.

## 2.4 Limit of quantification (LOQ)

According to the data provided by the applicant, the relative LOQ of the method is at least 0.09% in 200 ng of total maize DNA. The lowest relative GM content of the target sequence included in the international collaborative study was 0.09%.

## 2.5 Molecular specificity

The method exploits a unique DNA sequence in the region of recombination between the insert and the plant genome. The sequence is specific to event MON 88017 and thus imparts event-specificity to the method.

The specificity of MON 88017 assay (forward/reverse primers and probe) was experimentally tested in real-time PCR by the applicant against DNA extracted from samples containing Roundup Ready<sup>®</sup> maize MON 88017 (positive control), Roundup Ready<sup>®</sup> canola (RT200), Roundup Ready<sup>®</sup> canola (RT73), conventional canola, Roundup Ready<sup>®</sup> maize (GA21), Roundup Ready<sup>®</sup> maize (NK603), YieldGard<sup>®</sup> Corn Borer maize (MON810), YieldGard<sup>®</sup> Rootworm maize (MON863), Lysine maize (LY038), conventional maize, Roundup Ready<sup>®</sup> cotton (MON 1445), Bollgard<sup>®</sup> cotton (MON 531), Bollgard<sup>®</sup> cotton (MON 757), BollgardII<sup>®</sup> cotton (MON 15985), Roundup Ready<sup>®</sup> Flex cotton (MON 88913), conventional cotton, Roundup Ready<sup>®</sup> soybean (40-3-2), conventional soybean, Roundup Ready<sup>®</sup> wheat (MON 71800), conventional wheat, lentil, sunflower, buckwheat, rye berries and peanut.



According to the applicant, none of the GM lines tested, except the positive control MON 88017, produced amplification signals.

The specificity of the maize reference assay *hmg* was experimentally tested by the applicant against DNA extracted from samples containing Roundup Ready® corn MON 88017, Roundup Ready® canola (RT200), Roundup Ready® canola (RT73), conventional canola, Roundup Ready® maize (GA21), Roundup Ready® maize (NK603), YieldGard® Corn Borer maize (MON810), YieldGard® Rootworm maize (MON863), Lysine maize (LY038), conventional maize, Roundup Ready® cotton (MON 1445), Bollgard® cotton (MON 531), Bollgard® cotton (MON 757), BollgardII® cotton (MON 15985), Roundup Ready® Flex cotton (MON 88913), conventional cotton, Roundup Ready® soybean (40-3-2), conventional soybean, Roundup Ready® wheat (MON 71800), conventional wheat, lentil, sunflower, buckwheat, rye berries and peanut.

Only the positive control maize line MON 88017 and Roundup Ready® maize (GA21), Roundup Ready® maize (NK603), YieldGard® Corn Borer maize (MON810), YieldGard® Rootworm maize (MON863), Lysine maize (LY038) and conventional maize produced amplification signals.

### 3. Procedure

#### 3.1 General instructions and precautions

- The procedures require sterile conditions working experience.
- 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.
- Equipment used should be sterilised prior to use and any residue of DNA should be removed. All material used (e.g. vials, containers, pipette tips, etc.) should be suitable for PCR and molecular biology applications; it should 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 frequently.
- Laboratory benches and equipment should be cleaned periodically with 10% sodium hypochloride solution (bleach).
- Pipettes should be checked regularly for precision and calibrated, if necessary.

- All handling steps - unless specified otherwise - should be carried out at 0–4°C.
- In order to avoid repeated freeze/thaw cycles aliquots should be prepared.

## 3.2 Real-time PCR for quantitative analysis of MON 88017 maize

### 3.2.1 General

The PCR set-up for the taxon specific target sequence (*hmg*) and for the GMO (event MON 88017) target sequence should be carried out in separate vials. Multiplex PCR (using differential fluorescent labels for the probes) has not been tested or validated.

The use of maximum 200 ng of template DNA per reaction well is recommended.

The method is developed, for MON 88017, in a total volume of 50 µL per reaction mixture with the reagents as listed in Table 1 and, for *hmg*, in a total volume of 25 µL per reaction mixture with the reagents as listed in and Table 2.

### 3.2.2 Calibration

The calibration curves consist of five samples. The first point of the calibration curves is a 10% MON 88017 in non-GM maize DNA for a total of 200 ng of DNA (corresponding to approximately 73394 maize genome copies with one genome assumed to correspond to 2.725 pg of haploid maize genomic DNA) <sup>(1)</sup>.

A calibration curve is produced by plotting the Ct values against the logarithm of the target copy number for the calibration points. This can be done e.g. by means of spreadsheet software, e.g. Microsoft Excel, or directly by options available with the sequence detection system software.

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

### 3.2.3 Real-time PCR set-up

1. Thaw, mix gently and centrifuge the required amount of components needed for the run. **Keep thawed reagents at 1-4°C on ice.**
2. In two reaction tubes (one for the MON 88017 system and one for the *hmg* system) on ice, add the following components (Tables 1 and 2) in the order mentioned below (except DNA) to prepare the master mixes.

Table 1. Amplification reaction mixture in the final volume/concentration per reaction well for the MON 88017 specific system.

Component	Final concentration	µL/reaction
TaqMan® Universal PCR Master Mix (2x)	1x	25
MON 88017 AF (10 µM)	150 nM	0.75
MON 88017 AR (10 µM)	150 nM	0.75
MON 88017 AP (5 µM)	50 nM	0.50
Nuclease free water	#	19
Template DNA (max 200 ng)	#	4.0
Total reaction volume:		50

Table 2. Amplification reaction mixture in the final volume/concentration per reaction well for the maize *hmg* reference system.

Component	Final concentration	µL/reaction
Buffer A (10x)	1x	2.5
<i>Hmg</i> F (10 µM)	300 nM	0.75
<i>hmg</i> R (10 µM)	300 nM	0.75
<i>hmg</i> P ( 5 µM)	160 nM	0.80
MgCl <sub>2</sub> (25 mM)	6.5 mM	6.5
dNTPs mix (10 mM)	200 µM	0.5
Ampli TAQ Gold	1.25 U/rnx	0.25
Nuclease free water	#	8.95
Template DNA (max 200 ng)	#	4.0
Total reaction volume:		25

- Mix gently and centrifuge briefly.
- Prepare two reaction tubes (one for the MON 88017 and one for the *hmg* master mixes) for each DNA sample to be tested (standard curve samples, unknown samples and control samples).
- Add to each reaction tube the correct amount of master mix (e.g. 46 x 3 = 138 µL master mix for three PCR repetitions for MON 88017 and 21 x 3 = 63 µL master mix for three PCR repetitions for *hmg*). Add to each tube the correct amount of DNA (e.g. 4 x 3 = 12 µL DNA for three PCR repetitions). Vortex each tubes for approx. 10 sec. This step is mandatory to reduce the variability among the repetitions of each sample to a minimum.

6. Spin down the tubes in a microcentrifuge. Aliquot 50  $\mu\text{L}$  in each well for MON 88017 and 25  $\mu\text{L}$  for *hmg*. Seal the reaction plate with optical cover or optical caps. Centrifuge the plate at low speed (e.g. approximately 250 x *g* for 1 minute at 4 °C to room temperature) to spin down the reaction mixture.
7. Place the plate into the instrument.
8. Run the PCR with cycling conditions described in Table 3:

Table 3. Cycling program for MON 88017 and maize *hmg* system

Step	Stage	T °C	Time (sec)	Acquisition	Cycles	
1	UNG	50 °C	120	No	1	
2	Initial denaturation	95 °C	600	No	1	
3	Amplification	Denaturation	95 °C	15	No	45
		Annealing & Extension	60 °C	60	Yes	

### 3.3 Data analysis

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

- a) Set the threshold: display the amplification curves of one system (e.g. MON 88017) 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 Ct values. 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 geometric phase of the curves.
- b) Set the baseline: 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 Ct = 25, set the baseline crossing at Ct = 25 – 3 = 22).
- c) Save the settings.
- d) Repeat the procedure described in a) and b) on the amplification plots of the other system (e.g. *hmg* system).
- e) Save the settings and export all the data to a text file 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 Ct values for each reaction.

The standard curves are generated both for the *hmg* and the MON 88017 specific systems by plotting the Ct 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 copy numbers in the unknown sample DNA.

For the determination of the amount of event MON 88017 DNA in the unknown sample, the MON 88017 copy number is divided by the copy number of the maize reference gene (*hmg*) and multiplied by 100 to obtain the percentage value ( $GM\% = \text{MON 88017}/hmg \times 100$ ).

## 4. Materials

### 4.1 Equipment

- Real-time PCR instrument for plastic reaction vessels (glass capillaries are not recommended for the described buffer composition)
- Plastic reaction vessels suitable for real-time PCR instrument (enabling undisturbed fluorescence detection)
- Analysis software
- Microcentrifuge
- Micropipettes
- Vortex
- Rack for reaction tubes
- 1.5/2.0 mL reaction tubes

### 4.2 Reagents

- TaqMan<sup>®</sup> Universal PCR Master Mix (2X). Applied Biosystems Part No. 4304437
- 0.5 M EDTA. Sigma Cat. No. E-7647-01-0
- PCR Nucleotide Mix (10mM dNTPs). Promega Cat. No. C114G
- TaqMan<sup>®</sup> 1000X Rxn Gold/Buffer A Pack. Applied Biosystems Cat. No. 4304441
- AmpliTaq Gold Polymerase. Applied Biosystems Cat. No. N808-0244
- Nuclease-free water. Sigma Cat. No. W-4502
- 1 M Tris-HCl, pH 8.0. Sigma Cat. No. T-3038

### 4.3 Primers and Probes

Name	Oligonucleotide DNA Sequence (5' to 3')
MON 88017 target sequence	
MON 88017 AF	5' – GAG CAG GAC CTG CAG AAG CT – 3'
MON 88017 AR	5' – TCC GGA GTT GAC CAT CCA – 3'
MON 88017 AP (Probe)	6-FAM-TCC CGC CTT CAG TTT AAA CAG AGT CGG GT-TAMRA
Reference gene hmg target sequence	
<i>Hmg F</i>	5' – TTG GAC TAG AAA TCT CGT GCT GA– 3'
<i>Hmg R</i>	5' – GCT ACA TAG GGA GCC TTG TCC T– 3'
<i>hmg P</i> (Probe)	6-FAM- CAA TCC ACA CAA ACG CAC GCG TA -TAMRA

## 5. References

1. Arumuganathan K., Earle E. D., 1991. Nuclear DNA content of some important plant species. *Plant Molecular Biology Reporter* 9: 208-218.



EUROPEAN COMMISSION  
DIRECTORATE-GENERAL  
JOINT RESEARCH CENTRE  
Directorate F - Health, Consumers and Reference Materials  
Food & Feed Compliance



# **Report on the Validation of a DNA Extraction Method for Maize Seeds and Grains**

**13 October 2008  
Corrected version 2 – 26 July 2017**

**JOINT RESEARCH CENTRE  
Health, Consumers and Reference Materials  
Food & Feed Compliance**

## **Method development:**

Monsanto Company

## **Method testing and single laboratory validation:**

Community Reference Laboratory for GM Food and Feed (CRL-GMFF)  
Biotechnology & GMOs Unit

## **Modification from the previous version:**

At page 6:

### **5. PEG Precipitation Buffer (20% w/v) (store at room temperature)**

Changed to

### **5. PEG Precipitation Buffer (20% w/v) (store at room temperature)**

- 20% w/v PEG (MW 8000)

- 2.5 M NaCl

## **Note:**

Since 01/12/2009 the term "Community Reference Laboratory (CRL)" is changed into "European Union Reference Laboratory (EURL)".

Since 01/03/2009 to 31/06/2016 the JRC-unit that hosts the EURL GMFF is named "Unit for Molecular Biology and Genomics" instead of "Biotechnology and GMO Unit".

Since 01/07/2016 the JRC-unit that hosts the EURL GMFF is named "Food and feed compliance"



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## **Quality assurance**

The EURL GMFF is ISO 17025:2005 accredited [certificate number: Belac 268 TEST (Flexible Scope for DNA extraction, DNA identification and real Time PCR) and ISO 17043:2010 accredited (certificate number: Belac 268 PT, proficiency test provider).

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

### **Address of contact laboratory:**

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Functional mailbox: JRC-EURL-GMFF@ec.europa.eu

## 1 Introduction

This report describes the validation of a DNA extraction protocol to extract high quality genomic DNA from processed plant tissue (e.g., leaf, grain, or seed) and its applicability on the samples of food and feed provided by the applicant. This protocol can be used for the extraction of DNA from maize seeds and grains. It is a modified extraction method from Rogers and Bendich (1985)<sup>1</sup>.

The purpose of the DNA extraction method described is to provide DNA with purity suitable for real-time PCR based detection methods.

This protocol is recommended to be executed by skilled laboratory personnel since hazardous chemicals and materials are exploited at some steps. It is strongly advised to take particular notice of all product safety recommendations and guidelines.

## 2 Materials (Equipment/Chemicals/Plastic ware)

### 2.1 Equipment

The following equipment is used in the DNA extraction procedure described (equivalents may be used):

1. Centrifuge (Beckman Coulter Avanti J-251)
2. Shaker (LabLine Enviro 3527)
3. Thermometer (VWR Cat. No. 61222-504)
4. Vacufuge (Eppendorf 5301 22 82 010-9)
5. Water bath (Precision Cat. No. 51220046)
6. Microcentrifuge (Any appropriate model)

### 2.2 Chemicals

The following chemicals are used in the DNA extraction procedure described (equivalents may be used):

1. 24:1 chloroform:isoamyl alcohol (Sigma Cat. No. C-0549)
2. 25:24:1 phenol:chloroform:isoamyl alcohol (Sigma Cat. No. P-3803)
3. Ammonium acetate 7.5 M (Sigma Cat. No. A-2706)
4. CTAB (Sigma Cat. No. H-6269)
5. 0.5 M EDTA, pH 8.0 (GibcoBRL Cat. no. 15575-038)
6. 100% ethanol (AAPER)
7. NaCl (Sigma Cat. No. S-5150)
8. 2-mercaptoethanol (Bio-Rad Cat. no. 161-0710)
9. RNase A (Roche Cat. No. 10 109 196 001)
10. Isopropanol (EM Science Cat. No. PX1835-9)
11. 1 M Tris HCl pH 8.0 (Sigma Cat. No. T-3038)
12. Proteinase K (Roche Cat. No. 03 115 836 001)
13. Polyethylene Glycol (MW 8000) (Sigma Cat. No. P2139)

## 2.3 Solutions

The following buffers and solutions are used in the DNA extraction procedure described:

**1. CTAB Extraction Buffer (2%) (store at room temperature)**

- 2% w/v CTAB
- 100 mM Tris HCl pH 8.0
- 20 mM EDTA pH 8.0
- 1.4 M NaCl

**2. Tris-EDTA buffer (TE 1X) (store at room temperature)**

- 10 mM Tris HCl pH 8.0
- 1 mM EDTA pH 8.0

**3. Proteinase K (10 mg/mL) (store at -20 °C)**

**4. RNase A (10 mg/mL) (store at -20 °C)**

**5. PEG Precipitation Buffer (20% w/v) (store at room temperature)**

- 20% w/v PEG (MW 8000)
- 2.5 M NaCl

**6. Ethanol (70% v/v) (store at room temperature)**

**7. Ethanol (80% v/v) (store at room temperature)**

## 2.4 Plastic ware

1. 50 mL conical tubes (Corning Cat. No. 430290)
2. 13 mL Sarstedt tubes (Sarstedt Cat. No. 60.540)
3. 1.5 mL microcentrifuge tubes
4. filter tips

Note: All plastic ware has to be sterile and free of DNases, RNases and nucleic acids.

## 2.5 Precautions

- Phenol, chloroform, isoamyl alcohol, and isopropanol are hazardous chemicals; therefore, all manipulations have to be performed according to safety guidelines, under fume hood.
- It is recommended to use clean containers for Waring blenders for grinding the seed bulk samples.
- All tubes and pipette tips have to be discarded as biological hazardous material

## 2.6 Abbreviations

EDTA	ethylenediaminetetraacetic acid
PCR	polymerase chain reaction
RNase A	ribonuclease A
TE	Tris EDTA
Tris	Tris(hydroxymethyl)aminomethane

### **3 Description of the methods**

#### **3.1 Sampling**

For sampling methods, it is referred to the technical guidance documents and protocols described in Commission Recommendation 2004/787/EC on technical guidance for sampling and detection of genetically modified organisms and material produced from genetically modified organisms as or in products in the context of Regulation (EC) N. 1830/2003.

#### **3.2 Scope and applicability**

The method for DNA extraction described below is suitable for the isolation of genomic DNA from a wide variety of maize tissues and derived matrices. However, validation data presented here are restricted to ground maize seeds and grains. Application of the method to other matrices may require adaptation and possible further specific validation.

#### **3.3 Principle**

The basic principle of the DNA extraction consists of first releasing the DNA present in the matrix into aqueous solution and further purifying the DNA from PCR inhibitors. The present method starts with a lysis step (thermal lysis in the presence of Tris HCl, EDTA, CTAB and  $\beta$ -mercaptoethanol) followed by removal of contaminants such as lipophilic molecules and proteins by extraction with phenol and chloroform.

A DNA precipitate is then generated by using isopropanol. The pellet is dissolved in TE buffer. Remaining inhibitors are removed by PEG precipitation and re-suspension in TE buffer. Tissues crushing procedure

Tissues should be processed prior to extraction procedure. Possible methods of processing include a mortar and pestle with liquid nitrogen (leaf) or commercial blender (grain or seed).

#### **3.4 Samples grinding procedure**

Samples should be processed prior to extraction procedure. Possible methods of processing include a mortar and pestle with liquid nitrogen (leaf) or commercial blender (grain or seed).

#### **3.5 Extraction of genomic DNA from maize seeds/grains**

1. Weight out 6 g of processed tissue into a 50 mL conical tube appropriate for centrifugation. Note: For unprocessed tissue, weighing may occur prior to processing as long as entire processed sample is transferred to the conical tube.
2. For each 6 g sample add 25 mL of a solution consisting of 24.25 mL, pre-warmed CTAB extraction buffer, 0.5 mL 2- $\beta$ -mercaptoethanol (2-ME), and 0.25 mL of 10 mg/mL proteinase K for a final concentration of 2% (2-ME) and 100  $\mu$ g/mL (proteinase K).
3. Mix the tube vigorously by inversion for 45-60 seconds.
4. Incubate for 60 minutes at 55 °C and mix the tube vigorously for 40-60 seconds every 20 minutes. Cool the tube on bench for 10 minutes.
5. Add 20 mL of phenol:chloroform:isoamyl alcohol (PCI 25:24:1, pH 6.7). Cap the tube and mix vigorously by inversion at least for 1 minute.

6. Centrifuge for 10 minutes at 13000 x g at room temperature to separate the aqueous and organic phases. Transfer upper aqueous phase to a clean 50 mL conical tube.
7. Repeat extraction twice for a total of three extractions (step 5-6).
8. Transfer upper aqueous phase to a new tube, add 2/3 volume of -20 °C isopropanol and gently mix the tube by inversion.
9. To precipitate the DNA place the tube at -20 °C for 30 minutes. (DNA may be stored as isopropanol precipitate at -20 °C for up to 1 year).
10. To pellet the DNA, centrifuge the tubes at approximately 13000 x g for 20 minutes at 4 °C. Pour off isopropanol by pipette, and then perform a quick spin in the centrifuge to bring down the isopropanol from the side of the tube. Remove remaining isopropanol by pipette and ensure all residual isopropanol is removed before proceeding to the next step without over drying the pellet.
11. Re-dissolve the pellet in 4 mL of TE pH 8.0. Note: it may be necessary to incubate the tube at 60°C to resuspend the pellet.
12. Transfer the resuspended pellet to a 13-mL tube, add 40 µL of 10 mg/mL RNase and then incubate at 37°C for 30 minutes.
13. To extract the DNA, add 4 mL of chloroform:isoamyl alcohol (CIA 24:1), mix vigorously by inversion for 40-60 seconds and centrifuge for 10 minutes at 13000 x g at room temperature. Transfer the upper aqueous phase to a clean tube.
14. Repeat step 13 an additional time, then add half volume of 7.5 M ammonium acetate, gently mix by inversion and add 2 volumes of 100% ethanol. Mix by inversion and place at -20°C for 30 minutes. DNA may be stored as ethanol precipitate at -20 °C for up to 1 year.
15. Centrifuge at 13000 x g for 20 minutes at 4°C to pellet the DNA.
16. Rinse the DNA pellet twice with 10 mL of 70 % ethanol loosening the pellet from the side of the tube and remove residual ethanol by vacuum.
17. Re-suspend DNA in 1 mL TE, pH 8.0 and incubate at 65°C for at least 1 hour with periodic gentle mixing.
18. Centrifuge the DNA solution at 16000 x g for 10 minutes at 4°C. Transfer the aqueous portion to a clean tube without disturbing the pellet and store at 4°C.
19. Add equal volume of 20% PEG precipitation buffer (~1 mL) to the extracted DNA solution. Mix well by inversion.
20. Incubate the PEG/DNA mixture for 15 minutes at 37 °C.
21. Centrifuge the PEG/DNA mixture for 15 minutes at 15000 x g at room temperature.
22. Pour off supernatant. Wash the walls of the tube and DNA pellet with 1 mL of 80% ethanol loosening the pellet from the tube. Carefully pour off ethanol, centrifuge briefly and remove by pipetting any residual ethanol.
23. Repeat wash (step 22) for a total of two washes.
24. Completely dry any residual ethanol by vacuum at low heat.
25. Re-suspend the pellet in 1 mL TE or H<sub>2</sub>O. If necessary, incubate the sample at 60°C to dissolve the pellet.
26. Centrifuge the re-suspended DNA solution at 15000 x g for 15 minutes.
27. Transfer DNA solution to a clean tube without disturbing the pellet and store DNA at 4°C.

## **4 Testing of the DNA extraction method by the Community Reference Laboratory for GM Food and Feed**

The aim of the experimental testing was to verify that the DNA extraction method provides DNA of suitable quantity and quality for the intended purpose. The DNA extraction method should allow preparation of the analyte in quality and quantity appropriate for the analytical method used to quantify the event-specific analyte versus the reference analyte.

The CRL-GMFF tested the method proposed by the applicant on samples of food and feed consisting of ground maize seeds provided by the applicant.

To assess the suitability of the DNA extraction method for real-time PCR analysis, the extracted DNA was tested using a qualitative PCR run on the real-time PCR equipment.

### **4.1 Preparation of samples**

About 200 g of maize seed material were ground using a GRINDOMIX GM 200 (Retsch GmbH) mixer.

### **4.2 DNA extraction**

DNA was extracted following the method described above (see paragraph 3. "Description of the methods"); the DNA extraction was carried out on 6 test portions (replicates) and repeated over three different days, giving a total of 18 DNA extractions.

### **4.3 DNA concentration, yield and repeatability**

Concentration of the DNA extracted was determined by fluorescence detection using the PicoGreen dsDNA Quantitation Kit (Molecular Probes).

Each DNA extract was measured twice, and the two values were averaged. DNA concentration was determined on the basis of a five point standard curve ranging from 1 to 500 ng/ $\mu$ L using a Biorad VersaFluor fluorometer.

The DNA concentration for all samples is reported in the Table 1 below.

Table 1. DNA concentration (ng/ $\mu$ L) of eighteen samples extracted in three days: yellow boxes for samples extracted on day 1, green boxes for samples extracted on day 2 and blue boxes for samples extracted on day 3.

Sample	Concentration (ng/ $\mu$ L)
1	147.2
2	229.0
3	579.8
4	352.1
5	551.1
6	504.9
1	277.5
2	468.7
3	473.4
4	424.6
5	258.0
6	517.5
1	526.7
2	463.1
3	531.5
4	594.8
5	537.8
6	545.4

✓ DNA concentration (ng/ $\mu$ L)

Overall average	443.5 ng/ $\mu$ L
Standard deviation	133 ng/ $\mu$ L
Coefficient of variation	30 %

✓ Yield (total volume of DNA solution: 1 mL)

Overall average	443.5 $\mu$ g
Standard deviation	133 $\mu$ g
Coefficient of variation	30 %

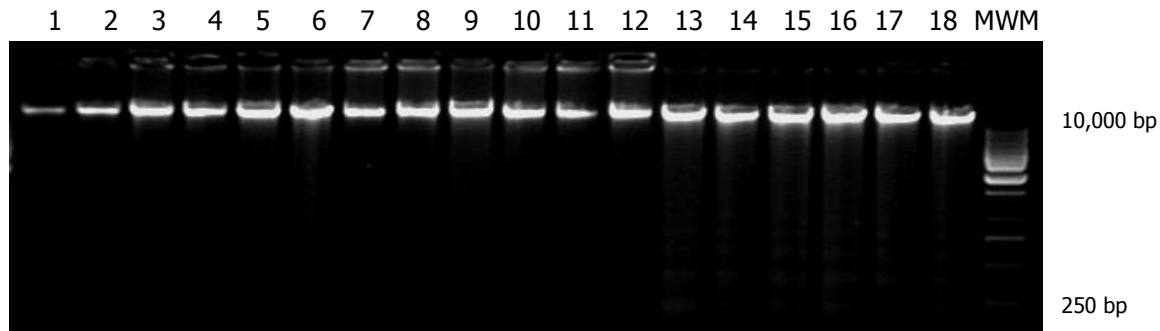
#### 4.4 Fragmentation state of DNA

The size of the extracted DNA was evaluated by agarose gel electrophoresis; 1  $\mu$ L of the DNA solution were analysed on a 1.0% agarose gel (Figure 1).

The eighteen genomic DNA samples extracted as described above appeared as distinct fluorescent banding patterns migrating through the gel corresponding to high molecular weight DNA. None of the DNA samples showed indications of significant degradation ('smearing').



Figure 1. Agarose gel electrophoresis of eighteen genomic DNA samples extracted from maize seeds. Lanes 1-6: samples extracted on day 1; lanes 7-12 samples extracted on day 2; lanes 13-18 samples extracted on day 3; lane 19: 1 kb DNA molecular weight marker (MWM).



#### 4.5 Purity / Absence of PCR inhibitors

In order to assess the purity and to confirm the absence of PCR inhibitors, the extracted DNA solutions were adjusted to a concentration of 50 ng/ $\mu$ L (hereafter referred as "undiluted" samples).

Subsequently fourfold serial dilutions of each extract were prepared with 0.2x TE buffer (1:4, 1:16, 1:64, 1:256) and analysed using a real-time PCR system detecting the target sequence of the maize endogenous control gene, hmg (high mobility group). The Ct values obtained for "undiluted" and diluted DNA samples are reported in the Table 2.

Table 2. Ct values of undiluted and fourfold serially diluted DNA extracts after amplification of the maize endogenous gene, hmg. Yellow boxes for samples extracted on day 1, green boxes for samples extracted on day 2 and blue boxes for samples extracted on day 3.

DNA extract	Undiluted (50 ng/ $\mu$ L)	Diluted			
		1:4	1:16	1:64	1:256
<b>1</b>	23.88	25.64	27.65	29.44	31.43
<b>2</b>	23.56	25.70	27.59	29.26	31.38
<b>3</b>	23.53	25.46	27.71	29.68	31.52
<b>4</b>	23.89	25.56	27.43	29.75	31.49
<b>5</b>	24.10	25.78	27.59	29.06	31.43
<b>6</b>	23.89	25.74	27.52	29.18	31.70
<b>1</b>	23.72	25.30	27.35	28.97	31.08
<b>2</b>	23.51	25.82	27.73	29.48	31.51
<b>3</b>	23.61	25.37	27.99	29.87	31.78
<b>4</b>	23.55	25.26	27.20	29.52	31.55
<b>5</b>	23.77	25.67	27.51	29.37	31.93
<b>6</b>	23.41	25.86	27.31	29.24	31.23
<b>1</b>	23.49	25.09	27.62	29.71	31.72
<b>2</b>	23.79	25.95	27.90	29.76	31.77
<b>3</b>	23.71	25.47	27.73	29.50	31.47
<b>4</b>	23.73	25.44	27.45	29.92	31.81
<b>5</b>	23.88	25.64	27.42	29.23	31.75
<b>6</b>	23.58	25.89	27.96	30.12	32.03

Table 3 below reports the comparison of extrapolated Ct values versus measured Ct values for all samples and the values of linearity (R<sup>2</sup>) and slope of all measurements.

To measure inhibition, the Ct values of the four diluted samples were plotted against the logarithm of the dilution and the Ct value for the "undiluted" sample (50 ng/μL) was extrapolated from the equation calculated by linear regression.

Subsequently the extrapolated Ct for the "undiluted" sample was compared with the measured Ct. The evaluation is carried out considering that PCR inhibitors are present if the measured Ct value for the "undiluted" sample is > 0.5 cycles compared the calculated Ct value ( $\Delta Ct > 0.5$ ). In addition, the slope of the curve should be between -3.6 and -3.1.

Table 3. Comparison of extrapolated Ct values versus measured Ct values (amplification of maize *hmg* gene).

DNA extraction	R <sup>2</sup>	Slope*	Ct extrapolated	mean Ct measured	$\Delta Ct^{**}$
1	0.998	-3.18	23.75	23.88	0.13
2	0.995	-3.11	23.79	23.56	0.23
3	0.997	-3.35	23.55	23.53	0.03
4	0.996	-3.34	23.53	23.89	0.36
5	0.987	-3.10	23.76	24.10	0.33
6	0.989	-3.25	23.64	23.89	0.24
1	0.997	-3.149	23.43	23.72	0.28
2	0.999	-3.127	23.93	23.51	0.42
3	0.992	-3.507	23.47	23.61	0.13
4	0.997	-3.516	23.09	23.55	0.46
5	0.991	-3.427	23.46	23.77	0.31
6	0.995	-2.995	23.90	23.41	0.49
1	0.995	-3.598	23.15	23.49	0.35
2	0.999	-3.212	24.01	23.79	0.22
3	0.996	-3.278	23.61	23.71	0.10
4	0.996	-3.582	23.26	23.73	0.46
5	0.991	-3.345	23.47	23.88	0.41
6	0.998	-3.412	23.87	23.58	0.28

Note: In yellow boxes samples from 1 to 6 extracted on day 1; in green boxes samples from 1-6 extracted on day 2; in blue boxes samples from 1-6 extracted on day 3.

\*The expected slope for a PCR with 100% efficiency is -3.32

\*\*delta Ct = abs (Ct extrapolated - Ct measured)

All  $\Delta Ct$  values of extrapolated versus measured Ct are < 0.5.

R<sup>2</sup> of linear regression is > 0.99 for all DNA samples except two samples extracted on day 1: the sample 5 (0.987) and the sample number 6 (0.989). The slopes of the curve are all between -3.1 and -3.6, with one exception: the sample number 6 extracted on day 2, with a value of -2.995.

## **5 Conclusion**

The data reported confirm that the extraction method, applied to samples of food and feed provided by the applicant, produces DNA of suitable quantity and quality for subsequent PCR based detection applications.

The method is consequently applicable to samples of maize seeds provided as samples of food and feed in accordance with the requirements of Annex I-2.C.2 to Commission Regulation (EC) No 641/2004.

## **6 Quality assurance**

The CRL-GMFF carries out all operations according to ISO 9001:2000 (certificate number: CH-32232) and ISO 17025:2005 (certificate number: DAC-PL-0459-06-00) [DNA extraction, qualitative and quantitative PCR in the area of Biology (DNA extraction and PCR method validation for the detection and identification of GMOs in food and feed materials)]

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