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METHODS AND MEASUREMENTS

# Event-specific Method for the Quantification of Soybean MON 87705 Using Real-time PCR

Validation Report and  
Validated Method

Christian Savini  
Marco Mazzara  
Chrystelee Delobel  
Gregor Pinski  
Guy Van den Eede

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European Commission  
Joint Research Centre  
Institute for Health and Consumer Protection

Contact information

Molecular Biology and Genomics Unit

Address: Joint Research Centre, Via Enrico Fermi 2749, TP 201, 21027 Ispra (VA), Italy

E-mail: [eurl-gmff@jrc.ec.europa.eu](mailto:eurl-gmff@jrc.ec.europa.eu)

Tel.: +39 0332 78 5165

Fax: +39 0332 78 9333

<http://ihcp.jrc.ec.europa.eu/>

<http://www.jrc.ec.europa.eu/>

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# **Event-specific Method for the Quantification of Soybean MON 87705 Using Real-time PCR**

## **Validation Report**

**17 January 2012**

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

### **Executive Summary**

The European Union Reference Laboratory for Genetically Modified Food and Feed (EU-RL 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 87705 transformation event in soybean DNA (unique identifier MON-87705-6). 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 (genomic DNA from soybean seeds harbouring the MON 87705 event and from conventional soybean seeds). The EU-RL GMFF 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 Regulation (EC) No 641/2004.

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

*Drafted by*

C. Savini (scientific officer)



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*Report review*

1) L. Bonfini



---

2) M. Querci



---

*Scientific and technical approval*

M. Mazzara (scientific officer)



---

*Compliance with EU-RL Quality System*

S. Cordeil (quality manager)



---

*Authorisation to publish*

G. Van den Eede (head of MBG Unit)



---

**Address of contact laboratory:**

European Commission, Joint Research Centre (JRC)  
Institute for Health and Consumer Protection (IHCP)  
Molecular Biology and Genomics Unit  
European Union Reference Laboratory for GM Food and Feed  
Via E. Fermi 2749, 21027 Ispra (VA) - Italy

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

Monsanto Company provided the detection method and the control samples for soybean event MON 87705 (unique identifier MON-877Ø5-6) 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 (EU-RL 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 EU-RL 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 (ENGL) 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, the scientific assessment was performed for soybean event MON 87705 and positively concluded in July 2010.

Between July 2010 and November 2010, the EU-RL GMFF verified the purity of the control samples provided. The method characteristics were verified by quantifying five blind GM levels within the range 0.1%-8.0% on a genome copy number basis ([step 3](#), experimental testing of samples and methods). The experiments were performed under repeatability conditions and demonstrated that the PCR (Polymerase Chain Reaction) efficiency, linearity, accuracy and precision of the quantifications were within the limits established by the ENGL. The DNA extraction module of the method was previously tested on samples of food and feed and a report was published on the EU-RL GMFF website on the 19<sup>th</sup> of September 2007 (<http://gmo-crl.jrc.ec.europa.eu/statusofdoss.htm>).

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

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## 1. Introduction

Monsanto Company provided the detection method and control samples for soybean event MON 87705 (unique identifier MON-87705-6) according to Articles 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 Genetically Modified Food and Feed established by Regulation (EC) No 1829/2003 organised the international collaborative study for the validation of the event-specific method for detection and quantification of soybean event MON 87705. The study involved twelve laboratories, among those listed in Annex II ("National reference laboratories assisting the EURL for testing and validation of methods for detection") of Regulation (EC) No 1981/2006 of 22 December 2006.

Upon reception of method, samples and related data (step 1), the EU-RL GMFF 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 evaluation of the method was carried out between July 2010 and November 2010.

Following the evaluation of the data and the results of the internal laboratory tests, the international collaborative study was organised (step 4) and took place in December 2010.

A method for DNA extraction from seeds and grains followed by PEG precipitation, submitted by the applicant, was evaluated by the EU-RL GMFF in order to confirm its performance characteristics. The protocol for DNA extraction and a report on method testing are available at <http://gmo-crl.jrc.ec.europa.eu/>.

The collaborative study aimed at assessing the performance of a quantitative real-time PCR (Polymerase Chain Reaction). The method is an event-specific quantitative real-time TaqMan<sup>®</sup> PCR procedure for the determination of the relative content of event MON 87705 DNA to total soybean DNA. The procedure is a simplex system, in which a soybean assay for the endogenous gene lectin 1 (*Le1*) and the target assay for the event MON 87705 are performed in separate wells.

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

- Accuracy (trueness and precision) of measurement methods and results. 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.

In November 2010, the EU-RL GMFF invited all National Reference Laboratories nominated under Regulation (EC) No 1981/2006 of 22 December 2006 and listed in Annex II ("National reference laboratories assisting the EURL 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 soybean event MON 87705.

Thirty-nine laboratories expressed in writing their willingness to participate, three declined the invitation, while twenty-seven did not answer. The EU-RL 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 soybean event MON 87705.

Laboratory	Country
State Office for Agriculture, Food Safety and Fisheries - Mecklenburg Western Pomerania	DE
Institute for Hygiene and Environment	DE
Landeslabor Schleswig-Holstein - Food, veterinary, and environmental diagnostic institute	DE
Laboratory of DNA analysis, Department of Gene Technology (GT), Tallinn University of Technology (TUT) <sup>1</sup>	EE
Service Commun des Laboratoires du MINEFI - Laboratoire de Strasbourg	FR
Italian National Institute for Health - Department of Veterinary Public Health and Food Safety - Unit GMOs and Mycotoxins	IT
E.N.S.E. - Seed Testing Station	IT
National Health Laboratory, Food Control Department	LU
National Veterinary Research Institute in Pulawy, Department of Feed Hygiene	PL
National Institute of Biological Resources- Laboratory for the Characterization of Plant Propagation Materials	PT
Agricultural Institute of Slovenia	SI
National Institute of Biology	SI

<sup>1</sup> The validation samples did not reach this laboratory in good conditions. Therefore the corresponding results were not taken into consideration in this study



### 3. Materials

For the validation of the quantitative event-specific method, control samples consisted of:

- i) genomic DNA extracted from homozygous soybean seeds harbouring the event MON 87705 (ID: MON87705-20091005), and
- ii) genomic DNA extracted from conventional soybean seeds (ID: C.SOY-20091005).

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 soybean MON 87705 and non-GM soybean genomic DNA at different GM percentages were prepared by the EU-RL GMFF, using the control samples provided, in a constant amount of total soybean DNA.

Participants received the following materials:

- ✓ Five calibration samples (140 µL of DNA solution each) for the preparation of the standard curve, labelled from S1 to S5.
- ✓ Twenty unknown DNA samples (70 µL of DNA solution each) labelled from U1 to U20.
- ✓ Reaction reagents:
  - universal PCR Master Mix (2x), three bottles: 5 mL each
  - distilled sterile water, one tube: 12 mL
- ✓ Primers and probes (1 tube each) as follows:
 

<i>Le1</i> reference system			
▪ <i>Le1</i> primer 1	(10 µM):	240 µL	
▪ <i>Le1</i> primer 2	(10 µM):	240 µL	
▪ <i>Le1</i> probe	(5 µM):	160 µL	
MON 87705 system			
▪ MON 87705 primer 1	(20 µM):	360 µL	
▪ MON 87705 primer 2	(20 µM):	360 µL	
▪ MON 87705 probe	(5 µM):	800 µL	

### 4. Experimental design

Twenty unknown samples (labelled from U1 to U20), representing five GM levels, were used in the validation study (Table 2). On each PCR plate, the samples were analysed for the MON 87705 specific system and for the *Le1* reference system. Two plates were run per participating laboratory with two replicates for each GM level. In total, 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.

Table 2. MON 87705 GM contents

MON 87705 GM% [GM copy number/maize genome copy number (x 100)]
0.1
0.5
0.9
5.0
8.0

#### 4. Method

For the detection of event MON 87705 genomic DNA, an 86-bp fragment of the region spanning the 3' plant-to-insert junction in soybean MON 87705 event is amplified using two 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 a reporter dye at its 5' end and TAMRA (carboxytetramethylrhodamine) as a quencher dye at its 3' end.

For the relative quantification of event MON 87705 DNA, a soybean-specific reference system amplifies a 74-bp fragment of the endogenous gene lectin (*Le1*), using two *Le1* specific primers and a *Le1* specific probe labelled with FAM as a reporter dye and TAMRA as a quencher dye.

Standard curves are generated for both the MON 87705 and the *Le1* 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 87705 DNA in a test sample, the MON 87705 copy number is divided by the copy number of the soybean reference gene (*Le1*) and multiplied by 100 to obtain the percentage value ( $GM\% = \text{MON 87705} / \text{Le1} \times 100$ ).

Calibration sample S1 was prepared by mixing the appropriate amount of MON 87705 DNA in control non-GM soybean DNA to obtain a 10% GM MON 87705. Sample S2 was prepared by serial dilution from the S1 sample by fourfold dilution as presented in Table 3.

The theoretical copy numbers of the calibration curve samples are calculated by dividing the sample DNA weight (nanograms) by the published average 1C value for soybean genome (1.13 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.

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

Sample code	S1	S2	S3	S4	S5
Total amount of DNA in reaction	200	50	10	5	1.67
Soybean genome copies	176991	44248	8850	4425	1475
MON 87705 GM soybean copies	17699	4425	885	442	147

## 6. Deviations reported

Nine laboratories reported no deviations from the protocol.

One laboratory reported the use of reaction volumes of 25 µL; one laboratory reported the use of reaction volumes of 20 µL.

## 7. 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 standard curve and of the  $R^2$  (expressing the linearity of the regression) reported by participating laboratories for the MON 87705 system and the *Le1* reference system are summarised in Table 4.

The mean PCR efficiency was 96% for the MON 87705 system and 95% for the *Le1* system; both values are within the European Network of GMO Laboratories (ENGL) acceptance criteria. The  $R^2$  was 0.99 and 1.00 for the MON 87705 and the *Le1* systems, respectively. Data reported confirm the appropriate performance characteristics of the method tested in terms of efficiency and linearity.

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

Lab	Plate	MON 87705			<i>Le1</i>		
		Slope	PCR Efficiency (%)	$R^2$	Slope	PCR Efficiency (%)	$R^2$
1	A	-3.23	104	1.00	-3.40	97	0.98
	B	-3.23	104	1.00	-3.48	94	1.00
2	A	-3.52	92	1.00	-3.49	93	1.00
	B	-3.45	95	1.00	-3.49	93	1.00
3	A	-3.44	95	1.00	-3.32	100	1.00
	B	-3.49	94	1.00	-3.33	100	0.99
4	A	-3.55	91	1.00	-3.44	95	1.00
	B	-3.50	93	1.00	-3.45	95	1.00
5	A	-3.29	101	0.96	-3.56	91	1.00
	B	-3.73	85	0.99	-3.51	93	1.00
6	A	-3.43	96	0.99	-3.51	93	0.99
	B	-3.62	89	0.99	-3.36	99	0.99
7	A	-3.54	92	0.97	-3.27	102	0.97
	B	-3.28	102	1.00	-3.30	101	0.98
8	A	-3.31	100	0.99	-3.35	99	1.00
	B	-3.37	98	1.00	-3.42	96	1.00
9	A	-3.29	102	1.00	-3.57	91	1.00
	B	-3.63	88	1.00	-3.53	92	1.00
10	A	-3.49	94	1.00	-3.55	91	1.00
	B	-3.41	96	1.00	-3.46	95	1.00
11	A	-3.30	101	1.00	-3.40	97	1.00
	B	-3.35	99	1.00	-3.35	99	1.00
	Mean	-3.44	96	0.99	-3.44	95	1.00

### ***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	GMO content (GMO% = GMO copy number/soybean genome copy number x 100)																			
	0.1				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	0.07	0.08	0.08	0.06	0.56	0.49	0.38	0.47	0.90	0.67	0.85	0.76	5.41	4.48	3.11	3.43	8.79	7.67	8.02	6.15
2	0.13	0.09	0.09	0.10	0.61	0.52	0.52	0.73	1.00	1.04	1.05	1.07	5.35	5.60	4.88	5.10	8.15	8.81	7.46	9.21
3	0.11	0.10	0.11	0.08	0.57	0.51	0.42	0.57	0.71	0.99	0.88	1.23	4.63	4.38	4.13	5.44	7.30	8.37	8.72	7.62
4	0.11	0.10	0.11	0.09	0.49	0.51	0.53	0.52	0.98	0.91	1.05	0.99	4.97	5.10	4.49	4.89	8.11	8.62	7.29	7.70
5	0.08	0.11	0.11	0.05	0.51	0.47	0.53	0.79	0.58	0.68	0.92	0.83	4.37	3.40	5.85	5.95	4.18	5.58	12.33	12.63
6	0.08	0.15	0.08	0.12	0.32	0.35	0.40	0.39	0.35	0.63	0.62	0.53	2.73	3.01	4.81	4.43	5.01	5.04	6.87	6.03
7	0.10	0.12	0.09	0.08	0.44	0.44	0.65	0.42	0.97	0.68	1.02	0.78	5.82	5.76	4.48	4.12	9.53	8.15	7.02	6.99
8	0.09	0.08	0.06	0.09	0.50	0.44	0.40	0.33	0.90	0.80	0.63	0.50	4.04	4.18	4.16	3.64	7.85	5.27	6.29	6.50
9	0.07	0.11	0.10	0.12	0.48	0.47	0.49	0.48	0.89	1.04	0.96	1.03	4.72	4.88	5.54	5.89	7.90	6.14	8.17	8.20
10	0.13	0.10	0.09	0.11	0.63	0.61	0.52	0.65	0.93	1.23	1.07	1.17	5.93	6.22	5.55	5.40	10.31	8.97	8.20	11.76
11	0.10	0.09	0.08	0.09	0.48	0.49	0.59	0.47	0.90	0.87	0.89	0.79	5.05	4.46	5.52	4.70	8.16	7.43	7.50	7.94

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 brown bar represents the overall mean for each GM level.

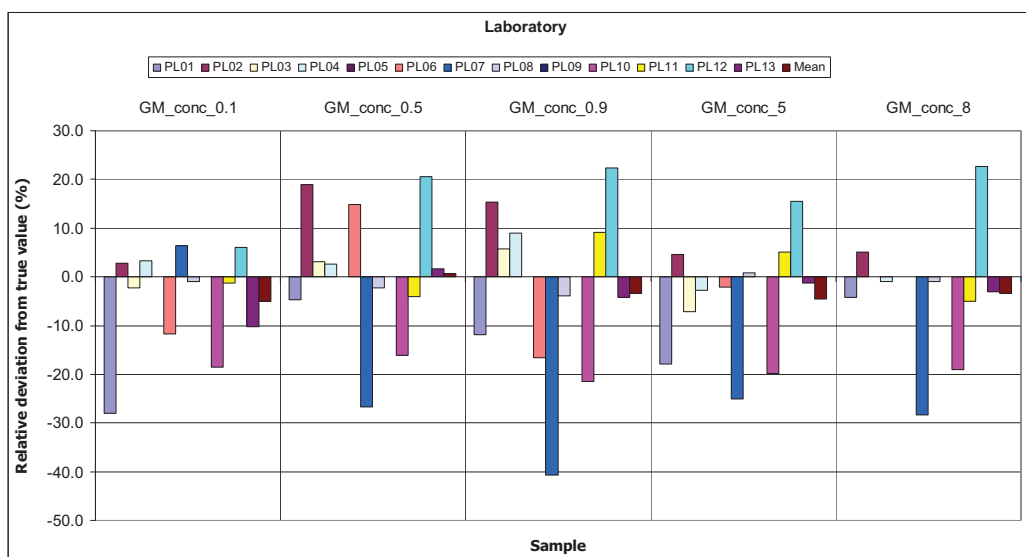


Figure 1. Relative deviation (%) from the true value of MON 87705 for all laboratories

As observed in Figure 1, the mean relative deviations from the true values are below 5 % in absolute value over the whole dynamic range. Overall, the average relative deviation is within the acceptance criterion at all GM levels tested, indicating a satisfactory trueness of the method.

## 8. Method performance requirements

Among the performance criteria established by ENGL and adopted by the EU-RL 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 ENGL 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% 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 6, the method satisfies this requirement at all GM levels tested. In fact, the highest value of  $RSD_R$  is 23% at the 0.9% GM level, thus within the acceptance criterion.

Table 6. MON 87705: summary of validation results.

unknown sample GMO %	Expected value (GMO%)				
	0.1	0.5	0.9	5.0	8.0
Laboratories having returned valid results	11	11	11	11	11
Samples per laboratory	4	4	4	4	4
Number of outliers	0	0	0	0	1
Reason for exclusion	-	-	-	-	1 C
Mean value	0.10	0.50	0.87	4.77	7.73
<b>Relative repeatability standard deviation, <math>RSD_r</math> (%)</b>	<b>20</b>	<b>15</b>	<b>15</b>	<b>15</b>	<b>13</b>
Repeatability standard deviation	0.02	0.08	0.13	0.72	0.97
<b>Relative reproducibility standard deviation, <math>RSD_R</math> (%)</b>	<b>21</b>	<b>19</b>	<b>23</b>	<b>18</b>	<b>18</b>
Reproducibility standard deviation	0.02	0.10	0.20	0.87	1.37
Bias (absolute value)	-0.005	0.004	-0.03	-0.23	-0.27
<b>Bias (%)</b>	<b>-4.96</b>	<b>0.71</b>	<b>-3.40</b>	<b>-4.54</b>	<b>-3.38</b>

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.

Table 6 further documents the relative repeatability standard deviation ( $RSD_r$ ), as estimated for each GM level. In order to accept methods for collaborative study evaluation, the EU-RL GMFF requires that the  $RSD_r$  value is below 25%, as indicated by ENGL (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 method showed a repeatability standard deviation below 25% at all GM levels, with the highest value of  $RSD_r$  (%) of 20% at the 0.1% 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. As reported in Table 6, the method satisfies this requirement across the dynamic range tested; in fact the highest value of bias % was equal to  $-4.96$  at the 0.1% GM level.

## 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 at <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.

Therefore, the method is considered 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 EU-RL GMFF operates according to ISO 9001:2008 (certificate number: CH-32232) and technical activities under ISO 17025:2005 [certificate number: ACCREDIA 1172, (Flexible Scope for DNA extraction and qualitative / quantitative PCR) – Accredited tests available at [http://www.accredia.it/accredia\\_labsearch.jsp?ID\\_LINK=293&area=7](http://www.accredia.it/accredia_labsearch.jsp?ID_LINK=293&area=7)]

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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. Royal Botanic Garden, Kew. Plant DNA c-values database. <http://data.kew.org/cvalues/>

## **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 the 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. cost/sample) of the method.

Acceptance criteria: The method should generally be practicable in line with other methods for a similar purpose. More specifically the method is deemed unacceptable, unless suitable justification is supplied, if:

- it requires a new type of apparatus (not generally available) or expensive equipment; or
- the resources required to perform the method (time, workload, reagents, costs) are considerably higher than the resources required to perform other methods for similar purpose.

Other practicability considerations may also deem the method impracticable.

#### ***DNA Extraction and Purification***

The aim of a DNA extraction procedure is to provide DNA of suitable quality for subsequent analysis. DNA quality depends on the average length, structural integrity and chemical purity of the extracted DNA.

It is recognised that highly fragmented DNA and co-extracted impurities of a DNA preparation may hinder the correct process of detecting and quantifying genetically modified DNA. Food and feed made



of various ingredients may exert a matrix effect, depending on the DNA extraction method employed, and impair the sensitivity of the following analytical approach. For this purpose, critical steps of DNA extraction and purification should be clearly highlighted in the technical documentation accompanying a method and acceptance criteria are established to allow objective determination of PCR quality of DNA extracts which can be considered suitable for subsequent detection experiments (e.g. qualitative and/or quantitative PCR).

DNA extraction procedures should result in repeatable recovery, fragmentation profile, concentration and PCR quality of DNA extracts. As such, it is recommended to process the given DNA extraction protocol on different days (e.g. 3 days) with an adequate number of test portions (e.g. 6 per day).

In agreement with international guidelines (e.g. EN ISO 21571<sup>Error! Reference source not found.</sup>, EN ISO 24276<sup>Error! Reference source not found.</sup>) the following criteria are used to assess method performance.

#### *a) DNA concentration*

Definition: amount of an analyte per unit volume of solution

Acceptance criterion: The DNA extraction method employed shall be appropriate to obtain the quantity of nucleic acid required for the subsequent analysis. The DNA concentration measured as weight of the analyte/volume of solution should be higher than the working concentration described in the protocol of the detection method.

Example: if the RT-PCR protocol indicates 40 ng/μL as the DNA concentration of the DNA solution to be added to the master-mix, the concentration of the DNA extract should be > 40 ng/μL.

#### *b) DNA fragmentation state*

Definition: Breakage of genomic (high molecular weight) DNA into smaller DNA fragments

Acceptance criterion: For quantitative (real time-based) analysis, the molecular weight of the extracted DNA sample should be at least higher than the amplicon size produced by the event specific and the taxon specific reference systems as established by comparison with a reference nucleic acid marker.

For qualitative analysis, in case of DNA suspensions to be used in qualitative analysis, the presence of a certain proportion of DNA molecules of molecular weight lower than the amplicon size produced by the method may be considered acceptable.

#### *c) Purity of DNA extracts*

Definition: the absence of co-extracted compounds in a DNA sample impairing the efficiency of the PCR reactions and leading to a delay in the onset of the exponential phase of the amplification profile

Acceptance criterion: The difference ( $\Delta Ct$ ) average between the measured Ct value and the extrapolated Ct value of the first diluted sample of the inhibition test should be <0.5. [(measured Ct – extrapolated Ct)] <0.5 and the slope of the inhibition curve should be within -3.6 and -3.1.

The preferred PCR assay for the inhibition test is the internal control assay (e.g. the taxon specific reference system). The total DNA amount in the first sample of the dilution series should be not less than the total DNA amount used in the submitted method (e.g. the DNA amount indicated in the PCR protocol of the taxon specific reference system).

**Specificity**

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

Acceptance Criterion: The method should not produce amplification signals with target sequences different for the target sequence for which the method was developed. This should be demonstrated by similarity searches against databases (e.g. EMBL, GenBank, Patent, etc.) and with empirical results from testing the method with non-target transgenic events and non-transgenic material.

For detection of specific GM events, the target sequence shall be event specific.

For taxon specific target sequences (target sequence), the absence of allelic and copy-number variation across a globally representative and diverse sample of the species variety shall be demonstrated. Allelic and/or copy-number variation in other lines shall be reported if such variation is known by the applicant. The specificity of the target sequence shall be verified by *in silico* studies against publicly available sequence databases (e.g. EMBL, GenBank, etc.) and experimentally by demonstrating the absence of amplification products when the target sequence specific assay is applied to individual PCRs of pure genomic DNA of a representative sample of the closest relatives to the target taxa as well as of the most important food crops.

**Dynamic Range**

Definition: The range of concentrations over which the method performs in a linear manner with an acceptable level of trueness 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 range of the standard curve(s) for real-time PCR should allow testing of blind samples throughout the entire dynamic range, including the lower (10%) and upper (500%) ends.

Example: 0.09% and 4.5% for a 0.9% GMO concentration or 50 and 2500 genome copies if the target is 500 copies.

**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 shall 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:

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

Acceptance Criterion: The average value of the slope of the standard curve shall be in the range of (-3.1  $\geq$  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> shall be  $\geq 0.98$ .

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

Definition: The relative 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  $\leq 25\%$  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 Error! Reference source not found..

### ***Limit of Quantification (LOQ)***

Definition: The limit of quantification 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.

Example: For a 0.9% nominal value LOQ  $< 0.09\%$ .

### ***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<sup>th</sup> 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.

Example: For a 0.9% nominal value LOD  $< 0.045\%$ .

### ***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.

The adequacy of the robustness testing needs to be demonstrated on a method-by-method basis. For instance, for a real-time PCR method, the following factors and their origin/source shall be taken into account: different thermal cycler models, DNA polymerase, uracyl-n-glycosylase, magnesium chloride concentration, primer forward and reverse concentration, probe concentration, temperature profile, time profile, dNTP including dUTP concentrations.

Acceptance Criterion: The response of an assay with respect to these small changes shall not deviate more than  $\pm 30\%$ .

Alternatively, robustness can be demonstrated through the application of formal robustness tests using factorial designs such as those published by Plackett Burman<sup>1</sup> or Yuden<sup>2</sup>

## **Method Performance Requirements**

### ***Precision - Relative Reproducibility Standard Deviation (RSD<sub>R</sub>)***

Definition: The relative 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  $RSD_R$  should be  $< 35\%$  over the whole dynamic range. However, at concentrations  $< 0.2\%$  then  $RSD_R$  values  $< 50\%$  are deemed acceptable.

### ***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.

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1) R.L. Plackett and J.P. Burman, "The Design of Optimum Multifactorial Experiments", *Biometrika* 33 (4), pp. 305-25, June 1946.

2) Statistical Manual of the AOAC, W.J. Youdens and E.H. Steiner, 1987.



# **Event-specific Method for the Quantification of Soybean MON 87705 Using Real-time PCR**

## **Protocol**

**17 January 2012**

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

### **Method development:**

Monsanto Company

### **Method validation:**

European Union Reference Laboratory for Genetically Modified Food and Feed  
(EU-RL GMFF)  
Molecular Biology and Genomics Unit

*Drafted by*

C. Savini (scientific officer)



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*Report Review*

1) M. Querci



---

2) L. Bonfini



---

*Scientific and technical approval*

M. Mazzara (scientific officer)



---

*Compliance to EURL Quality System*

S. Cordeil (quality manager)



---

*Authorisation to publish*

G. Van den Eede (head of MBG Unit)



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**Address of contact laboratory:**

European Commission, Joint Research Centre (JRC)  
Institute for Health and Consumer Protection (IHCP)  
Molecular Biology and Genomics Unit  
European Union Reference Laboratory for GM Food and Feed  
Via E. Fermi 2749, 21027 Ispra (VA) - Italy

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## 1. General information and summary of the methodology

This protocol describes an event-specific quantitative real-time TaqMan® PCR (polymerase chain reaction) procedure for the determination of the relative content of soybean event MON 87705 DNA to total soybean 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 soybean event MON 87705 DNA, an 86-bp fragment of the region spanning the 3' plant-to-insert junction in soybean MON 87705 event is amplified using specific primers. PCR products are measured at each cycle (real-time) by means of a target-specific oligonucleotide probe labelled with the fluorescent dye FAM (6-carboxyfluorescein), as a reporter at its 5' end, and TAMRA (carboxytetramethylrhodamine) as a quencher dye at its 3' end.

For the relative quantification of soybean event MON 87705, a soybean-specific reference system amplifies a 74-bp fragment of *Le1*, a soybean endogenous gene encoding lectin, using specific primers and a *Le1* gene-specific probe labelled with FAM as a reporter dye at its 5' end, and TAMRA as a 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 "Ct" value. For quantification of the amount of MON 87705 DNA in a test sample, Ct values for the MON 87705 and *Le1* systems are determined for the sample. Standard curves are then used to estimate the relative amount of MON 87705 DNA to total soybean DNA.

## 2. Validation and performance characteristics

### 2.1 General

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

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 EU-RL GMFF. The study was undertaken with twelve participating laboratories in December 2010.



Each participant received twenty blind samples containing soybean MON 87705 genomic DNA at five GM contents, ranging from 0.1% 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 event MON 87705 in four unknown samples. Two 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 method developer, the relative LOD of the method is  $\leq 0.04\%$  in 200 ng of total soybean 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  $\leq 0.085\%$  in 200 ng of total soybean DNA. The lowest relative GM content of the target sequence included in the collaborative trial was 0.09%.

### **2.5 Molecular specificity**

According to the method developer, the method exploits a unique DNA sequence in the region of recombination between the insert and the plant genome; the sequence is specific to soybean event MON 87705 and thus imparts event-specificity to the method.

The specificity of both the event-specific and the soybean-specific assays was assessed by the method developer in real-time PCR against DNA extracted from plant materials containing the specific targets of maize GA21, NK603, MON810, MON863, MON88017, LY038, MON88034, MON87460 and conventional maize; canola RT73, RT200 and conventional canola; soybean GTS 40-3-2, MON89788, MON87769 and conventional soybean; wheat MON71800 and conventional wheat; rice, lentils, Buckwheat, peanuts (shelled), quinoa; cotton MON531, MON 15985, MON1445, MON88913 and conventional cotton.

According to the method developer, the MON 87705 assay did not react with any of the plant materials tested, except the MON 87705 positive control; the soybean-specific reference system reacted only with conventional soybean and with the soybean GM events tested.

The EU-RL GMFF assessed *in silico* the specificity of the event-specific assay by running similarity searches against the Central DNA Core Sequence Information System (CCSIS). The CCSIS contains non-publicly available DNA sequences of GM events from applications for authorisation according to Regulation No (EC) 1829/2003 on GM Food and Feed. The sequence records are stored locally on a dedicated server and are accessible with restricted user-access

integrated with common bioinformatics applications (BLAST, ClustalW, EMBOSS package) for immediate bioinformatics analyses.

The results of the bioinformatics analysis showed that part of the 5' flanking region is duplicated from the 3' flanking region. The reverse primer (MON 87705 primer 2) is located in this flanking region, i.e. it is complementary to both the 5' and 3' flanking region. Nevertheless no significant sequence similarity for the reverse primer was found in the CCSIS. The forward primer (MON 87705 primer 1) is complementary to a sequence of the left border region of the T-DNA, i.e. it matches many sequences of GM events containing the left border region. The probe is located on the junction between the insert and the duplicated 3' flanking region, covering just 2 nucleotides of the insert and 28 nucleotides of the duplicated flanking sequence.

The EU-RL GMFF consulted with the European Food Safety Authority (EFSA) on the findings of the bioinformatics analysis; after the assessment of the EFSA Molecular Characterisation Working Group of the GMO Panel, EFSA concluded that it could not find evidence for instability in event MON 87705.

### **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 used should be sterilised prior to use and any residue of DNA has to be 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 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 soybean event MON 87705

#### 3.2.1 General

The PCR set-up for the taxon specific target sequence (*Le1*) and for the GMO (event MON 87705) 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 a total volume of 50 µL per reaction mixture with the reagents as listed in Table 1 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 87705 DNA in non-GM soybean DNA for a total of 200 ng of DNA (corresponding to approximately 176991 soybean genome copies with one genome assumed to correspond to 1.13 pg of haploid soybean genomic DNA)<sup>(1)</sup>. The other four standards are prepared by serial dilution.

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 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 each 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 on ice.
2. To prepare the amplification reaction mixtures add the following components (Tables 1 and 2) in two reaction tubes (one for the MON 87705 assay and one for the *Le1* assay) on ice in the order mentioned below (except DNA).
3. Mix gently and centrifuge briefly.
4. Prepare two reaction tubes (one for the soybean MON 87705 and one for the *Le1* reaction mix) for each DNA sample to be tested (standard curve samples, unknown samples and controls).

Table 1. Amplification reaction mixture in the final volume/concentration per reaction well for the MON 87705 assay.

Component	Final concentration	µL/reaction
TaqMan® Universal PCR Master Mix (2x)	1x	25
MON 87705 forward primer (20 µM)	450 nM	1.125
MON 87705 reverse primer (20 µM)	450 nM	1.125
MON 87705 probe (5 µM)	250 nM	2.5
Nuclease free water	#	16.25
Template DNA (max 200 ng)	#	4
Total reaction volume:		50

Table 2. Amplification reaction mixture in the final volume/concentration per reaction well for the soybean *Le1* assay.

Component	Final concentration	µL/reaction
TaqMan® Universal PCR Master Mix (2x)	1x	25
<i>Le1</i> primer 1 (10 µM)	150 nM	0.75
<i>Le1</i> primer 2 (10 µM)	150 nM	0.75
<i>Le1</i> probe (5 µM)	50 nM	0.5
Nuclease free water	#	19
Template DNA (max 200 ng)	#	4
Total reaction volume:		50

- Add to each reaction tube the correct amount of reaction mix (e.g. 46 µL x 3 = 138 µL reaction mix for three PCR repetitions). Add to each tube the correct amount of DNA (e.g. 4 µL x 3 = 12 µL DNA for three PCR repetitions). Vortex each tube for approx. 10 sec. This step is mandatory to reduce to a minimum the variability among the repetitions of each sample.
- Spin down the tubes in a micro-centrifuge. Aliquot 50 µL in each well. 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.
- Place the plate into the instrument.
- Run the PCR with the cycling program described in Table 3.

Table 3. Cycling program for MON 87705/*Le1* assays.

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

### 3.3 Data analysis

After 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 87705) 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. *Le1* 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 *Le1* and the MON 87705 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 DNA copy numbers in the unknown sample.

To obtain the percentage value of event MON87705 DNA in the unknown sample, the MON 87705 copy number is divided by the copy number of the soybean reference gene (*Le1*) and multiplied by 100 (GM% = MON 87705/*Le1* x 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)
- Software for run analysis (mostly integrated in the software of the real-time PCR instrument)
- Microcentrifuge
- Micropipettes
- Vortex
- Rack for reaction tubes
- 0.2/1.5/2.0 mL reaction tubes

### 4.2 Reagents

- TaqMan<sup>®</sup> Universal PCR Master Mix (2X). Applied Biosystems Part No 4304437.

### 4.3 Primers and Probes

Name	Oligonucleotide DNA Sequence (5' to 3')	Length (nt)
MON 87705 target sequence		
MON 87705 forward primer	5' – TTC CCg gAC ATg AAg CCA TTT AC - 3'	23
MON 87705 reverse primer	5' – ACA ACg gTg CCT Tgg CCC AAA g - 3'	22
MON 87705 probe	6-FAM 5' – AAg AgA CTC Agg gTg TTg TTA TCA CTg Cgg - 3' TAMRA	30
Taxon specific <i>le1</i> target sequence		
<i>Le1</i> primer 1	5' - CCA gCT TCg CCg CTT CCT TC - 3'	20
<i>Le1</i> primer 2	5' - gAA ggC AAg CCC ATC TgC AAg CC - 3'	23
<i>Le1</i> probe	6-FAM 5' - CTT CAC CTT CTA TgC CCC TgA CAC -3' TAMRA	24

FAM: 6-carboxyfluorescein; TAMRA: tetramethylrhodamine



## 5. References

1. Royal Botanic Garden, Kew. Plant DNA c-values database. <http://data.kew.org/cvalues/>



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#### Abstract

The European Union Reference Laboratory for Genetically Modified Food and Feed (EU-RL 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 87705 transformation event in soybean DNA (unique identifier MON-87705-6). The collaborative trial was conducted according to internationally accepted guidelines (1, 2).

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 (genomic DNA from soybean seeds harbouring the MON 87705 event and from conventional soybean seeds). The EU-RL GMFF 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 Regulation (EC) No 641/2004.

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

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Key policy areas include: environment and climate change; energy and transport; agriculture and food security; health and consumer protection; information society and digital agenda; safety and security, including nuclear; all supported through a cross-cutting and multi-disciplinary approach.

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