

JRC VALIDATED METHODS, REFERENCE
METHODS AND MEASUREMENTS REPORTS

Event-specific Method for the Quantification of Maize Event 3272 Using Real-time PCR

*Validation Report
And*

Validated Method

Corrected version 1 – 11 November 2014

Replace version – 7 November 2008

2014



This document replaces a document with the same title with ISBN number 978-92-79-11045-0 and PUBSY request JRC48922. The correction made in the new document is a correction in the Validated Method (Protocol), Page 7/11 Table 1 and Table 2, column "Components ": Sigma Jumpstart ReadyMix (2x) replaced by Supplemented 2x Sigma JumpStart ReadyMix.

European Commission

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JRC94616

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Printed in Italy

Event-specific Method for the Quantification of Maize Event 3272 Using Real-time PCR

Validation Report

7 November 2008

**Joint Research Centre
Institute for Health and Consumer Protection
Biotechnology & GMOs Unit**

Executive Summary

The JRC as Community Reference Laboratory for GM Food and Feed (CRL-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 3272 transformation event in maize DNA (unique identifier SYN-E3272-5). 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", Syngenta Seeds S.A.S. provided the detection method and the samples (genomic DNA of conventional maize and of maize event 3272). The JRC prepared the validation samples (calibration samples and blind samples at unknown GM percentage [DNA/DNA]). The collaborative trial involved twelve laboratories from eleven 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.it/>.


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Report on Steps 1-3 of the Validation Process

Syngenta Seeds S.A.S. submitted the detection method and control samples for maize event 3272 (unique identifier SYN-E3272-5) 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 Community Reference Laboratory for Genetically Modified Food and Feed (CRL-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 to 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 CRL-GMFF Validation Process", <http://gmo-crl.jrc.it/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.it/guidancedocs.htm>) (see Annex 1 for a summary of method acceptance criteria and method performance requirements). During step 2, four scientific assessments were performed and requests of complementary information addressed to the applicant. The scientific assessment of the detection method for event 3272 was positively concluded in December 2007.

In December 2007, the CRL-GMFF verified experimentally the method characteristics (step 3, experimental testing of the samples and methods) by quantifying five blind GM levels within the range 0.09%-8.00% on a DNA/DNA ratio. The experiments were performed under repeatability conditions and demonstrated that the PCR 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 of the same matrix and a report published on the CRL-GMFF web site on 20th April 2007 (<http://gmo-crl.jrc.it/statusofdoss.htm>).

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

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1. Introduction

Syngenta Seeds S.A.S. submitted the detection method and control samples for maize event 3272 (unique identifier SYN-E3272-5) 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, Biotechnology and GMOs Unit of the Institute for Health and Consumer Protection) as Community Reference Laboratory for Genetically Modified Food and Feed (see Commission Regulation EC No 1829/2003) organised the international collaborative study for the method of detection and quantification of 3272 maize. The study involved twelve laboratories from eleven European countries, among those listed in Annex II ("National reference laboratories assisting the CRL 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 in-house experimental evaluation of the method was carried out in December 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 January 2008.

A method for DNA extraction from maize seeds, submitted by the applicant, was previously evaluated by the CRL-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.it/>.

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® PCR procedure for the determination of the relative content of event 3272 DNA to total maize DNA. The procedure is a simplex system, in which a maize *alcohol dehydrogenase (adh1)* endogenous assay (reference gene) and the target assay (3272) 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.

In January 2008 the CRL-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 CRL 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 event 3272.

Thirty-four laboratories expressed in writing their willingness to participate, two declined the invitation, while thirty-six did not answer. The CRL-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 event 3272.

Laboratory	Country
Central Agricultural Office, Food and Feed Safety Directorate, 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
Groupe d'Intérêt Public – Groupe d'Etude et de contrôle des Variétés et des Semences	FR
Institute for Agricultural and Fisheries Research (ILVO)	BE
Institute of Biochemistry and Biophysics Polish Academy of Sciences, Genetic Modifications Analysis Laboratory	PL
National Centre for Food, Spanish Food Safety Agency	ES
National Food Institute, Dept. of Toxicology and Risk Assessment	DK
National Institute of Biology	SI
National Institute of Chemical Physics and Biophysics (NICPB), the Laboratory of Molecular Genetics (LMG)	EE
State Institute of Chemical and Veterinarian Analysis	DE
Veterinary Public Health Institute for Lazio and Toscana Regions; National Reference Centre for GMO Analysis	IT

3. Materials

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

- i) genomic DNA extracted from maize leaf tissue harbouring the event 3272 (NPH8431AMY/NP911AMY)
- and
- ii) genomic DNA extracted from non-GM maize leaf tissue (NPH8431/NP911)

were provided by the applicant in accordance to the provisions of Commission 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% maize event 3272 and non-GM maize genomic DNA at different GMO concentrations were prepared by the CRL-GMFF, using the control samples provided, in a constant amount of total maize DNA.

Participants received the following materials:

- ✓ Five calibration samples (200 µL of DNA solution each) for the preparation of the standard curve, labelled from S1-0306 to S5-0306.
- ✓ Twenty unknown DNA samples (100 µL of DNA solution each), labelled from U1-0306 to U20-0306.
- ✓ Amplification reagent control for use on each PCR plate.
- ✓ Reaction mix components:

<input type="checkbox"/> Sigma Jumpstart Ready mix 2x, 1 vial:	8 mL
<input type="checkbox"/> Sulforhodamine 1.5 mM, 1 vial:	200 µL
<input type="checkbox"/> Distilled sterile water, 1 vial:	4 mL

Sulforhodamine was provided for equipment calibration purposes

- ✓ Primers and probes (1 tube each) as follows:

<input type="checkbox"/> Zm <i>adh1</i> Endogenous Assay Stock (50x):	160 µL
<input type="checkbox"/> Event 3272 Assay Stock (50x):	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 for the 3272 specific system and the *Adh1* 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. 3272 GM contents

3272 GM% (GM DNA/Non-GM DNA x 100)
0.09
0.40
0.90
5.00
8.00

5. Method

Description of operational steps followed

For the specific detection of event 3272 DNA, a 95-bp fragment of the integration region of the construct inserted into the plant genome (5' 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 3272 DNA, a maize-specific reference system amplifies a 135-bp fragment of the maize endogenous gene *adh1* (*alcohol dehydrogenase*), using two *Adh1* gene-specific primers and an *Adh1* gene-specific probe labelled with VIC and TAMRA.

For relative quantification of event 3272 DNA in a test sample, the normalised ΔC_t values of calibration samples are used to calculate, by linear regression, a standard curve (plotting ΔC_t values against the logarithm of the amount of event 3272 DNA). The normalised ΔC_t values of the unknown samples are measured and, by means of the regression formula, the relative amount of event 3272 DNA is estimated.

Calibration samples denominated from S1-0306 to S5-0306 were prepared by mixing the appropriate amount of 3272 DNA from the stock solution with non-GM maize DNA to obtain the following relative contents of 3272: 10%, 5.0%, 1.0%, 0.5% and 0.08%. The total DNA amount per reaction was 250 ng, with 5 μ L of a DNA solution at the concentration of 50 ng/ μ L for each reaction.

The GM contents of the calibration samples and the total DNA quantity used in PCR are provided in Table 3.

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

Sample code	S1-0306	S2-0306	S3-0306	S4-0306	S5-0306
Total amount (ng) of DNA in reaction	250	250	250	250	250
GM% (DNA/DNA)	10.00	5.00	1.00	0.50	0.08

6. Deviations reported

Eight laboratories reported no deviations from the protocol.

One laboratory did not use the manual threshold setting but the automatic one of ABI Prism 7900 instrument.

One laboratory received two tubes U16-3272 and decided to label one of them U3-3272. The same laboratory received an empty tube for S4-0306.

One laboratory performed all tests are done on a ABI Prism 7000 instrument with "ROX" as the passive reference dye instead of sulforhodamine.

One laboratory performed all tests in 20 µL reactions (due to the use of 384-well plates on ABI Prism 7900 instrument). PCR reagents volumes were re-calculated to achieve the final concentration written in the protocol.

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 are summarised in Table 4.

The mean PCR efficiency was 102%, and the average linearity of the method was 1.00. Data reported in Table 4 confirm the appropriate performance characteristics of the method in terms of efficiency and linearity.

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

LAB	PLATE	Slope	PCR Efficiency (%)	Linearity (R^2)
1	A	-3.54	91	1.00
	B	-3.42	96	0.99
2	A	-3.40	97	1.00
	B	-3.27	102	1.00
3	A	-3.32	100	1.00
	B	-3.37	98	1.00
4	A	-3.22	105	1.00
	B	-3.28	102	1.00
5	A	-3.21	105	1.00
	B	-3.19	106	1.00
6	A	-3.30	101	1.00
	B	-3.41	97	1.00
7	A	-2.73	132	0.97
	B	-3.29	101	0.99
8	A	-3.21	105	1.00
	B	-3.20	105	1.00
9	A	-3.26	102	0.99
	B	-3.34	99	1.00
10	A	-3.32	100	1.00
	B	-3.26	103	1.00
11	A	-3.30	101	1.00
	B	-3.32	100	1.00
12	A	-3.28	102	1.00
	B	-3.29	101	1.00
Mean		-3.28	102	1.00

GMO quantification

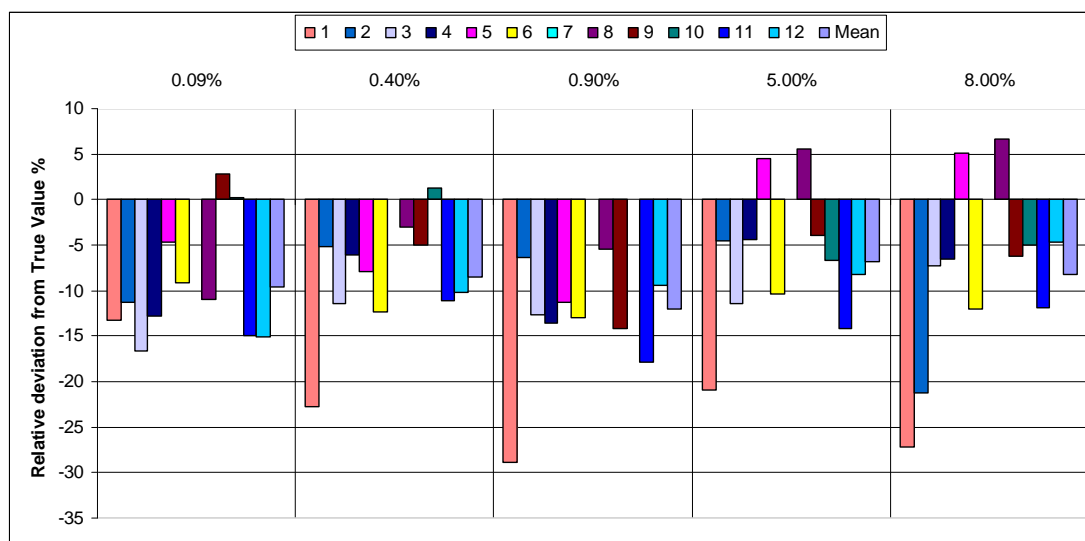
Table 5 shows the mean values of the four replicates for each GM level as provided by all laboratories. Each mean value is the average of three PCR repetitions.

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

	GMO content (%)																			
LAB	0.09				0.4				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	0.09	0.05	0.10	0.40	0.27	0.30	0.27	0.67	0.70	0.55	0.64	4.17	3.88	3.82	2007.00	2007.00	7.96	4.85	4.65
2	0.08	0.05	0.09	0.11	0.32	0.38	0.42	0.40	0.87	0.83	0.73	0.93	4.57	5.29	4.73	4.51	2.05	7.39	7.65	8.14
3	0.08	0.07	0.08	0.07	0.33	0.35	0.40	0.34	0.86	0.74	0.78	0.76	4.62	4.35	4.29	4.45	7.53	8.01	6.83	7.29
4	0.09	0.06	0.09	0.08	0.38	0.40	0.39	0.32	0.73	0.81	0.84	0.73	4.73	4.70	4.99	4.72	7.83	7.55	6.90	7.66
5	0.09	0.08	0.09	0.08	0.35	0.39	0.36	0.37	0.82	0.82	0.79	0.76	4.60	5.79	5.25	5.26	8.93	8.03	8.49	8.19
6	0.10	0.08	0.07	0.08	0.34	0.38	0.36	0.32	0.77	0.82	0.79	0.76	5.04	4.24	4.51	4.13	6.79	7.14	7.19	7.00
7	0.13	0.06	0.12	0.05	0.64	0.27	0.27	0.43	1.73	1.32	1.28	0.91	5.40	4.04	5.84	8.61	16.95	9.37	10.63	9.37
8	0.08	0.08	0.09	0.08	0.30	0.45	0.40	0.39	0.97	0.80	0.73	0.91	4.62	5.44	5.52	5.53	9.98	7.34	7.79	9.03
9	0.11	0.08	0.09	0.09	0.38	0.44	0.36	0.34	0.74	0.79	0.79	0.77	5.04	4.52	4.60	5.07	7.56	7.65	6.92	7.90
10	0.07	0.09	0.09	0.11	0.44	0.38	0.39	0.40	0.92	0.93	0.87	0.88	4.78	4.72	4.56	4.59	7.42	7.67	7.58	7.74
11	0.08	0.08	0.08	0.08	0.38	0.37	0.39	0.28	0.78	0.73	0.76	0.68	4.80	3.99	4.38	3.98	6.65	7.39	7.20	6.97
12	0.08	0.08	0.08	0.07	0.37	0.34	0.36	0.36	0.80	0.84	0.78	0.84	4.67	4.50	4.45	4.72	7.59	7.71	7.50	7.70

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 bar represents the overall mean for each GM level (%) tested.

Figure 1. Relative deviation (%) from the true value of 3272 for all laboratories



On average, the true value was underestimated at all GM levels. But only one laboratory reported a relative deviation from the true value > 25%, at GM levels 0.4%, 0.9% and 8.0%.

On average, the relative deviations from the true values are below 10% (absolute value) for GM levels 0.09%, 0.4%, 5% and 8%. The relative deviation from the true value at GM level 0.9% is -12%.

Overall, the bias was well within the acceptance criterion (25%) at all GM levels tested, indicating a satisfactory trueness of the method.

8. Method performance requirements

Among the performance criteria established by the ENGL and adopted by the CRL-GMFF (<http://gmo-crl.jrc.it/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 17% at the 8.00% GM level.

Table 6. Summary of 3272 validation results.

Unknown sample GM%	Expected value (GM%)				
	0.09	0.40	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	1	1
Reason for exclusion	1 C. test	1 C. test	1 C. test	1 C. test	1 C. test
Mean value	0.08	0.37	0.79	4.66	7.35
Relative repeatability standard deviation, RSD_r (%)	16	11	7.1	6.7	15
Repeatability standard deviation	0.01	0.04	0.06	0.31	1.09
Relative reproducibility standard deviation, RSD_R (%)	16	12	10	9.9	17
Reproducibility standard deviation	0.01	0.04	0.08	0.46	1.22
Bias (absolute value)	-0.01	-0.03	-0.11	-0.34	-0.65
Bias (%)	-9.6	-8.5	-12	-6.8	-8.2

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 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 CRL-GMFF requires that 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.it/guidancedocs.htm>)).

As can be observed from the values reported in Table 6, the method provided a relative repeatability standard deviation below 25% at all GM levels, with the highest value of RSD_r (%) equal to 16% at the 0.09% 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. In this case the method fully satisfies this requirement across the entire dynamic range tested; with the highest value of bias (%) is -12% at the 0.9% GM 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.it/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.

The method is therefore 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 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)].

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 E. D., 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: $\text{Efficiency} = [10^{(-1/\text{slope})}] - 1$

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

R² Coefficient

Definition: the R² coefficient is the correlation coefficient of a standard curve obtained by linear regression analysis.

Acceptance Criterion: the average value of R² should be ≥ 0.98 .

Repeatability Standard Deviation (RSD_r)

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 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 $1/10^{\text{th}}$ of the value of the target concentration with an $\text{RSD}_r \leq 25\%$. 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.



EUROPEAN COMMISSION
JOINT RESEARCH CENTRE
Institute for Health and Consumer Protection
Molecular Biology and Genomics Unit



Event-specific Method for the Quantification of Maize Event 3272 Using Real-time PCR

Validated Method

7 November 2008

Corrected version 1 – 11 November 2014

Method development:

Syngenta Seeds S.A.S.

Method validation:

European Union Reference Laboratory for GM Food and Feed (EU-RL GMFF)

Quality assurance

The EU-RL GMFF is ISO 17025:2005 accredited [certificate number: ACCREDIA 1172, (Flexible Scope for DNA extraction and qualitative/quantitative PCR) - Accredited tests are available at http://www.accredia.it/accredia_labsearch.jsp?ID_LINK=293&area=7].

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

The EU-RL GMFF is also ISO 17043:2010 accredited (proficiency test provider) and applies the corresponding procedures and processes for the management of ring trials during the method validation.

The EU-RL GMFF conducts its activities under the certification ISO 9001:2008 of the Institute for Health and Consumer Protection IHCP provided by CERMET.

Modifications from the previous version:

Page 7/11 Table 1 and Table 2, column "Components ":
Sigma Jumpstart ReadyMix (2x) replaced by Supplemented 2x Sigma JumpStart ReadyMix

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1. General information and summary of the methodology

This protocol describes an event-specific real-time quantitative TaqMan® PCR procedure for the determination of the relative content of event 3272 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 the 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 event 3272 DNA, a 95-bp fragment of the integration region of the construct inserted into the plant genome (located at the 5' 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 two fluorescent dyes: FAM as a reporter dye at its 5' end and TAMRA as a quencher dye at its 3' end.

For the relative quantification of event 3272 DNA, a maize-specific reference system amplifies a 135-bp fragment of the maize endogenous *alcohol dehydrogenase 1* gene (*adh1*), using two specific primers and an *adh1* gene-specific probe labelled with VIC 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 3272 DNA in a test sample, the normalised ΔC_t values of the calibration samples are used to calculate by linear regression a reference curve ΔC_t -formula. The normalised ΔC_t values of the unknown samples are measured and, by means of the regression formula, the relative amount of event 3272 DNA is estimated.

2. Validation status and performance characteristics

2.1 General

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

The reproducibility and trueness of the method were tested through an international collaborative study 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 January 2008.

Each participant received twenty unknown samples containing 3272 maize 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 3272 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.it/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 0.04% in 250 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 < 0.09% in 250 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

According to the applicant, 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 3272 and thus imparts event-specificity to the method.

The specificity of the 3272 assay (forward/reverse primers and probe) was experimentally tested by the applicant in real-time PCR against DNA extracted from samples containing GM maize Bt11, Bt176, GA21, NK603, MON810, MON863, MON810 x MON863, non-GM 3272.

According to the applicant, none of the above mentioned GM lines tested, except the positive control 3272, produced amplification signals in replicated samples when 250 ng total DNA per reaction were used.

3. Procedure

3.1 General instructions and precautions

- The procedures require sterile conditions working experience.
- Laboratory organisation, e.g. “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 hypochlorite solution (bleach).
- Pipettes should be checked regularly for precision and calibrated, if necessary.
- All handling steps - unless specified otherwise - should be carried out at 0 - 4°C.
- In order to avoid repeated freeze/thaw cycles aliquots should be prepared.

3.2 Real-time PCR for quantitative analysis of maize 3272

3.2.1 General

The PCR set-up for the taxon specific target sequence (*adh1*) and for the GMO (3272) 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 250 ng of template DNA per reaction well is recommended.

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

3.2.2 Calibration

The calibration curve consists of five samples containing fixed percentages of 3272 DNA in a total amount of 250 ng maize DNA. The GM content of the standard samples ranges from 10% to 0.08%.

A calibration curve is produced by plotting the ΔC_t values of calibration samples against the logarithm of the respective GM% contents; the slope (a) and the intercept (b) of the calibration curve ($y = ax + b$) are then used to calculate the mean GM% content of the blind samples based on their normalised ΔC_t values.

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. In two reaction tubes (one for the 3272 system and one for the *adh1* 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 maize *adh1* reference system.

Component	Final concentration	$\mu\text{L}/\text{reaction}$
Supplemented 2x Sigma JumpStart ReadyMix	1x	12.5
50x Zm Adh1 Assay Stock	1x	0.5
Nuclease free water	#	7
Template DNA (max 250 ng)	#	(5)
Total reaction volume:		25

Table 2. Amplification reaction mixture in the final volume/concentration per reaction well for the 3272 specific system.

Component	Final concentration	$\mu\text{L}/\text{reaction}$
Supplemented 2x Sigma JumpStart ReadyMix	1x	12.5
50x 3272 Assay Stock	1x	0.50
Nuclease free water	#	7
Template DNA (max 250 ng)	#	(5)
Total reaction volume:		25

3. Mix gently and centrifuge briefly.
4. Prepare two reaction tubes (one for the 3272 and one for the *adh1* master mixes) for each DNA sample to be tested (standard curve samples, unknown samples and control samples).

5. Add to each reaction tube the correct amount of master mix (e.g. $20 \times 3 = 60 \mu\text{L}$ master mix for three PCR repetitions). Add to each tube the correct amount of DNA (e.g. $5 \times 3 = 15 \mu\text{L}$ DNA for three PCR repetitions). Vortex each tubes for approx. 10 sec. This step is mandatory to reduce to a minimum the variability among the repetitions of each sample.
6. Spin down the tubes in a microcentrifuge. Aliquot 25 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.
7. Place the plate into the instrument.
8. Run the PCR with the cycling program described in Table 3

Table 3. Cycling program for maize 3272/*adh1* systems

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	No	40
		Annealing & Extension	60°C	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. 3272) 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 (or apply)" 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 $\text{Ct} = 25 - 3 = 22$).
- c) Save the settings.
- d) Repeat the procedure described in a) and b) on the amplification plots of the other system (e.g. *adh1* system).
- e) Save the settings and export all the data into an Excel 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 reference Δ Ct-curve is generated by plotting the Δ Ct-values measured for the calibration points against the logarithm of the GM% content, and by fitting a linear regression line into these data.

Thereafter, the regression formula is used to estimate the relative amount (%) of 3272 event in the unknown samples of DNA.

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
- 1.5/2.0 mL reaction tubes

4.2 Reagents and solutions

- Sigma JumpStart Taq ReadyMix (2x), Sigma Aldrich Ltd Cat No P-2893
- Sulforhodamine 101, Sigma Cat No S-7635
- 1 M MgCl₂, Sigma Aldrich Ltd Cat No M-1028

10000x Sulforhodamine 101 stock:

Resuspend 227.5 mg of Sulforhodamine 101 in 250 mL nuclease free water to make a 1.5 mM stock solution.

Vortex well and store at -20 °C.

Supplemented 2x Sigma JumpStart ReadyMix:

For 50 mL: to Sigma Jumpstart Taq ReadyMix (2X), add:

- 550 µL of 1 M MgCl₂

- 20 µL 10000x Sulforhodamine 101.
- Vortex well and store at 4 °C for up to 1 year.

4.3 Primers and Probes

Name	Oligonucleotide DNA Sequence (5' to 3')
3272 target sequence	
ES3272-F	5' – TCA TCA GAC CAG ATT CTC TTT TAT GG -3'
ES3272-R	5' – CGT TTC CCG CCT TCA GTT TA -3'
ES3272-P	FAM 5'- ACT GCT GAC GCG GCC AAA CAC TG -3' TAMRA
Reference gene <i>adh1</i> target sequence	
Zm <i>adh1</i> -F	5' – CGT CGT TTC CCA TCT CTT CCT CC-3'
Zm <i>adh1</i> -R	5' – CCA CTC CGA GAC CCT CAG TC -3'
Zm <i>adh1</i> -P	VIC 5' – AAT CAG GGC TCA TTT TCT CGC TCC TCA-3' TAMRA

50x Zm *adh1* Endogenous Assay Stock:

For 1 mL add:

- 15 µL of ZmAdh1-F (1000 µM)
 - 15 µL of ZmAdh1-R (1000 µM)
 - 100 µL of ZmAdh1-P (100 µM)
 - 870 µL of nuclease-free water
- Vortex well and store at 4 °C for up to 1 year.

50x Event 3272 Assay Stock:

For 1 mL add:

- 2.5 µL of ES3272-F (1000 µM)
 - 45 µL of ES3272-R (1000 µM)
 - 100 µL of ES3272-P (100 µM)
 - 852.5 µL of nuclease-free water
- Vortex well and store at 4 °C for up to 1 year.

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European Commission

Joint Research Centre – Institute for Health and Consumer Protection

Title: Event-specific Method for the Quantification of Maize Event 3272 Using Real-time PCR

Author(s): European Union Reference Laboratory for Genetically Modified Food and Feed

2014 – 28 pp. – 21.0 x 29.7 cm

Abstract

The JRC as European Union Reference Laboratory for GM 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 3272 transformation event in maize DNA (unique identifier SYN-E3272-5). 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*, Syngenta Seeds S.A.S. provided the detection method and the samples (genomic DNA of conventional maize and of maize event 3272). The JRC prepared the validation samples (calibration samples and blind samples at unknown GM percentage [DNA/DNA]). The collaborative trial involved twelve laboratories from eleven 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.

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