



EUROPEAN COMMISSION
JOINT RESEARCH CENTRE

Directorate F – Health, Consumers and Reference
Materials

Food & Feed Compliance (F.5)



Event-specific Method for the Quantification of maize MZIR098 by Real-time PCR

Validated Method

Method development:

Syngenta Crop Protection NV/SA

1. General information and summary of the methodology

This protocol describes an event-specific real-time quantitative TaqMan[®] PCR (polymerase chain reaction) procedure for the determination of the relative content of maize event MZIR098 (unique identifier SYN-ØØØ98-3) DNA to total maize DNA in a sample.

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

For the detection of GM event MZIR098, a 73 bp fragment of the region spanning the 5' plant-to-insert junction in maize MZIR098 is amplified using specific primers. PCR products are measured during each cycle (real-time) by means of a target-specific oligonucleotide probe labelled with FAM (6-carboxyfluorescein) as reporter dye at its 5' end and BHQ-1 (Black Hole Quencher[®] 1) as non-fluorescent quencher dye at its 3' end.

For the relative quantification of GM event MZIR098, an maize taxon-specific system amplifies a 135 bp fragment of a maize *alcohol dehydrogenase 1 (adh1)* endogenous gene (Accession number, GeneBank: AY691949.1), using *adh1* gene-specific primers and a *adh1* gene-specific probe labelled with VIC[®] as reporter dye at its 5' end and TAMRA (6-carboxytetramethylrhodamine) as quencher dye at its 3' end.

The measured fluorescence signal passes a threshold value after a certain number of cycles. This threshold cycle is called the "Cq" value. For quantification of the amount of MZIR098 DNA in a test sample, Cq values for the MZIR098 and the *adh1* systems are determined for the sample. Standard curves are then used to estimate the relative amount of MZIR098 DNA to total maize DNA.

2. Validation and performance characteristics

2.1 General

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

2.2 Collaborative trial

The method was validated in an international collaborative study by the European Union Reference Laboratory for GM Food and Feed (EURL GMFF). The study was undertaken with twelve participating laboratories in May-June 2018.

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

2.3 Limit of detection (LOD)

According to the method developer, the relative LOD of the method is at least 0.01 % (copies GM/total haploid genome copies) in 200 ng of total suitable maize DNA. The relative LOD was not assessed in the collaborative study.

2.4 Limit of quantification (LOQ)

According to the method developer, the relative LOQ of the method is at least 0.063 % (copies GM/total haploid genome copies) in 200 ng of total suitable maize DNA. The lowest relative GM content of the target sequence included in the collaborative trial was 0.1 % (mass fraction of GM-material).

2.5 Molecular specificity

The method exploits a unique DNA sequence in the region spanning the 5' plant-to-insert junction in maize MZIR098 and is therefore event-specific for the event MZIR098. This was confirmed in the validation study.

3. Procedure

3.1 General instructions and precautions

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

3.2 Real-time PCR for quantitative analysis of maize event MZIR098

3.2.1 General

The real-time PCR set-up for the taxon (*adh1*) and the GMO (event MZIR098) target sequences are carried out in separate vials. Multiplex qPCR (using differential fluorescent labels for the probes) has not been tested or validated by the EURL GMFF.

The method is developed for a total volume of 25 µL per reaction mixture for the GM (event MZIR098) and the taxon (*adh1*) assay with the reagents as listed in Table 2 and Table 3.

3.2.2 Calibration

The calibration curves have to be established on at least five samples. The first point of the calibration curve (S1) should be established for a sample containing 10 % maize MZIR098 DNA in a total of 250 ng of maize DNA (corresponding to 91575 maize haploid genome copies with one haploid genome assumed to correspond to 2.73 pg of maize genomic DNA)⁽¹⁾. Standards S2 to S5 are to be prepared by serial dilutions (dilution factor 5.0 for samples S2-S4 and dilution factor 4.0 for standard S5) according to Table 1 below.

Table 1. Copy number values of the standard curve samples

Sample code	S1	S2	S3	S4	S5
Total amount of maize DNA in reaction (ng)*	250	50	10	2	0.50
Maize haploid genome copies	91575	18315	3663	733	183
MZIR098 copies	9158	1832	366	73	18

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

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

3.2.3 Real-time PCR set-up

1. Thaw, mix and centrifuge the components needed for the run. Keep thawed reagents on ice.
2. In two tubes on ice, add the components in the order mentioned below (except DNA) to prepare the reaction mixes for the MZIR098 maize specific system (Table 2) and the *adh1* reference gene system (Table 3). Please note that additional volume is included in the total to cover pipetting variability due to the viscosity of the solution.

Table 2. Amplification reaction mixture in the final volume/concentration per reaction well for the MZIR098 assay.

Component	Final concentration	µL/reaction
Supplemented Jumpstart™ Taq ReadyMix™ (2x)	1x	12.5
MZIR098 forward primer (10 µM)	300 nM	0.75
MZIR098 reverse primer (10 µM)	300 nM	0.75
MZIR098 probe* (10 µM)	100 nM	0.25
Nuclease free water	-	5.75
DNA	-	5.0
Total reaction volume:		25 µL

*TaqMan® probe labelled with 6-FAM at its 5'-end and BHQ-1 at its 3'-end

Table 3. Amplification reaction mixture in the final volume/concentration per reaction well for the maize *adh1* assay.

Component	Final concentration	µL/reaction
Supplemented Jumpstart™ Taq ReadyMix™ (2x)	1x	12.5
Zm <i>adh1</i> primer F (10 µM)	300 nM	0.75
Zm <i>adh1</i> primer R (10 µM)	300 nM	0.75
Zm <i>adh1</i> probe* (10 µM)	200 nM	0.50
Nuclease free water	-	5.5
DNA	-	5.0
Total reaction volume:		25 µL

*TaqMan® probe is labelled with VIC® at its 5'-end and TAMRA at its 3'-end

3. Mix well and centrifuge briefly.
4. Prepare two 0.5 mL reaction tubes (one for the maize MZIR098 and one for the *adh1* system) for each DNA sample to be tested (standard curve samples, unknown samples and control samples).
5. Add an optical cover on the reaction plate and briefly centrifuge the plate.

6. Place the reaction plate in the real-time PCR apparatus (possibly apply a compression pad, depending on the model), according to the manufacturer's instructions and your Standard Operating Procedures and start the run.
7. Select FAM as reporter dye for the MZIR098 and VIC[®] for the *adh1* reference system. Define BHQ-1 or non-fluorescent as quencher dye for MZIR098 specific system and TAMRA for *adh1* reference system. Select Sulforhodamine as the passive reference dye. Enter the correct reaction volume (25 µL).
8. Run the PCR with the cycling program described in Table 4. Those using the second derivative maximum analysis method (an option e.g. on Roche LC480 instruments) are advised to program 45 cycles instead of 40, in order to be able to quantify down to Cq 40.

Table 4. Cycling program for MZIR098/*adh1* assays.

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

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

3.3 Data analysis

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

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

3.4 Calculation of results

After having defined a threshold value within the logarithmic phase of amplification as described above, the instrument's software calculates the Cq values for each reaction.

The standard curves are generated both for the *adh1* and the MZIR098 specific assays by plotting the Cq values measured for the calibration points against the logarithm of the DNA copy numbers and by fitting a linear regression line into these data.

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

To obtain the percentage value of event MZIR098 DNA in the unknown sample, the MZIR098 copy number is divided by the copy number of the maize endogenous gene *adh1* and multiplied by 100 ($GM\% = MZIR098/adh1 \times 100$).

4. Equipment and Materials

4.1 Equipment

- Real-time PCR instrument for plastic reaction vessels (glass capillaries are not recommended for the described buffer composition) and appropriate analysis software
- 96-well reaction plates
- Optical caps/adhesion covers

- Microcentrifuge
- Micropipettes
- Standard bench top centrifuge with rotor or standard microfuge fit for 0.5 mL reaction tubes, centrifuge for 96-Well reaction plates
- Vortex
- Racks for reaction tubes, also cooled
- 0.5, 1.5 mL and 5 or 15 mL DNase free reaction tubes

4.2 Reagents

- JumpStart™ Taq ReadyMix™ (requires supplement, see below) Sigma-Aldrich® Catalogue Number P2893
- 1X TE buffer pH 8.0 Sigma-Aldrich® catalogue Number 93283
- Nuclease-free Water (e.g. HPLC Gradient Grade) Ambion® Product Number AM9937
- 1 M MgCl₂ Sigma-Aldrich® catalogue Number M1028
- Sulforhodamine 101 Sigma-Aldrich® catalogue Number S7635

10.000X 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 JumpStart™ Taq ReadyMix™ (2X)

For 50 mL: to 49.43 mL of 2X JumpStart™ Taq ReadyMix™ add:

- 550 µL of 1 M MgCl₂ (11 mM final concentration)
- 20 µL 10000X Sulforhodamine 101 stock (600 nM final concentration)

Vortex well and store at 4°C for up to 1 year.

4.3 Primers and Probes

Table 5. Primers and probes for the MZIR098 and *adh1* methods

	Name	DNA Sequence (5' to 3')	Length (nt)
<i>MZIR098</i>			
Forward primer	MZIR098 forward primer	ATC TCA GAC ACC AAA CCG AGA TC	23
Reverse primer	MZIR098 reverse primer	ACA CCG TTA GGC TAG TGC CAG T	22
Probe	MZIR098 probe	FAM-CAA GTG ACA GCG AAC GGA GCT GGT TT- BHQ-1	26
<i>adh1</i>			
Forward primer	Zm <i>adh1</i> primer F	CGT CGT TTC CCA TCT CTT CCT CC	23
Reverse primer	Zm <i>adh1</i> primer R	CCA CTC CGA GAC CCT CAG TC	20
Probe	Zm <i>adh1</i> probe	VIC-AAT CAG GGC TCA TTT TCT CGC TCC TCA-TAMRA	27

FAM: 6-carboxyfluorescein; BHQ-1: black hole quencher 1; VIC: VIC[®]; TAMRA: carboxytetramethylrhodamine.

5. References

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