Joint Research Centre

Conversion factors in GMO measurements: the past and the future

Buttinger, G., Broothaerts, W.

2025

Contact information
Name: EU Reference Laboratory for GM Food and Feed
Address: JRC-Geel
Email: jrc-eurl-gmff@ec.europa.eu

The Joint Research Centre: EU Science Hub
https://joint-research-centre.ec.europa.eu

JRC144947

Geel: European Commission, 2025

How to cite this report: Buttinger, G. and Broothaerts, W., *Conversion factors in GMO measurements: the past and the future,* European Commission, Geel, 2025, JRC144947.

Contents

Abstract

Conversion factors are the key link in GMO measurements for the conversion of a result obtained in a GM copy number per haploid genome ratio into the legally required GM mass fraction expressed per mass of the ingredient or species.

Therefore, we propose in this report to attribute a fixed, common conversion factor to each GMO CRM, considering the zygosity and type of plant material used for the production of the CRM, the biology of the seed, and the parental origin of the GM DNA.

Authors

Gerhard Buttinger, Wim Broothaerts

Executive summary

Conversion factors are the key link in GMO measurements for the conversion of a result obtained in a GM copy number per haploid genome ratio into the legally required GM mass fraction expressed per mass of the ingredient or species.

This is in particular the case for digital PCR measurements where no calibration with CRMs is necessary and results are obtained as copy number ratios. The conversion factor allows not only expressing the result as a mass fraction but is also the crucial link to the established metrological anchor point for GMO measurements, the CRM.

Currently 73 conversion factors have been determined. These factors were established experimentally from the results of 3 or 4 laboratories. We have reviewed the results obtained in the last 6 years for several crops. We observed that the conversion factors were in most cases very well in agreement with the expected value based on the type of plant material, the plant species and the zygosity and parental origin of the GM material used for the production of the CRM.

Therefore, we propose in this report to attribute a fixed, common conversion factor to each CRM, taking into account the zygosity and type of plant material used for the production of the CRM, the biology of the seed, and the parental origin of the GM DNA. Based on these factors, we present a flow chart for prediction of the conversion factor for different types of CRMs. To confirm the predictions, the conversion factor will be experimentally verified by the JRC. This experimental verification can be part of the agreed procedure to assess the appropriateness of each of the CRMs prior to their commercial release.

This makes the use of conversion factors in GMO analysis more predictable and avoid attributing slightly modified values for new batches that may be attributable to experimental variations.

1 Introduction

Current EU legislation regarding the expression of the measurement results on the genetically modified (GM) content in food, feed and seeds prescribes mass fraction (m/m %) as the measurement unit. Although not all GMO regulations specify that the results should be expressed as a GM mass fraction, it is understood that mass fraction is the unit of choice [1]. The GM mass fraction is expressed as the percentage of the masses of the GM material versus the total material of the species. This report focuses on the official control based on EU legislation. Therefore, the data is solely based on measurements of CRMs produced for the official control within the EU.

The measurement of the GM content in a sample is routinely performed by applying a quantitative real-time polymerase chain reaction (qPCR) method calibrated with CRMs. These GMO CRMs are certified for their GM mass fraction. However, digital polymerase chain reaction (dPCR) has emerged as a new promising technique that starts to be used in official control laboratories [2], [3], [4]. Such dPCR methods target the same amplicons as those validated for the qPCR assays and use the same primers and probes. However, the experimental conditions for dPCR need to be verified and in some cases optimised [5]. The full validation of a dPCR method for MON810 maize has been recently performed by the EURL GMFF [6].

Regarding the expression of the results, the two PCR techniques have one major difference. The qPCR assay has to be calibrated with CRMs used to prepare standard curves with known content of GM and endogene DNA. The calibrator is a CRM with a property value certified as a mass fraction. Two of these GMO CRMs have additionally been certified for their DNA copy number ratio, i.e. for MON810 (ERM®-BF413ek) and NK603 (ERM®-BF415e). Depending on the calibrator used for qPCR, the result is either expressed as mass fraction or DNA copy number ratio. In contrast, the dPCR assay does not need a CRM calibration and delivers a result expressed as DNA copy number ratio.

As pointed out in several publications [1], [7], there is no metrological sound way of converting a result expressed in mass fraction to one expressed in DNA copy number ratio and vice versa, unless a reference system is established.

In the EU, the reference point for qPCR results is the legally prescribed CRM. To achieve a unique reference point for qPCR and dPCR measurements, the dPCR result needs to be linked to the same CRM. This can be achieved by establishing a conversion factor (CF) for each CRM [8]. This CF is determined on the CRM certified with the largest GM mass fraction, preferably ~1000 g/kg (100 m/m %), as it is assumed that this CRM will usually be used for preparing the calibration curves.

Currently 73 CFs have been established [9] and are available for the GMO testing community through the EURL GMFF website. These factors have been determined experimentally from results of 3 or 4 laboratories. Also, every new batch of the same CRM is tested in this way, and the newly determined CF may be slightly different from the one attributed to the previous batch. This procedure is not very efficient neither time nor cost wise. Furthermore, it may be confusing to the laboratories when CFs change for newly released CRM batches.

Based on the CFs determined so far and evaluation of the biological factors that may affect the CFs for CRMs, we propose here an alternative approach, consisting of 1) attributing a common, predicted CF to similar types of CRMs; 2) performing an in-house experimental verification of the copy number ratio for every new CRM and new CRM batch; and 3) conducting an interlaboratory study only in case the measured copy number ratio deviates significantly from the predicted CF.

2 CFs assigned on the basis of an interlaboratory study

The CF assignment by interlaboratory testing was started in 2018, when the use of dPCR started to gain in popularity. Three laboratories participated in the CF studies and followed a strict measurement protocol. In case of disagreement between the results or omitted measurement results, a fourth laboratory was asked to perform additional measurements.

The protocol prescribed 3 DNA extraction replicates for each powder material. Each extract had to be measured in two dilutions in triplicate. CRMs consisting of DNA solutions had to be measured in two dilutions in triplicate. The results were averaged and corrected for the certified CRM content to calculate the CF. Additionally, a measurement uncertainty was estimated, based on contributions from the certified GM content and the within and between laboratory repeatability. The study design and the evaluation of the results has been described in detail in [8].

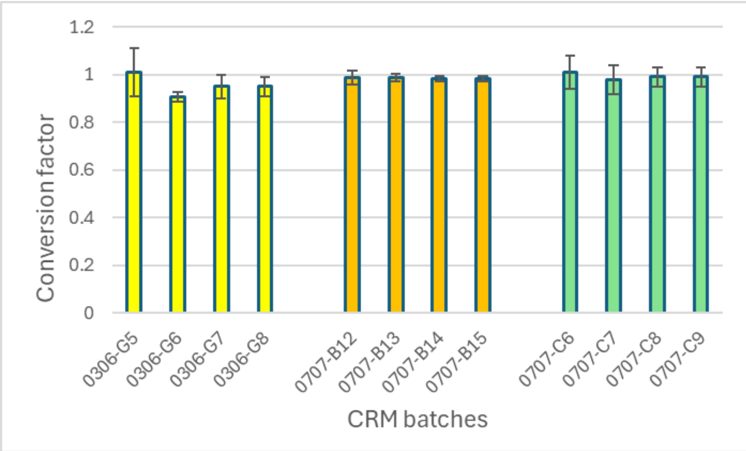
The first CF list was published in the autumn of 2019, the latest version 12 was published in December 2024. Nearly every 6 months the list was updated with the CFs for new CRMs or new batches of CRMs or corrected due to a modified uncertainty of the certified value. Because laboratories should use the current commercially available CRMs for all measurements, only the CFs of the latest CRMs or CRM batches are shown in the list and only the most recent list is available from the website.

Updates due to new certificates or new batches of CRMs were normally minor and within the experimental measurement variability (a few examples are shown in Figure 1). However, in some cases the difference between CRM batches was significant. For instance, for maize event MON89034, the female GM donor parent for the hybrid seeds changed to a male GM donor from one batch to another, leading to a significant change of the CF (from 0.58 ± 0.04 for 0906-E to 0.36 ± 0.05 for 0906-E2).

Over the years, it was noted that batches of CRMs consisting of DNA solutions, generally produces from leaves, are frequently renewed. For these CRMs, it was decided in 2022 to only confirm the CF for each batch by single-laboratory measurements in the EURL GMFF laboratory to minimise the time and costs. The CF was measured and if it was in agreement with the CF of the previous batch a weighted mean of these two values was defined as the new CF. This resulted in only slight CF differences in the order of < 10 %.

Figure 1. Conversion factors determined on subsequent CRM batches for RF3 oilseed rape (0306-G), A2704 soybean (0707-B) and A5547 soybean (0707-C)

Source: JRC analysis



3 Biological factors affecting the CF

The CF is determined on the basis of the DNA copies of the transgene and the DNA copies of the endogene. These copy numbers depend on the zygosity of the plant material. Assuming that both the transgene and endogene are single copy genes, a homozygous plant has an equal number of GM copies compared to endogene copies. In a diploid genome, this means two copies of the transgene target and two copies of the endogene target. The CF will, therefore, be 1, when measured on any (vegetative or reproductive) plant tissue used for processing into a CRM. Similarly, a plant that is hemizygous for the transgene insertion, i.e. the transgene is present on only one chromosomal copy of a diploid plant, while the endogene is present on both, will have a CF of 0.5 in all vegetative tissues of the plant such as leaves, tubers, roots, etc. In the reproductive tissues like seeds, however, the situation largely depends on the taxonomic group to which the plant belongs, as it is linked to the morphology of the seeds. Seeds of flowering plants (Angiosperms) develop encapsulated within a maternal seed coat and are composed of several tissues with a different parental origin, basically the seed coat, embryo and endosperm. Such seeds result from a characteristic double fertilisation process, in which one male sperm nucleus fertilises the egg cell, creating the embryo (diploid, 2n), while the other sperm nucleus fertilises the (maternal) central cell, which is itself diploid (as a result of the fusion of two polar nuclei). The latter fertilisation leads to the development of the endosperm, a nourishing tissue for the developing embryo. The endosperm (3n), therefore, contains twice as much maternal genome (2n) as paternal genome (1n).

But there is an important difference in seed structure between the two major taxonomic groups of the Angiosperms, the monocots and dicots: the seed of monocots, including important crops like maize, rice and wheat, have well-developed endosperms constituting the most part of the seed in volume. In contrast, in dicots, the mature seeds bear only little remaining endosperm, as most of it has already been consumed by the growing embryo, storing the nutrients in the two cotyledons that take up the largest part of the seed's volume.

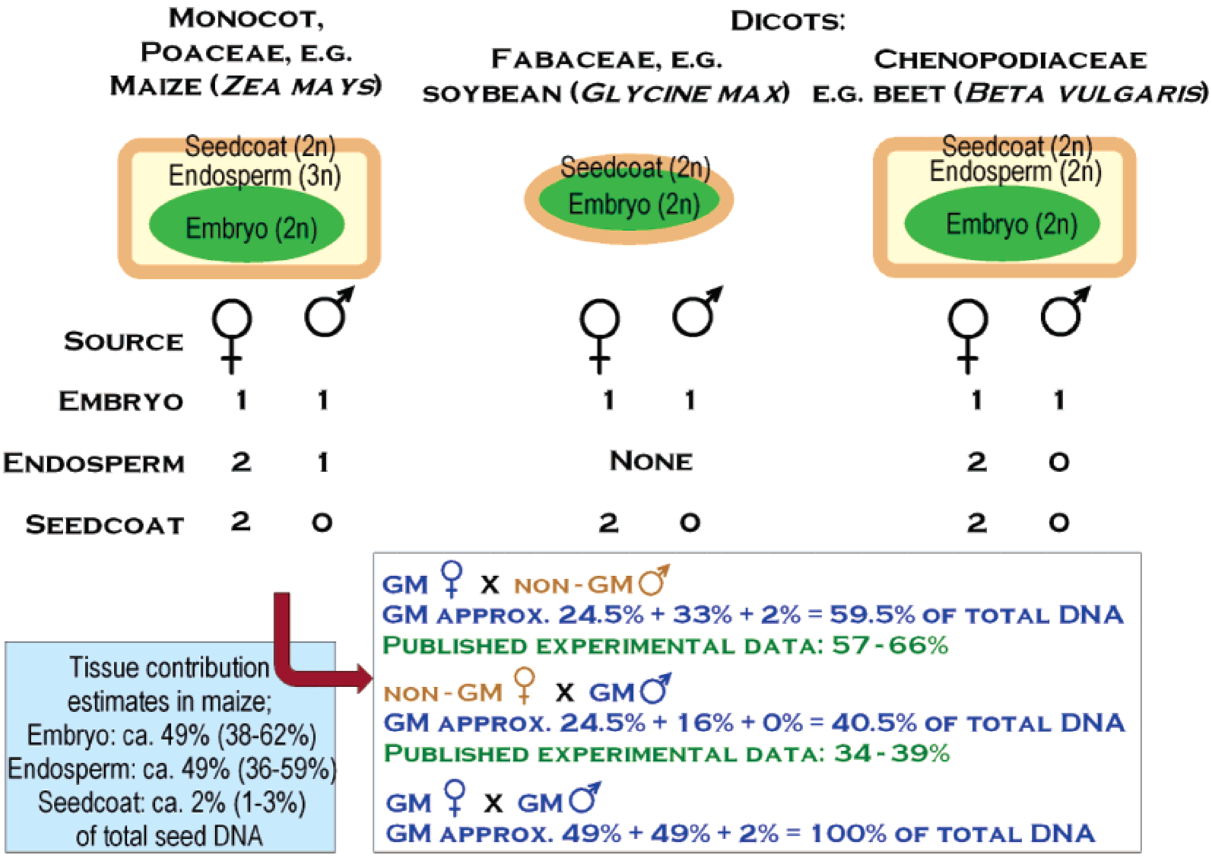
Additionally, each of the seed tissues contributes differently to the extracted DNA from seeds: in maize, on average over different varieties and experiments, half of the seed DNA was shown to be derived from the embryo, and the other half from the endosperm, while the seed coat contributes only a little (about 2 %) DNA [10]. In contrast, in most dicots, all the DNA (except the little DNA from the seed coat) derives from the embryo with its two cotyledons. Seeds from some dicot families, including the one to which sugar beet belongs (Amaranthaceae), are an exception, as the seed is composed of an embryo surrounded by the maternal perisperm (2n) and seed coat, and embedded in (maternal) fruit tissues (pericarp) [11].

The seed morphology of different taxonomic groups affects the DNA copy number in extracted seed DNA and thus the CF.

— In most hemizygous dicot seeds (except e.g. sugar beet), composed mainly of the embryo, regardless of the male or female origin of the transgene, the transgene versus endogene copy number, and thus the CF, is expected to be close to 0.5;

— In monocot seeds, the parental origin of the transgene affects its DNA copy number contribution in the endosperm, i.e. if the transgene derives from the (homozygous) male parent, the endosperm of the hybrid seed will have one paternal transgene copy versus two maternal haploid genomes; in contrast, if the transgene originates from the (homozygous) maternal plant, the endosperm will bear two transgene copies from the mother and 1 paternal genome. Holst-Jensen et al. [10] estimated, for maize, the transgene versus endogene copy numbers in case of male or female GM donors as close to 0.4 and 0.6, respectively (**Figure 2**).

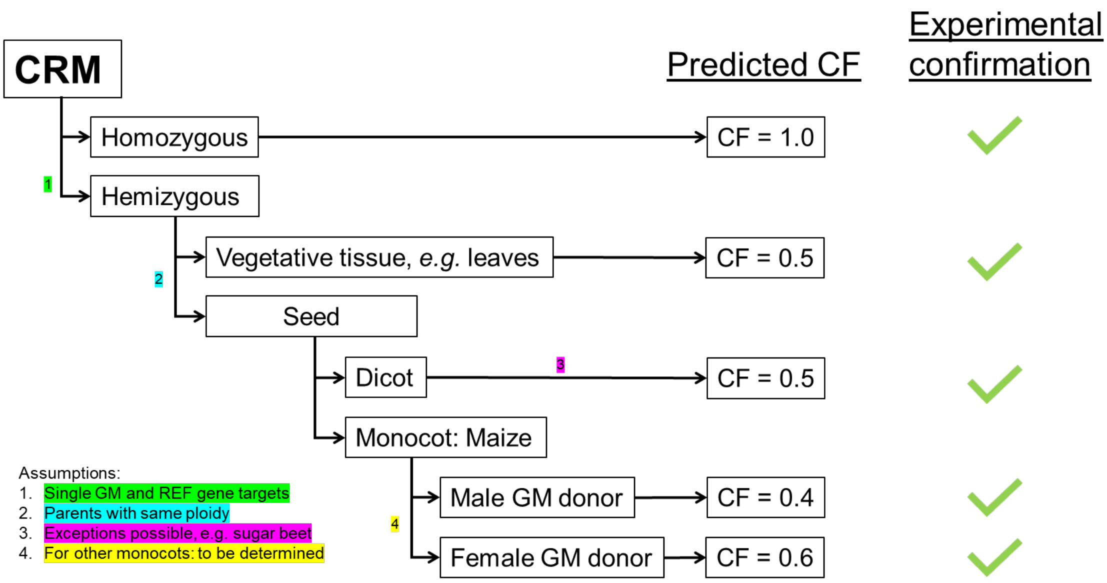
Figure 2. Expected copy number ratio in seeds based on zygosity and plant taxonomy.



Source: From: Holst-Jensen et al., J. Agric. Food Chem. ***2006,*** *54, 2799-2809*

Taken into account the effects of the major biological factors on the copy number measurements, we developed a decision tree showing the predicted CFs for different types of CRMs (**Figure 3**). In the following chapter, we will analyse to what extent the experimentally derived CFs established so far match with the predicted CFs.

Figure 3. Decision tree to assign a CF to a CRM.



Source: JRC analysis

4 Comparison of measured versus predicted CFs

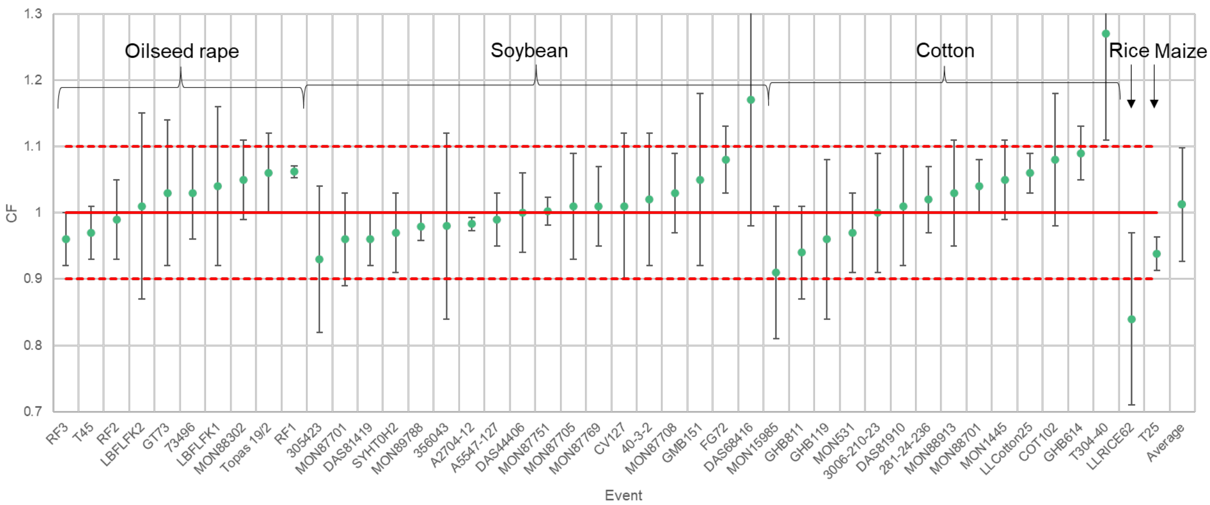
In order to evaluate to what extent, the measured CFs correspond with the predicted ones, considering the biological parameters affecting the DNA copy numbers, we established a fixed measurement uncertainty around the predicted CFs corresponding to 10 m/m %. This expanded measurement uncertainty is close to the average uncertainty determined experimentally for the CFs so far. In the analysis below, we included all CRMs for which a CF was published in version 12 of the CF list (Annex 1), including some that correspond to GM events that are not authorised in the EU (e.g. 98140, VCO-1981, Bt176, MON863 maize, 356043 soybean).

4.1 CRMs made from homozygous plants

The expected ratio between transgenic and endogenous target is 1 for homozygous plants independent of the taxon or plant material used for the production of the CRM. All current CRMs for GM soybean and cotton events are homozygous as well as most of the GM oilseed rape events (except the male sterility lines MS1, MS8 and MS11 and the new event MON94100). In addition, there is one CRM from homozygous GM maize (event T25), consisting of genomic DNA extracted from leaves. In the past, also a rice GM event (LLRice62), produced from homozygous seeds, was temporarily authorised in the EU.

The average of the over 40 CFs measured for CRMs made from homozygous plants is 1.0, which is in perfect agreement with the theoretical value of 1. Considering an expanded measurement uncertainty of 10 %, which is in good agreement with the measured values (Figure 3, mean and U shown at the right), only one CF is statistically significantly different from 1. The CF of T304-40 cotton measured on ERM®-BF429c, a nominal 10 % CRM, is with 1.27 ± 0.16 statistically different from 1.0 ± 0.1. The reason could be a slightly different DNA extraction efficiency or DNA content between the non-GM cotton and the 100 % GM cotton used to produce the 10 % material. This was already noted in the certification report for this CRM. Therefore, this CF will be kept at the current level, while for the other CRMs a fixed, theoretical CF of 1.0 ± 0.1 would be a good approximation of what has been experimentally determined.

Figure 4. CRMs made from homozygous plants (in solid red the new CF and in dashed red its uncertainty).



Source: JRC analysis

4.2 CRMs made from hemizygous plants

4.2.1 CRMs made from vegetative tissues

As explained before, all vegetative tissues from hemizygous plants (monocots and dicots) have a 1:1 ratio of GM versus endogene DNA and the expected GM copy number ratio is, therefore, 0.5.

Among the tested CRMs, three have been processed from oilseed rape leaves (available as genomic DNA solution) and one from sugar beet roots (powder). The average of the four CFs measured for CRMs made from hemizygous vegetative plant material is 0.49, which is in good agreement with a theoretical value of 0.50 ± 0.05.

Figure 5. CRMs made from hemizygous plants. (in solid red the new CF and in dashed red its uncertainty).

Source: JRC analysis

4.2.2 CRMs made from hemizygous dicot seeds

As explained before, the seeds of most dicot plants are mainly composed of the embryo with its cotyledons and little endosperm is remaining. In CRMs made from hemizygous dicot seeds, the copy number ratio between transgene and endogene targets is, therefore, expected to be close to 0.5.

The CF experimentally determined for the CRM from MON94100 oilseed rape is 0.46, which is close to the predicted value of 0.5.

A special case is sugar beet seeds. The sugar beet seed has a substantial mass of pericarp tissue receiving its genome set only from the female parent, however, the embryo contributes most of the extractable DNA from the seed. Sugar beet exists in triploid and diploid varieties. Based on experimental measurements of the mass of each of the seed tissues and their DNA content [11], it appears that the GM copy number, and hence CF, averages to a value of 0.5 for triploid varieties, independent of the GM donor parent. For diploid varieties the CF is estimated as 0.4 if the GM trait is received via the male parental line and 0.6 if it is received via the maternal line [11]. We will use these predictions to assign a CF for CRMs made from sugar beet seeds, such as the event KWS20-1 for which an authorisation application has recently been submitted.

4.2.3 CRMs made from hemizygous monocot seeds

Currently, the only crop from the monocot taxonomic lineage with EU-authorised GM events is maize, which is generally commercialised as hybrid crop (hemizygous for the transgene). Maize is also the only crop for which the DNA contribution from embryo and endosperm has been assessed [10]. The value of the CF depends on the parental origin of the GM insert and may be different for other monocot crops.

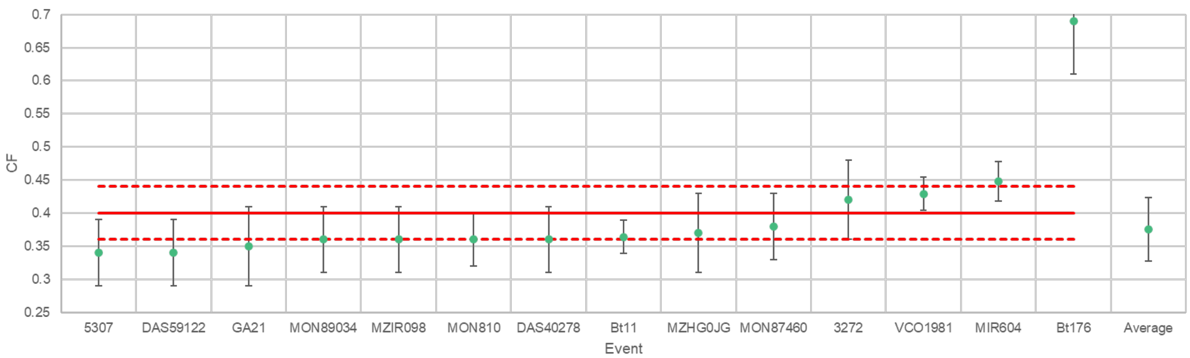
4.2.3.1 CRMs from hemizygous maize seeds with male GM donor

The expected ratio transgenic to endogenic target is predicted to be around 0.4 for hemizygous maize seeds receiving the GM trait from the male parent.

The average of the 13 CFs measured for CRMs (excluding the CF for ERM®-BF411g for Bt176 maize) made from hemizygous maize seeds with male GM donor was 0.38, which is in good agreement with the predicted value of 0.4 [10].

Only one CF is statistically significantly different from 0.40. The CF for the expired GM event Bt176, measured on ERM®-BF411g (nominal 100 m/m % Bt176) was 0.69 ± 0.08, which is statistically different from 0.40 ± 0.04. The reason is not known and the company confirmed that the seeds were produced with a male GM donor. No further investigation will be conducted as the event's authorisation expired more than 5 years ago. If this CRM is used, the experimentally derived CF should be applied.

Figure 6. CRMs from hemizygous maize seeds: male parent (average shown excludes Bt176) (in solid red the new CF and in dashed red its uncertainty).



Source: JRC analysis

4.2.3.2 CRMs from hemizygous maize seeds with female GM donor

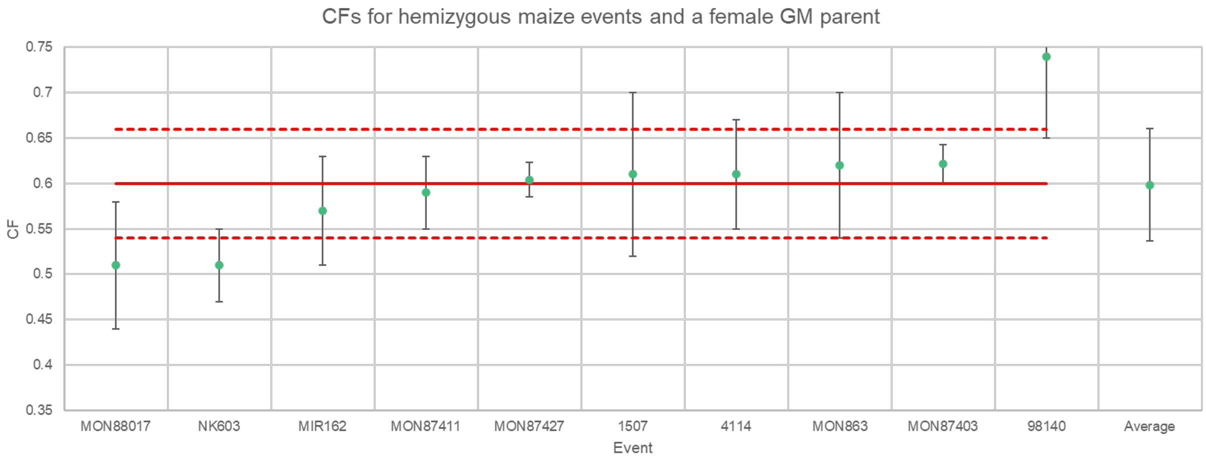
The expected ratio of the transgenic to endogenous target is 0.6 for hemizygous maize seeds receiving the trait from the female parent [10].

The average of the 10 CFs measured for CRMs made from hemizygous maize seeds with female GM donor was 0.6, which is in perfect agreement with the predicted value. Considering an uncertainty of 10 %, which is also in good agreement with the measured values, two CFs are statistically significantly different from 0.6. Both of these cases refer to CRMs produced as mixture of GM and non-GM seeds (the pure GM CRM was not available at the time of testing).

— The CF for NK603 measured on ERM®-BF415f, a nominal 5 % CRM, is with 0.51 ± 0.04 statistically different from 0.60 ± 0.06. The lower CF may be the consequence of a different DNA extractability between GM and non-GM seeds

— The CF for 98140 measured on ERM®-BF427d, a nominal 10 % CRM, is with 0.74 ± 0.09 also statistically different from 0.60 ± 0.06. A higher DNA extractability from the GM seeds compared to the non-GM seeds may also here explain the larger CF. As 98140 maize is not an authorised event, quantification of the 98140 content in marketed products is not required under European legislation, therefore, a CF is not relevant for this event

Figure 7. CRMs from hemizygous maize seeds: female parent (in solid red the new CF and in dashed red its uncertainty).



Source: JRC analysis

5 Conclusions

We evaluated the CF results obtained in the last 6 years using interlaboratory studies among 3 or 4 laboratories. We show here that the measured CFs are in most cases in agreement with the predicted values (± 10 % expanded uncertainty, k = 2), based on the origin, type and the zygosity of the raw material used for the production of the CRMs. These predicted factors can be summarised as follows:

- 1.00 ± 0.10 for CRMs produced from plants with homozygous GM inserts;
- 0.50 ± 0.05 for CRMs produced from vegetative tissues of hemizygous plants;
- 0.50 ± 0.05 for CRMs produced from seeds of dicot plants (with exceptions, e.g. sugar beet);
- 0.40 ± 0.04 for CRMs produced from hemizygous maize seeds with a male GM donor;
- 0.60 ± 0.06 for CRMs produced from hemizygous maize seeds with a female GM donor.

The CFs for a few CRMs deviated from the predicted ratios. This was observed for CRMs processed as mixtures of GM and non-GM seeds, for which a different DNA extractability from GM and non-GM seeds could be the cause. Another exemption was the CRM for the expired GM maize event Bt176, which was much larger than predicted.

Based on this large-scale assessment, and considering the agreement of the results for similar types of CRMs, we decided to follow a different approach for assigning a CF to a CRM: instead of conducting interlaboratory studies for new CRMs or new batches of CRMs, the EURL GMFF will experimentally verify whether the copy number ratio falls within the predicted CF interval. If confirmed, the predicted CF will be assigned to the CRM and published on the EURL GMFF website. This experimental assessment will be done during the appropriateness testing procedure for new CRMs. Only in case of significant differences, an interlaboratory study will be set up and the CFs for which such a difference has already been confirmed by interlaboratory comparison will continue to be available as such. Unless the calculated CF would significantly deviate, the common CFs should be applied for the conversion of a result in GM copy number ratio into a result in GM mass fraction (m/m %).

This will make the use of CFs in GMO analysis more predictable and avoid changes in CFs for new batches that may be attributable to experimental variations.

References

[1] Corbisier, P., Barbante, A., Broothaerts, W., De Loose, M., Emons, H.,. et al., 'Recommendation for the unit of measurement and the measuring system to report traceable and comparable results expressing GM content in accordance with EU legislation', Publication Office of the European Union, Luxembourg, 2017.

[2] Corbisier, P., Bhat, S., Partis, L., Xie, V. R. and Emslie, K. R., 'Absolute quantification of genetically modified MON810 maize (*Zea mays L.*) by digital polymerase chain reaction', *Analytical and Bioanalytical Chemistry,* Vol. 396, pp. 2143-2150, 2010.

[3] Köppel, R and Bucher, T., 'Rapid establishment of droplet digital PCR for quantitative GMO analysis', *European Food Research Technologies,* Vol. 241, pp. 427-439, 2015.

[4] Dobnik, D., Spilsberg, B., Bogožalec Koširt, A., Holst-Jensen, A. and Žel, J., 'Multiplex quantification of 12 European Union authorized genetically modified maize lines with droplet digital polymerase chain reaction', *Analytical Chemistry, V*ol. 87, pp. 8218-8226, 2015.

[5] Pecoraro, S., Berben, G., Burns, M., Corbisier, P., De Giacomo, M. et al., 'Overview and recommendations for the application of digital PCR', Publication Office of the European Union, Luxembourg, 2019.

[6] Gatto, F., Savini, C., Sacco, M. G., Vinciguerra, D., Buttinger, G. et al., 'Single and multi-laboratory validation of a droplet digital PCR method', *Food Control, V*ol. 140, 109117, 2022.

[7] Corbisier, P. and Emons, H., 'Towards metrologically traceable and comparable results in GM quantification', *Analytical and Bioanalytical Chemistry*, Vol. 411, pp. 7-11, 2019.

[8] Corbisier, P., Buttinger, G., Savini, C., Sacco, M. G., Gatto, F. and Emons, H., 'Expression of GM content in mass fraction from digital PCR data', *Food Control*, Vol. 133, 108626, 2022.

[9] 'Conversion factors (CF) for certified reference materials (CRM) (version 12 - 06/11/2024)', [Online], accessed 28 July 2025, gmo-crl.jrc.ec.europa.eu/doc/CF-CRM-values.pdf.

[10] Holst-Jensen, A., De Loose, M. and Van den Eede, G., 'Coherence between legal requirements and approaches for detection of genetically modified organisms (GMOs) and their derived products', *Journal of Agricultural and Food Chemistry*, Vol. 54, pp. 2799-2809, 2006.

[11] Papazova, N., Taverniers, I., van Bockstaele, E. and de Loose, M., 'Sugar beet seed architecture and genetics - influence on DNA-based GM quantification', *Seed Science and Technology,* Vol. 36, no. 3, pp. 546-554, 2008.

List of abbreviations and definitions

Abbreviations	Definitions
CF	Conversion factor
CRM	Certified reference material
dPCR	Digital polymerase chain reaction
EURL-GMFF	European reference laboratory for genetically modified food and feed
GM	Genetically modified
GMO	Genetically modified organism
NRL	National reference laboratory
PCR	Polymerase chain reaction
qPCR	Quantitative polymerase chain reaction

List of figures

Annexes

Annex 1. CF list version 12

EUROPEAN COMMISSION
JOINT RESEARCH CENTRE

Directorate F - Health, Consumers and Reference Materials (Geel/Ispra)
Food & Feed Compliance

European Union Reference Laboratory for GM Food & Feed

The table below provides conversion factors (CF_{CRM}) experimentally determined on certified reference materials (CRM) by using digital PCR by at least three and up to four independent expert laboratories. The expanded uncertainty (U) estimated for each CF_{CRM} has been calculated to allow expressing dPCR results in mass fraction with a reliable uncertainty estimate.

See also : Corbisier P. and Emons H. (2019) and Corbisier P. et al. (2022)

CRM	Species	Event	Transgene method	Endogene method	CF CRM	U (k=2)	Zygosity
ERM®-BF419b	Beta vulgaris (sugar beet)	H71	QT-EVE-BV-001	QT-TAX-BV-013	0.48	0.05	Heterozygous / transgenic parent male
0117-E	Brassica napus (oilseed rape)	LBFLFK1	QT-EVE-BN-012	QT-TAX-BN-001	1.04	0.12	Homozygous
0117-E	Brassica napus (oilseed rape)	LBFLFK2	QT-EVE-BN-013	QT-TAX-BN-001	1.01	0.14	Homozygous
0208-A7	Brassica napus (oilseed rape)	T45	QT-EVE-BN-001	QT-TAX-BN-001	0.97	0.04	Homozygous
0304-B3	Brassica napus (oilseed rape)	GT73	QT-EVE-BN-004	QT-TAX-BN-001	1.03	0.11	Homozygous
0306-F9	Brassica napus (oilseed rape)	MS8	QT-EVE-BN-002	QT-TAX-BN-001	0.484	0.017	Hemizygous
0306-G8	Brassica napus (oilseed rape)	RF3	QT-EVE-BN-003	QT-TAX-BN-001	0.96	0.04	Homozygous
0421-A	Brassica napus (oilseed rape)	MON94100	QT-EVE-BN-014	QT-TAX-BN-001	0.46	0.05	Heterozygous / transgenic parent female
1011-A2	Brassica napus (oilseed rape)	MON88302	QT-EVE-BN-010	QT-TAX-BN-001	1.05	0.06	Homozygous
1116-A	Brassica napus (oilseed rape)	MS11	QT-EVE-BN-011	QT-TAX-BN-001	0.470	0.012	Hemizygous
ERM®-BF434b	Brassica napus (oilseed rape)	73496	QT-EVE-BN-009	QT-TAX-BN-001	1.03	0.07	Homozygous
0711-A4	Brassica napus (swede-rape)	MS1	QT-EVE-BN-005	QT-TAX-BN-001	0.526	0.022	Hemizygous
0711-B3	Brassica napus (swede-rape)	RF1	QT-EVE-BN-006	QT-TAX-BN-001	1.062	0.009	Homozygous
0711-C3	Brassica napus (swede-rape)	RF2	QT-EVE-BN-007	QT-TAX-BN-001	0.99	0.06	Homozygous
0711-D5	Brassica napus (swede-rape)	Topas 19/2	QT-EVE-BN-008	QT-TAX-BN-001	1.04	0.04	Homozygous
0112-A2	Glycine max (soybean)	SYHT0H2	QT-EVE-GM-017	QT-TAX-GM-009	0.97	0.06	Homozygous
0210-A2	Glycine max (soybean)	MON87705	QT-EVE-GM-003	QT-TAX-GM-009	1.01	0.08	Homozygous
0215-A	Glycine max (soybean)	MON87751	QT-EVE-GM-016	QT-TAX-GM-009	1.002	0.021	Homozygous
0311-A2	Glycine max (soybean)	MON87708	QT-EVE-GM-012	QT-TAX-GM-009	1.03	0.06	Homozygous
0610-A7	Glycine max (soybean)	FG72	QT-EVE-GM-001	QT-TAX-GM-009	1.07	0.05	Homozygous
0707-B15	Glycine max (soybean)	A2704-12	QT-EVE-GM-004	QT-TAX-GM-009	0.983	0.010	Homozygous

CRM	Species	Event	Transgene method	Endogene method	CF CRM	U (k=2)	Zygosity
0707-C9	Glycine max (soybean)	A5547-127	QT-EVE-GM-007	QT-TAX-GM-009	0.99	0.04	Homozygous
0809-A2	Glycine max (soybean)	MON87701	QT-EVE-GM-010	QT-TAX-GM-009	0.96	0.07	Homozygous
0809-B2	Glycine max (soybean)	MON87769	QT-EVE-GM-002	QT-TAX-GM-009	1.01	0.06	Homozygous
0906-B2	Glycine max (soybean)	MON89788	QT-EVE-GM-006	QT-TAX-GM-009	0.979	0.021	Homozygous
0911-D	Glycine max (soybean)	CV127	QT-EVE-GM-011	QT-TAX-GM-009	1.01	0.11	not known
ERM®-BF410bp	Glycine max (soybean)	40-3-2	QT-EVE-GM-005	QT-TAX-GM-009	1.02	0.10	Homozygous
ERM®-BF425d	Glycine max (soybean)	356043	QT-EVE-GM-009	QT-TAX-GM-009	0.98	0.14	Homozygous
ERM®-BF426d	Glycine max (soybean)	305423	QT-EVE-GM-008	QT-TAX-GM-009	0.93	0.11	Homozygous
ERM®-BF432d	Glycine max (soybean)	DAS68416	QT-EVE-GM-013	QT-TAX-GM-009	1.17	0.19	Homozygous
ERM®-BF436b	Glycine max (soybean)	DAS44406	QT-EVE-GM-015	QT-TAX-GM-009	1.00	0.06	Homozygous
ERM®-BF437b	Glycine max (soybean)	DAS81419	QT-EVE-GM-014	QT-TAX-GM-009	0.96	0.04	Homozygous
ERM®-BF443b	Glycine max (soybean)	GMB151	QT-EVE-GN-018	QT-TAX-GM-009	1.05	0.13	Homozygous
0113-A2	Gossypium hirsutum (cotton)	MON88701	QT-EVE-GH-010	QT-TAX-GH-018	1.04	0.04	Homozygous
0306-E4	Gossypium hirsutum (cotton)	LLCotton25	QT-EVE-GH-002	QT-TAX-GH-018	1.06	0.03	Homozygous
0804-B2	Gossypium hirsutum (cotton)	MON1445	QT-EVE-GH-003	QT-TAX-GH-018	1.05	0.06	Homozygous
0804-C2	Gossypium hirsutum (cotton)	MON531	QT-EVE-GH-004	QT-TAX-GH-018	0.97	0.06	Homozygous
0804-D2	Gossypium hirsutum (cotton)	MON15985	QT-EVE-GH-005	QT-TAX-GH-018	0.91	0.10	Homozygous
0906-D2	Gossypium hirsutum (cotton)	MON88913	QT-EVE-GH-007	QT-TAX-GH-018	1.03	0.08	Homozygous
1012-C2	Gossypium hirsutum (cotton)	COT102	QT-EVE-GH-012	QT-TAX-GH-018	1.08	0.10	Homozygous
1108-A7	Gossypium hirsutum (cotton)	GHB614	QT-EVE-GH-006	QT-TAX-GH-018	1.09	0.04	Homozygous
ERM®-BF422b	Gossypium hirsutum (cotton)	281-24-236	QT-EVE-GH-001a	QT-TAX-GH-018	1.02	0.05	Homozygous
ERM®-BF422b	Gossypium hirsutum (cotton)	3006-210-23	QT-EVE-GH-001b	QT-TAX-GH-018	1.00	0.09	Homozygous
ERM®-BF428c	Gossypium hirsutum (cotton)	GHB119	QT-EVE-GH-008	QT-TAX-GH-018	0.96	0.12	Homozygous
ERM®-BF429c	Gossypium hirsutum (cotton)	T304-40	QT-EVE-GH-009	QT-TAX-GH-018	1.27	0.16	Homozygous
ERM®-BF440b	Gossypium hirsutum (cotton)	DAS81910	QT-EVE-GH-011	QT-TAX-GH-018	1.01	0.09	Homozygous
ERM®-BF442b	Gossypium hirsutum (cotton)	GHB811	QT-EVE-GH-013	QT-TAX-GH-018	0.94	0.07	Homozygous
0306-I9	Oryza sativia (rice)	LLRICE62	QT-EVE-OS-002	QT-TAX-OS-017	0.84	0.13	Homozygous
0215-B	Zea mays (maize)	MON87411	QT-EVE-ZM-024	QT-TAX-ZM-002	0.59	0.04	Heterozygous / transgenic parent female
0216-A	Zea mays (maize)	MON87403	QT-EVE-ZM-025	QT-TAX-ZM-002	0.622	0.021	Heterozygous / transgenic parent female

CRM	Species	Event	Transgene method	Endogene method	CF CRM	U (k=2)	Zygosity
0306-H11*	Zea mays (maize)	T25	QT-EVE-ZM-011	QT-TAX-ZM-002	0.938	0.025	Homozygous
0406-D2	Zea mays (maize)	MON88017	QT-EVE-ZM-016	QT-TAX-ZM-002	0.51	0.07	Heterozygous / transgenic parent female
0407-B	Zea mays (maize)	GA21	QT-EVE-ZM-007	QT-TAX-ZM-002	0.35	0.06	Heterozygous / transgenic parent male
0411-D2	Zea mays (maize)	5307	QT-EVE-ZM-002	QT-TAX-ZM-002	0.34	0.05	Heterozygous / transgenic parent male
0512-A2	Zea mays (maize)	MON87427	QT-EVE-ZM-003	QT-TAX-ZM-002	0.604	0.019	Heterozygous / transgenic parent female
0709-A2	Zea mays (maize)	MON87460	QT-EVE-ZM-005	QT-TAX-ZM-002	0.38	0.05	Heterozygous / transgenic parent male
0906-E2	Zea mays (maize)	MON89034	QT-EVE-ZM-018	QT-TAX-ZM-002	0.36	0.05	Heterozygous / transgenic parent male
1114-B2	Zea mays (maize)	MZIR098	QT-EVE-ZM-028	QT-TAX-ZM-002	0.36	0.05	Heterozygous / transgenic parent male
1114-C	Zea mays (maize)	MZHG0JG	QT-EVE-ZM-027	QT-TAX-ZM-002	0.37	0.06	Heterozygous / transgenic parent male
ERM®-BF411g	Zea mays (maize)	Bt176	QT-EVE-ZM-023	QT-TAX-ZM-002	0.69	0.08	Heterozygous / transgenic parent male
ERM®-BF412bk	Zea mays (maize)	Bt11	QT-EVE-ZM-015	QT-TAX-ZM-002	0.364	0.025	Heterozygous / transgenic parent male
ERM®-BF413gk	Zea mays (maize)	MON810	QT-EVE-ZM-020	QT-TAX-ZM-002	0.36	0.04	Heterozygous / transgenic parent male
ERM®-BF415f	Zea mays (maize)	NK603	QT-EVE-ZM-008	QT-TAX-ZM-002	0.51	0.04	Heterozygous / transgenic parent female
ERM®-BF416d	Zea mays (maize)	MON863	QT-EVE-ZM-009	QT-TAX-ZM-002	0.62	0.08	Heterozygous / transgenic parent female
ERM®-BF418d	Zea mays (maize)	1507	QT-EVE-ZM-010	QT-TAX-ZM-002	0.61	0.09	Heterozygous / transgenic parent female
ERM®-BF420c	Zea mays (maize)	3272	QT-EVE-ZM-019	QT-TAX-ZM-002	0.42	0.06	Heterozygous / transgenic parent male
ERM®-BF423d	Zea mays (maize)	MIR604	QT-EVE-ZM-013	QT-TAX-ZM-002	0.448	0.030	Heterozygous / transgenic parent male
ERM®-BF424d	Zea mays (maize)	DAS59122	QT-EVE-ZM-012	QT-TAX-ZM-002	0.34	0.05	Heterozygous / transgenic parent male
ERM®-BF427d	Zea mays (maize)	98140	QT-EVE-ZM-021	QT-TAX-ZM-002	0.74	0.09	Heterozygous / transgenic parent female
ERM®-BF433d	Zea mays (maize)	DAS40278	QT-EVE-ZM-004	QT-TAX-ZM-002	0.36	0.05	Heterozygous / transgenic parent male
ERM®-BF438b	Zea mays (maize)	VCO1981	QT-EVE-ZM-001	QT-TAX-ZM-002	0.429	0.025	Heterozygous / transgenic parent male
ERM®-BF439b	Zea mays (maize)	4114	QT-EVE-ZM-026	QT-TAX-ZM-002	0.61	0.06	Heterozygous / transgenic parent female
ERM®-BF446b	Zea mays (maize)	MIR162	QT-EVE-ZM-022	QT-TAX-ZM-002	0.57	0.06	Heterozygous / transgenic parent female

Version: 12 Data for CRMs marked in red is either new or has been updated

* The CF_{CRM} for T25 has been established using the ddPCR Supermix for Probes (No dUTP) (Bio-Rad®)

Getting in touch with the EU

In person

All over the European Union there are hundreds of Europe Direct centres. You can find the address of the centre nearest you online (european-union.europa.eu/contact-eu/meet-us_en).

On the phone or in writing

Europe Direct is a service that answers your questions about the European Union. You can contact this service:

— by freephone: 00 800 6 7 8 9 10 11 (certain operators may charge for these calls),
— at the following standard number: +32 22999696,
— via the following form: european-union.europa.eu/contact-eu/write-us_en.

Finding information about the EU

Online

Information about the European Union in all the official languages of the EU is available on the Europa website (european-union.europa.eu).

EU publications

You can view or order EU publications at op.europa.eu/en/publications. Multiple copies of free publications can be obtained by contacting Europe Direct or your local documentation centre (european-union.europa.eu/contact-eu/meet-us_en).

EU law and related documents

For access to legal information from the EU, including all EU law since 1951 in all the official language versions, go to EUR-Lex (eur-lex.europa.eu).

EU open data

The portal data.europa.eu provides access to open datasets from the EU institutions, bodies and agencies. These can be downloaded and reused for free, for both commercial and non-commercial purposes. The portal also provides access to a wealth of datasets from European countries.

Science for policy

The Joint Research Centre (JRC) provides independent, evidence-based knowledge and science, supporting EU policies to positively impact society

Scan the QR code to visit:

The Joint Research Centre: EU Science Hub
https://joint-research-centre.ec.europa.eu