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CONFERENCE OF THE PARTIES TO THE CONVENTION
ON BIOLOGICAL DIVERSITY SERVING AS THE
MEETING OF THE PARTIES TO THE CARTAGENA
PROTOCOL ON BIOSAFETY

Tenth meeting

Kunming, China, 11-15 October 2021

and dates to be confirmed

Agenda item 15

SUMMARY OF THE ONLINE DISCUSSIONS OF THE NETWORK OF LABORATORIES FOR THE DETECTION AND IDENTIFICATION OF LIVING MODIFIED ORGANISMS

Note by the Executive Secretary

I. BACKGROUND

1. In decision [CP-9/11](#), the Conference of Parties serving as the meeting of the Parties to the Cartagena Protocol on Biosafety requested the Executive Secretary to continue facilitating online discussions of the Network of Laboratories for the Detection and Identification of Living Modified Organisms (LMOs). Further, in decision [14/19](#) on synthetic biology, the Conference of Parties to the Convention on Biological Diversity requested the Executive Secretary to collaborate and convene discussions, including through the Network of Laboratories for the Detection and Identification of Living Modified Organisms, for sharing experiences on the detection, identification and monitoring of organisms, components and products of synthetic biology, and to continue inviting laboratories, including analytical laboratories, to join the Network.

2. Based on the above, the Secretariat convened online discussions of the Network of Laboratories for the Detection and Identification of Living Modified Organisms from 28 October to 11 November 2019. The discussions were moderated by Ms. Shakirat Ajenifujah-Solebo from Nigeria. Overall, 67 interventions from 35 experts¹ were made, under the following three topics:

Topic 1: Current techniques used in the detection and identification of LMOs, with special consideration of any new technique that is currently in use since the last discussion of the Network of Laboratories in April 2018;

Topic 2: Sharing of experiences on the detection, identification, and monitoring of organisms, components and products of synthetic biology;

Topic 3: Overview of current capacity for the detection and identification of living modified organisms.

¹ In total 23 Parties: Belarus, Bhutan, Brazil, Cameroon, Costa Rica, Democratic Republic of the Congo, Denmark, Ethiopia, European Union, Germany, Iran (Islamic Republic of), Latvia, Lebanon, Malaysia, Mexico, Nigeria, Republic of Korea, South Africa, Thailand, Tunisia, Uganda, Uruguay, Venezuela (Bolivarian Republic of); 2 organizations: BASF, GenØk Centre for Biosafety.

3. The following table provides an overview of the interventions per topic:

Topic number	Number of interventions	Number of participants
1	28	22
2	10	10
3	29	22

4. The present document provides a summary of the views presented in the online discussions. For a full account of all views, it is recommended that the original online interventions be viewed through the Biosafety Clearing-House (http://bch.cbd.int/onlineconferences/portal_detection/2019discussions.shtml). A list of resources shared by the participants, including publications, websites and standards, can be found in annexes I and II below.

II. SUMMARY OF INTERVENTIONS

Topic 1: Current techniques used in the detection and identification of LMOs, with special consideration of any new technique that is currently in use since the last discussion of the Network of Laboratories in April 2018

5. Under this topic, participants were requested to provide examples of the techniques that are currently in use, as well as to highlight any new technique or approach that is either in use or under development. Participants were encouraged to consider this with respect to LMOs that are currently on the market, as well as those that are under research and development.

6. Participants highlighted that current detection and identification of LMOs rely on polymerase chain reaction (PCR),² which is applicable for modified crops because most modified plants contain the following genetic elements: *Cauliflower mosaic virus* (CaMV) 35S protomer, CaMV 35S terminator, *Agrobacterium tumefaciens* nopaline synthase terminator, *Escherichia coli* neomycin phosphotransferase II and/or *Streptomyces hygroscopicus* phosphinothricin N-acetyltransferase. Participants stated that PCR screens are accurate for testing foodstuffs and are commonly used in matrix approaches to determine the identity of a modified plant. Some highlighted quantitative PCR (qPCR) as the best option for modified crops and grains due to its reliability, reproducibility, precision and cost-effectiveness. However, one participant noted that matrix approaches may not be applicable for modified animals, as standard genetic elements similar to plant genetic elements would be unlikely and introduced elements would be taxon-specific.³

7. For developing countries, protein-based techniques were suggested as an economical option for when testing for modified products. One participant suggested that protein and PCR techniques could be used in parallel to complement each other.

8. One participant highlighted the involvement of the International Organization for Standardization (ISO) in the development of several standards relevant for detection and identification, including qualitative, quantitative, protein-based and nucleic acid-based methods. Further, the participant mentioned new standards being developed for isothermal techniques and detection from animal species. These standards can be found in annex II to this document.

9. For new techniques in use since April 2018, some participants mentioned implementing digital PCR (dPCR), which was touted as an improvement from qPCR because dPCR offers lower detection limits,⁴ as well as improved precision and accuracy. Another advantage was that dPCR does not require a calibration curve, thus differences between the test and the calibrant of qPCR can be avoided.

² Polymerase chain reaction is a molecular biology technique used to amplify specific segments of DNA and allows researchers to obtain sufficient quantities of DNA for experiments.

³ Taxon-specific genetic elements may be specific for a particular taxonomic group or rank.

⁴ Ability to detect lower quantities of the target.

10. It was also mentioned that another new technique that some laboratories were beginning to implement was next-generation sequencing (NGS).⁵ which was also described by the experts as a more accurate technique than to qPCR. However, participants mentioned that NGS is more costly than qPCR, especially considering an increased number of samples, and unlike qPCR, validated methodologies have not been established thus far. Further, there will be a need to consider different sampling approaches due to the nature of the technology, which is applied to single organism samples (e.g. one seed), and thus may not be suitable for mixed samples. Additionally, some participants noted that NGS cannot distinguish between traditional breeding techniques using mutagenesis and genome editing.

Topic 2: Sharing of experiences on the detection, identification, and monitoring of organisms, components and products of synthetic biology

11. Following the request in decision 14/19 of the Conference of the Parties, an online forum on synthetic biology had taken place from 4 to 31 March 2019, and had shared experiences under topic 6, “Sharing of experiences on detection, identification and monitoring of organisms, components and products of synthetic biology”. Additional discussions were subsequently hosted under the online discussions of the Network of Laboratories for the Detection and Identification of LMOs held from 28 October to 11 November 2019. Participants in the latter discussions were invited to take into account the discussions held earlier under topic 6 of the online forum on synthetic biology,⁶ and to share information along the same lines.

12. The following guiding questions were proposed:

(a) Which tools are currently available for detecting, identifying and monitoring organisms, components and products of synthetic biology?

(b) Does the novelty that some organisms, components and products of synthetic biology might present, require the development of additional detection, identification and monitoring tools, other than those that already exist?

(c) Could the current analytical techniques be used to distinguish between products of synthetic biology and their naturally occurring or chemically synthesized counterparts?

13. Regarding the current tools and methodologies to detect, identify and monitor the organisms, components and products of synthetic biology, participants shared the following techniques:

- Polymerase chain reaction (PCR);
- Quantitative (real-time) PCR;
- Nested PCR;
- Next-generation sequencing;
- Immunological strip tests;
- Enzyme-linked immunosorbent assay (ELISA).

14. Some participants believed that there is no need for the development or modification of the existing tools for the organisms, components and products of synthetic biology and that current methods would be sufficient. For plants containing multiple events or new biochemical pathways, one participant suggested the use of multiplexing samples and digital PCR.

15. However, other participants believed that new techniques will need to be developed. In particular, one participant highlighted the fact that current methodologies rely on insertion of a transgene, which may not be present in an organism, component or product of synthetic biology, and changes in DNA sequences could also be found in non-modified organisms. Thus, indicating that there will need to be a change in the

⁵ Next-generation sequencing is high-throughput, massively parallel genomic sequencing technologies that allow for increased scalability and speed compared to Sanger (chain-termination) sequencing technology.

⁶ See <https://bch.cbd.int/synbio/open-ended/discussion/?threadid=9603>.

methodological approach to avoid reliance on a single target. Further, considering that genetic modifications will also be likely in other species apart from plants, another participant mentioned that common plant-related promoters and terminators would not exist in other organisms, such as animals, rendering the current methodologies based on the detection of these aforementioned genetic elements not applicable. Furthermore, due to differences in the genetics of animals, regulatory elements may additionally be more taxon- or species-specific. Thus, laboratories may be required to routinely provide a larger array of tests, which would require additional reagents and could cause strains for laboratories unequipped for larger volumes of testing.

16. For genome editing techniques, when the modification involves the incorporation of DNA of sufficient size, PCR-based methods can be applied, similar to those used for transgenic varieties. However, when genome editing involves single base pair changes without other genetic changes, detection and identification become technically challenging. When the change is known, it was suggested that a combination of PCR and Sanger sequencing could be applied. However, when the genetic edit is unknown, the challenge becomes distinguishing between an engineered and a natural change. Next-generation sequencing could be applied, but detection may depend on disclosure of information and regulatory tools rather than technical methodologies. Additional considerations include the size and complexity of plant genomes, bulk shipments and grain samples. Other participants stated that current methodologies are insufficient or not applicable for organisms produced through new breeding techniques, such as genome editing.

17. Participant's opinions diverged on whether current analytical techniques could be applied to distinguish between the products of synthetic biology and their naturally occurring or chemically synthesized counterparts. One suggested that current techniques may need updating as single target detection may no longer be suitable. However, the feasibility of PCR and qPCR was noted provided that transgenes or transgene junctions were present. Another participant suggested that mass spectrometry⁷ and glycan profiling⁸ could be applied to detect subtle molecular differences between natural products and products produced through different synthetic biology applications. For example, some products may have co-purified contaminants that may suggest the origin of the material. However, for certain highly purified products, such as sugar, no DNA or protein may be present to detect modified material and thus impossible to distinguish.

Topic 3: Overview of current capacity for the detection and identification of living modified organisms

18. Participants shared their views on the current capacity for the detection and identification of LMOs, described current challenges and considered how efforts can be focused for future capacity-building activities. The aim of this discussion was to complement the information provided by Parties (34 submissions) in response to a survey prepared pursuant to the request in paragraph 5 of decision CP-9/11.⁹

19. The following guiding questions were suggested to guide participants interventions under this topic:

- (a) Is there sufficient capacity in your country or region to carry out detection and identification of LMOs?
- (b) What are the challenges that are currently being faced (if any)?
- (c) Have there been recent efforts and/or collaborations with other countries and/or organizations to improve the capacity for detection and identification of LMOs?

⁷ Mass spectrometry is an analytical tool used for measuring the mass-to-charge ratio of compounds in a given sample. The technique is used for the identification of unknown compounds by their molecular weight, the quantification of known compounds and to determine structure and chemical properties of molecules present.

⁸ Glycan profiling refers to techniques used to analyse the structure of glycans (polysaccharides).

⁹ Results are summarized at [Microsoft Forms online survey](#); see also synthesis in CBD/CP/MOP/10/INF/4.

(d) Who are the relevant organizations involved in improving global capacity for detection and identification?

(e) Where should efforts be focused to improve the global capacity on detection and identification of LMOs?

20. Overall, some participants stated that there was sufficient national capacity for detection and identification of LMOs in their home countries, while others believed there were challenges still to be overcome. The following challenges were identified by participants:

- Lack of adequate laboratory infrastructure and reagents;
- Lack of technical expertise;
- Lack of access and availability to certified reference materials;
- Difficulty implementing of International Organization for Standardization (ISO) standards;
- Lack of standardized and validated methodologies;
- Rapid development and commercialization of new LMOs and biotechnologies, including new modified crop species, fish and animals;
- Detection of unknown LMOs or LMOs with unknown sequences;
- Lack of quantitative detection methodologies;
- High financial costs for laboratory operations and capacity-building abroad.

21. Participants also shared examples of recent collaborations with other countries and organizations, which have been effective at improving the capacity for detection and identification. Examples included:

- Regional networks of laboratories to collaborate and exchange information:
 - West African Network of GMO Laboratories,
 - Middle East and North Africa regional laboratories,
 - Latin America and Caribbean Network of GMO analysis;
- National Reference Center for GMO Detection and the National Metrology Center of Mexico collaborated to generate 9 certified reference materials for products of agriculture;
- The United Nations Environment Programme - Global Environment Facility (UNEP-GEF) “Multi-Country Project to Strengthen Institutional Capacity on LMO Testing in Support of National Decision-making”;¹⁰
- UNEP-GEF project in Tunisia for the establishment of a regulatory framework, network of laboratories and a reference laboratory at the National Gene Bank of Tunisia;¹¹
- The Government of the Republic of Korea created the Korea Biosafety Capacity-Building Initiative through which the Secretariat of the Convention on Biological Diversity has organized global capacity-building activities on detection and identification.

22. Furthermore, the following organizations were identified as being involved in improving global capacity:

- Secretariat of the Convention on Biological Diversity ([SCBD](#));
- The Global Environment Facility ([GEF](#));
- European Commission Joint Research Centre ([JRC](#))
 - Institute for Reference Materials and Measurements (IRMM);
- European Food Safety Authority ([EFSA](#));
- EU Reference Laboratory for GM food and feed ([EU-RL GMFF](#));
- United States Food and Drug Administration ([US FDA](#));

¹⁰ Participating countries: Angola, Democratic Republic of the Congo, Lesotho, Madagascar, Malawi and Mozambique; Executing Agencies - Participating Laboratories: Angola, Democratic Republic of the Congo, Lesotho, Madagascar, Malawi, Namibia and RAEIN-Africa; <https://www.thegef.org/project/multi-country-project-strengthen-institutional-capacity-lmo-testing-support-national>.

¹¹ <https://www.thegef.org/project/capacity-building-implementation-national-biosafety-framework>.

- International Centre for Genetic Engineering and Biotechnology ([ICGEB](#));
- International Organization for Standardization ([ISO](#));
- International Life Sciences Institute ([ILSI](#));
- American Oil Chemists' Society ([AOCS](#));
- [Cereal and Grains Association](#);
- Regional Agricultural and Environmental Innovations Network–Africa ([RAEIN-Africa](#)).

23. When considering how efforts could be focused to improved global capacity, some participants suggested the following:

- Establishment of regional and global networks of laboratories;
- New detection methodologies for organisms produced through genome editing and synthetic biology;
- Standardization, harmonization and validation of analytical methodologies;
- Access to and development of certified reference materials and information regarding LMOs, particularly for newly developed LMOs;
- Further development of quantitative methods (qPCR and dPCR);
- Development of DNA chips to detect multiple lines simultaneously;
- Development of guidance documents;
- Online webinars and discussions;
- Development of locally relevant approaches;
- Technology transfer;
- Training more laboratory personnel;
- Improve DNA extraction protocols and develop additional quality control measures;
- Promote open access to sequence information;
- Including further sampling training in workshops.

Annex I

**LIST OF RESOURCES SHARED DURING THE ONLINE DISCUSSIONS OF THE NETWORK
OF LABORATORIES FOR THE DETECTION AND IDENTIFICATION OF LIVING
MODIFIED ORGANISMS**

I. ARTICLES AND PUBLICATIONS

1. S. Z. Agapito-Tenfen, A. S. Okoli, M. J. Bernstein, O.-G. Wikmark, A. I. Myhr, Revisiting risk governance of GM plants: the need to consider new and emerging gene-editing techniques. *Front. Plant Sci.* 9 (2018), doi:10.3389/fpls.2018.01874
2. S. Z. Agapito-Tenfen, F. Wickson, Challenges for transgene detection in landraces and wild relatives: learning from 15 years of debate over GM maize in Mexico. *Biodivers. Conserv.* 27, 539–566 (2018), doi: 10.1007/s10531-017-1471-0
3. C. M. Alarcon, G. Shan, D. T. Layton, T. A. Bell, S. Whipkey, R. D. Shillito, Application of DNA- and protein-based detection methods in agricultural biotechnology. *J. Agric. Food Chem.* 67, 1019–1028 (2019), doi: 10.1021/acs.jafc.8b05157
4. K. Amanuma, N. Nakajima, A. H. Hashimoto, Y. Aoki, Genetically modified, red fluorescent zebrafish: detection, crossing, inheritance of red fluorescence, and tolerance to low temperatures. *J. Environ. Biotechnol.* 8, 105–110 (2008). <https://www.jseb.jp/wordpress/wp-content/uploads/08-02-105.pdf>
5. W. Arber, Genetic engineering compared to natural genetic variations. *N. Biotechnol.* 27, 517–521 (2010). doi: 10.1016/j.nbt.2010.05.007
6. Y. Bertheau, in *Encyclopedia of Food Chemistry* (Elsevier, 2019; <https://linkinghub.elsevier.com/retrieve/pii/B9780081005965218349>), pp. 320–336.
7. K. Canckar, M. Ravnikar, J. Žel, K. Gruden, N. Toplak, Real-time polymerase chain reaction detection of cauliflower mosaic virus to complement the 35S screening assay for genetically modified organisms. *J. AOAC Int.* 88, 814–822(9) (2005). <https://aoac.publisher.ingentaconnect.com/contentone/aoac/jaoac/2005/00000088/00000003/art00020>
8. Central Committee on Biological Safety, On the Identifiability of Genome Editing in plants - Commentary of the ZKBS on Y. Bertheau (2019) (2019), (available at [http://www.zkbs-online.de/ZKBS/EN/01_Aktuelles/ZKBS-commentary on Y. Bertheau \(2019\)/ZKBS-commentary on Y. Bertheau \(2019\)_basepage.html?nn=8569050](http://www.zkbs-online.de/ZKBS/EN/01_Aktuelles/ZKBS-commentary%20on%20Y.%20Bertheau%20(2019)/ZKBS-commentary%20on%20Y.%20Bertheau%20(2019)_basepage.html?nn=8569050)).
9. R. Custers, J. M. Casacuberta, D. Eriksson, L. Sági, J. Schiemann, Genetic alterations that do or do not occur naturally; consequences for genome edited organisms in the context of regulatory oversight. *Front. Bioeng. Biotechnol.* 6 (2019), doi: 10.3389/fbioe.2018.00213.
10. T. Demeke, D. Dobnik, Critical assessment of digital PCR for the detection and quantification of genetically modified organisms. *Anal. Bioanal. Chem.* 410, 4039–4050 (2018), doi: 10.1007/s00216-018-1010-1
11. D. Dobnik, D. Štebih, A. Blejec, D. Morisset, J. Žel, Multiplex quantification of four DNA targets in one reaction with Bio-Rad droplet digital PCR system for GMO detection. *Sci. Rep.* 6, 35451 (2016), doi: 10.1038/srep35451
12. European Network of GMO Laboratories (ENGL), “Definition of Minimum Performance Requirements for Analytical Methods of GMO Testing” (Ispra, Italy, 2015), (available at [https://gmo-crl.jrc.ec.europa.eu/doc/MPR Report Application 20_10_2015.pdf](https://gmo-crl.jrc.ec.europa.eu/doc/MPR%20Report%20Application%2020_10_2015.pdf)).

13. European Network of GMO Laboratories (ENGL), “Detection of food and feed plant products obtained by new mutagenesis techniques” (Ispra, Italy, 2019), (available at <https://gmo-crl.jrc.ec.europa.eu/doc/JRC116289-GE-report-ENGL.pdf>).
14. Food and Agriculture Organization of the United Nations, Guidelines on Performance Criteria and Validation of Methods for Detection, Identification and Quantification of Specific DNA Sequences and Specific Proteins in Foods (2010), p. 22. http://www.fao.org/fileadmin/user_upload/gmfp/resources/CXG_074e.pdf
15. L. Freese, J.-W. Chen, R. D. Shillito, Sampling of grain and seed to estimate the adventitious presence of biotechnology-derived seeds in a lot. *Cereal Foods World*. 60, 9–15 (2015), doi: 10.1094/CFW-60-1-0009
16. L. Grantina-Ievina, B. Ievina, V. Evelone, S. Berga, L. Kovalcuka, I. Bergspica, A. Jakovele, A. Malisevs, O. Valcina, I. Rodze, N. Rostoks, Potential risk evaluation for unintended entry of genetically modified plant propagating material in Europe through import of seeds and animal feed – the experience of Latvia. *GM Crops Food*. 10, 159–169 (2019), doi: 10.1080/21645698.2019.1638721
17. L. Grohmann, J. Keilwagen, N. Duensing, E. Dagand, F. Hartung, R. Wilhelm, J. Bendiek, T. Sprink, Detection and identification of genome editing in plants: challenges and opportunities. *Front. Plant Sci*. 10 (2019), doi:10.3389/fpls.2019.00236.
18. L. Hougs, F. Gatto, O. Goerlich, L. Grohmann, K. Lieske, M. Mazzara, F. Narendja, J. Ovesná, N. Papazova, I. Scholtens, J. Žel, “Verification of analytical methods for GMO testing when implementing interlaboratory validated methods” (Ispra, Italy, 2017), doi:10.2760/645114, <https://gmo-crl.jrc.ec.europa.eu/ENGL/docs/WG-MV-Report-version-2.pdf>
19. I. Huber, A. Block, D. Sebah, F. Debode, D. Morisset, L. Grohmann, G. Berben, D. Štebih, M. Milavec, J. Žel, U. Busch, Development and validation of duplex, triplex, and pentaplex real-time PCR screening assays for the detection of genetically modified organisms in food and feed. *J. Agric. Food Chem*. 61, 10293–10301 (2013), doi: 10.1021/jf402448y
20. A. B. Košir, B. Spilsberg, A. Holst-Jensen, J. Žel, D. Dobnik, Development and inter-laboratory assessment of droplet digital PCR assays for multiplex quantification of 15 genetically modified soybean lines. *Sci. Rep*. 7, 8601 (2017), doi: 10.1038/s41598-017-09377-w
21. H. Rehbein, J. Bogerd, Identification of genetically modified zebrafish (*Danio rerio*) by protein- and DNA-analysis. *J. für Verbraucherschutz und Leb*. 2, 122–125 (2007), doi: 10.1007/s00003-007-0179-6
22. N. Rostoks, L. Grantina-Ievina, B. Ievina, V. Evelone, O. Valcina, I. Aleksejeva, Genetically modified seeds and plant propagating material in Europe: potential risks of entrance and current status. *Heliyon*. 5, e01242 (2019), doi: 10.1016/j.heliyon.2019.e01242
23. J. Schnell, M. Steele, J. Bean, M. Neuspiel, C. Girard, N. Dormann, C. Pearson, A. Savoie, L. Bourbonnière, P. Macdonald, A comparative analysis of insertional effects in genetically engineered plants: considerations for pre-market assessments. *Transgenic Res*. 24, 1–17 (2015), doi: 10.1007/s11248-014-9843-7
24. G. Shan, Ed., *Immunoassays in Agricultural Biotechnology* (John Wiley & Sons, Inc., Hoboken, NJ, USA, 2011; <http://doi.wiley.com/10.1002/9780470909935>).
25. S. Trapman, M. Burns, H. Broll, R. Macarthur, R. Wood, J. Zel, “Guidance Document on Measurement Uncertainty for GMO Testing Laboratories” (Luxembourg, 2009), doi:10.2787/18988.

26. United Nations Conference on Trade and Development, “Synthetic Biology and its potential Implications for Biotrade and Access and Benefit-Sharing” (2019), https://unctad.org/en/PublicationsLibrary/ditctedinf2019d12_en.pdf.
27. N. Weber, C. Halpin, L. C. Hannah, J. M. Jez, J. Kough, W. Parrott, Editor’s choice: crop genome plasticity and its relevance to food and feed safety of genetically engineered breeding stacks. *Plant Physiol.* 160, 1842–1853 (2012), doi: 10.1104/pp.112.204271

II. WEBSITES

American Oil Chemists’ Society

<https://www.aocs.org/>

Biosafety Clearing-House (BCH; Secretariat of the Convention on Biological Diversity)

<http://bch.cbd.int>

Bundesinstitut für Risikobewertung (BfR) Reference Laboratory of the network on genetically modified organisms (GVO) [English|German]

https://www.bfr.bund.de/en/reference_laboratory_of_the_network_on_genetically_modified_organisms_gvo_-10524.html

Centro Nacional de Metrología (el CENAM): Ensayos de aptitud técnica [Spanish]

<http://www.cenam.mx/servicios/paptitudtecnica/>

Cereals & Grains Association

<https://www.cerealsgrains.org/Pages/default.aspx>

CropLife International Detection Methods Database

<http://www.detection-methods.com/>

European GMO database (EUropean GMO INitiative for a Unified database System)

<http://www.euginius.eu/euginius/pages/home.jsf>

European Union Reference Laboratory for Genetically Modified Food and Feed

<https://gmo-crl.jrc.ec.europa.eu/default.htm>

European Union Science Hub – IRMM reference materials catalogue

<https://ec.europa.eu/jrc/en/science-update/welcome-irrm-reference-materials-catalogue>

GenBit GM Crop Database

<https://www.genbitgroup.com/en/gmo/gmodatabase/index.php>

International Life Sciences Institute

<https://ilsi.org/>

International Seed Testing Association – Analytical Methods

<https://www.seedtest.org/en/analytical-methods-content---1--1477.html>

Ministério da Agricultura, Pecuária e Abastecimento – Brazilian Detection Laboratories [Portuguese]

<http://www.agricultura.gov.br/assuntos/laboratorios/laboratorios-credenciados/biotecnologia-e-organismos-geneticamente-modificados>

Annex II

INTERNATIONAL ORGANIZATION FOR STANDARDIZATION (ISO) STANDARDS

Current standards

ISO TC34/SC16 - Horizontal methods for molecular biomarker analysis, <https://www.iso.org/committee/560239.html>

ISO/TC 16393:2019 - Molecular biomarker analysis — Determination of the performance characteristics of qualitative measurement methods and validation of methods, <https://www.iso.org/standard/67450.html>

ISO 16577:2016 - Molecular biomarker analysis — Terms and definitions, <https://www.iso.org/standard/57184.html>

ISO 16578:2013 - Molecular biomarker analysis — General definitions and requirements for microarray detection of specific nucleic acid sequences, <https://www.iso.org/standard/57185.html>

ISO/CD 20813:2019 - Molecular biomarker analysis — Methods of analysis for the detection and identification of animal species in foods and food products (nucleic acid-based methods) — General requirements and definitions, <https://www.iso.org/standard/69297.html>

ISO 21570:2005 - Foodstuffs — Methods of analysis for the detection of genetically modified organisms and derived products — Quantitative nucleic acid based methods, <https://www.iso.org/standard/34615.html>

ISO 21571:2005 - Foodstuffs — Methods of analysis for the detection of genetically modified organisms and derived products — Nucleic acid extraction, <https://www.iso.org/standard/34616.html>

ISO 21572:2019 - Foodstuffs — Molecular biomarker analysis — Immunochemical methods for the detection and quantification of proteins, <https://www.iso.org/standard/77325.html>

ISO 24276 - Foodstuffs — Methods of analysis for the detection of genetically modified organisms and derived products — General requirements and definitions, <https://www.iso.org/standard/37125.html>

Under development

ISO/AWI 22753 - Molecular biomarker analysis — Methods of analysis for the detection of genetically modified organisms — Semi-quantitative method for the statistical evaluation of weight/weight GMO content in seeds and grains, <https://www.iso.org/standard/73822.html>

ISO/NP 22942-1 - Molecular biomarker analysis in foodstuffs — Nucleic acid isothermal nucleic acid amplification based methods — Part 1: General requirements, <https://www.iso.org/standard/74245.html>
