



ATTN: Bernadette Juarez
APHIS Deputy Administrator
Biotechnology Regulatory Services
RSRrequests@usda.gov,

July 14, 2023

Subject: Regulatory Status Review (RSR) Request for the Determination of Nonregulated Status of the Soybean Edited for Drought Stress Tolerance from Regulations under 7 CFR Part 340.4

Dear Bernadette Juarez,

GDM Seeds and its affiliate GDM Genética do Brazil Ltda., request from the Biotechnology Regulatory Services (BRS) an Regulatory Status Review (RSR) to Exempt a soybean plant edited for drought stress tolerance, generated by two repairs of double-strand break from regulations in 7 CFR part 340.4. We provided the information related to the development of this plant below, including Confidential Business Information (CBI), as recommended in the Guide for Requesting a RSR under 7 CFR part 340.

We utilized a CRISPR-Cas system without a DNA repair template to induce mutations that could be caused by conventional breeding. We confirmed that (i) the desired change in the target gene was obtained, (ii) no exogenous DNA was present in the generated plant, and (iii) no off-target mutations were generated. Moreover, we provide evidence from the scientific literature that multiple SNP and insertions/deletions (indels) polymorphisms are commonly found in native and bred soybean genotypes, demonstrating that more than one mutation in a gene occurs in nature and by conventional breeding. Therefore, given that multiple polymorphisms in the same gene already exist in natural germplasm, these changes would fall in the natural range for the species.

Furthermore, we would like to provide additional background information on the regulatory status of this soybean plant and its mutations in other countries. The induced mutations were exempted from GMO regulations in Brazil by CTNBio on May 5th, 2022 (Appendix 1), and in Argentina by CONABIA on November 25th, 2022 (Appendix 2).

We would appreciate your attention to this request, and please do not hesitate to contact us with any questions or requirements for additional information.

Sincerely,

Mirta Antongiovanni
Global Regulatory Affairs Manager
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Information about requestor

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Confidential Business Information (CBI) statement

This RSR request does contain CBI.

CBI justification

GDM Seeds and its affiliate GDM Genética do Brazil Ltda., act in a very competitive segment of the agriculture science and technology business. Any knowledge about strategic development of traits and technology can provide competitors with an advantage that can directly influence the results of competing products, technology, and its competitiveness along the time. This happens because the timely development and launching of products greatly impact revenues and market share of the developed products.

Therefore, we request that the information related to the gene that we have modified to generate a soybean plant for enhanced drought stress tolerance remain confidential.

To maintain the confidentiality of the gene we deleted the Confidential Business Information that could allow anyone to identify the gene, or the new allele created. These include the name identification, the literature that would allow the identification of the gene, and the sequences of the gene, its coding region sequence, and its protein sequence.

Description of the comparator plants

Scientific name (genus, species, subspecies)

Glycine max (L.) Merr.

Ploidy

Diploidized tetraploid ($2n=40$).

Common Name

Soybean.

Cultivar

Private conventional non-GMO soybean line named GDMNBT16.



Genotype of the modified plant

The genome edited soybean plant contains two small deletions in the gene [] created by induced repair of two DNA breaks, resulting in the loss-of-function allele of the protein with the goal of conferring drought stress tolerance. The mutations generated the desired knockout of the protein by creating a premature stop codon. The whole genome DNA sequence of the resulting soybean plant was analyzed and confirmed to match the intended modification, no foreign DNA remained, and no off-target mutations were generated.

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The gene target is called [], according to the Williams 82 soybean genome reference sequence (Schmutz et al. 2010).

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To develop the soybean plant more tolerant to drought stresses we knocked out the target gene. Initially, a conventional non-GMO soybean plant was transformed by *Agrobacterium tumefaciens* containing a vector with a CRISPR-Cas system and two gRNAs (Hsu, Lander, and Zhang 2014) targeting the same target gene at different positions. DNA sequence of the regenerated plant was analyzed to identify mutations in the target gene to select the intended mutations.

The repair of the first induced DNA break resulted in a deletion of three DNA base pairs (**Table 1 and Table 3**) that changed two amino acids of the protein to another amino acid (**Table 4 and Table 5**) and the repair of the second induced DNA break resulted in the deletion of four DNA base pairs (**Table 1 and Table 3**), causing the early truncation of protein by the creation of a premature termination (stop) codon and knockout of the target gene (**Table 4 and Table 5**). The analysis of the DNA sequence of the modified gene (**Table 1 and Table 3**) and its predicted protein translation (**Table 4 and Table 5**) indicated that we obtained the intended modification(s), which was the knockout of the gene to impair its protein function, and which should result in the enhanced drought stress tolerance of the soybean plants.

The transformation plasmid was removed through self-fertilization and posterior selection of the progenies by marker-assisted breeding. To confirm none of the components present in the vector remained, we sequenced the whole genome of the soybean plant obtained and the non-edited version with paired-end reads of 100 nucleotides each. The final sequencing coverage was ~53x for the original non-edited genotype and ~60x for the edited plant. The reads had high quality, with more than 93% of bases with quality higher than Q30, and were mapped to the Williams 82 soybean genome reference (Schmutz et al. 2010) and the sequence of the vector that contained the CRISPR-Cas system by using the BWA algorithm (H. Li and Durbin 2010; H. Li 2013). The whole genome DNA sequence analysis showed that no fragment of the plasmid or T-DNA remained, and that no off-target mutations were created. The regions with the highest homology to the gRNAs recognition sites have only up to 19 identical nucleotides out of the 23 nucleotides of the gRNA (**Table 2**). The possible off-target region of the gRNAs used to induce the target DNA breaks were identified by using the CRISPR/Cas9 target online predictor service at <https://crispr.cos.uni-heidelberg.de/>.

Sequence of the Modification

The sequence of the gRNAs and distinct protein alleles created are shown in **Table 1**.

Table 1: DNA sequencing and amino acid translations of the targeted PCR amplicons and the later whole genome sequencing of the original and edited soybean plants validated the intended mutations.

gRNA/plant	[]	Alleles (DNA 5'-3')	
gRNA 1	[[CBI, CBI-Deleted
Original plant				
Edited plant]]	
gRNA 2	[[CBI, CBI-Deleted
Original plant				
Edited plant]]	

No off-target differences were identified between the edited and original plants (**Table 2**).

Table 2: Sequence alignment of possible off-target regions identified by their similarity to the gRNAs used.

Oligonucleotide or genomic interval	Sequences*	
gRNA1 sequence matches/mismatches	[CBI-Deleted
[]	CBI-Deleted
gRNA1 sequence matches/mismatches	[CBI-Deleted
[]	CBI-Deleted
gRNA2 sequence matches/mismatches	[CBI-Deleted
[]	CBI-Deleted
gRNA2 sequence matches/mismatches	[CBI-Deleted
[]	CBI-Deleted

Obs. (*) Identity of the DNA bases are represented by “.”.



Sequence comparison

The genomic sequences of the original and edited soybean plants are shown in **Table 3**.

Table 3. Full gene alignment of sequences of the original plant, edited plant, and gRNAs used.

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The protein sequences of the original plant and the predicted translated protein sequence of the edited plant are shown in **Tables 4 and 5**.

Table 4: Proteins predicted for both original and edited alleles.

Plant	Predicted translation of the proteins
Original plant	[]
Edited plant	[]

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Obs. (*) termination codon, which results in the early termination of the protein (knockout with loss-of-function).

Table 5. Alignment of predicted protein sequences. The early termination of the predicted protein results in a protein with [] amino acids while the native protein from the Williams 82 and the original plant has a protein with [] amino acids.

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In our view, the obtained gene sequence could be achieved in nature or by conventional breeding by the accumulation of mutations in the same gene or by the repeated mutation of the gene by successive natural or induced mutations and targeted DNA breaks in separate generations or experiments. In both cases, the outcome matches what happens to most of the natural soybean genes as commonly identified in allelic differences among genotypes or varieties of the same species (Martínez-Fortún, Phillips, and Jones 2022). The scientific literature has shown that more than one polymorphism, either SNPs or insertions/deletions (indels) are commonly found in soybeans (Torkamaneh et al. 2021). The authors re-sequenced 1,007 soybean accessions and identified several natural alleles present among genotypes illustrating the range of natural variation already present within the soybean genome. The authors used the SNP subset of polymorphisms to create SNP haplotypes, which they called Gene-Centric Haplotypes (GDH)s and showed that 95% of the soybean genes have more than one haplotype per gene (only 2,766 out of the 55,589 have one haplotype per gene) (**Figure 1**). They demonstrated that there is a large amount of variation present in the soybean germplasm, but more interestingly, many of these haplotypes have more than one SNP. To quantify the proportion of haplotypes that have at least two SNPs, we counted the number of SNPs that each haplotype has in comparison to one of the haplotypes arbitrarily chosen as a reference. We identified that most of the 445,147 haplotypes (306,049 corresponding to 77.9% of the alternative haplotypes), including the reference haplotype of each gene, have more than one SNP (**Figure 2**). Moreover, the data show that the presence of only one SNP per gene is the minority of the cases (86,794 corresponding to approximately 22% of the alleles).

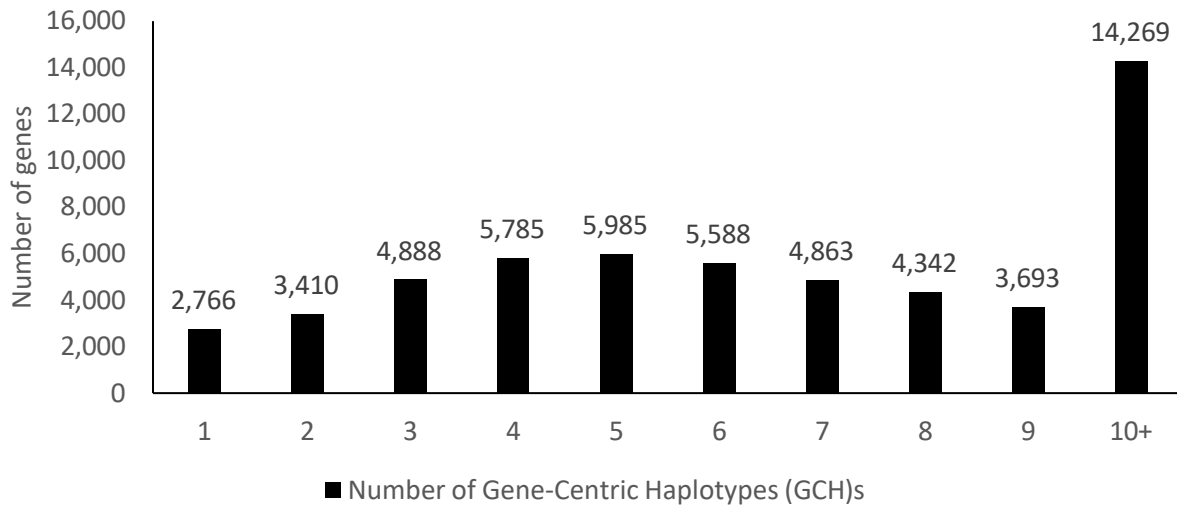


Figure 1. Number of soybean genes distributed according to the number of Gene-Centric Haplotypes (GCHs). Modified from Torkamaneh et al. 2021.

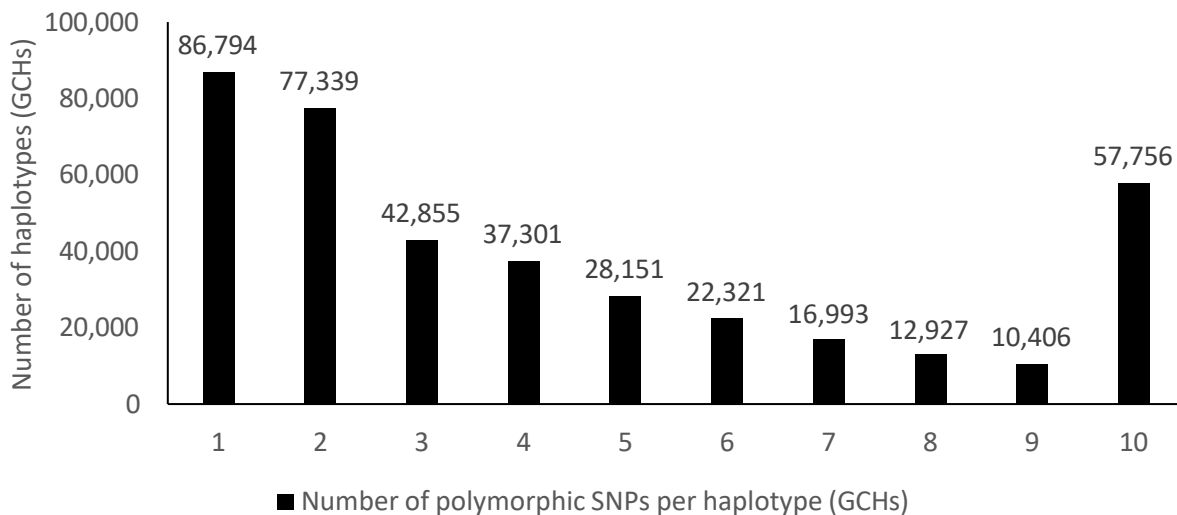


Figure 2. Number of Gene-Centric Haplotypes (GCHs) of all soybean genes distributed by the number of SNP polymorphisms that each CGH has in comparison to its reference haplotype. Estimated from data deposited by Torkamaneh et al. 2021 in www.soybase.org.

To understand the presence of multiple indels in each gene, we performed the same analysis of the data generated by Torkamaneh et al. 2021. In their dataset the authors considered indels as deletions of up to 50 nucleotides or insertions of up to 32 nucleotides and found 1,873,299 indels in the 1,007 samples re-sequenced. The results were that 92% of the genes have two or more haplotypes (**Figure 3**). Only 4,396 out of 50,125 with indels had a single haplotype per gene. Moreover, we identified that 72% of the haplotypes have two or more indels (462,037 out of 636,903) (**Figure 4**). Like SNP polymorphisms, the data shows that only the minority of the soybean alleles have one indel per gene (28%). It is noteworthy

that if the SNP and indels polymorphisms were analyzed together, the proportion of alleles per gene and the proportion of alleles with more than one polymorphism would increase.

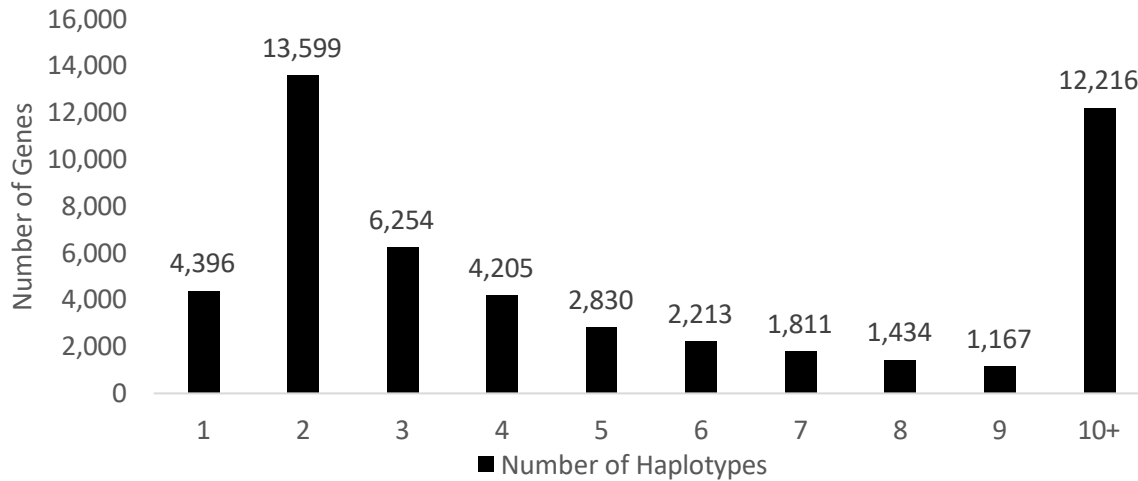


Figure 3. Number of soybean genes distributed according to the number of alleles containing at least 1 indel (–50 bp to +32 bp). Estimated from data deposited by Torkamaneh et al. 2021 in www.soybase.org.

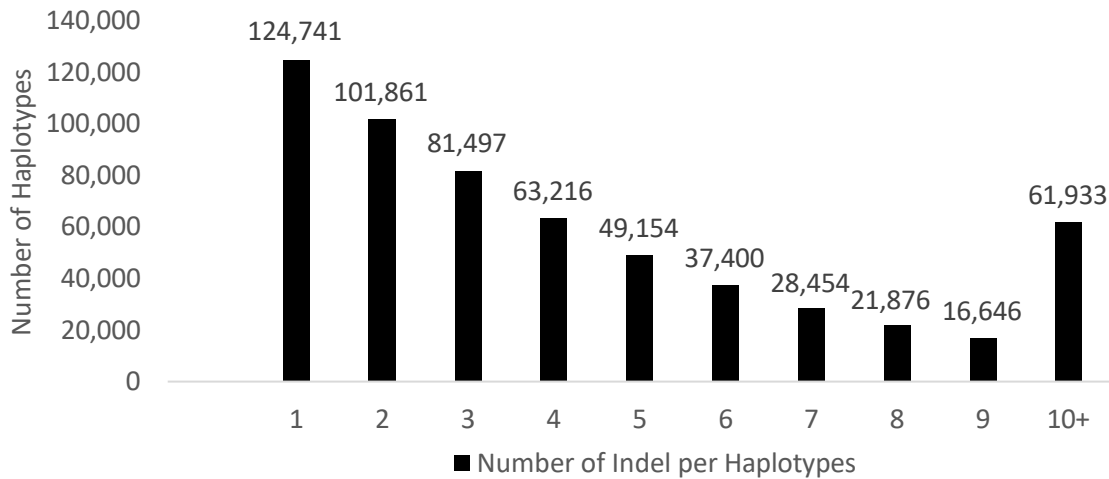


Figure 4. Number of haplotypes/alleles of all soybean genes distributed by the number of indels in comparison to the reference genome. Estimated from data deposited by Torkamaneh et al. 2021 in www.soybase.org.

Several independent studies have also reported comparable results, which show the significant heterogeneity among soybean subpopulations' genomes (Qiu et al. 2014; Zhou et al. 2015; Sedivy, Wu,



and Hanzawa 2017; Kim et al. 2021). Therefore, we understand that the natural and artificial variation of the soybean germplasm created by the domestication and conventional breeding of soybean is enormous and that the most common scenario is the presence of more than a single polymorphism per gene.

Specifically for the gene [] that we edited, there is no natural allele with deletions in the dataset of Torkamaneh et al. 2021, but there are three distinct natural SNP haplotypes/alleles, all of them distinguishable from each other by two or more SNPs (data in Torkamaneh et al. 2021).

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In our soybean plant, the additional mutation did not affect the intended molecular phenotype, which was supposed to lead to the protein knockout. These intended mutations resulted in the early terminated protein by the generation of a stop codon that caused a loss-of-function of the gene (knockout), which could be caused by conventional breeding.

Description of new trait

Intended trait

Abiotic drought stress tolerance.

Intended phenotype

The intended phenotype is the increase of the drought stress tolerance of soybean plants in the vegetative stage.

Description of the MOA

The gene [] encodes a protein that is [] family of proteins involved in the signaling of various cellular pathways (Adams, Ron, and Kiely 2011). In plants, []. The silencing of [] in rice resulted in an increase in drought tolerance (D. Li et al. 2009). The silencing of [] in soybeans by transgenesis resulted in an increase in the tolerance to flooding (Komatsu, Hiraga, and Nouri 2014) and drought (D.-H. Li et al. 2018). The accumulation of evidence shows that [] plays an important role in the modulation of the plant responses to several types of abiotic stress but mainly in the increase of drought tolerance when it has its expression decreased or eliminated [(D.-H. Li et al. 2018; Zheng et al. 2019)].

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In soybeans, []

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References

- [] CBI-Deleted
- Hsu, Patrick D., Eric S. Lander, and Feng Zhang. 2014. "Development and Applications of CRISPR-Cas9 for Genome Engineering." *Cell* 157 (6): 1262–78. <https://doi.org/10.1016/j.cell.2014.05.010>.
- Kim, Myung-Shin, Roberto Lozano, Ji Hong Kim, Dong Nyuk Bae, Sang-Tae Kim, Jung-Ho Park, Man Soo Choi, et al. 2021. "The Patterns of Deleterious Mutations during the Domestication of Soybean." *Nature Communications* 12 (1): 97. <https://doi.org/10.1038/s41467-020-20337-3>.
- [] CBI-Deleted
- [] CBI-Deleted
- [] CBI-Deleted
- [] CBI-Deleted
- Li, Heng. 2013. "Aligning Sequence Reads, Clone Sequences and Assembly Contigs with BWA-MEM," March. <https://doi.org/10.48550/arXiv.1303.3997>.
- Li, Heng, and Richard Durbin. 2010. "Fast and Accurate Long-Read Alignment with Burrows–Wheeler Transform." *Bioinformatics* 26 (5): 589–95. <https://doi.org/10.1093/bioinformatics/btp698>.
- Martínez-Fortún, Jorge, Dylan W. Phillips, and Huw D. Jones. 2022. "Natural and Artificial Sources of Genetic Variation Used in Crop Breeding: A Baseline Comparator for Genome Editing." *Frontiers in Genome Editing* 4 (August): 937853. <https://doi.org/10.3389/fgeed.2022.937853>.
- Qiu, Jie, Yu Wang, Sanling Wu, Ying-Ying Wang, Chu-Yu Ye, Xuefei Bai, Zefeng Li, et al. 2014. "Genome Re-Sequencing of Semi-Wild Soybean Reveals a Complex Soja Population Structure and Deep Introgression." *PLOS ONE* 9 (9): e108479. <https://doi.org/10.1371/journal.pone.0108479>.
- Schmutz, Jeremy, Steven B. Cannon, Jessica Schlueter, Jianxin Ma, Therese Mitros, William Nelson, David L. Hyten, et al. 2010. "Genome Sequence of the Palaeopolyploid Soybean." *Nature* 463 (7278): 178–83. <https://doi.org/10.1038/nature08670>.
- Sedivy, Eric J., Faqiang Wu, and Yoshie Hanzawa. 2017. "Soybean Domestication: The Origin, Genetic Architecture and Molecular Bases." *New Phytologist* 214 (2): 539–53. <https://doi.org/10.1111/nph.14418>.
- Torkamaneh, Davoud, Jérôme Laroche, Babu Valliyodan, Louise O'Donoghue, Elroy Cober, Istvan Rajcan, Ricardo Vilela Abdelnoor, et al. 2021. "Soybean (*Glycine Max*) Haplotype Map (GmHapMap): A Universal Resource for Soybean Translational and Functional Genomics." *Plant Biotechnology Journal* 19 (2): 324–34. <https://doi.org/10.1111/pbi.13466>.
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Zhou, Zhengkui, Yu Jiang, Zheng Wang, Zhiheng Gou, Jun Lyu, Weiyu Li, Yanjun Yu, et al. 2015. "Resequencing 302 Wild and Cultivated Accessions Identifies Genes Related to Domestication and Improvement in Soybean." *Nature Biotechnology* 33 (4): 408–14. <https://doi.org/10.1038/nbt.3096>.

Appendices

Appendix 1. Brazilian Official Diary with communication of exemption of soybean edited for drought tolerance to GMO regulations (*in Portuguese* and freely translated to English).

5/9/22, 1:05 PM

EXTRATO DE PARECER TÉCNICO Nº 8.013/2022 - EXTRATO DE PARECER TÉCNICO Nº 8.013/2022 - DOU - Imprensa Nacional

DIÁRIO OFICIAL DA UNIÃO

Publicado em: 09/05/2022 | Edição: 86 | Seção: 1 | Página: 23

Orçã: Ministério da Ciência, Tecnologia e Inovações/Comissão Técnica Nacional de Biosseguranc

EXTRATO DE PARECER TÉCNICO Nº 8.013/2022

A Presidência da Comissão Técnica Nacional de Biossegurança - CTNBio, no uso de sua atribuições e de acordo com o artigo 14, inciso XIX, da Lei 11.105/05 e do Art. 5º, inciso XIX do Decreto 5.591/05, torna público que na 251ª Reunião Ordinária da CTNBio, realizada em 05 de maio de 2022, a CTNBio apreciou e emitiu parecer técnico para o seguinte processo:

Processo: 01245.003707/2022-81

Requerente: GDM - Genética do Brasil S.A

COR: 367/15

Assunto: Carta Consulta TIMP

A CTNBio, após análise do requerimento de Consulta Prévia a respeito do Enquadramento Regulatório de soja com tolerância a seca editada por CRISPR-Cas no Brasil, concluiu que o produto proposto está de acordo com a Resolução Normativa Nº 16, de 15 de janeiro de 2018 por considerar que as TIMP abrangem um conjunto de novas metodologias e abordagens que diferem da estratégia de engenharia genética por transgenia, por resultar na ausência de ADN/ARN recombinante no produto final. A proposta em questão se enquadra em um dos exemplos de Técnicas Inovadoras de Melhoramento de Precisão (TIMP) constantes no ANEXO I da referida Resolução Normativa: produto obtido por técnica que introduz mutações sítio dirigidas, gerando ganho ou perda de função gênica, com a ausência comprovada de ADN/ARN recombinante no produto. Portanto, a CTNBio considerou não se tratar de um novo organismo geneticamente modificado à luz da Lei 11.105/05.

No âmbito das competências dispostas na Lei 11.105/05 e seu decreto 5.591/05, a CTNBio concluiu que o presente pedido atende às normas e legislação pertinentes que visam garantir a biossegurança do meio ambiente, agricultura, saúde humana e animal.

A CTNBio esclarece que este extrato não exime a requerente do cumprimento das demais legislações vigentes no país, aplicáveis ao objeto do requerimento.

Este é um extrato do Parecer Técnico da CTNBio. Sua íntegra, assim como todos os documentos referentes à solicitação, constam do processo armazenado na CTNBio. Informações complementares poderão ser solicitadas por meio do Serviço de Informação ao Cidadão - SIC ou pelo sistema FALABR, pelo site eletrônico <https://esic.cqn.gov.br/>.

PAULO AUGUSTO VIANNA BARROSO
Presidente da Comissão

Este conteúdo não substitui o publicado na versão certificada.

DIÁRIO OFICIAL DA UNIÃO

Published: 05/09/2022 | Edition: 86 | Section: 1 | Page: 23

Office: *Ministério da Ciência, Tecnologia e Inovações/Comissão Técnica Nacional de Biossegurança*
(Ministry of Science, Technology and Innovation/ National Biosafety Technical Commission)

Technical Opinion Extract Nº 8.013/2022

The Presidency of the *Comissão Técnica Nacional de Biossegurança - CTNBio* (National Biosafety Technical Commission), in the exercise of its attributions and following article 14, item XIX, of Law 11.105/05 and Art. 5, item XIX of Decree 5.591/05, makes public that at the 251st Ordinary Meeting of CTNBio, held on May 5, 2022, CTNBio assessed and issued a technical opinion for the following process:

Process: 01245.003707/2022-81

Applicant: GDM - Genética do Brasil S.A

CQB: 367/13

Subject: Innovative and Precise Breeding Techniques Consultation Letter.

CTNBio, after analyzing the request for Prior Consultation regarding the Regulatory Framework for drought-tolerant soy edited by CRISPR-Cas in Brazil, concluded that the proposed product is in compliance with Normative Resolution No. 16, of January 15, 2018, considering that Innovative and Precise Breeding Technique encompasses a set of new methodologies and approaches that differ from the genetic engineering strategy by transgenics, as it results in the absence of recombinant DNA/RNA in the final product. The question falls within one of the examples of Innovative and Precise Breeding Technique contained in ANNEX I of the aforementioned Normative Resolution: product obtained by a technique that introduces site-directed mutations, generating gain or loss of gene function, with the proven absence of recombinant DNA/RNA on the product. Therefore, CTNBio considered that it was not a new genetically modified organism regulated under Law 11.105/05.

Within the scope of the Law 11,105/05 and its decree 5,591/05, CTNBio concluded that the present request complies with the pertinent norms and legislation that aim to guarantee the biosafety of the environment, agriculture, human and animal health.

CTNBio clarifies that this extract does not exempt the applicant from complying with other laws in force in the country, applicable to the object of the application.

This is an extract of the Technical Opinion of CTNBio. Its entirety and all documents related to the request are part of the process stored at CTNBio. Additional information may be requested through the *Serviço de Informação ao Cidadão - SIC* (Citizen Information Service) or through the FALABR system, through the website <https://esic.cgu.gov.br/>.

PAULO AUGUSTO VIANNA BARROSO

Presidente da Comissão (Commission President)

Appendix 2. Letter from CONABIA from Argentina exempting the soybean edited for drought tolerance from GMO regulations (*in Spanish* and freely translated to English).



República Argentina - Poder Ejecutivo Nacional
Las Malvinas son argentinas

Nota

Número: NO-2022-127455998-APN-DNB#MAGYP

CIUDAD DE BUENOS AIRES
Viernes 25 de Noviembre de 2022

Referencia: Ex-2022-119785920 ICP Soja NBT16_001/HO_001

A: Ing. Agr. Ignacio BARTOLOMÉ (GDM),

Con Copia A: Gladys Huerga (DNB#MAGYP), Luciano Pardo Funes (DNB#MAGYP), Maria de los Angeles Primo (DNB#MAGYP), Florencia Goberna (DNB#MAGYP),

De mi mayor consideración:

En relación al expediente EXP. 2022- 119785920 para soja NBT16_001/HO_001 con fenotipo tolerancia a sequía, presentado como Instancia de Consulta Previa (ICP) ante la Coordinación de Innovación y Biotecnología el 07 de noviembre del 2022, se le informa que la CONABIA procedió a su evaluación del producto final y consideró que dicho producto, no contienen una nueva combinación de material genético.

Por tal motivo, el desarrollo del producto tal como fue descrito en la ICP remitida, no se encuentra alcanzado por la Resolución N 763/11 del ex-Ministerio de Agricultura, Ganadería y Pesca, pudiendo ser manejado como material no regulado.

Sin otro particular saluda atte.



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Date: 2022.11.25 14:34:28 -03:00

Perla Godoy
Coordinadora
Dirección Nacional de Bioeconomía
Secretaría de Agricultura, Ganadería y Pesca

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Date: 2022.11.25 14:34:29 -03:00



República Argentina - Poder Ejecutivo Nacional (Argentinean Republic – National Executive Office)
Las Malvinas son argentinas (The Maldivas are Argentinean)

Notification

Number: NO-2022-12455998-APN-DNB MAGYP

Buenos Aires

Friday, November 25, 2022

Reference: Ex-2022-119785920 ICP Soja NBT16_001/HO_001

To: Ing Agr. Ignacio BARTOLOMÉ (GDM),

Cc: Gladys Huerga (DNB-MAGYP), Luciano Pardo Funes (DNB-MAGYP), Maria de los Angeles Primo (DNB=MAGYP), Florencia Goberna (DNB=MAGYP),

With my highest consideration,

In relation to the dossier EXP.2022-119785920 for NBT16_001/HO_001 soybean with a drought tolerance phenotype, presented as a Prior Consultation Instance (ICP) to the *Coordinación de Innovación y Biotecnología* (Innovation and Biotechnology Coordination) office on November 7, 2022, it is informed that CONABIA proceeded with the final product evaluation and considered that the product does not contain a new combination of genetic material.

For this reason, the development of the product as described in the ICP submitted, is not covered by Resolution No. 763/11 of the *ex-Ministerio de Agricultura, Ganadería y Pesca* (former Ministry of Agriculture, Livestock and Fisheries), and can be handled as non-regulated.

Without further ado, sincerely

Perla Godoy

Coordinator

Dirección Nacional de Bioeconomía (Directorship of National Bioeconomy)

Secretaría de Agricultura, Ganadería y Pesca (Secretary of Agriculture, Livestock, and Fisheries)