Novel Food Information: Insect Resistant and Herbicide Tolerant DP-915635 Maize

On this page

Background:

Health Canada has notified Pioneer Hi-Breed Canada Company that it has no objection to the food use of insect resistant and herbicide tolerant DP-915635 maize. Health Canada conducted a comprehensive assessment of this variety according to its *Guidelines for the Safety Assessment of Novel Foods*. These Guidelines are based upon internationally accepted principles for establishing the safety of foods with novel traits.

The following provides a summary of the notification from Pioneer Hi-Breed Canada Company and the evaluation by Heath Canada and contains no confidential business information.

1. Introduction

Pioneer Hi-Breed Canada Company developed DP-915635 maize to resist corn rootworm pest pressures and glufosinate herbicide application.

The safety assessment performed by Food Directorate evaluators was conducted according to Health Canada's *Guidelines for the Safety Assessment of Novel Foods*. These Guidelines are based on harmonization efforts with other regulatory authorities and reflect international guidance documents in this area (e.g., Codex Alimentarius). The assessment considered: how DP-915635 maize was developed; how the composition and nutritional quality of DP-915635 maize compared to non-modified corn varieties; and the potential for DP-915635 maize to be toxic or cause allergic reactions. Pioneer Hi-Breed Canada Company provided data that demonstrates that DP-915635 maize is as safe and of the same nutritional quality as traditional corn varieties used as food in Canada.

The Food Directorate has a legislated responsibility for pre-market assessment of novel foods and novel food ingredients as detailed in the *Food and Drug Regulations* (Division B.28). Food use of DP-915635 maize is considered a novel food under the following part of the definition of novel foods:

- "c) a food that is derived from a plant, animal or microorganism that has been genetically modified such that
  (i) the plant, animal or microorganism exhibits characteristics that were not previously observed in that plant, animal or microorganism."

2. Development of the Modified Plant

DP915635-4 corn was created by site-specific integration of the DNA sequence encoding three expression cassettes. This site-specific integration was achieved using two sequential transformation steps: (1) insertion of a 'landing pad' sequence at a specific location in the plant genome, achieved using biolistics and CRISPR-Cas9-mediated insertion, and (2) insertion of the intended expression cassettes, containing the genes for insect protection and herbicide tolerance, into the landing pad. This second step was accomplished by *Agrobacterium*-mediated transformation.

The first transformation step was accomplished by biolistic co-bombardment with four plasmids (PHP73878, PHP70605, PHP21193 and PHP21875). This co-bombardment delivered the components needed for plant transformation and improved plant regeneration, as well as the landing pad sequence. The landing pad sequence was inserted into the plant genome using a CRISPR-Cas9-mediated targeted insertion.

The landing pad sequence itself consists of the *lox*P site, *ubi*ZM1 promoter including the 5' UTR and intron, FRT1 recombination target site, *nptII* gene, *pin*II terminator, and FRT6 recombination site.

The plasmids that were co-bombarded with the landing pad sequence resulted in the transient expression of *zm*-41CR1 guide RNA and the *cas9* gene (PHP70605), the *zm-wus2* gene (PHP21139), and the *zm-odp2* gene (PHP21875).

Transient expression of *zm-wus2* and the *zm-odp2* genes generate the WUS and ODP2 proteins respectively, which result in improved plant transformation and regeneration.

Transient expression of *zm*-41CR1 guide RNA (gRNA) directs the Cas9 protein, an RNA-guided DNA endonuclease, to produce a double-stranded DNA break between the endogenous *zm*-SEQ-158 and *zm*-SEQ159 sequences, which are adjacent on the corn genome.

The landing pad is integrated in a site-specific manner between the *zm*-SEQ158 and *zm*-SEQ159 sites in the corn genome. The sequences of these sites are identical to the sequences that flank the landing pad sequence from PHP73878 plasmid. The CRISPR-Cas9 system enables incorporation of the landing pad at the target site through homology-directed DNA repair.

A corn line containing the landing pad, but no other unintended DNA sequences, was selected and advanced to the next transformation.

Agrobacterium-mediated transformation of the corn event containing the landing pad was performed using the PHP83175 T-DNA containing plasmid. This allowed for the transport of the T-DNA into the plant nucleus but, in the selected event, the full T-DNA sequence was not incorporated into the corn

genome. The *nptII* gene and *pin*II terminator in the landing pad sequence, which was in the corn genome from the first transformation, was exchanged for the *pmi*, *mo-pat*, and *ipd072Ea* gene cassettes from PHP83175 T-DNA. The result of this exchange generated the intended genetic modification.

The *pmi* gene from the PHP83175 T-DNA codes for a phosphomannose isomerase. When expressed, this protein allows for positive selection and recovery of transformed plant cells. This protein has been introduced into 5 products [1] that have been previously reviewed by Health Canada that have all received letters of no objection.

The *mo-pat* gene from the PHP83175 T-DNA encodes a phosphinothricin N-acetyl transferase. When expressed, this protein confers glufosinate herbicide tolerance to the plant as a weed management tool for corn cultivation. This protein has been introduced to 14 products [2] that have been previously authorized by Health Canada.

The *ipd079Ea* gene from the PHP83175 T-DNA encodes an insecticidal protein. When expressed, this protein confers corn rootworm (*Diabrotica* spp.) insect pest resistance. This protein has not been previously reviewed by Health Canada for its safety in food.

3. Characterization of the Modified Plant

The number of T-DNA inserts in DP915635-4 corn was characterized by using High Throughput Sequencing, following the Southern by Sequencing methodology. The results of the analyses demonstrated that there is a single, intact integration site in DP915635-4 corn at the intended genomic locus between the *zm*-SEQ158 and *zm*-SEQ159 sequences.

Because the *zm*-SEQ158 and *zm*-SEQ159 sequences are contiguous and non-genic, endogenous corn genes were not disrupted.

A bioinformatics analysis was performed to search for open reading frames (ORFs) both within the DNA insert and across the insert-genome junctions. These searches looked for sequences that encode proteins of at least 30 amino acids (AA) which share sequence similarity to known toxins or allergens. Ninety-two (92) putative ORFs greater than or equal to 30 AA were identified for DP915635-4 corn.

The predicted ORFs were further screened for similarity to known allergens and toxins. To screen for possible toxins, the 92 ORFs were assessed against an annually updated internal toxin database made up a subset of UniProtKB/Swiss-Prot database, filtered by keywords that imply toxicity or adverse health effects (e.g. toxin, hemagglutinin, vasoactive, etc.). No alignment matches were found. Based on this analysis, it is reasonable to conclude that no putative toxins would be generated.

To screen for possible allergens, the same amino acid sequences were used to search the Comprehensive Protein Allergen Resource 2021 database, which contains 2248 sequences. The first search looked for protein homologies with E-values <0.0001 and >35 % identity over the protein length (>80AA) to known allergens. The second search looked for open reading frames with predicted peptide sequences with any 8 perfect (100 %) AA residue matches to an allergen. Only one hit was yielded for 8 identical, contiguous amino acid residues (DLSDKETT) between the PMI protein sequence in DP915635-4 corn and the sequence of an allergen (alpha-parvalbumin from frog,

GenBank Accession CAC83047.1). It is unlikely that these identical, contiguous residues reflect an allergenic hazard given that the PMI protein has been previously reviewed by Health Canada for safety in other products.

Generational stability of the inserted DNA was assessed by Southern blot analysis over five generations of DP915635-4 corn. The results of these analyses demonstrated that the event-specific bands across generations had consistent genomic border regions, as evidenced by the consistent signal sizes across generations, and therefore the insert was stably inherited.

To evaluate the mode of inheritance, 100 maize plants from each of five generations of DP915635-4 corn (F1, T2, T3, T4 and T5) were evaluated using genotyping and phenotyping. Genotypic study used qPCR to evaluate the presence/absence of the DP915635-4 *ipd079Ea*, *mo-pat* and *pmi* genes. The phenotypic analysis used visual herbicide injury to confirm the presence/absence for tolerance to glufosinate-ammonium herbicide in each plant. The phenotypic results were compared to genotypic results to evaluate the co-segregation of genotype with phenotype. No statistical differences were noted between observed and expected segregation ratios for each of the segregating generations. As a result, the phenotypes co-segregate with the inserted DNA locus, and that the inserted DNA locus segregates according to Mendelian rules of inheritance.

Expression of transgenic IPD079Ea protein in DP915635-4 corn was evaluated using enzyme-linked immunosorbent assay. In grain, IPD079Ea protein was measured at 0.18 (± 0.065) ng/mg dry weight, PAT protein was measured at 6.4 (±1.5) ng/mg dry weight and PMI protein was measured at 3.1 (± 1.1) ng/mg dry weight.

To assess IPD079Ea protein safety, recombinant IPD079Ea was used as a surrogate for DP915635-4 corn expressed IPD079Ea. Recombinant IPD079Ea was generated in *E. coli* as an N-terminal poly-histidine fusion protein and was subsequently purified using nickel affinity chromatography. The poly-histidine tag was cleaved using thrombin, and thrombin was removed using heparin sepharose column chromatography. This recombinant protein was compared with IPD079Ea protein that partially purified from DP915635-4 corn leaf using immuno-affinity chromatography to establish protein equivalency, and suitability of the recombinant protein for protein safety studies.

Characterization to establish equivalence between microbe-produced and plant-produced DP915635-4 IPD079Ea proteins was performed using 1) sodium dodecylsulfate polyacrylamide gel electrophoresis (SDS-PAGE), 2) western blot analysis, 3) glycosylation analysis, 4) mass spectrometry, and 4) N-terminal amino acid sequence analysis. By SDS-PAGE, both plant- and microbe-derived IPD079Ea proteins migrated to an MW of approximately 52 kDa. The western blot analysis showed that both plant- and microbe-derived IPD079Ea proteins are immunoreactive, revealing bands that migrated to an MW of approximately 52 kDa. Protein glycosylation analysis confirmed that neither version of IPD079Ea protein contained post-translational glycosylation modifications. Mass spectrometry peptide mapping was carried out by excising the relevant bands from Coomassie-stained SDS-PAGE gels for each sample. The proteins extracted from these bands were digested with trypsin or chymotrypsin, and resulting peptide fragments were evaluated using UPLC-MS. The resulting MS data was used to search and match against the expected IPD079Ea protein sequence, and a coverage percentage was calculated. The coverage of the mapped corn-derived IPD079Ea protein was 94.8 % while the coverage of the mapped microbe-derived IPD079Ea protein was 91 %. The deduced amino acid sequences were identical between the two samples.

Based on the equivalency studies, bacterially produced IPD079Ea can serve as a suitable surrogate for plant produced IPD079Ea in terms of protein safety studies.

No protein equivalency data was presented for PAT and PMI; instead, a rationale was presented for the safety of these proteins in food based on their both having been reviewed as part of prior authorizations, and the history of their presence in the food supply. The *mo-pat* gene in DP915635 maize encodes the identical PAT protein found in a number of Novel Foods reviewed previously by Health Canada, and that have a history of safe use (Hérouet et al., 2005) [3]. Similarly, the *pmi* gene in DP915635 maize encodes the same PMI protein found in a number of Novel Foods reviewed previously by Health Canada.

Based on the available data provided, the BMH has no safety concerns regarding DP-915635-4 maize from a molecular biology perspective.

4. Dietary Exposure

It is expected that DP915635-4 maize will be consumed similarly to corn currently sold in the Canadian marketplace.

In terms of expected expression patterns: IPD079Ea expression is driven by root specific promoters and enhancers; PAT expression is driven by a constitutive promoter; the *pmi* expression cassette lacks a promoter, but it is expected that due to the proximity to the FRT1 that expression of *pmi* will be controlled by an unspecified proximal promoter.

Tissue samples were harvested at 6 different sites during the 2019 growing season in the United States and Canada. Tissue samples were collected for root (V6, V9, R1, and R4), leaf (V9, R1, and R4), pollen (R1), forage (R4), and grain (R6). Protein abundances for IPD079Ea, PAT and PMI proteins were determined using ELISA.

Maize grain is the part of the plant used for human food. IPD079Ea protein was observed in grain at 0.18 (± 0.065) ng/mg dry weight. PAT protein was observed at 6.4 (± 1.5) ng/mg dry weight. PMI protein was observed at 3.1 (± 1.1) ng/mg dry weight.

No food safety concerns were raised by the information provided by the petitioner in relation to dietary exposure.

5. Nutrition

The petitioner provided compositional data for DP-915635-4 maize, a non-GM near-isoline control maize (control), and four non-GM reference varieties collected from eight field trials in the United States and Canada during the 2019 growing season. In each trial, four replicates of each entry were planted in a randomized complete block design. Typical commercial agriculture production practices were used for the field trials.

Grain samples were harvested and analysed using acceptable methods for moisture, crude protein, crude fat, acid detergent fibre, total dietary fibre, neutral detergent fibre, crude fibre, ash, carbohydrates, calcium, copper, iron, magnesium, manganese, phosphorous, potassium, sodium, zinc, β-carotene, thiamine, niacin, pantothenic acid, vitamin B6, folic acid, tocopherols, amino acids, fatty acids, p-Coumaric acid, ferulic acid, inositol, phytic acid, raffinose, trypsin inhibitor, and furfural.

The data provided was for all key nutrients and anti-nutrients as described in the Organization for Economic Co-Operation and Development (OECD) "Consensus Document on Compositional Considerations for New Varieties of Maize (*Zea Mays*): Key Food and Feed Nutrients, Anti-nutrients and Secondary Plant Metabolites" (2002).

Statistically significant differences between the conventional control and DP-915635-4 were noted when *P*-values were < 0.05. When a statistical difference was identified, the nutritional relevance of these differences were further examined by comparing the results to expected ranges for conventional maize as described in the OECD consensus document (2002), the in-study reference range, and the tolerance interval which was based on proprietary accumulated data from 31 multi-site field studies between 2003 and 2018 consisting of a total of 167 non-GM commercial reference maize lines and 171 unique environments representative of commercial maize-growing regions in the United States, Canada, Chile, Brazil, and Argentina.

Statistically significant differences compared to the control were observed for the following components (control vs DP-915635-4): palmitoleic acid (0.119 vs 0.122 % total fatty acids), stearic acid (1.98 vs 2.02 % total fatty acids), oleic acid (24.1 vs 23.8 % total fatty acids), linoleic acid (58.8 vs 59.2 % total fatty acids), lignoceric acid (0.301 vs 0.294 % total fatty acids), methionine (0.214 vs 0.200 % dw), and α-tocopherol (3.67 vs 3.97 mg/kg dw). In all cases the composition of DP915635 was within the reference ranges provided by the petitioner and the expected range for conventional maize. There were no differences in proximate, fibre, mineral, anti-nutrient, or secondary metabolite content between the DP915635 and the control maize.

No nutritional concerns were identified with the food use of insect resistant and herbicide tolerant DP915635 maize.

6. Chemistry

Data for toxic trace elements were not provided by the petitioner. However, the petitioner provided the results of a compositional assessment comparing samples of grain and forage from DP915635-4 maize, its non-genetically modified (GM) counterpart and reference varieties, where samples were assessed for levels of various nutrients, including minerals (calcium, copper, iron, magnesium, manganese, phosphorus, potassium, sodium, zinc), anti-nutrients, and secondary metabolites. The petitioner determined that mineral levels were similar between DP915635-4, the non-GM counterpart and reference varieties. Based on the above information, there is no indication that the modifications would affect the transport and uptake or result in significant differences in the concentrations of other trace elements in DP915635-4 maize relative to conventional corn.

Data for mycotoxins were also not provided by the petitioner. However, a qualitative assessment was conducted comparing responses to naturally occurring insects, diseases and abiotic stressors for DP915635-4 maize, its non-GM counterpart, and reference varieties. Information in the submission indicates that DP915635-4 maize did not exhibit any major differences in responses to naturally occurring insects, diseases, or abiotic stressors. Since infection from pests, disease and abiotic stressors can increase the susceptibility of a plant to mycotoxin-producing fungi, it can be inferred that the modifications to DP915635-4 maize are unlikely to increase its susceptibility to mycotoxins compared to conventional varieties of corn.

Data comparing agronomic characteristics of DP915635-4 maize, its non-GM counterpart and reference varieties were provided by the petitioner. The petitioner indicated in the submission that the majority of characteristics measured in the various types of maize as part of the agronomic evaluation did not demonstrate any statistically significant differences. For the two characteristics where a difference was observed (i.e., early stand count and days to flowering) between DP915635-4 maize and the control, the petitioner indicated that these were likely false positives and not biologically meaningful as they were well within the range of natural variation observed in other reference varieties. Increased uptake of chemical contaminants and greater susceptibility to mycotoxins would potentially impact plant growth and yield. The above information suggests that the genetic modification in DP915635-4 maize is not expected to have a negative impact on crop yield relative to other conventional corn varieties.

The molecular characterization assessment did not identify any concerns that would make DP915635-4 maize different when compared to conventional corn in relation to increased ability to uptake chemical contaminants or greater susceptibility to mycotoxin-producing fungi relative to non-GM maize.

7. Toxicology

The host organism, maize (*Zea mays*), has a long history of safe food use in Canada, and is not associated with toxicological concerns. The source of the *ipd079Ea* gene (producing the novel IPD079Ea protein) is from the fern *Ophioglossum pendulum.* The petitioner stated that there were no reports identified in the literature of *Ophioglossum* being poisonous to humans or livestock.

No test substance-related mortality was observed (LD_{50} > 5000 mg/kg bw in mice) in an OECD guideline acute oral toxicity study of the novel IPD079Ea protein produced in a microbial expression system. There were no test substance-related clinical observations, and the animals gained weight during the 2-week observation period prior to sacrifice.

A bioinformatics analysis of the amino acid sequence of the novel IPD079Ea protein was conducted using the UniProtKB/Swiss-Prot database. There were no matches for IPD079Ea with any proteins associated with toxicity or adverse health effects.

The source of the *mo-pat* gene (producing the PAT protein) is a non-pathogenic bacteria.

No treatment-related effects were observed (up to 5050 mg/kg bw in mice) in a previously-conducted OECD guideline acute oral toxicity study of the PAT protein. [4]

A bioinformatics analysis of the amino acid sequence of the PAT protein was conducted using the UniProtKB/Swiss-Prot database. There were no matches for PAT with any proteins associated with toxicity or adverse health effects.

PAT protein has also been approved in several different crops in Canada (e.g., LLRICE62, TC6275 maize, MS3 maize, DBT418 maize, 7MS8/RF3 canola).

PMI is an enzyme that is widely present in nature. Soybeans and several other legumes have also been reported to contain the enzyme.

The PMI protein was found to have low acute oral toxicity based on a previously-conducted study [5]. No clinical signs of toxicity or effects on body weight gain were identified, and no gross abnormalities were observed at necropsy, when tested at 3030 mg/kg bw in mice.

A bioinformatics analysis of the amino acid sequence of the PMI protein was conducted using the UniProtKB/Swiss-Prot database. There were no matches for PMI with any proteins associated with toxicity or adverse health effects.

PMI protein has also been used as a selectable marker in several different crops authorized by Health Canada (e.g., MIR162, Golden Rice, MIR604 maize, 5307 maize, 3272 maize).

The dietary exposures for the IPD079Ea, PAT and PMI proteins are expected to be low, and are likely overestimates because it is assumed that all corn products eaten would be derived from this variety, and furthermore did not account for any reductions from food processing.

No toxicological concerns were identified for the IPD079Ea, PAT or PMI proteins. It was concluded that DP915635 maize would be as safe as conventional maize.

8. Allergenicity

The host organism, maize (*Zea mays*), has a long history of safe food use in Canada and is not associated with allergenic concerns.

The novel IPD079Ea protein is sensitive to heat at temperatures of ≥ 50°C, suggesting that this protein would be denatured during cooking/processing, rendering it more susceptible to digestion.

Incubation of the novel IPD079Ea protein in simulated gastric fluid (SGF), followed by simulated intestinal fluid (SIF), and resulted in complete degradation with 0.5 minutes. This result suggests that the protein is completely and rapidly digested under conditions simulating the digestive tract.

The amino acid sequence for the novel IPD079Ea protein was compared to the sequences for known or suspected allergens [6]. No sequence similarity was identified over 80 amino acids (with homology ≥ 35%) for known allergen sequences [7]. No contiguous 8-amino acid exact matches between the IPD079Ea protein sequence and known allergen sequences were identified, suggesting that IPD079Ea is unlikely to cross-react with known or suspected allergens.

Evidence [8] was presented showing that the PAT protein is completely degraded (within 0.5 minutes) in a SGF assay and a SIF assay. This result suggests that the protein is completely and rapidly digested under conditions simulating the digestive tract.

The amino acid sequence for PAT was compared to the sequences for known or suspected allergens. No sequence similarity or exact matches were identified, suggesting that PAT is unlikely to cross-react with known or suspected allergens.

The petitioner presented evidence [9] that the PMI protein is completely degraded (within 2 minutes) in a SGF assay and a SIF assay. These findings suggest that the protein is completely and rapidly digested under conditions simulating the digestive tract.

The amino acid sequence for PMI was compared to the sequences for known or suspected allergens. No sequence similarity greater than 35 % over 80 or more amino acids was identified. One contiguous 8-amino acid match was identified for the CAC83047.1 alpha-parvalbumin frog allergen.

An acceptable scientific rationale was provided for this match as being a false positive.

In a previously-assessed corn event containing the identical PMI protein (Health Canada, 2010) [10], an exact match of 8 contiguous amino acids for alpha-parvalbumin from frog was also identified. IgE binding using the serum of the single individual known to have this allergy was determined to be negative for cross-reactivity.

No allergenic concerns were identified for the IPD079Ea, PAT or PMI proteins. The PTAS concludes that DP915635 maize would be as safe as conventional maize.

Taken together, the information presented supports the conclusion that the DP915635-4 maize would be just as safe as conventional corn in terms of potential chemical contaminants, toxicants and allergens.

Conclusion:

Health Canada's review of the information presented in support of the food use of DP915635-4 maize does not raise concerns related to food safety. Health Canada is of the opinion that food derived from DP915635-4 maize is as safe and nutritious as food from current commercial corn varieties.

Health Canada's opinion concerns only with the food use of DP915635-4 maize.

This Novel Food Information document has been prepared to summarize the opinion regarding the subject product provided by the Food Directorate, Health Products and Food Branch, Health Canada. This opinion is based upon the comprehensive review of information submitted by the petitioner according to the *Guidelines for the Safety Assessment of Novel Foods*.

(Également disponible en français)

For further information, please contact:

Health Canada
Novel Food Section
Food Directorate
Health Products and Food Branch
251 Sir Frederick Banting Driveway
PL2204E
Ottawa, Ontario, K1A 0K9
bmh-bdm@hc-sc.gc.ca

---

1 PMI protein has been reviewed by Health Canada during the evaluation of several other events; Golden Rice (2018), MIR604 maize (2007), MIR162 maize (2010), 5307 maize (2013), 3272 maize (2008).

2 The PAT protein has been reviewed during the evaluation of several other events; LLRICE62 (2006), TC6275 maize (2006), MS3 maize (1997), DLL5 maize (1996), DBT418 maize (1997),Bt176 maize (1996), T304-40 cotton (2011), MON88701 cotton (2014), LLCotton25 cotton (2004), GHB119 cotton (2011), MS8/RF3 canola (1997), MS11 (2018), MS1/RF2 (1995), HCN92 canola (1995).

3 Hérouet, Corinne, et al. "Safety evaluation of the phosphinothricin acetyltransferase proteins encoded by the pat and bar sequences that confer tolerance to glufosinate-ammonium herbicide in transgenic plants." Regulatory Toxicology and Pharmacology 41.2 (2005): 134-149.

4 Organisation for Economic Co-operation and Development. 1999. Consensus document on general information concerning the genes and their enzymes that confer tolerance to phosphinothricin herbicide. Series on harmonization of regulatory oversight in biotechnology, No. 11. ENV/JM/MONO(99)13.

5 Reed, J., Privalle, L., Powell, M.L., Meghi, M., Dawson, J., Dunder, E., Suttie, J., Wenk, A., Launis, K., Kramer, C., Chang, Y., Hansen, G., Wright, M. 2001. Phosphomannose isomerase: an efficient selectable marker for plant transformation. In vitro Cellular & Developmental Biology-Plant, 37, 127-132.

6 Comprehensive Protein Allergen Resource (COMPARE), January, 2020: 2248 sequences.

7 Codex Alimentarius Commission, 2009; FAO/WHO, 2001.

8 Hérouet, C., Esdaile, D.J., Mallyon, B.A., Debruyne, E., Schulz, A., Currier, T., Hendrickx, K., van der Klis, R-J., Rouan, D. 2005. Safety evaluation of the phosphinothricin acetyltransferase proteins encoded by the pat and bar sequences that confer tolerance to glufosinate-ammonium herbicide in transgenic plants. Regulatory Toxicology and Pharmacology, 41: 134-149.

9 Reed, J., Privalle, L., Powell, M.L., Meghi, M., Dawson, J., Dunder, E., Suttie, J., Wenk, A., Launis, K., Kramer, C., Chang, Y., Hansen, G., Wright, M. 2001. Phosphomannose isomerase: an efficient selectable marker for plant transformation. In vitro Cellular & Developmental Biology-Plant, 37, 127-132.

10 Health Canada. 2010. “Novel Food Information – Insect Resistant Corn Event MIR162” Available: https://www.canada.ca/en/health-canada/services/food-nutrition/genetically-modified-foods-other-novel-foods/approved-products/novel-food-information-insect-resistant-corn-event-162.html

---

Date modified:

2022-06-16