Application for authorization to place on the market MON 15985 × MON 1445 cotton in the European Union, according to Regulation (EC) No 1829/2003 on genetically modified food and feed

Part II

Summary

A. GENERAL INFORMATION

1. Details of application

a)	**Member State of application** United Kingdom
b)	**Application number** Not available at the time of application
c)	**Name of the product (commercial and other names)** The Monsanto development code for the genetically modified cotton product is MON 15985 × MON 1445. In countries where MON 15985 × MON 1445 is being cultivated, packages of these cottonseeds are marketed under the name of the variety, in association with the trademark Bollgard II® with Roundup Ready®, indicating clearly to growers that the cotton is protected from specific lepidopteran insect pests and tolerant to Roundup® herbicide, containing the active ingredient glyphosate.
d)	**Date of acknowledgement of valid application** Not available at the time of application

2. Applicant

a)	**Name of applicant** Monsanto Company, represented by Monsanto Europe S.A.
b)	**Address of applicant** Monsanto Europe S.A. Avenue de Tervuren 270-272 B-1150 Brussels BELGIUM Monsanto Company 800 N. Lindbergh Boulevard St. Louis, Missouri 63167 U.S.A
c)	**Name and address of the person established in the Community who is responsible for the placing on the market, whether it be the manufacturer, the importer or the distributor, if different from the applicant (Commission Decision 2004/204/EC Art 3(a)(ii))** MON 15985 × MON 1445 will be traded and used in the E.U. in the same manner as the equivalent products from current commercial cotton and by the same operators currently involved in the trade and use of traditional cotton.

3. Scope of the application

® Bollgard II®, Roundup Ready® and Roundup® are registered trademarks of Monsanto Technology LLC.

( ) GM plants for food use
( ) Food containing or consisting of GM plants
(X) Food produced from GM plants or containing ingredients produced from GM plants
( ) GM plants for feed use
( ) Feed containing or consisting of GM plants
(X) Feed produced from GM plants
(X) Import and processing (Part C of Directive 2001/18/EC)
( ) Seeds and plant propagating material for cultivation in Europe (Part C of Directive 2001/18/EC)

4. Is the product being simultaneously notified within the framework of another regulation (*e.g.* seed legislation)?

Yes ( )	**No (x)**
If *ye*s, specify	

5. Has the GM plant been notified under Part B of Directive 2001/18/EC and/or Directive 90/220/EEC?

Yes ( )	**No (x)**
If *n*o, refer to risk analysis data on the basis of the elements of Part B of Directive 2001/18/EC *See* following sections	

6. Has the GM plant or derived products been previously notified for marketing in the Community under Part C of Directive 2001/18/EC or Regulation (EC) 258/97?

Yes ( )	**No (x)**
If *ye*s, specify	

7. Has the product been notified in a third country either previously or simultaneously?

Yes (x)	No ( )

If *yes*, specify

Outside the E.U., such as in U.S. and Australia, MON 15985 × MON 1445 is authorized for all uses, corresponding to the full range of used of traditional cotton. The scope of the approvals already granted for this genetically modified cotton product and the status of pending regulatory reviews, which are currently in progress in numerous countries around the world, depend on the country and its local regulatory framework. Final approvals wherein countries require specific approvals are posted by these regulatory agencies on their official websites.

8. General description of the product

a) Name of the recipient or parental plant and the intended function of the genetic modification

MON 15985 × MON 1445 has been produced by the traditional breeding of MON 15985 and MON 1445. Although genetic modification was used in the development of MON 15985 and MON 1445, no additional genetic modifications were involved for the production of MON 15985 × MON 1445.

MON 15985 has been developed to produce the Cry1Ac and Cry2Ab2 proteins that confer protection against feeding damage caused by major lepidopteran insect pests of cotton, including the cotton cotton bollworm (CBW, *Helicoverpa armigera*), tobacco budworm (TBW, *Heliothis virescens*) and pink bollworm (PBW, *Pectinophora gossypiella*). It was produced by stable insertion of the coding sequence for Cry2Ab2 protein from *Bacillus thuringiensis* subsp. *kurstaki* into the genome of an existing genetically modified cotton, MON 531 (Bollgard® cotton), which expresses the Cry1Ac protein.

MON 1445 contains the genetic material necessary to express the CP4 EPSPS protein which imparts tolerance to glyphosate and the NPTII selectable marker protein.

As MON 15985 × MON 1445 inherits the introduced traits from its parental inbreds, it is protected against targeted lepidopteran insect pests and it is tolerant to glyphosate.

The use of MON 15985 × MON 1445 enables the farmer to effectively control the targeted lepidopteran pests in cotton, ensuring maximum realization of yield potential, while removing the environmental burden of the production, packaging and transport of insecticides, previously used to control lepidopteran pests. In addition, growers will have the ability to apply glyphosate over the top of cotton crop.

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b) Types of products planned to be placed on the market according to the authorisation applied for

The scope of the current application covers the import of MON 15985 × MON 1445 for processing and the use of food and feed produced from MON 15985 × MON 1445 in the E.U. Neither the use of the whole cottonseed as such nor the cultivation of MON 15985 × MON 1445 varieties in the E.U. are included in this application.

c) Intended use of the product and types of users

MON 15985 × MON 1445 will be traded and used in the E.U. in the same manner as the equivalent products from current commercial cotton varieties and by the same operators currently involved in the trade and use of conventional cotton.

d) Specific instructions and/or recommendations for use, storage and handling, including mandatory restrictions proposed as a condition of the authorisation applied for

MON 15985 × MON 1445 is substantially equivalent to other cotton varieties except for the inherited lepidopteran-protection and glyphosate-tolerance traits, which are traits of agronomic interest. MON 15985 × MON 1445 was shown to be as safe and as nutritious as traditional cotton. Therefore, MON 15985 × MON 1445 and the food and feed products produced from MON 15985 × MON 1445 will be stored, packaged, transported, used and handled in the same manner as current commercial cotton, and the measures for waste disposal and treatment of MON 15985 × MON 1445 products are the same as those of conventional cotton.

e) Any proposed packaging requirements

MON 15985 × MON 1445 is substantially equivalent to traditional cotton varieties (except for the protection from targeted lepidopteran insect pests and tolerance to glyphosate). Therefore, MON 15985 × MON 1445 and the food and feed products produced from MON 15985 × MON 1445 will be used in the same manner as other cotton and no specific packaging is foreseen. (For labelling, *See* question 8.(f)).

f) A proposal for labelling in accordance with Articles 13 and Articles 25 of Regulation (EC) 1829/2003. In the case of GMOs, food and/or feed containing, consisting of GMOs, a proposal for labelling has to be included complying with the requirements of Article 4, B(6) of Regulation (EC) 1830/2003 and Annex IV of Directive 2001/18/EC.

In accordance with Regulations (EC) No 1829/2003 and 1830/2003, a labelling threshold of 0.9% is applied for the placing on the market of MON 15985 × MON 1445 and derived products.

Operators shall be required to label foods and feeds derived from

MON 15985 × MON 1445 with the words "produced from genetically modified cotton". In the case of products for which no list of ingredients exists, operators shall ensure that an indication that the food or feed product is produced from GMOs is transmitted in writing to the operator receiving the product.

Operators handling or using MON 15985 × MON 1445 cottonseed and derived foods and feeds in the E.U. are required to be aware of the legal obligations regarding traceability and labelling of these products. Given that explicit requirements for the traceability and labelling of GMOs and derived foods and feeds are laid down in Regulations (EC) No 1829/2003 and 1830/2003, and that authorized foods and feeds shall be entered in the Community Register, operators in the food/feed chain will be fully aware of the traceability and labelling requirements for MON 15985 × MON 1445. Therefore, no further specific measures are to be taken by the applicant.

g) Unique identifier for the GM plant (Regulation (EC) 65/2004; does not apply to applications concerning only food and feed produced from GM plants, or containing ingredients produced from GM plants)

MON-15985-7 × MON-Ø1445-2

h) If applicable, geographical areas within the EU to which the product is intended to be confined under the terms of the authorisation applied for. Any type of environment to which the product is unsuited

The use in foods and feeds produced from MON 15985 × MON 1445 is suitable throughout the E.U.

9. Measures suggested by the applicant to take in case of unintended release or misuse as well as measures for disposal and treatment

Because this application is for consent to import MON 15985 × MON 1445 for processing and to use food and feed produced from MON 15985 × MON 1445 as any other cotton product, not including the cultivation of varieties of MON 15985 × MON 1445 in the E.U., environmental release would more likely occur through incidental release during import, handling, storage and processing. However, modern methods of transporting and handling minimize such losses of cottonseed, so there is little chance of germination, growth and reproduction of cotton destined for processing in the E.U. In practice, the cottonseed will mostly be confined to fixed locations (seaports, seed elevators and processing facilities) and enclosed to minimize or prevent spillage (transport vehicles including trucks and railroad cars). Such conditions significantly limit entry into the environment. Moreover, in the event of incidental spillage, the establishment of volunteer plants would be unlikely, since cotton cannot survive without human assistance and is not capable of surviving as a weed. Although cottonseed could over-winter in mild conditions and germinate the following year, cotton does not persist as a weed. The appearance of cotton volunteers in rotational fields is highly unlikely under European conditions and, if they occur, they can be easily

controlled by current agronomic practices, including cultivation or the use of appropriate herbicides such as glufosinate and paraquat.

In addition, the information presented in this application established that MON 15985 × MON 1445 is unlikely to be different from other cotton, and therefore, is unlikely to pose any threat to the environment or to require special measures for its containment.

No specific conditions are warranted or required for the import of MON 15985 × MON 1445 for processing and for the use of foods and feeds produced from MON 15985 × MON 1445.

B. INFORMATION RELATING TO THE RECIPIENT OR (WHERE APPROPRIATE) PARENTAL PLANTS

1. Complete name

a)	**Family name** Malvaceae
b)	**Genus** *Gossypium*
c)	**Species** *hirsutum* (4n = 52)
d)	**Subspecies** N/A
e)	**Cultivar/breeding line or strain** MON 15985 × MON 1445
f)	**Common name** Cotton

2. a) Information concerning reproduction

(i)	***Mode(s) of reproduction*** Cotton production is generally carried out with seeds. Cotton is a perennial plant that is harvested and planted annually. Cross-pollination can occur, but cotton is normally considered to be a self-pollinating crop.
(ii)	***Specific factors affecting reproduction*** Although natural crossing can occur, cotton is considered to be a self-pollinating crop. The pollen is heavy and sticky and transfer by wind is unlikely. Regardless, there are no morphological barriers to cross-pollination based on flower structure. Pollen is transferred instead by insects, in particular by various wild bees, bumble bees (*Bombus* sp.), and honeybees (*Apis mellifera*).
(iii)	***Generation time*** The cultural cycle for cotton ranges from 120 to 200 growing days from seedling emergence to maturity.

2 b) Sexual compatibility with other cultivated or wild plant species

The scope of the current application does not include the environmental release of MON 15985 × MON 1445.

Gene transfer to cultivated genotypes

In as much as similar cotton genotypes are fully compatible, any pollen that is transferred has the potential to produce a hybrid seed. The degree of out-crossing in a production field is strongly dependent upon the geographic location of the field, which means upon the crop ecology.

Cross-pollination decreased from five to less than one percent from one to seven meters, respectively, away from the source plot.

Gene transfer to wild plant species

The criterion of sexual compatibility greatly limits the potential of gene flow from cultivated *Gossypium* in the geopolitical boundaries of the E.U. No genera in the Gossypieae tribe occur naturally in this region.

3. Survivability

a) Ability to form structures for survival or dormancy

Cotton is a perennial plant that is harvested and planted annually and is not considered to have weedy characteristics.

b) Specific factors affecting survivability

Cultivated cotton does not possess any of the attributes associated with long term survivability such as seed dormancy, long soil persistence, germination under diverse environmental conditions, rapid vegetative growth, a short life cycle, high seed output, high seed dispersal or long distance dispersal of seeds. In most cotton growing areas of the E.U. some of the seed remaining in the field following harvest and cultivation may germinate in the autumn if conditions are favourable. The seeds not germinating are likely to rot and die. In cotton growing regions with mild and dry winters, such as in Spain and Greece, cottonseed may over-winter and germinate the following spring. These cotton volunteers can be easily controlled by current agronomic practices including cultivation and the use of appropriate herbicides. However, it should be noted that cultivation of MON 15985 × MON 1445 is not in the scope of this application.

4. Dissemination

a) Ways and extent of dissemination

Cotton is a perennial plant that is harvested and planted annually. Dissemination occurs only by means of seeds. Genetic material can be disseminated by pollen movement.

b) Specific factors affecting dissemination

Seed dissemination is impacted by mechanical harvesting and transport as well as wind damage, which may cause some mature bolls to fall to the ground. Pollen dispersal is influenced by insect vectors, particularly, bumble bees (*Bombus* spp.) and honey bees (*Apis mellifera*), with the former being the most efficient pollinator.

5. Geographical distribution and cultivation of the plant, including the distribution in Europe of the compatible species

There are five prominent types of cotton being grown commercially around the world including Egyptian, Sea Island, American Pima, Asiatic and Upland. Cotton is grown worldwide between latitudes of 45° north and 30° south, in areas that have at least 160 frost free days. Cotton is a 'heat loving' plant, however more than 50% of the world crop is grown in temperate zones above 30° N latitude. Additionally, cotton is grown under similar climatic and soil constraints. The majority of cotton is grown in areas that receive between 50 and 150 cm of rainfall per year.

The major cotton producing countries in the world include the United States, Peoples Republic of China, India, Pakistan and the Republic of Uzbekistan. Brazil, Australia, Egypt, Argentina, Turkey, Greece, Syria and others produces significant, but lesser amounts.

There are no close wild relatives of cotton in the E.U.

6. In the case of plant species not normally grown in the Member State(s), description of the natural habitat of the plant, including information on natural predators, parasites, competitors and symbionts

In the E.U., cotton is commercially grown in Spain and Greece, however cotton cultivation of MON 15985 × MON 1445 in the E.U. is not within the scope of this application.

7. Other potential interactions, relevant to the GM plant, of the plant with organisms in the ecosystem where it is usually grown, or used elsewhere, including information on toxic effects on humans, animals and other organisms

Cotton is known to interact with other organisms in the environment including a range of beneficial and pestiferous arthropods, fungal diseases and surrounding weed species. Cotton is cultivated in Spain and Greece and

has a history of safe use in those countries. Cotton is not considered harmful nor pathogenic to humans, however the plant does produce gossypol and cyclopropenoid fatty acids, which are natural toxicants. Both gossypol and cyclopropenoid fatty acids contents are reduced via processing of the cottonseed into oil or meal.

C. INFORMATION RELATING TO THE GENETIC MODIFICATION

Information on MON 15985 and MON 1445 have been previously described in the application for authorization of MON 15985 in the E.U. according to Regulation (EC) No 1829/2003 and the notification for MON 1445 pursuant to Regulation (EC) No 258/97, respectively.

1. Description of the methods used for the genetic modification

MON 15985 × MON 1445 was produced by crossing inbred plants of MON 15985 and MON 1445, using traditional breeding methods. Although genetic modification was used in the development of MON 15985 and MON 1445, no additional genetic modifications were involved for the production of MON 15985 × MON 1445.

MON 15985 is produced by the transformation of MON 531, which was previously genetically modified via *Agrobacterium tumefaciens* mediated transformation. MON 15985 was generated using the particle acceleration transformation system.

Agrobacterium-mediated transformation of cotton cells was used to develop MON 1445. DNA containing the *cp4 epsps* expression cassette was integrated into the genome of conventional cotton.

2. Nature and source of the vector used

MON 15985 × MON 1445 has been obtained by traditional breeding of MON 15985 and MON 1445. Although transformation vectors were used in the development of MON 15985 and MON 1445, no additional vectors were involved for the production of MON 15985 × MON 1445.

MON 15985 is produced by the transformation of MON 531. The plasmid vector used to generate MON 15985, PV-GHBK11, is an 8.7 kb high copy number, pUC-based plasmid. It contains well-characterized DNA elements for selection (*nptII*) and replication (ori-pUC) of the plasmid in bacteria.

The plasmid vector used to produce MON 1445, PV-GHGT07, is a 12 kb single border binary transformation vector. It contains well-characterised DNA segments required for selection and replication of the plasmid in bacteria as well as a right border for initiating the region of DNA (T-DNA) integrated into the plant genomic DNA.

3. Source of donor DNA, size and intended function of each constituent fragment of the region intended for insertion

MON 15985 × MON 1445 has been produced by the traditional breeding of MON 15985 and MON 1445. The inserted DNA fragment from both parental

lines are inherited in MON 15985 × MON 1445.

The individual components and the size, source and function of these inherited DNA sequences are given in Tables 1 and 2.

Table 1. Summary of genetic elements of the inserts in MON 15985.

Genetic Element	Approximate Size (Kb)[1]	Description/source
Genetic elements associated to the functional *cry1Ac* insert (MON 531)		
cry1Ac cassette		
7S 3'	0.44	3' nontranslated region from soybean 7S seed storage protein gene which terminates transcription and directs polyadenylation of the *cry1Ac* mRNA
cry1Ac	3.54	DNA sequence coding for a synthetic variant of the Cry1Ac protein of *Bacillus thuringiensis*
e35S	0.6	Cauliflower mosaic virus (CaMV) promoter with the duplicated enhancer region used to drive expression of the *cry1Ac* coding sequence.
aad gene		
aad	0.79	Bacterial gene comprising its own regulatory elements and coding for an aminoglycoside-modifying enzyme, 3'(9)-O-nucleotidyltransferase from the transposon Tn7
nptII cassette		
NOS 3'	0.24	3' nontranslated region of the nopaline synthase (*nos*) gene from *Agrobacterium tumefaciens* which terminates transcription and directs polyadenylation
nptII	0.97	DNA sequence isolated from the bacterial transposon Tn5 coding for neomycin phosphotransferase type II. Expression of this sequence in plant cells confers resistance to kanamycin and serves as a selectable marker for transformation. The *nptII* cassette also contains a 153 bp portion of the 378 bp (*ble*) gene encoding the bleomycin binding protein.
35S	0.32	Cauliflower mosaic virus (CaMV) promoter
ori-V	0.39	Origin of replication for *Agrobacterium* derived from the broad host range plasmid RK2.
Genetic elements associated to the *cry2Ab2* insert (MON 15947)		
uidA cassette		
e35S	0.3	Cauliflower mosaic virus (CaMV) promoter with a duplicated enhancer region used to drive expression of the *uidA* coding sequence.
uidA	1.8	DNA sequence coding for the ß-D-glucuronidase (GUS) protein from *E. coli*
NOS 3'	0.26	3' nontranslated region of the nopaline synthase (*nos*) gene from *Agrobacterium tumefaciens* which terminates transcription and directs polyadenylation
cry2Ab2 cassette		
e35S	0.6	Cauliflower mosaic virus (CaMV) promoter with the duplicated enhancer region used to drive expression of the *cry2Ab2* gene.
HSP70	0.1	Petunia heat shock protein 70 5' untranslated leader sequence.
ctp2	0.23	DNA sequence coding for the N-terminal chloroplast transit peptide from *Arabidopsis thaliana epsps* gene.
cry2Ab2	1.9	DNA sequence coding for a synthetic Cry2Ab2 protein of *Bacillus thuringiensis*.
NOS 3'	0.26	3' nontranslated region of the nopaline synthase (NOS) gene from *Agrobacterium tumefaciens* which terminates transcription and directs polyadenylation.

[1] Sizes of the same genetic element may differ slightly between the *cry1Ac* and *cry2Ab2* coding regions due to revisions in the annotation of the Monsanto proprietary sequence database.

Table 2. Summary of genetic elements of the insert in MON 1445.

Genetic Element	Approximate Size (Kb)	Description/source (Reference)
Right Border	0.02	DNA sequence derived from *Agrobacterium* containing the right border essential for transfer of the T-DNA.
cp4 epsps cassette		
E9 3'	0.64	3' nontranslated region of the pea ribulose-1,5-bisphosphate carboxylase small subunit (rbcS) E9 gene, terminates transcription and directs polyadenlyation of the mRNA.
cp4 epsps	1.37	DNA sequence coding for the synthetic CP4 EPSPS protein (5-enolpyruvylshikimate-3-phosphate synthase) from *Agrobacterium* sp. strain CP4 (*aroA* gene).
ctp2	0.29	DNA sequence coding for the N-terminal chloroplast transit peptide from *Arabidopsis thaliana* EPSPS gene.
FMV	0.56	35S promoter derived from figwort mosaic virus.
aad gene		
aad	0.83	Bacterial gene comprising its own regulatory elements and coding for an aminoglycoside-modifying enzyme, 3'(9)-O-nucleotidyltransferase from the transposon Tn7
nptII cassette		
NOS 3'	0.25	3' nontranslated region of the nopaline synthase (NOS) gene from *Agrobacterium tumefaciens* which terminates transcription and directs polyadenylation.
nptII	0.79	DNA sequence isolated from the bacterial transposon Tn5 (Beck *et al.*, 1982) coding for neomycin phosphotransferase type II. Expression of this sequence in plant cells confers resistance to kanamycin and serves as a selectable marker for transformation.
35S	0.32	Cauliflower mosaic virus (CaMV) promoter.
ori-V	0.22	Origin of replication for *Agrobacterium* derived from the broad host range plasmid RK2.

D. INFORMATION RELATING TO THE GM PLANT

Information on MON 15985 and MON 1445 have been previously described in the application for authorization of MON 15985 in the E.U. according to Regulation (EC) No 1829/2003 and the notification for MON 1445 pursuant to Regulation (EC) No 258/97, respectively.

1. Description of the trait(s) and characteristics which have been introduced or modified

MON 15985 × MON 1445 has been produced by the traditional breeding of MON 15985 and MON 1445. MON 15985 × MON 1445 expresses the insect-protection traits found in MON 15985, as well as the CP4 EPSPS protein which confers tolerance to glyphosate. The insect protection traits provide effective control of lepidopteran insects which are economically damaging pests in most cotton growing regions, such as cotton bollworm (CBW, *Helicoverpa armigera*), pink bollworm (PBW, *Pectinophora gossypiella*) and tobacco budworm (TBW, *Heliothis virescens*). The glyphosate-tolerance trait provides a novel, highly efficacious weed control option for farmers, and allows the farmer to take advantage of the favorable environmental properties exhibited by glyphosate.

MON 15985 × MON 1445 is also expected to provide an additional tool to delay the development of lepidopteran resistance in cotton, because MON 15985 × MON 1445 produces both the Cry1Ac and Cry2Ab2 proteins. MON 15985 × MON 1445 provides equivalent or increased control of the major insect pests of cotton (tobacco budworm, pink bollworm, and cotton bollworm) compared to MON 531, with additional control of secondary lepidopteran insect pests such as beet and fall armyworm.

2. Information on the sequences actually inserted or deleted

a) The copy number of all detectable inserts, both complete and partial

To confirm that the DNA inserts in MON 15985 × MON 1445 are the same as those that occur in MON 15985 and MON 1445, a Southern blot analysis was conducted to confirm the presence of the product-specific fingerprints for both MON 15985 and MON 1445 in MON 15985 × MON 1445.

The fingerprint analyses indicate that each of the parental inserts are present in MON 15985 × MON 1445.

Tables 1 and 2 summarize the genetic elements of the DNA inserts in MON 15985 and MON 1445.

b) In case of deletion(s), size and function of the deleted region(s)

Not applicable.

c) Chromosomal location(s) of insert(s) (nucleus, chloroplasts, mitochondria, or maintained in a non-integrated form), and methods for its determination

The traditionally bred MON 15985 × MON 1445 contains the DNA inserts from both MON 15985 and MON 1445 at separate sites in the nuclear genome, as they were inherited from the MON 15985 and MON 1445 single trait material.

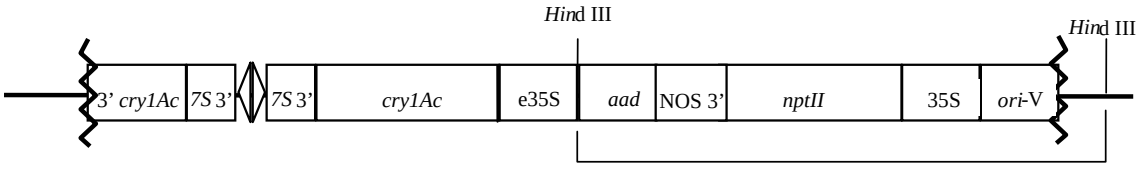
d) The organisation of the inserted genetic material at the insertion site

MON 15985 × MON 1445 is the result of traditional breeding of MON 15985 and MON 1445. There is no indication that the location of the inserts and the 5' and 3' flanking sequences have been altered during the breeding process; the molecular analysis of MON 15985 × MON 1445 confirms the presence of both inserts.

A schematic representation of the MON 15985 and MON 1445 inserts is given in Figures 1 and 2.

Figure 1. Schematic representation of the inserts in MON 15985

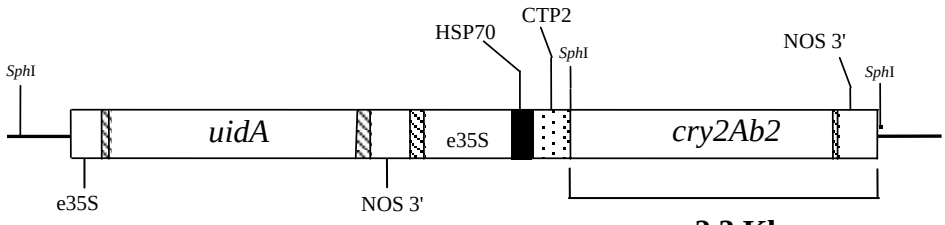
a/ MON 531 insert



~4.0 Kb

Schematic representation of the functional *cry1Ac* insert denoting the expected fingerprint band that should be detected by probing *Hin*d III digested MON 531 DNA with the ^{32}P-labeled *ori*-V element.

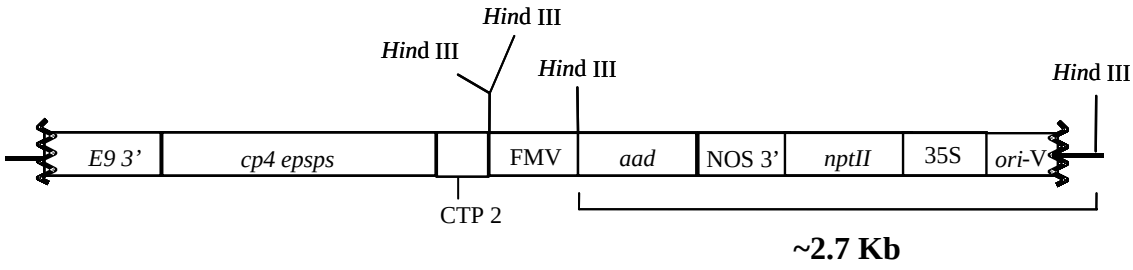
b/ MON 15947 insert



~2.3 Kb

Schematic representation of the *cry2Ab2* insert denoting the expected fingerprint band that should be detected by probing *Sph* I digested MON 15985 DNA with the ^{32}P-labeled *cry2Ab2* element.

Figure 2. Schematic representation of the *cp4 epsps* insert in MON 1445.



Schematic representation of the *cp4 epsps* insert denoting the expected fingerprint band that should be detected by probing *Hin*d III digested MON 1445 DNA with the ^{32}P-labeled *ori*-V element.

3. Information on the expression of the insert

a) Information on developmental expression of the insert during the life cycle of the plant

A study was conducted to measure the amount of Cry1Ac, Cry2Ab2, CP4 EPSPS, NPTII, and GUS proteins in various tissues collected from test and control cotton varieties grown in U.S. field trials conducted in 2001. The test for this study was MON 15985 × MON 1445, expressing the Cry1Ac, Cry2Ab2, CP4 EPSPS, NPTII, and GUS proteins. There were three types of controls used for this study consisting of 1) MON 15985 expressing Cry1Ac, Cry2Ab2, NPTII, and GUS proteins; 2) MON 1445 expressing CP4 EPSPS and NPTII proteins; and 3) a traditional cotton control. The background genetics of the test and controls were similar.

Enzyme-Linked Immunosorbent Assay (ELISA) methods were developed and validated to quantify the Cry1Ac, Cry2Ab2, CP4 EPSPS, NPTII, and GUS protein levels in seed and leaf tissues. Seed and leaf tissues were analyzed for all five proteins, seeds being the only relevant tissue to food and feed product safety. Tissue samples were collected from five locations in 2001. The sites included in the production year provided a variety of environmental conditions representative of regions where cotton is grown for commercial use.

Table 3 presents a summary of Cry1Ac, Cry2Ab2, CP4 EPSPS, NPTII and GUS proteins on a fresh weight basis in cottonseed samples collected from the 2001 field season.

The mean levels of the Cry1Ac, Cry2Ab2, CP4 EPSPS, NPTII and GUS proteins were 1.5, 45, 160, 17 and 45 µg/g respectively in MON 15985 × MON 1445. The Cry1Ac levels in MON 15985 was similar to those found in MON 15985 × MON 1445. Additionally, the Cry2Ab2 and GUS protein levels in MON 15985 were similar to those found in MON 15985 × MON 1445. CP4 EPSPS protein levels were slightly higher in MON 15985 × MON 1445 compared to MON 1445. The levels of Cry1Ac, Cry2Ab2, CP4 EPSPS, NPTII and GUS proteins were below the limits of detection in the traditional cotton control.

In conclusion, Cry1Ac, Cry2Ab2, CP4 EPSPS, NPTII and GUS protein levels between the test and cotton controls were generally very similar for a given protein. Where a slight expression difference occurred, the differences are not considered to be meaningful from a safety perspective considering the low levels of protein expression, the protein safety characteristics and the absence of detectable level of protein in refined oil.

Table 3. Summary of Cry1Ac, Cry2Ab2, CP4 EPSPS, NPTII, and GUS protein levels (µg/g fw)[1] measured in cottonseed samples collected in the 2001 field season Mean ± Std Dev. (n = 5)[2] - (Range)[3].

	Cry1Ac	Cry2Ab2	CP4 EPSPS	NPTII[4]	GUS
Traditional control	N.D.[5]	N.D.[5]	N.D.[5]	N.D.[5]	N.D.[5]
MON 15985	1.6 ± 0.23 (1.3-1.9)	44 ± 10 (34-60)	N.D.[5]	5.5 ± 0.59 (4.8-6.2)	46 ± 13 (27-59)
MON 1445	N.D.[5]	N.D.[5]	110 ± 6.8 (100-120)	16 ±2.0 (13-17)	N.D.[5]
MON 15985 × MON 1445	1.5 ± 0.095 (1.3-1.6)	45 ± 5.7 (39-53)	160 ± 28 (130-200)	17 ± 2.6 (14-20)	45 ± 16 (29-67)

[1] Protein levels are expressed as µg/g fw of tissue. Cry2Ab2, CP4 EPSPS, NPTII, and GUS protein levels were corrected for assay bias. Cry1Ac protein levels were corrected for trypsinization using the trypsinization factor.

[2] The mean and SD were calculated across sites from the analyses of plant samples from four plots (i.e. replicates) at each of five field sites.

[3] Minimum and maximum values from the analyses of samples across sites.

[4] The LOQ for the NPTII ELISA in seed tissue is 4.1 µg/g fw.

[5] Not detectable. The LODs for the Cry1Ac, Cry2Ab2, CP4 EPSPS, NPTII, and GUS ELISAs in seed tissue are 0.10, 3.4, 6.8, 1.3, and 6.5 µg/g fw, respectively.

b) Parts of the plant where the insert is expressed

MON 15985 × MON 1445 expresses the insect protection proteins Cry1Ac and Cry2Ab2 and the CP4 EPSPS protein that provides tolerance to glyphosate. The expression of these proteins in seed was measured by ELISA analysis and was previously reported in this document (*See* Section 3.a))

4. Information on how the GM plant differs from the recipient plant in

a) Reproduction

Comparative assessments of the phenotypic and agronomic characteristics of MON 15985 × MON 1445 and traditional cotton have been conducted at multiple sites in the U.S. since development of this product began. Further, MON 15985 × MON 1445 is currently registered and grown commercially in the U.S., Australia and elsewhere. The extensive experience from commercial use of these products has demonstrated that, except for the lepidopteran-protection and glyphosate-tolerance traits, there are no biologically significant differences in the reproductive capability, dissemination or survivability of MON 15985 × MON 1445 compared to traditional cotton.

b) Dissemination

The inherited traits have no influence on cotton reproductive morphology or dissemination.

c) Survivability

Cotton is known to be a weak competitor in the wild, which cannot survive outside cultivation without the aid of human intervention. Field observations have demonstrated that MON 15985 × MON 1445 has not been altered in its survivability when compared to traditional cotton.

d) Other differences

Comparative assessments in the field did not reveal any biologically significant differences between MON 15985 × MON 1445 and traditional cotton, except for the inherited traits that are of agronomic interest.

5. Genetic stability of the insert and phenotypic stability of the GM plant

MON 15985 × MON 1445 is produced by crossing MON 15985 and MON 1445 parental inbred lines (made homozygous) by traditional breeding. Thereby, each parental line passes on its inserted DNA sequence to the resulting MON 15985 × MON 1445 progeny.

The presence of the parental inserts in MON 15985 × MON 1445 was demonstrated using DNA material extracted at the 8th generation (BC_2F_6) of the plant expressing the combined traits. The fact that the functional inserts are still present after this high number of generations indicate that, as expected, each of them is stable even when combined over multiple generations.

6. Any change to the ability of the GM plant to transfer genetic material to other organisms

a) Plant to bacteria gene transfer

None of the genetic elements inherited in MON 15985 × MON 1445 carries a genetic transfer function. Therefore, no changes are expected in the ability of this cotton to transfer genetic material to bacteria.

b) Plant to plant gene transfer

Not applicable. The scope of the current application does not include the cultivation of MON 15985 × MON 1445 varieties in the E.U.

7. Information on any toxic, allergenic or other harmful effects on human or animal health arising from the GM food/feed

7.1 Comparative assessment

Choice of the comparator

MON 15985 × MON 1445 was compared with a traditional cotton control and other commercially available cotton.

7.2 Production of material for comparative assessment

a) number of locations, growing seasons, geographical spreading and replicates

A study was conducted on the compositional analysis of cottonseed from the test, MON 15985 × MON 1445, and a control cotton. The control cotton was a traditional cotton variety. Additionally, eleven different traditional cotton varieties were included as reference varieties to provide data for the development of a 99% tolerance interval for each component analyzed. The study was conducted at five sites across the U.S. during the 2001 field season. All sites were replicated using a randomized complete block design, with each site having four blocks or replicates of the control, test and reference substance.

b) the baseline used for consideration of natural variations

The test MON 15985 × MON 1445 was compared to a traditional, non-transgenic control. Eleven different non-transgenic commercial varieties were included as reference lines to provide data for the development of a 99% tolerance interval for each component analyzed. Where statistical differences occurred, the measured analyte was compared to a confidence interval developed from the reference varieties. Differences were also compared to historical ranges and ranges reported in literature.

7.3 Selection of material and compounds for analysis

The compounds that were selected for analysis in the compositional studies were chosen on the basis of internationally accepted guidance,

and animal feed manufacturers specifications.

The results of the compositional analyses conducted for MON 15985 × MON 1445 in comparison to control cotton demonstrate equivalence and do not indicate a need for further analysis of selected compounds in these cotton products.

7.4 Agronomic traits

The results from field trials and the experience from commercial planting in North America has provided a weight of evidence that when compared with traditional cotton varieties, MON 15985 × MON 1445 has:

- equivalent growth, developmental and morphological characteristics;
- equivalent plant health, vigour and pest susceptibility (except for predation by specific leptidopteran insect pests);
- equivalent agronomic performance, including yield potential.

These results also infer that MON 15985 × MON 1445 has equivalent biological fitness, dissemination and survival characteristics (*i.e.* similar lack of persistence in the field and lack of invasiveness into natural environments) as any other cotton.

7.5 Product specification

MON 15985 × MON 1445 comprises all traditionally bred cotton produced by the combinations of MON 15985 and MON 1445. As MON 15985 × MON 1445 is the result of a traditional cross of MON 15985 and MON 1445, it contains all the respective DNA inserts from both single trait cotton products. Therefore, MON 15985 × MON 1445 is detectable using either the product-specific PCR method for detecting the introduced DNA present in MON 15985 or the equivalent method for MON 1445. However, as for all plants in which one or more genetically modified traits are combined by traditional breeding, unambiguous detection of MON 15985 × MON 1445 can only occur with seeds from the MON 15985 × MON 1445, by using a combination of the provided PCR methods on a single seed.

7.6 Effect of processing

As MON 15985 × MON 1445 is substantially equivalent and as safe and nutritious as traditional cotton, the use of MON 15985 × MON 1445 seed for the production of foods and feeds is no different from that of traditional cotton. Consequently, any effects of the processing of MON 15985 × MON 1445 is not expected to be any different from the processing of the equivalent foods and feeds, originating from traditional cottonseed.

7.7 Anticipated intake/extent of use

There are no anticipated changes in the intake and/or extent of use of cotton-derived foods or feeds as a result of the addition of MON 15985 × MON 1445 varieties to the traditional cotton supply.

MON 15985 × MON 1445 is expected to replace a portion of current cotton such that its intake or use will represent some fraction of the total products derived from cotton.

7.8 Toxicology

7.8.1 Safety assessment of newly expressed proteins

MON 15985 × MON 1445 was produced by the traditional crossing of MON 15985 and MON 1445. The introduced traits present in MON 15985 and MON 1445 are inherited in MON 15985 × MON 1445. This resulted in the combined expression of the Cry1Ac, Cry2Ab2, NPTII, GUS and CP4 EPSPS proteins in the same plant.

The conclusion of safety to humans of those proteins was based upon the following considerations:

- The protein has a demonstrated history of safe use;
- The protein has no structural similarity to known toxins or other biologically active proteins that could cause adverse effects in humans or animals;
- The protein does not exert any acute toxic effects to mammals.

In addition, the low concentration of introduced proteins in tissues that are consumed and the rapid digestibility in simulated digestive fluids provide additional assurance for their safety.

It is therefore highly unlikely that the Cry1Ac, Cry2Ab2, NPTII, GUS and CP4 EPSPS proteins would cause any toxic effects on human or animal health.

7.8.2 Testing of new constituents other than proteins

The introduced genes are not intended to produce new constituents other than the Cry1Ac, Cry2Ab2, NPTII, GUS and CP4 EPSPS proteins.

Since cotton is known as a common source of food and feed products with a centuries-long history of safe use and consumption around the world, and as MON 15985 × MON 1445 was shown to be substantially equivalent to traditional cotton, no toxicological testing of any constituents, other than the introduced proteins is warranted.

7.8.3 Information on natural food and feed constituents

Cotton is known as a common source of human food and feed products, with a long history of safe use and consumption around the world. All cotton contains cyclopropenoid fatty acids (CPFA) and gossypol, natural compounds that are considered to be undesirable and anti-nutritional. The steps taken during cottonseed processing, in order to produce cottonseed oil, detoxify gossypol and greatly reduce the CPFA content. No other

particular natural constituents of cotton are considered to be of significant concern to require additional information or further risk assessment.

7.8.4 Testing of the whole GM food/feed

Compositional analyses and comparative phenotypic assessments have demonstrated that MON 15985 × MON 1445 is substantially equivalent to traditional cotton, with the exception of the inherited lepidopteran-protection and glyphosate-tolerance traits.

The human and animal safety of the Cry1Ac, Cry2Ab2, NPTII, GUS and CP4 EPSPS proteins was demonstrated on the basis of a) an extensive characterization of each protein, b) comparison of these proteins to known protein toxins and allergens, c) their digestion in simulated gastric and intestinal fluids, and d) the assessment of each protein for evidence of any acute toxicity in oral gavage studies in rodents. All these studies confirmed the absence of any toxic effects associated to the introduced proteins and confirmed the absence of any unanticipated or pleiotropic effects of the genetic modification. The introduced proteins in MON 15985 and MON 1445 have shown no evidence of adverse effects on human or animal safety.

The conclusions of the safety assessments for the individual proteins are unaffected when their combined expression in MON 15985 × MON 1445 is considered.

7.9 Allergenicity

7.9.1 Assessment of allergenicity of the newly expressed protein

Absence of any allergenic potential associated with the introduced Cry1Ac, Cry2Ab2, NPTII, GUS and CP4 EPSPS proteins expressed in MON 15985 × MON 1445 has previously been demonstrated.

These proteins were assessed for their potential allergenicity by a variety of tests, including a) whether the genes came from allergenic or non-allergenic sources, b) sequence similarity to known allergens, and c) pepsin stability of the protein in an *in vitro* digestion assay. In all cases, the proteins did not exhibit properties characteristic of allergens.

7.9.2 Assessment of allergenicity of the whole GM plant or crop

As the introduced proteins do not have any allergenic potential, it was concluded that the use of MON 15985 × MON 1445 for food or feed does not lead to an increased risk for allergenic reactions compared to the equivalent range of food and feed uses of traditional cotton.

7.10 Nutritional assessment of GM food/feed

7.10.1 Nutritional assessment of GM food

MON 15985 × MON 1445 expresses the inherited lepidopteran-protection and glyphosate-tolerance traits, which are agronomic traits and not intended to change any nutritional aspects of this cotton. Hence MON 15985 × MON 1445 is not expected to be more or less attractive for use as food (or feed), for processing, or as a food (or feed) ingredient. Therefore, anticipated dietary intake of cotton-derived foods and feeds is not expected to be altered upon commercialisation of MON 15985 × MON 1445, and no nutritional imbalances are expected as a result of the use of MON 15985 × MON 1445.

7.10.2 Nutritional assessment of GM feed

Once compositional equivalence has been established in GM feed modified for agronomic input traits, nutritional equivalence can be assumed. The results of the compositional analyses have established the compositional equivalence of these cottonseed and traditional cottonseed, and as a consequence, no further nutritional assessments of MON 15985 × MON 1445 for use in feed are considered necessary.

7.11 Post-market monitoring of GM food/feed

The assessment of the human and animal safety of MON 15985 × MON 1445 was conducted on the basis of this product's substantial equivalence to traditional cotton (except for the introduced traits) and by extensive characterisation of the introduced traits, which are of agronomic interest, resulting in the expression of the Cry1Ac, Cry2Ab2, NPTII, GUS and CP4 EPSPS proteins.

There are no intrinsic hazards related to MON 15985 × MON 1445 as no signs of adverse or unanticipated effects have been observed in a number of safety studies. The pre-market risk assessment of MON 15985 × MON 1445 has demonstrated that the risks of consumption of foods and feeds produced from MON 15985 × MON 1445 are negligible and no different than the risks associated with the consumption of traditional cotton and cotton-derived products. Therefore, specific risk management measures are not warranted for MON 15985 × MON 1445, and post-market monitoring of the use of this cotton for food and feed products is not considered appropriate.

8. Mechanism of interaction between the GM plant and target organisms (if applicable)

MON 15985 × MON 1445 carries three traits, which protect against targeted lepidopteran insect pests and it confer tolerance to glyphosate. As there are no target organisms for the CP4 EPSPS protein, target organisms for the combined trait product will be the same as those for the Cry1Ac and Cry2Ab2

proteins together.

The Cry1Ac and Cry2Ab2 proteins produced in MON 15985 × MON 1445 provide protection from feeding damage caused by a wide spectrum of lepidopteran insect pests. Those lepidopteran insects may be considered the target organisms which interact with MON 15985 × MON 1445.

A generalized mode of action of Cry1Ac and Cry2Ab2 proteins includes the following steps: ingestion of the protoxin crystal by the insect, solubilization of the crystal in the insect midgut, proteolytic processing of the released Cry protein by digestive enzymes to produce an active toxin termed delta-endotoxin, binding of the endotoxin to receptors on the surface of midgut epithelial cells of target organisms, formation of membrane ion channels or pores, and consequent disruption of cellular homeostasis. Electrolyte imbalance and pH changes render the gut paralyzed, which causes the insect to stop eating and die.

Any significant interactions of MON 15985 × MON 1445 with its target pest organisms are limited to those countries where the cultivation of this cotton has been authorized. The cultivation of MON 15985 × MON 1445 varieties in the E.U. is not within the scope of this application. In the context of the current application, the likelihood is negligible that the import of MON 15985 × MON 1445 will result in plants of this cotton being present in the environment, and the potential for interactions between MON 15985 × MON 1445 and its target organisms is, therefore, considered to be minimal

9. Potential changes in the interactions of the GM plant with the biotic environment resulting from the genetic modification

This application is limited to the import of MON 15985 × MON 1445 for processing and use of food and feed produced from MON 15985 × MON 1445, but it does not cover the cultivation of MON 15985 × MON 1445 varieties in the E.U. As such, exposure to the environment will be rare, occurring only through incidental release during shipment and handling. The conditions where incidental release could occur are not conducive to establishment of cotton.

9.1 Persistence and invasiveness

Like for conventional cotton, the likelihood of MON 15985 × MON 1445 spreading in the environment is negligible, as cotton is neither persistent nor invasive and these parameters are unaltered in MON 15985 × MON 1445 when compared to conventional cotton. In the event MON 15985 × MON 1445 cottonseed is spilt in the environment, its inherited traits would have negligible consequences for the environment. Hence the risk of establishment and spreading of MON 15985 × MON 1445 in the environment is negligible.

9.2 Selective advantage or disadvantage

Compared with conventional cotton, the presence of the lepidopteran-protection and glyphosate-tolerance traits confers a selective advantage only under specific conditions (*i.e.* upon attack by the target insects or upon treatment with glyphosate), which are short in duration. The advantage is of purely agronomic interest and presents negligible risk to the non-agricultural

environments because of the poor survival characteristics of cotton under most European conditions. The potential for the lepidopteran-protection and glyphosate-tolerance traits in MON 15985 × MON 1445 to cause a selective advantage of cotton outside an agro-ecosystem is exceedingly low. Therefore, the risk of adversely impacting the receiving environment is negligible under the intended use for processing.

9.3 Potential for gene transfer

MON 15985 × MON 1445 is unchanged in its potential for gene transfer compared to conventional cotton. There is no potential for gene transfer from MON 15985 × MON 1445 to wild plant species and negligible likelihood for gene transfer to other cotton crops, as this application is not for consent to cultivate MON 15985 × MON 1445 varieties in the E.U.

In the highly unlikely event that the inherited genes outcross to another cotton plant, their transfer would, in any event, have negligible consequences for the environment. The environmental risk posed by this transfer, and hence by the intended import of MON 15985 × MON 1445 for processing, is negligible.

9.4 Interactions between the GM plant and target organisms

The (intended) insecticidal action of the Cry proteins for the control of pest species is not considered adverse to the environment in an agro-ecosystem. In any case, since the likelihood is negligible that the import of MON 15985 × MON 1445 for processing will result in plants of this cotton being present in the environment at meaningful levels, it is not expected that the target organisms will be exposed to Cry1Ac and/or Cry2Ab2 proteins. Therefore, it is highly unlikely that the target organisms could develop resistance to the Cry1Ac and/or Cry2Ab2 proteins. As a consequence, there is negligible risk for harmful effects on the environment posed by the import of MON 15985 × MON 1445 for processing.

9.5 Interactions of the GM plant with non-target organisms

Given the scope of the current application, which does not include the cultivation of MON 15985 × MON 1445 varieties in the E.U., the likelihood for direct or indirect interactions of this cotton with non-target organisms is considered to be negligible. In addition, the newly expressed proteins present a negligible hazard to non-target organisms, even if incidental spillage of MON 15985 × MON 1445 cottonseed during import, storage, transport or processing leads to the short survival of MON 15985 × MON 1445 plants in the environment. As a consequence, there is negligible risk for harmful effects of MON 15985 × MON 1445 on non-target organisms, either through direct or indirect interactions with this cotton or through contact with the newly expressed proteins. Furthermore, no adverse effects were brought forward by the people handling these products during the extensive field trials conducted in the U.S.A.

9.6 Effects on human health

The likelihood for any adverse effects occurring in humans as a result of their contact with this cotton is no different from conventional cotton, as MON 15985 × MON 1445 contains the Cry1Ac, Cry2Ab2, NPTII, GUS and

CP4 EPSPS proteins, which have negligible potential to cause any toxic or allergenic effects in humans. Therefore, the risk of changes in the occupational health aspects of this cotton is negligible.

9.7 Effects on animal health

The likelihood of potential adverse effects in animals fed on MON 15985 × MON 1445 and in humans consuming those animals, is negligible (*see* Sections D.7.8, D.7.9 and D.7.10 of this document). Therefore, the risk of MON 15985 × MON 1445 for the feed/food chain is also negligible.

9.8 Effects on biogeochemical processes

In the event of an incidental release of MON 15985 × MON 1445 in the environment, the risk for direct or indirect, immediate or delayed adverse effects on biogeochemical processes can be considered as negligible. There is no evidence that MON 15985 × MON 1445 plants would be any different from conventional cotton regarding their direct influence on biogeochemical processes or nutrient levels in the soil, as MON 15985 × MON 1445 is compositionally equivalent to conventional cotton and presents no biologically meaningful differences in its growth and development, morphology, yield, plant health and survival characteristics (*see* Sections D.4, D.7.1 and D.7.4 of this document). Furthermore, any indirect interactions of the GMHP and non-target organisms in the vicinity of an incidental release of the cottonseed are not likely to cause hazardous effects on the biogeochemical processes in the soil.

9.9 Impacts of the specific cultivation, management and harvesting techniques

Not applicable. This application is for consent to import MON 15985 × MON 1445 in the E.U. for processing and for the use of food and feed produced from this cotton as any other cotton, excluding the use for cultivation of varieties in the E.U. The above data requirement is meant to evaluate the cultivation of a GMHP in the E.U.

10. Potential interactions with the abiotic environment

As MON 15985 × MON 1445 was shown to be substantially equivalent to conventional cotton, except for the inherited lepidopteran-protection and glyphosate-tolerance traits, imparted by the expression of the Cry1Ac, Cry2Ab2 and CP4 EPSPS proteins, there is no evidence that this cotton would be any different from conventional cotton with regard to its baseline interactions with the abiotic environment. Although Cry1Ac, Cry2Ab2 and CP4 EPSPS are introduced proteins in cotton, they have a safe history of use and no known negative effects on biochemical processes (*see* Sections D.7.8.1 and D.9.8 in this document). Therefore, no adverse impact on the abiotic environment is expected to result from the import of MON 15985 × MON 1445 for processing and for use of food and feed products derived from MON 15985 × MON 1445 in the E.U.

11. Environmental monitoring plan (not if application concerns only food and feed produced from GM plants, or containing ingredients produced from GM plants and if the applicant has clearly shown that environmental exposure is absent or will be at levels or in a form that does not present a risk to other living organisms or the abiotic environment)

11.1 General (risk assessment, background information)

As required by Article 5(5)(b) and 17(5)(b) of Regulation (EC) No. 1829/2003 the proposed monitoring plan for MON 15985 × MON 1445 has been developed according to the principles and objectives outlined in Annex VII of Directive 2001/18/EC and Decision 2002/811/EC

11.2 Interplay between environmental risk assessment and monitoring

An environmental risk assessment (ERA) of MON 15985 × MON 1445 was undertaken in the context of the scope of the application, that is for MON 15985 × MON 1445 import and processing, and food and feed use of MON 15985 × MON 1445 derived products in the E.U., but excluding the cultivation of MON 15985 × MON 1445 varieties in the E.U.

Analysis of the characteristics of MON 15985 × MON 1445 has shown that the risk for potential adverse effects on human health and the receiving environment, resulting from the import of MON 15985 × MON 1445 and food and feed use of MON 15985 × MON 1445 derived products in the E.U. is consistently negligible. Therefore, the overall environmental risk posed by this genetically modified higher plant is negligible, and no specific strategies for risk management and no case-specific post-marketing monitoring actions are considered required.

11.3 Case-specific GM plant monitoring (approach, strategy, method and analysis)

As discussed in Section D.11.2, the scientific evaluation of the characteristics of MON 15985 × MON 1445 in the ERA has shown that the risk for potential adverse effects on human and animal health or the environment is negligible in the context of the intended uses of MON 15985 × MON 1445. It is therefore considered that there is no need for case-specific monitoring.

11.4 General surveillance of the impact of the GM plant (approach, strategy, method and analysis)

In accordance with Council Decision 2002/811/EC, general surveillance is not based on a particular hypothesis and it should be used to identify the occurrence of unanticipated adverse effects of the viable GMO or its use for human and animal health or the environment that were not predicted in the e.r.a.

The authorisation holder is not involved in commodity trade with MON 15985 × MON 1445. The monitoring methodology hence needs to be predominantly based on collaboration with third parties, such as

operators involved in the import, handling and processing of viable MON 15985 × MON 1445. They are exposed to the imported viable MON 15985 × MON 1445 and therefore are the best placed to observe and report any unanticipated adverse effects in the framework of their routine surveillance of the commodities they handle and use.

The general surveillance information reported to and collected by the authorisation holder from the European trade associations or other sources will be analysed for its relevance. Where information indicates the possibility of an unanticipated adverse effect, the authorisation holder will immediately investigate to determine and confirm whether a significant correlation between the effect and MON 15985 × MON 1445 can be established. If the investigation establishes that MON 15985 × MON 1445 was present when the adverse effect was identified, and confirms that MON 15985 × MON 1445 is the cause of the adverse effect, the authorisation holder will immediately inform the European Commission, as described in Section D.11.5.

11.5 Reporting the results of monitoring

The authorisation holder will submit an annual monitoring report containing information obtained from participating networks, and/or in case of an effect that was confirmed. If information that confirms an adverse effect which alters the existing risk assessment becomes available, Monsanto will submit a report, consisting of a scientific evaluation of the potential adverse effect and a conclusion on the safety of the product. The report will also include, where appropriate, the measures that were taken to ensure the safety of human or livestock health and/or the environment.

12. Detection and event-specific identification techniques for the GM plant

As MON 15985 × MON 1445 is the result of a traditional cross of MON 15985 and MON 1445, it contains both inserts. Therefore, MON 15985 × MON 1445 is detectable using either the event-specific PCR method for detecting the introduced DNA present in MON 15985 or the equivalent method for MON 1445. However, as for all plants in which one or more events are combined by traditional breeding, the unambiguous detection of MON 15985 × MON 1445 in mixed consignments will require single seeds to be subjected to detection methods for both MON 15985 and MON 1445, and to test positive for both.

E. INFORMATION RELATING TO PREVIOUS RELEASES OF THE GM PLANT AND/OR DERIVED PRODUCTS

1. History of previous releases of the GM plant notified under Part B of the Directive 2001/18/EC and under Part B of Directive 90/220/EEC by the same notifier

a)	**Notification number** Not applicable
b)	**Conclusions of post-release monitoring** Not applicable
c)	**Results of the release in respect to any risk to human health and the environment (submitted to the Competent Authority according to Article 10 of Directive 2001/18/EC)** Not applicable

2. History of previous releases of the GM plant carried out outside the Community by the same notifier

a)	**Release country** Since its commercial introduction in the U.S. and in Australia, MON 15985 × MON 1445 has been grown on more than 0.5 million hectares. Field tests of MON 15985 × MON 1445 in countries such as the U.S. and Australia have been conducted since 1999.
b)	**Authority overseeing the release** MON 15985: U.S.: Environmental Protection Agency; Australia: Office of Gene Technology Regulator.
c)	**Release site** Selected sites based on where MON 15985 × MON 1445 would be grown.
d)	**Aim of the release** Since 2003, MON 15985 × MON 1445 is grown commercially in the U.S. and in Australia.
e)	**Duration of the release** Please see question E.2.(a)
f)	**Aim of post-releases monitoring** Insect resistance management
g)	**Duration of post-releases monitoring** Insect resistance management is an annual condition of the registrations.

h)	**Conclusions of post-release monitoring** No stable insect resistance has been detected.
i)	**Results of the release in respect to any risk to human health and the environment** No evidence of any adverse effect to human or animal health and the environment.

3. Links (some of these links may be accessible only to the competent authorities of the Member States, to the Commission and to EFSA):

a)	**Status/process of approval** The JRC websites http://gmoinfo.jrc.it/gmc_browse.asp and http://gmo-crl.jrc.it/statusofdoss.htm and the EFSA website http://www.efsa.europa.eu/en/science/gmo/gm_ff_applications.html provide publicly accessible links to up-to-date databases on the regulatory progress of notifications under Directive 2001/18/EC and applications under Regulation (EC) No 1829/2003, including the Monsanto dossier for MON 15985 × MON 1445.
b)	**Assessment Report of the Competent Authority (Directive 2001/18/EC)** Not applicable
c)	**EFSA opinion** No EFSA opinion is available at the time of this application.
d)	**Commission Register (Commission Decision 2004/204/EC)** http://ec.europa.eu/food/dyna/gm_register/index_en.cfm
e)	**Molecular Register of the Community Reference Laboratory/Joint Research Centre** Information on detection protocols is posted at http://gmo-crl.jrc.it/
f)	**Biosafety Clearing-House (Council Decision 2002/628/EC)** The publicly accessible portal site of the Biosafety Clearing-House (BCH) can be found at http://bch.biodiv.org/
g)	**Summary Notification Information Format (SNIF) (Council Decision 2002/812/EC)** EFSA provides a link to the publicly accessible summary of this application under Regulation (EC) No 1829/2003 at http://www.efsa.europa.eu/en/science/gmo/gm_ff_applications.html.