



FOOD STANDARDS
Australia New Zealand
Te Mana Kounga Kai - Ahitereiria me Aotearoa

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8 August 2007

DRAFT ASSESSMENT REPORT

APPLICATION A592

FOOD DERIVED FROM GLYPHOSATE-TOLERANT SOYBEAN MON 89788

DEADLINE FOR PUBLIC SUBMISSIONS: 6pm (Canberra time) 19 September 2007
SUBMISSIONS RECEIVED AFTER THIS DEADLINE
WILL NOT BE CONSIDERED

(See 'Invitation for Public Submissions' for details)

For Information on matters relating to this Assessment Report or the assessment process generally, please refer to <http://www.foodstandards.gov.au/standardsdevelopment/>

Executive Summary

An Application has been received from Monsanto Australia Limited to amend the *Australia New Zealand Food Standards Code* (the Code) to approve food derived from genetically modified (GM) herbicide-tolerant soybean MON 89788. Standard 1.5.2 – Food Produced using Gene Technology, requires that GM foods undergo a pre-market safety assessment before they may be sold in Australia and New Zealand.

Soybean MON 89788 has been genetically modified to be tolerant to the herbicide glyphosate. FSANZ has undertaken a safety assessment of glyphosate-tolerant soybean MON 89788. If approved, food derived from glyphosate-tolerant soybean MON 89788 may enter Australia and New Zealand as imported products. It is not intended that MON 89788 be cultivated in Australia or New Zealand

The herbicide tolerance trait introduced into glyphosate-tolerant soybean MON 89788 is conferred by expression in the plant of an enzyme, CP4 EPSPS, derived from a common soil bacterium. No marker genes are present in glyphosate-tolerant soybean MON 89788.

Safety assessment

FSANZ has completed a comprehensive safety assessment of food derived from glyphosate-tolerant soybean MON 89788, as required under Standard 1.5.2. The assessment included consideration of (i) the genetic modification to the plant; (ii) the potential toxicity and allergenicity of the novel protein; and (iii) the composition of glyphosate-tolerant soybean MON 89788 compared with that of conventional soybean.

The assessment of this Application identified no public health and safety concerns. On the basis of the available evidence, including detailed studies provided by the Applicant, food derived from glyphosate-tolerant MON 89788 is considered as safe and wholesome as food derived from commercial soybean varieties.

Labelling

Foods derived from glyphosate-tolerant soybean MON 89788 will be required to be labelled as genetically modified if novel DNA and/or novel protein is present in the final food. Studies conducted by the Applicant show that the novel protein is present in the unprocessed grain. Highly processed products that do not contain novel protein or DNA, such as soybean oil, do not have to be labelled.

Labelling addresses the requirement of paragraph 18(1)(b) of the *Food Standards Australia New Zealand Act 1991*; provision of adequate information relating to food to enable consumers to make informed choices.

Impact of regulatory options

Two regulatory options were considered in the assessment: (1) no approval; or (2) approval of food derived from glyphosate-tolerant soybean MON 89788 based on the conclusions of the safety assessment.

Following analysis of the potential costs and benefits of each option on affected parties (consumers, the food industry and government), approval of this Application is the preferred option as the potential benefits to all sectors outweigh the costs associated with the approval.

Purpose

The Applicant seeks amendment to Standard 1.5.2 to include food derived from glyphosate-tolerant soybean MON 89788 in the Table to clause 2.

Preferred Approach

Amend Standard 1.5.2 - Food Produced using Gene Technology, to include food derived from glyphosate-tolerant soybean MON 89788 in the Table to clause 2.

Reasons for Preferred Approach

An amendment to the Code approving food derived from glyphosate-tolerant soybean MON 89788 in Australia and New Zealand is recommended on the basis of the available scientific evidence, for the following reasons:

- the safety assessment did not identify any public health and safety concerns associated with the genetic modification used to produce glyphosate-tolerant soybean MON 89788;
- food derived from glyphosate-tolerant soybean MON 89788 is equivalent to food from other commercially available soybean varieties in terms of its safety for human consumption and nutritional adequacy;
- labelling of certain food fractions derived from glyphosate-tolerant soybean MON 89788 will be required if novel DNA and/or protein is present in the final food; and
- a regulation impact assessment process has been undertaken that also fulfils the requirement in New Zealand for an assessment of compliance costs. The assessment concluded that the most appropriate option is option 2, an amendment to the Code.

Consultation

The Initial Assessment was advertised for public comment between 13 December 2006 and 7 February 2007. A total of six submissions were received during this period and a summary of these is provided in **Attachment 3** to this Report. The submitters indicated that they will review the Draft Assessment Report and Safety Assessment when available and provide further comment at that time.

Public submissions are now invited on this Draft Assessment Report.

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INVITATION FOR PUBLIC SUBMISSIONS

FSANZ invites public comment on this Draft Assessment Report based on regulation impact principles and the draft variation to the Code for the purpose of preparing an amendment to the Code for approval by the FSANZ Board.

Written submissions are invited from interested individuals and organisations to assist FSANZ in preparing the Final Assessment of this Application. Submissions should, where possible, address the objectives of FSANZ as set out in section 18 of the FSANZ Act. Information providing details of potential costs and benefits of the proposed change to the Code from stakeholders is highly desirable. Claims made in submissions should be supported wherever possible by referencing or including relevant studies, research findings, trials, surveys etc. Technical information should be in sufficient detail to allow independent scientific assessment.

The processes of FSANZ are open to public scrutiny, and any submissions received will ordinarily be placed on the public register of FSANZ and made available for inspection. If you wish any information contained in a submission to remain confidential to FSANZ, you should clearly identify the sensitive information and provide justification for treating it as confidential commercial information. Section 114 of the FSANZ Act requires FSANZ to treat in-confidence, trade secrets relating to food and any other information relating to food, the commercial value of which would be, or could reasonably be expected to be, destroyed or diminished by disclosure.

Submissions must be made in writing and should clearly be marked with the word 'Submission' and quote the correct project number and name. Submissions may be sent to one of the following addresses:

Food Standards Australia New Zealand
PO Box 7186
Canberra BC ACT 2610
AUSTRALIA
Tel (02) 6271 2222
www.foodstandards.gov.au

Food Standards Australia New Zealand
PO Box 10559
The Terrace WELLINGTON 6036
NEW ZEALAND
Tel (04) 473 9942
www.foodstandards.govt.nz

Submissions need to be received by FSANZ by 6pm (Canberra time) 19 September 2007.

Submissions received after this date will not be considered, unless agreement for an extension has been given prior to this closing date. Agreement to an extension of time will only be given if extraordinary circumstances warrant an extension to the submission period. Any agreed extension will be notified on the FSANZ website and will apply to all submitters.

While FSANZ accepts submissions in hard copy to our offices, it is more convenient and quicker to receive submissions electronically through the FSANZ website using the Standards Development tab and then through Documents for Public Comment. Questions relating to making submissions or the application process can be directed to the Standards Management Officer at the above address or by emailing slo@foodstandards.gov.au.

Assessment reports are available for viewing and downloading from the FSANZ website. Alternatively, requests for paper copies of reports or other general inquiries can be directed to FSANZ's Information Officer at either of the above addresses or by emailing info@foodstandards.gov.au.

INTRODUCTION

An Application was received from Monsanto Australia Limited on 19 October 2006 seeking approval for food derived from glyphosate-tolerant soybean (*Glycine max*) line MON 89788 under Standard 1.5.2 – Food produced using Gene Technology, in the Code.

The genetic modification involved the transfer of the *cp4 epsps* gene into soybean. This gene is from a common soil bacterium and encodes the protein CP4-EPSPS (5-enolpyruvyl-3-shikimate phosphate synthase), which confers tolerance to the herbicide glyphosate.

A Draft Assessment of the Application has been completed, including a comprehensive safety assessment, and public comment is now being sought prior to Final Assessment of the Application.

1. Background

The genetic modification in glyphosate-tolerant soybean MON 89788 involves the introduction of the *cp4 epsps* gene derived from *Agrobacterium* sp. strain CP4. The *cp4 epsps* gene codes for an enzyme, 5-enolpyruvyl-3-shikimate phosphate synthase (EPSPS), which confers tolerance to the herbicide glyphosate. The EPSPS enzyme is present in all plants, bacteria and fungi and is essential for aromatic amino acid biosynthesis. The normal mode of action of glyphosate is to inhibit the endogenous plant EPSPS, thus blocking the synthesis of aromatic amino acids in cells which subsequently leads to the death of the plant. In contrast to the plant EPSPS, the bacterial EPSPS is able to function in the presence of glyphosate, therefore expression of CP4 EPSPS in the plant allows continued production of aromatic amino acids in the presence of the herbicide.

The purpose of the modification is to provide growers with an effective method for controlling weeds, together with enhanced yield potential relative to their previous herbicide tolerant product, soybean line 40-3-2. Food from soybean line 40-3-2 was approved in Australia and New Zealand in 2000. The Applicant states that soybean line MON 89788 has equivalent herbicide tolerance, and thus the same weed control benefits, as soybean 40-3-2. However, soybean line MON 89788 is reported to have a yield advantage due to improvements in transformation technology that have allowed the gene cassette to be directly transformed into an elite soybean line, thus accelerating further breeding improvements.

Glyphosate-tolerant soybean is not intended to be grown in Australia or New Zealand at this time and therefore food from MON 89788 will be present in imported foods only.

The Applicant made submissions for food and feed use to the US Food and Drug Administration and the USDA-Animal and Plant Health Inspection Service in mid-2006. Regulatory submissions for import approvals have been or will be made to countries that import significant soybean or soybean products, including China, Japan, Canada, Korea, the Philippines and Taiwan.

1.1 Current Standard

Standard 1.5.2 requires that genetically modified foods undergo a pre-market safety assessment before they may be sold in Australia and New Zealand. Foods that have been assessed under the Standard, if approved, are listed in the Table to clause 2 of the Standard.

2. The Issue / Problem

Before food derived from soybean line MON 89788 can enter the food supply in Australia and New Zealand, it must first be assessed for safety and an amendment to the Code must be approved by the FSANZ Board, and subsequently be notified to the Australia and New Zealand Food Regulation Ministerial Council (Ministerial Council). An amendment to the Code may only be gazetted, once the Ministerial Council process has been finalised.

Monsanto Australia Limited has therefore applied to have Standard 1.5.2 amended to include food derived from soybean line MON 89788.

3. Objectives

The objective of this assessment is to determine whether it would be appropriate to amend the Code to approve the use of food derived from soybean line MON 89788 under Standard 1.5.2. In developing or varying a food standard, FSANZ is required by its legislation to meet three primary objectives, which are set out in section 18 of the FSANZ Act. These are:

- the protection of public health and safety;
- the provision of adequate information relating to food to enable consumers to make informed choices; and
- the prevention of misleading or deceptive conduct.

In developing and varying standards, FSANZ must also have regard to:

- the need for standards to be based on risk analysis using the best available scientific evidence;
- the promotion of consistency between domestic and international food standards;
- the desirability of an efficient and internationally competitive food industry;
- the promotion of fair trading in food; and
- any written policy guidelines formulated by the Ministerial Council.

4. Key Assessment Questions

Based on information provided by the Applicant on the nature of the genetic modification, the molecular characterisation, the characterisation of the novel protein, the compositional analysis and any nutritional issues, is food derived from soybean line MON 89788 as safe as that derived from conventional varieties of soybean?

Is there other available information, including from the scientific literature, general technical information, independent scientists, other regulatory agencies and international bodies, and the general community that needs to be considered?

Are there any other considerations that would influence the outcome of this assessment?

RISK ASSESSMENT

Food from soybean line MON 89788 has been evaluated according to the safety assessment guidelines prepared by FSANZ¹. The summary and conclusions from the full safety assessment report (at **Attachment 2**) are presented below. In addition to information supplied by the Applicant, other available resource material including published scientific literature and general technical information was used for the assessment.

5. Risk Assessment Summary

In conducting a safety assessment of food derived from glyphosate-tolerant soybean MON 89788, a number of criteria were addressed including:

- (i) characterisation of the transferred genes, their origin, function and stability;
- (ii) changes at the level of DNA, protein and in the whole food;
- (iii) compositional analyses, and an evaluation of intended and unintended changes; and
- (iv) potential for the newly expressed proteins to be either allergenic or toxic in humans.

Detailed molecular and genetic analyses of glyphosate-tolerant soybean MON 89788 indicate that the transferred gene is stably integrated into the plant genome as a single copy at one insertion site, and is inherited in subsequent generations according to predicted patterns of inheritance. There was no transfer of bacterial antibiotic resistance marker genes in this modification.

The EPSPS protein present in glyphosate-tolerant soybean MON 89788 has been assessed previously for safety. These assessments have shown that CP4 EPSPS administered directly to animals at high doses is not toxic, and the evidence indicates no potential for this protein to be allergenic to humans. The novel EPSPS protein is expressed at moderate levels in glyphosate-tolerant MON 89788.

Compositional analyses of soybean grain did not reveal any meaningful differences between glyphosate-tolerant MON 89788 and its non-GM counterpart. The use of MON 89788 for food would be expected to have minimal nutritional impact.

Overall, no potential public health and safety concerns have been identified in the comprehensive assessment of glyphosate-tolerant soybean MON 89788. On the basis of the data provided in the present application, and other available information, food derived from glyphosate-tolerant soybean MON 89788 is considered as safe and wholesome as food derived from other soybean varieties.

¹ FSANZ (2003) Information for Applicants – Format for applying to amend the Australian New Zealand Food Standards Code – Food Produced using Gene Technology.

RISK MANAGEMENT

6. Options

FSANZ is required to consider the impact of various regulatory (and non-regulatory) options on all sectors of the community, which includes consumers, food industries and governments in Australia and New Zealand.

The two regulatory options available for this Application are:

6.1 Option 1 – *Status quo*

Maintain the *status quo* by not amending Standard 1.5.2 to approve the sale and use of food derived from glyphosate-tolerant soybean line MON 89788.

6.2 Option 2 – Approve food derived from soybean line MON 89788

Amend Standard 1.5.2 to permit the sale and use of food derived from glyphosate-tolerant soybean line MON 89788, with or without listing special conditions in the Table to clause 2 of Standard 1.5.2.

7. Impact Analysis

7.1 Affected Parties

The affected parties to this Application include the following:

- consumers, particularly those who have concerns about biotechnology;
- food importers and distributors of wholesale ingredients;
- the manufacturing and retail sectors of the food industry; and
- Government generally, where a regulatory decision may impact on trade or WTO obligations and enforcement agencies in particular who will need to ensure that any approved products are correctly labelled.

The cultivation of soybean line MON 89788 may have an impact on the environment, which would need to be assessed by the Office of the Gene Technology Regulator in Australia and by various New Zealand Government agencies including the Environmental Risk Management Authority and the Ministry of Agriculture and Forestry before cultivation in either of these countries could be permitted. At this stage, the Applicant has no plans for cultivation in either country.

7.2 Benefit Cost Analysis

In the course of developing food regulatory measures suitable for adoption in Australia and New Zealand, FSANZ is required to consider the impact of all options on all sectors of the community, including consumers, the food industry and governments in both countries.

The regulatory impact assessment identifies and evaluates, though is not limited to, the costs and benefits of the regulation, and its health, economic and social impacts.

Following public consultation on the Initial Assessment, FSANZ has identified the following potential costs and benefits of the two regulatory options:

7.2.1 Option 1 – status quo

Consumers: Cost in terms of a possible reduction in the availability of certain food products.

Cost associated with higher retail prices for segregated foods.

Benefit to consumers if there are potential public health and safety issues.

No impact on consumers wishing to avoid GM foods, as food from glyphosate-tolerant soybean MON 89788 is not currently permitted in the food supply. However, food derived from glyphosate-tolerant soybean line 40-3-2 is permitted.

Government: No immediate impact.

Potential impact if considered inconsistent with WTO obligations but impact would be in terms of trade policy rather than in government revenue.

Industry: No immediate impact.

Cost in terms of restricting innovation in food/crop production for both growers and other sectors of the food industry. Cost to the food industry to source either segregated or non-GM supplies.

Potential longer-term impact - any successful WTO challenge has the potential to impact adversely on food industry.

7.2.2 Option 2 – approve food derived from glyphosate-tolerant soybean MON 89788

Consumers: No direct impact.

Possible benefit of lower prices, to the extent that savings from production efficiencies are passed on.

Benefit of access to a greater range of products including imported food products containing ingredients derived from soybean MON 89788.

Possible cost to consumers wishing to avoid GM food by a potential restriction of choice of products, or increased prices for non-GM food, although impact expected to be minimal as glyphosate-tolerant soybean line 40-3-2 is already widely cultivated.

Government: No direct impact.

This decision is likely to impact on monitoring resources of state, territory and New Zealand enforcement agencies, as certain foods derived from glyphosate-tolerant MON 89788 would be required to be labelled as genetically modified, increasing the costs incurred in monitoring for the presence of GM foods.

Industry: No direct impact.

Benefit to importers and distributors of overseas food products as the product range is extended.

Benefit for food manufacturers in that the choice of raw ingredients is extended.

Benefit to food retailers in an increased product range.

Possible cost to food industry as some food ingredients derived from soybean MON 89788 will be required to be labelled as genetically modified.

7.3 Comparison of Options

Option 2 is the preferred option as glyphosate-tolerant soybean MON 89788 has been found to be safe for human consumption. This option is also unlikely to disadvantage those consumers wishing to avoid GM foods as soybean MON 89788 is intended to supersede glyphosate-tolerant soybean 40-3-2, which is already widely cultivated and likely to be present in imported food products.

The proposed amendment to Standard 1.5.2, giving approval to food from glyphosate-tolerant soybean MON 89788, is therefore considered appropriate.

COMMUNICATION AND CONSULTATION STRATEGY

8. Communication

This is a routine approval matter. As a result, FSANZ has applied a basic communication strategy to Application A592. This involves advertising the availability of assessment reports for public comment in the national press and making the reports available on the FSANZ website. We will issue a media release drawing journalists' attention to the matter.

The Applicant and individuals and organisations who make submissions on this Application will be notified at each stage of the Application. If approval is recommended, once the FSANZ Board has approved the Final Assessment Report, we will notify the Ministerial Council. The Applicant and Stakeholders, including the public, will be notified of the gazettal of changes to the Code in the national press and on the website.

FSANZ provides an advisory service to the jurisdictions on changes to the Code.

9. Consultation

9.1 Public Consultation

The Initial Assessment was advertised for public comment between 13 December 2006 and 7 February 2007.

Six submissions were received during this period and a summary of these is included in **Attachment 3** to this Report. The submitters indicated that they will review the Draft Assessment Report and Safety Assessment and provide further comment at that time. One submitter made a specific comment related to enforcement costs.

9.1.1 Enforcement costs

The NSW Food Authority has indicated that there are extensive costs incurred in monitoring for the presence of GM food, particularly taking into account labour and reagent costs, methodology validation and competency maintenance. The NSW Food Authority believes these costs should be factored into the benefit cost analysis and that there is a need to consider a national enforcement strategy surrounding GM food approvals.

9.1.1.1 Response

Costs associated with the enforcement by jurisdictions of any new food regulatory measure are considered by FSANZ in the Regulatory Impact Statement (RIS) and are not unique to GM foods. Australia and New Zealand's current system of food regulation provides for the discussion of such issues by the Implementation Sub-Committee (ISC). Inevitably, enforcement costs would be expected to rise over time as a result of the need to regulate an ever-increasing number of new food additives, processing aids and novel technologies in the Code.

9.2 World Trade Organization (WTO)

As members of the World Trade Organization (WTO), Australia and New Zealand are obligated to notify WTO member nations where proposed mandatory regulatory measures are inconsistent with any existing or imminent international standards and the proposed measure may have a significant effect on trade.

Guidelines for assessing the safety of GM foods have been developed by the Codex Alimentarius Commission and have the status of standards for WTO purposes. The proposed amendment to Standards 1.5.2 of the Code to allow food derived from soybean MON 89788 may be of interest to other WTO member nations because it pertains to the safety of GM food and is likely to have a liberalising effect on international trade.

For these reasons, FSANZ will be recommending to the agencies responsible that the WTO be notified under the Sanitary and Phytosanitary Measures (SPS) Agreement, in order to enable other member nations to comment on the proposed changes to standards that may have a significant impact on them.

CONCLUSION

10. Conclusion and Preferred Approach

An amendment to the Code to give approval to the sale and use of food derived from glyphosate-tolerant soybean MON 89788 in Australia and New Zealand is proposed on the basis that food derived from glyphosate-tolerant soybean MON 89788 is as safe and wholesome for human consumption as food from other soybean varieties.

Preferred Approach

Amend Standard 1.5.2 - Food Produced using Gene Technology, to include food derived from glyphosate-tolerant soybean MON 89788 in the Table to clause 2.

Reasons for Preferred Approach

An amendment to the Code approving food derived from glyphosate-tolerant soybean MON 89788 in Australia and New Zealand is recommended on the basis of the available scientific evidence, for the following reasons:

- the safety assessment did not identify any public health and safety concerns associated with the genetic modification used to produce glyphosate-tolerant soybean MON 89788;
- food derived from glyphosate-tolerant soybean MON 89788 is equivalent to food from other commercially available soybean varieties in terms of its safety for human consumption and nutritional adequacy;
- labelling of certain food fractions derived from glyphosate-tolerant soybean MON 89788 will be required if novel DNA and/or protein is present in the final food; and
- a regulation impact assessment process has been undertaken that also fulfils the requirement in New Zealand for an assessment of compliance costs. The assessment concluded that the most appropriate option is option 2, an amendment to the Code.

11. Implementation and Review

It is proposed that the draft variation come into effect on the date of gazettal.

ATTACHMENTS

1. Draft variation to the *Australia New Zealand Food Standards Code*
2. Safety Assessment Report
3. Summary of issues raised in public submissions

**DRAFT VARIATION TO THE AUSTRALIA NEW ZEALAND FOOD STANDARDS
CODE**

To commence: on gazettal

[1] *Standard 1.5.2 of the Australia New Zealand Food Standards Code is varied by inserting in the Table to clause 2 –*

Food derived from glyphosate-tolerant soybean line MON 89788	
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SAFETY ASSESSMENT

APPLICATION A592: FOOD DERIVED FROM GLYPHOSATE-TOLERANT SOYBEAN MON 89788

SUMMARY AND CONCLUSIONS

Background

Glyphosate-tolerant soybean MON 89788 has been genetically modified for tolerance to the broad-spectrum herbicide glyphosate. Tolerance is conferred by expression of the *cp4 epsps* gene in the soybean crop.

An earlier version of glyphosate-tolerant soybean, line 40-3-2, is already approved under Standard 1.5.2. Soybean line 40-3-2 currently accounts for 60% of the global production of soybean. Glyphosate-tolerant soybean MON 89788 is claimed to provide enhanced yield potential relative to soybean line 40-3-2. Glyphosate-tolerant soybean MON 89788 was developed primarily for cultivation in the United States and is not intended for cultivation in Australia or New Zealand. Australia and New Zealand import a considerable quantity of soybean and soybean products from the United States. Therefore, it is likely that, if approved, imports of soybean and soybean products into Australia and New Zealand will contain MON 89788.

In conducting a safety assessment of food derived from glyphosate-tolerant soybean MON 89788, a number of criteria have been addressed including: a characterisation of the transferred genes, their origin, function and stability in the soybean genome; the changes at the level of DNA, protein and in the whole food; compositional analyses; evaluation of intended and unintended changes; and the potential for the newly expressed proteins to be either allergenic or toxic in humans.

This safety assessment report addresses only food safety and nutritional issues. It therefore does not address: environmental risks related to the environmental release of GM plants used in food production; the safety of animal feed or animals fed with feed derived from GM plants; or the safety of food derived from the non-GM (conventional) plant.

History of Use

The cultivated soybean, *Glycine max* (L.) Merr., is an annual crop grown commercially in over 35 countries. Soybean is the dominant oilseed traded in international markets (OECD, 2001). There are three major soybean products — beans, meal and oil. The primary use of soybean meal is in animal feed, although a proportion is also used for human food products. The principle processed fraction used by the food industry is soybean oil. There are no human food uses for raw unprocessed soybeans as they contain high levels of trypsin inhibitor which has anti-nutritional properties. A significant proportion of the trypsin inhibitor is destroyed by heat treatment.

Description of the Genetic Modification

Glyphosate-tolerant soybean MON 89788 was generated through the transfer of the *cp4 epsps* gene to the elite soybean line, A3244. Direct transfer into elite germplasm accelerates subsequent introgression of the trait into other soybean varieties and is reported to provide a yield advantage compared to the already approved glyphosate-tolerant soybean 40-3-2.

The *cp4 epsps* gene is derived from the soil bacterium *Agrobacterium sp.* strain CP4 which encodes a version of the enzyme 5-enolpyruvyl-3-shikimatephosphate synthase (CP4 EPSPS). Unlike the plant's own EPSPS, CP4 EPSPS continues to function in the biochemical pathway producing aromatic amino acids in a plant that has been treated with glyphosate. There was no transfer of bacterial antibiotic resistance marker genes in this modification.

Detailed molecular and genetic analyses of glyphosate-tolerant soybean MON 89788 indicate that the transferred gene is stably integrated into the plant genome as a single copy and is inherited in subsequent generations according to predicted patterns of inheritance.

Characterisation of Novel Protein

The mature CP4 EPSPS in glyphosate-tolerant soybean MON 89788 is identical to the bacterial enzyme of 455 amino acids and is targeted to the plant chloroplast, the site of synthesis of essential aromatic compounds.

The novel protein is expressed at moderate levels in glyphosate-tolerant MON 89788 soybean plants. The mean level of CP4 EPSPS in grain (seed) was 140 µg/g fresh weight and 150 µg/g dry weight. This is lower than the level of CP4 EPSPS protein in the previous glyphosate-tolerant soybean 40-3-2 (average 288 µg/g fresh weight).

Potential toxicity and allergenicity

The novel protein present in glyphosate-tolerant soybean MON 89788 has been assessed previously for safety; the CP4 EPSPS protein is present in approved lines of canola, cotton, soybean, potato, corn and lucerne. Previous assessments have shown that CP4 EPSPS administered directly to animals at a high dose is not toxic, and the evidence does not indicate any potential for this protein to be allergenic in humans. Given its widespread use in approved glyphosate-tolerant crops, CP4 EPSPS now has a history of safe use in food over 10 years.

Compositional Analyses

Compositional studies were conducted to establish the nutritional adequacy of glyphosate-tolerant soybean MON 89788 compared to the non-GM control and conventionally produced commercial soybean varieties. Components measured in grain samples were proximates (protein, fat, ash and moisture), acid detergent fibre (ADF), neutral detergent fibre (NDF), amino acids, fatty acids (C8-C22), phytic acid, trypsin inhibitor, isoflavones, lectins, farinose, stachyose, vitamin E and carbohydrates (by calculation).

In general, no differences of biological significance were observed between glyphosate-tolerant soybean MON 89788 and its non-GM counterpart. Food from glyphosate-tolerant soybean MON 89788 is therefore considered to be compositionally equivalent to food from the control and commercially available soybean varieties.

Soybean is known to be one of the major allergenic foods. The potential allergenicity of soybean MON 89788 was compared to that of commercially available soybean varieties by assessing IgE binding responses using sera from known soybean allergic patients. These studies indicated that soybean MON 89788 does not have any greater potential to be allergenic than commercially available soybean varieties.

Nutritional Impact

The detailed compositional studies are considered adequate to establish the nutritional adequacy of food derived from glyphosate-tolerant soybean MON 89788. The introduction of glyphosate-tolerant soybean MON 89788 into the food supply would be expected to have minimal nutritional impact. This was supported by the results of a broiler feeding study, where no difference was found between birds fed diets containing MON 89788 soybean meal and those birds fed conventional soybean meal diets.

Conclusion

No potential public health and safety concerns have been identified in the comprehensive assessment of glyphosate-tolerant soybean MON 89788. On the basis of the data provided in the present application, and other available information, food derived from glyphosate-tolerant soybean MON 89788 is considered as safe and wholesome as food derived from other soybean varieties.

1. INTRODUCTION

Monsanto Australia Ltd is seeking approval in Australia and New Zealand for food derived from a genetically modified herbicide-tolerant soybean MON 89788 under Standard 1.5.2 – Food Produced using Gene Technology in the *Food Standards Code*. Soybean MON 89788 has been modified for tolerance to the broad-spectrum herbicide glyphosate. The intended product name for this soybean is Roundup RReady2Yield™.

Soybean (*Glycine max* (L.) Merr) is an annual crop grown for meal and oil. The primary use of soybean meal is in animal feed, although a proportion can also be used for human food products. The principle processed fraction used by the food industry is soybean oil. There are no human food uses for unprocessed soybeans as they contain high levels of trypsin inhibitor which has anti-nutritional properties. A significant proportion of the trypsin inhibitor is destroyed by heat treatment.

The glyphosate tolerance trait in soybean MON 89788 is due to the expression of the bacterial enzyme 5-enolpyruvyl-3-shikimate phosphate synthase (EPSPS) from *Agrobacterium sp.* strain CP4. The EPSPS enzyme is present in all plants, bacteria and fungi and is essential for aromatic amino acid biosynthesis. The normal mode of action of glyphosate is to bind to the endogenous plant EPSPS, blocking its enzymatic activity which subsequently leads to the death of the plant.

The bacterial EPSPS enzyme has a lower binding affinity for glyphosate, and therefore expression of CP4 EPSPS in the plant allows continued production of aromatic amino acids in the presence of the herbicide.

Glyphosate-tolerant soybean enables the use of herbicides to provide effective weed control during forage and seed production. An existing glyphosate-tolerant soybean, 40-3-2, currently accounts for 60% of the global soybean area and is the most cultivated genetically modified plant product to date. This new version of glyphosate-tolerant soybean exploits improvements in biotechnology and molecular-assisted breeding to enhance yield by 4-7% compared to the existing variety, while maintaining effective weed control. This was achieved by directly transforming the glyphosate-tolerant trait into an elite soybean variety with favourable agronomic characteristics and high yields, allowing more efficient introgression of the trait into other soybean varieties.

2. HISTORY OF USE

2.1 Donor organisms

Agrobacterium sp. strain CP4 produces a naturally glyphosate-tolerant EPSPS enzyme and was therefore chosen as a suitable gene donor for the herbicide tolerance trait (Padgett *et al.*, 1996). The bacterial isolate CP4 was identified in the American Type Culture Collection as an *Agrobacterium* species. *Agrobacterium* species are known soil-borne plant pathogens but are not pathogenic to humans or other animals.

2.2 Host organism

Cultivated soybean (*Glycine max* (L.) Merr) is a diploidised tetraploid ($2n=40$) of the Leguminosae family. Soybean is an annual crop that is grown commercially in over 35 countries world-wide. Soybean is the major oilseed crop in terms of world production and trade in international markets. In 2005-2006 global production exceeded 219 million metric tons. The major producers are the US, Argentina, Brazil and China; these countries account for 87% of total production (OECD, 2001). In 2005, glyphosate-tolerant soybean line 40-3-2 accounted for 60% of global soybean production (James, 2005).

The majority of soybean is processed for soybean meal used in animal feed, and soybean oil for human food uses. Soybeans are a traditional source of protein and oil for human consumption. Foods that contain soybean protein include bakery products, confections, meat products, textured foods and nutritional supplements. Soybean protein isolate is also the protein source for soy-based infant formula, where the amino acid and fatty acid profile is very important (OECD, 2001). The oil is typically used in margarine, shortening, cooking oil, salad oil and mayonnaise. Lecithin, derived from crude soybean oil, is used as a natural emulsifier, lubricant and stabilising agent.

There are no human food uses for raw unprocessed soybeans as they contain high levels of trypsin inhibitor and lectins, both of which have anti-nutritional properties. A significant proportion of both trypsin inhibitor and lectins is destroyed by heat treatment. Phytic acid present in soybean can reduce bioavailability of some mineral nutrients (OECD, 2001).

Soybean also contains phytoestrogens, naturally occurring isoflavone compounds that have a number of biochemical activities in mammals. The low molecular weight carbohydrates stachyose and raffinose are the cause of gas production resulting in flatulence and are considered to be anti-nutrients.

Soybeans contain several allergenic proteins that can cause severe adverse reaction when present in the diet of hypersensitive individuals (OECD, 2001).

3. DESCRIPTION OF THE GENETIC MODIFICATION

3.1 Method used in the genetic modification

MON 89788 was generated by *Agrobacterium*-mediated transformation of meristem tissue of Asgrow soybean variety A3244, based on the method developed by Martinell et al. (Martinell et al., 2002).

The *Agrobacterium*-mediated DNA transformation system is the basis of natural plasmid-induced crown-gall formation in many plants and is well understood (Zambryski, 1992). The genes of interest were inserted into the plasmid between DNA sequences known as the Left and Right Borders (LB and RB). These border sequences were isolated from the Ti plasmid of *Agrobacterium* and normally delimit the DNA sequence (T-DNA) transferred into the plant.

A double border, binary vector PV-GMGOX20, was used to generate transformation event MON 89788. This vector contains the *cp4 epsps* coding region under the control of a constitutive promoter. PV-GMGOX20 also contains both the left and right transfer-DNA (T-DNA) border sequences to facilitate transformation. The genetic elements present in PV-GMGOX20 are shown in Table 1. *Agrobacterium tumefaciens* strain ABI was used as it contains a disarmed Ti plasmid that is incapable of inducing tumour formation because of the deletion of the phytohormone genes originally present in the *Agrobacterium* Ti plasmid.

Table 1: Genetic elements in plasmid PV- GMGOX20

Genetic element	Size in base pairs (position in plasmid)	Function
Intervening sequence	51 (1-51)	Sequences used in DNA cloning
<i>FMV/Tsfl</i>	1040 (52-1091)	Chimeric promoter consisting of the enhance sequences from the 35S promoter of the Figwort Mosaic virus (Richins et al., 1987) and the promoter from <i>Tsfl</i> of <i>Arabidopsis thaliana</i> encoding elongation factor EF-1 alpha (Axelos et al., 1989)
<i>Tsfl</i>	46 (1092-1137)	5' non-translated leader (exon 1) from <i>Tsfl</i> of <i>Arabidopsis thaliana</i> encoding elongation factor EF-1 alpha (Axelos et al., 1989)
<i>Tsfl</i>	622 (1138-1759)	Intron from <i>Tsfl</i> of <i>Arabidopsis thaliana</i> encoding elongation factor EF-1 alpha (Axelos et al., 1989)
Intervening sequence	9 (1760-1768)	Sequences used in DNA cloning
<i>CTP2</i>	228 (1769-1996)	Chloroplast transit peptide sequence from the ShkG gene of <i>A. thaliana</i> (Klee et al., 1987)

Genetic element	Size in base pairs (position in plasmid)	Function
<i>cp4 epsps</i>	1368 (1997-3364)	Codon optimised coding sequence of the <i>aroA</i> (<i>epsps</i>) gene from <i>Agrobacterium</i> sp. Strain CP4 (Padgett <i>et al.</i> , 1996; Barry <i>et al.</i> , 1997)
Intervening Sequence	42 (3365-3406)	Sequences used in DNA cloning
<i>E9</i>	643 (3407-4049)	3' untranslated sequence from the ribulose-1,5-bisphosphate carboxylase small subunit (<i>RbcS2</i>) <i>E9</i> gene from pea (<i>Pisum sativum</i>). Transcriptional termination sequence and polyadenylation signal sequence (Coruzzi <i>et al.</i> , 1984)
Intervening sequence	43 (4050-4092)	Sequences used in cloning
Left Border	442 (4093-4534)	Left border sequence essential for T-DNA transfer (Barker <i>et al.</i> , 1983)
Intervening sequence	86 (4535-4620)	Sequences used in cloning
<i>ori-V</i>	397 (4621-5017)	Origin of replication for maintenance of the plasmid in <i>Agrobacterium</i> (Stalker <i>et al.</i> , 1981)
Intervening sequence	1508 (5018-6525)	Sequences used in cloning
<i>rop</i>	192 (6526-6717)	Coding sequence for repressor of primer protein for maintenance of plasmid copy number in <i>E. coli</i> (Giza and Huang, 1989)
Intervening sequence	417 (6718-7134)	Sequences used in cloning
<i>ori-PBR322</i>	629 (7135-7763)	Origin of replication from pBR322 for maintenance of plasmid in <i>E. coli</i> (Sutcliffe, 1978)
Intervening sequence	500 (7764-8263)	Sequences used in cloning
<i>aadA</i>	889 (8264-9152)	Bacterial promoter and coding sequence for an aminoglycoside modifying enzyme, 3'(9)-O-nucleotidyltransferase from the transposon Tn7 (Fling <i>et al.</i> , 1985)
Intervening sequence	136 (9153-9288)	Sequences used in cloning
Right Border	357 (9289-9645)	Right border sequence essential for T-DNA transfer (Depicker <i>et al.</i> , 1982)
Intervening sequence	19 (9646-9664)	Sequences used in cloning

Following transformation, the meristems were placed on selection media containing glyphosate to inhibit the growth of untransformed plant cells. Carbenicillin and Claforan were used to prevent the growth of remaining *Agrobacterium*. The meristems were then placed in media conducive to root and shoot formation, and only those plants with normal phenotypic characteristics were selected and transferred to soil for growth and further assessment.

R0 plants were self-pollinated and the subsequent R1 plants screened for the presence of the CP4-EPSPS protein, tolerance to glyphosate and for the homozygosity of the inserted gene. The progeny of the glyphosate-tolerant, homozygous plants were subjected to further molecular and phenotypic analysis. Based on its superior phenotypic characteristics and molecular profile, MON 89788 was selected for further characterisation.

These steps are summarised in Figure 1. The breeding tree of MON 89788 is shown in Figure 2.

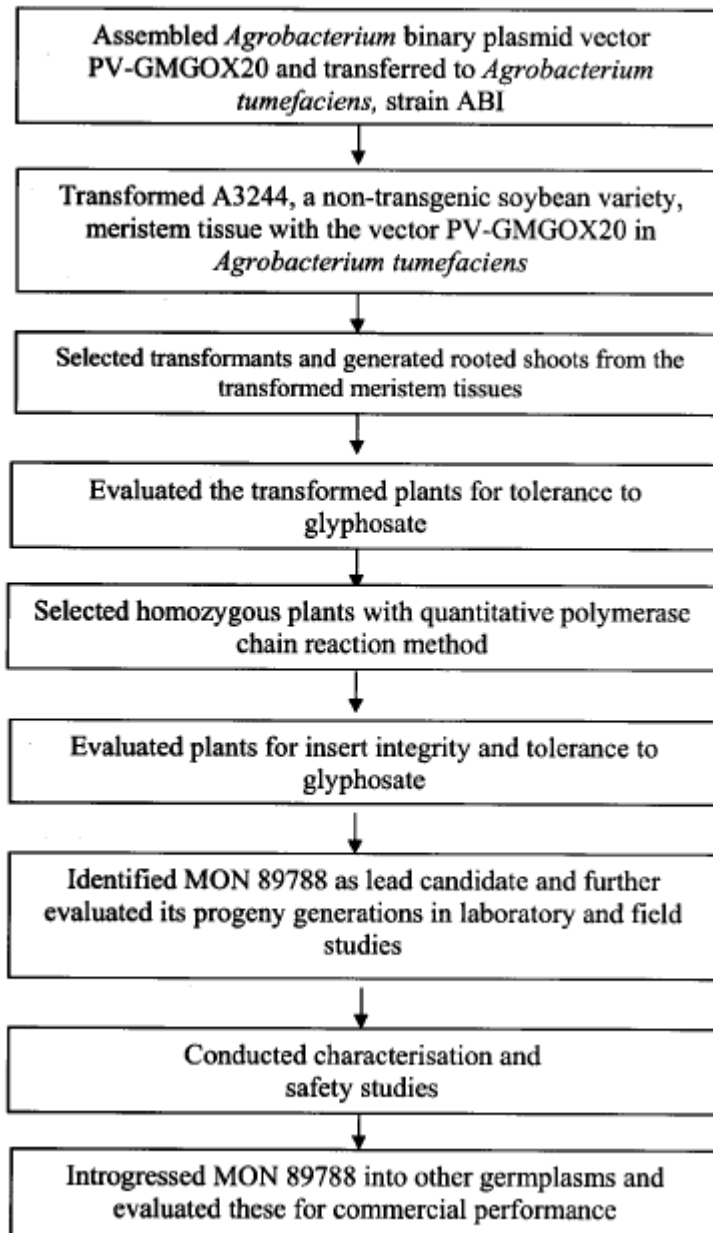


Figure 1: Development of MON 89788

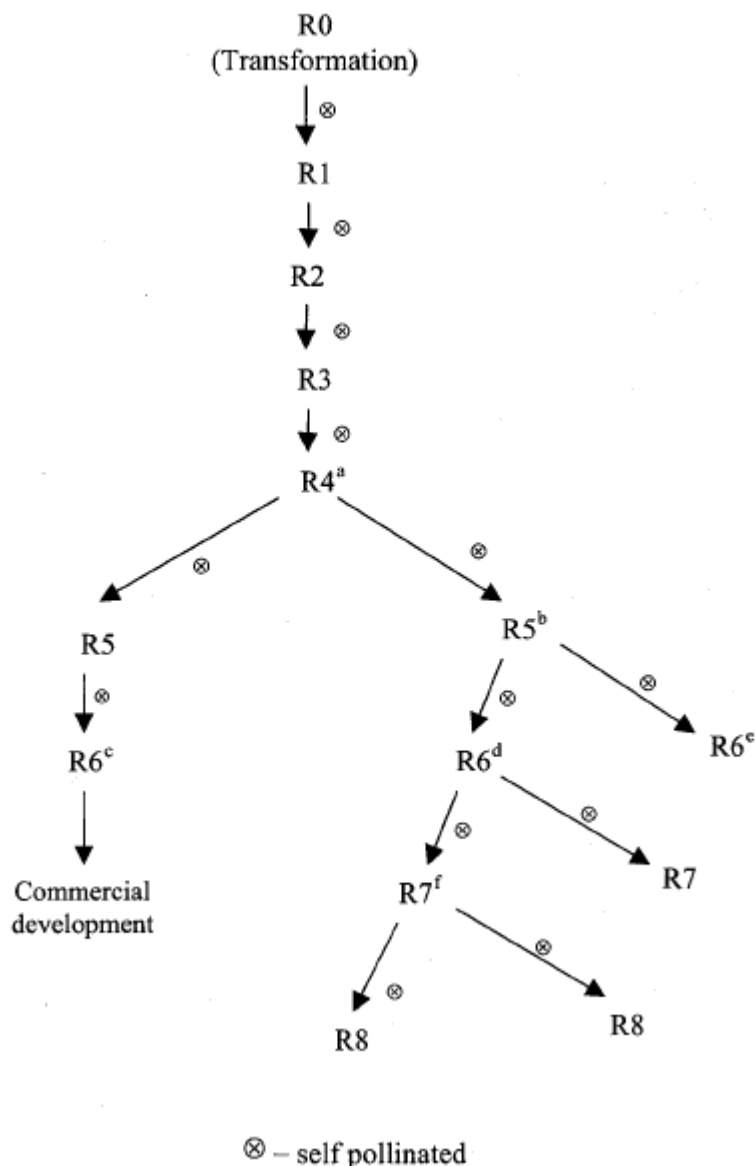


Figure 2: Breeding tree of MON 89788

Molecular characterisation was performed using R5^b generation. Generational stability analyses were performed on R4^a, R5^b, R6^c, R6^d, R6^e and R7^f.

3.2 Genetic elements in vector

Plasmid PV-GMGOX20 is approximately 9.7 kb and contains a *cps-epsps* gene expression cassette within the left and right border regions. Approximately 5.4 kb of this vector is backbone DNA and is not intended for incorporation into the soybean genome.

The *cp4-epsps* expression cassette T-DNA contains a chimeric transcriptional promoter (P-*FMV/Tsf1*), and leader and an intron sequence derived from the *Tsf1* gene (L-*Tsf1* and I-*Tsf1*), a chloroplast transit peptide sequence (TS-*CTP2*), the *cp4 epsps* coding sequence (CS-*cp4 epsps*), and a polyadenylation sequence from the *RbcS2* gene (T-*E9*). This expression cassette is identical to that used in the transformation of Roundup Ready Flex cotton MON 88913, which was approved by FSANZ in 2006 (Application A553).

All genetic elements are shown in Table 1.

3.3 Function and regulation of the novel genes

The only novel gene introduced into soybean MON 89788 is *cp4 epsps*. Expression of the *cp4 epsps* gene in the soybean plants confers tolerance to the herbicide glyphosate.

Since the early 1990s it has been known that the *cp4 epsps* gene from *Agrobacterium* sp. strain CP4 has the potential to provide high levels of tolerance to glyphosate when introduced into plants. Glyphosate normally binds to the plant EPSPS enzyme, blocking biosynthesis of essential aromatic amino acids by the shikimate pathway, which is common to plants, bacteria and fungi. The bacterial CP4 EPSPS protein has a lower binding affinity with glyphosate compared to most other EPSPS enzymes and therefore retains its high catalytic efficiency in the presence of the herbicide. The bacterial *cp4 epsps* gene has been modified to optimise codon usage, which allows for higher expression in plants. These changes to the DNA sequence produce an identical CP4 EPSPS protein (Harrison *et al.*, 1996) and do not affect the functional activity of the expressed protein.

Expression of *cp4-epsps* is regulated by the chimeric promoter *FMV/Tsf1*, which directs constitutive expression of *cp4 epsps* in soybean, conferring tolerance to the herbicide at the whole plant level.

The activity of the EPSPS enzyme in higher plants occurs in the chloroplast (Ia-Cioppa *et al.*, 1986). The CP4 EPSPS protein is produced in the cytoplasm and then targeted to the chloroplasts via an N-terminal fusion with a chloroplast transit peptide sequence (CTP2). The CTP is typically cleaved on uptake of the mature protein into the chloroplast, and is subsequently rapidly degraded.

The *cp4 epsps* gene together with these plant regulatory elements has been used previously to confer glyphosate-tolerance in a range of food crops including canola, cotton, soybean, sugarbeet, and corn.

3.4 Characterisation of the novel gene in soybean MON 89788

Studies submitted:

Dickinson, E.C., N.G. Pineda, N.K. Scanlon, A.J. Whetsell and J.D. Masucci (2006) Molecular Analysis of Glyphosate-Tolerant Soybean MON 89788. Unpublished Monsanto Report MSL-20160

Masucci, J.D. (2006) Alignment of the MON 89788 Insert DNA Sequence to the PV-GMGOX20 Transformation Vector DNA Sequence. Unpublished Monsanto Report 06-RA-30-01

Insert and copy number

Analysis of the DNA introduced into glyphosate-tolerant soybean MON 89788 was undertaken using a range of established molecular techniques. Southern blot analyses were performed on genomic DNA extracted from soybean MON 89788 and the parent soybean cultivar A3244 as a control to assess the following:

- (i) number of insertions of the expression cassette;
- (ii) number of copies of the expression cassette;
- (iii) integrity of the inserted gene expression cassette;

- (iv) presence or absence of plasmid backbone; and
- (v) stability of the inserted DNA with conventional breeding over several generations.

Genomic DNA from soybean MON 89788 and A3244 was digested with a variety of restriction endonucleases and subjected to Southern blot analyses. The plasmid PV-GMGOX20 was used as a reference substance serving as a positive hybridisation control. The Southern blot hybridisations, based on the method described by Southern (Southern, 1975), involved both short and long gel runs in order to improve the resolution of different size molecular fragments. Individual Southern blots were tested with probes corresponding to *cp4 epsps*, the promoter and polyadenylation sequence, and the transforming plasmid backbone. In all, ten radiolabelled probes corresponding to segments of DNA spanning the entire length of the plasmid PV-GMGOX20 were used in the analyses.

The combined results from these multiple Southern blot analyses indicate that glyphosate-tolerant soybean MON 89788 is characterised by the presence of one copy of the gene cassette, inserted at a single locus in the soybean genome. No unexpected hybridisation bands were detected. These results suggest that soybean MON 89788 does not contain any additional DNA elements other than those expected from the insertion of the *cp4 epsps* expression cassette. Fragments corresponding to partial genes, regulatory elements or backbone sequences derived from the transforming plasmid were not detected. A map of the inserted DNA presented below (Figure 3).

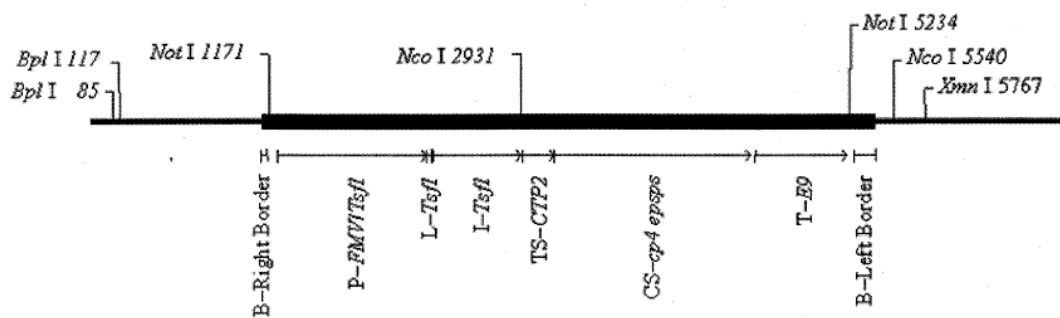


Figure 3: Map of the insertion event in glyphosate-tolerant soybean MON 89788

The bold heavy line represents the genetic material inserted into the soybean genome. The lighter line to the left and right of the insert represents genomic DNA. Individual genetic elements are identified below the insert. The map was developed on the basis of Southern blot characterisation data and confirmed by DNA sequence analysis.

PCR and sequence analysis

The organisation of the elements within the MON 89788 insert was confirmed by PCR analysis of three overlapping regions of DNA that span the entire length of the insert and soybean genomic flanking regions. Sequence analysis demonstrated that the sequence of the insert (4303 base pairs) is identical to that of the gene construct in the transforming plasmid. The insert begins at base 9604 of plasmid PV-GMGOX20, located in the right border region, and ends at base 4242 in the left border region. This sequence analysis confirmed the presence and organisation of the insert as shown in Figure 3.

Flanking regions and putative Open Reading Frame (ORF) analysis

Studies submitted:

Dickinson and Masucci (2006) PCR and DNA Sequence Analysis of Conventional Soybean to Examine the MON 89788 Insertion Site. Unpublished Monsanto Technical Report MSL-20320.

Soybean genomic DNA on either side of the MON 89788 *cp4 epsps* insert was also sequenced. Such alignment can reveal potential deletion or addition of DNA sequence in comparison to the wild-type genome at the site of the insertion event. PCR amplification of soybean A3244 genomic DNA using primers that flank the *cp4 epsps* insertion site of MON 89788 yielded a DNA product of ~650 base pairs which was sequenced using the same primers used for amplification. The A3244 sequence was compared to 1103 base pairs of MON 89788 genomic DNA at the 5' end of the transgene insert and 1060 base pairs at the 3' end of the insert. Results from the DNA sequence comparison indicated that 40 base pairs of parental genomic DNA were deleted from the site of the T-DNA insertion. In addition, there are ten bases at the 5' end and six bases at the 3' end of the insert that are not present in this region of the parental soybean genome. This minor deletion and insertion of DNA can occur due to double strand break repair mechanisms in the plant during the *Agrobacterium*-mediated transformation process (Salomon and Puchta, 1998). Based on this analysis, it can be concluded that there is minor rearrangement of the endogenous soybean genomic DNA at the MON 89788 insertion site, and that the DNA sequences flanking the insert are native to the soybean genome. The junction regions between the insert and genomic DNA were further analysed for their potential to be involved in the production of chimeric proteins.

The production of unexpected chimeric proteins as a result of transgene insertion is of particular relevance to food safety. In cases where there is 100% molecular identity between the plasmid T-DNA and inserted DNA in the plant, and all regulatory elements including termination and polyadenylation signals are intact, there is little likelihood of unintended formation of gene fragments that are transcriptionally active or likely to produce a chimeric protein.

In the case of glyphosate-tolerant soybean MON89788, the transformation event has not resulted in any additions, deletions, rearrangements or partial insertions of the gene of interest, or its regulatory elements, as determined by the Southern blot, PCR analyses and direct DNA sequencing of the entire insert region. Nonetheless, the applicant has provided a bioinformatic evaluation of DNA sequences flanking the junctions of the inserted DNA in MON 89788 for assessment of putative polypeptides. Two of the novel open reading frames between stop codons were less than eight amino acids, so bioinformatics analysis of the other ten putative open reading frames was performed using the ALLPEPTIDES, TOXIN5 and AD6 (the allergen database) databases. This is discussed further in section 4.6.

3.5 Stability of the genetic changes

Segregation data

During the development of MON 89788, R0 plants were self-pollinated and the resulting R1 plants segregated with the expected 3:1 ratio based on the glyphosate tolerance phenotype. Selected R1 plants that survived glyphosate treatment were subjected to quantitative PCR analysis and a single plant that was homozygous for the *cp4 epsps* expression cassette was selected.

Self pollination of this plant gave rise to the R2 generation, with an expected segregation ratio for this and subsequent self pollinated generations of 100% positive for glyphosate tolerance. Phenotypic frequency was compared by Chi square analysis, which confirmed that the inserted *cp4 epsps* cassette was segregating as expected (Table 2). These results are consistent with a single insertion event segregating according to Mendel's laws of genetics.

Table 2: Genotypic Segregation Data for MON 89788

Generation	No. of Plant (% germ) ¹	Expected ²		Observed ³		χ^2
		Positive	Negative	Positive	Negative	
R1	43	32.25	10.75	29	14	1.31 ⁴
R2	58	58	0	58	0	Fixed
R3	240 (80%)	192	0	192 ⁵	0	Fixed
R3	240 (85%)	204	0	204 ⁵	0	Fixed
R3	240 (85%)	204	0	204 ⁵	0	Fixed

¹ Percent germination

² Expected number of glyphosate tolerant plants

³ Observed number of glyphosate tolerant plants by ELISA and glyphosate application

⁴ Not significant at $p \leq 0.05$ (Chi-square = 3.84 at 1 df)

⁵ Number of plants (observed positives) was calculated based on number of seeds planted x percent germination

Stability of the inserted DNA

In order to demonstrate the stability of the genetic change in MON 89788 over multiple generations, additional Southern blot analyses were performed. Genomic DNA from four generations of MON 89788 was examined (R4 – R7, see Figure 2). Genomic DNA from the parental line A3244 and plasmid PV-GMGOX20 were used as negative and positive controls respectively.

Probes were used that spanned the insert region and the plasmid backbone region. The hybridisation patterns indicated that the insert in MON 89788 is stably integrated into the soybean genome. No plasmid backbone DNA was detected in any of the four generations assessed.

3.6 Antibiotic resistance genes

No antibiotic marker genes are present in glyphosate-tolerant soybean MON89788. The molecular characterisation shows that the region outside the T-DNA of plasmid PV-GMGOX20 was not integrated into the soybean genome during transformation. Consequently, the bacterial selectable marker gene, *aad* (which confers resistance to the antibiotics spectinomycin and streptomycin), is not present in glyphosate-tolerant soybean MON 89788. The absence of the bacterial marker gene in the plant was confirmed by Southern hybridisation analysis using a probe encompassing the *aad* gene.

4. CHARACTERISATION OF NOVEL PROTEINS

4.1 Function and phenotypic effects

Expression of the CP4 EPSPS protein in MON 89788 plants confers tolerance to the herbicide glyphosate. This protein is one of many EPSPS proteins found in nature in a broad range of organisms including plants, bacteria and fungi. The bacterial CP4 EPSPS is naturally highly tolerant to inhibition by glyphosate and continues to have high catalytic efficiency in the presence of the herbicide. Plant cells producing the CP4 EPSPS protein are therefore tolerant to glyphosate because the enzyme continues to function when the plant's own EPSPS has been inactivated by the herbicide.

Several glyphosate-tolerant varieties of corn, canola and soybean expressing CP4 EPSPS have been assessed for safety previously and are permitted on the market for use in food.

The mature 47.6 kDa CP4 EPSPS protein consists of a single polypeptide of 455 amino acids.

4.2 Protein Expression Analysis

Study submitted:

Pineda N.G. and A. Silvanovich (2006) Assessment of CP4 EPSPS Protein Quantities in Leaf, Seed, Root, and Forage Tissues from Second Generation Glyphosate-Tolerant Soybean MON 89788 Produced in the U.S. During 2005. Unpublished Monsanto study report MSL-20182

The levels of the CP4 EPSPS protein in leaf, seed, root and forage tissue of soybean MON 89788 were estimated using an enzyme-linked immunosorbent assay (ELISA). For capture of CP4 EPSPS, mouse monoclonal antibodies were used. A goat polyclonal CP4 EPSPS antibody was used for detection, with quantitation of protein levels accomplished by interpolation from a CP4 EPSPS protein standard curve. The limit of detection of the ELISA was estimated to be 0.26 µg/g fresh weight.

To produce the material for analysis, MON 89788 was planted at five field sites in the 2005 growing season. Sites represented geographies where soybean is typically grown in the United States – York County (Nebraska), Clinton County (Illinois), Warren County (Illinois), Jackson County (Arkansas), and Fayette County (Ohio).

Leaf tissue was collected four times over the growing period: OSL1 (over-season leaves V3-V4 growth stage); OSL2 (V6-V8 growth stage); OSL3 (V10-V12); an OSL4 (V14-V16 growth stage). Grain, root and forage were collected at one time point only. 15 samples were analysed for each tissue, except for forage, where only 14 samples were analysed. The mean levels of the CP4 EPSPS protein across the sites for OSL1, OSL2, OSL2, OSL4, grain, root and forage were 300, 340, 330, 290, 150, 74 and 220 µg/g dry weight respectively (Table 3).

The levels of CP4 EPSPS from the control soybean (conventional parental variety A3244) were less than the assay limit of detection in all tissue types.

Table 3: Summary of CP4 EPSPS protein levels in tissues collected from MON 89788 produced in the US during 2005

Tissue Type	CP4 EPSPS µg/g FW (SD)¹	Range² (µg/g FW)	CP4 EPSPS µg/g DW (SD)³	Range (µg/g DW)	LOQ / LOD (µg/g FW)
OSL1⁴	54 (7.8)	40 – 66	300 (51)	220 – 380	0.57 / 0.26
OSL2⁴	60 (10)	42 – 80	340 (55)	250 – 440	0.57 / 0.26
OSL3⁴	58 (11)	40 – 79	330 (94)	200 – 520	0.57 / 0.26
OSL4⁴	75 (17)	60 – 110	290 (48)	210 – 390	0.57 / 0.26
Grain	140 (20)	98 – 170	150 (22)	110 – 180	0.34 / 0.26
Root	22 (6.0)	13 – 38	74 (27)	41 – 150	0.57 / 0.11
Forage	59 (14)	41 – 94	220 (51)	140 – 330	0.57 / 0.10

1. Protein quantities are expressed as mean µg of CP4 EPSPS/g tissue on a fresh weight (FW) basis. The mean and standard deviation (SD) were calculated across all sites.
 2. Minimum and maximum values across all sites.
 3. Protein quantities are expressed as mean µg of CP4 EPSPS/g tissue on a dry weight (DW) basis. The dry weight values were calculated by dividing the fresh weight values by the dry weight conversion factors obtained from moisture analysis data.
 4. OSL1 to OSL4 represent over-season leaves collected at the following developmental stages: OSL1: V3-V4 growth stage; OSL2: V6-V8 growth stage; OSL3: V10-V12 growth stage; OSL4: V14-V16 growth stage.
- Note: Sample number is 14 for forage, and 15 each for OSL1 to OSL4, grain, and root.

4.3 Characterisation of the novel protein in MON 89788

Studies submitted:

Kurunanandaa K, B.E. Goertz, J.J. Thorp, S.H. Elliot, and M. Alibhai (2006) Characterization of the CP4 EPSPS Protein Purified from the Seed of MON 89788 and Assessment of the Physicochemical and Functional Equivalence of the Plant and *E. coli*- Produced CP4 EPSPS Proteins. Unpublished Monsanto Study Report, MSL-20178.

The CP4 EPSPS protein produced in MON 89788 was characterised to determine that the expected protein was being produced. The *cp4 epsps* gene encodes a 47.7 kDa protein (calculated based on predicted amino acid sequence) consisting of a single polypeptide of 455 amino acids. The CP4 EPSPS protein in MON 89788 is translocated to the chloroplasts via an N-terminal fusion with CTP2 to form the CTP2-CP4 EPSPS precursor protein. This protein is then processed to remove the transit peptide, resulting in the mature functional CP4 EPSPS protein. The molecular identity and biochemical characteristics of the CP4 EPSPS protein expressed *in planta* were examined using a variety of biochemical techniques.

SDS-PAGE and Western blot analysis of the MON 89788 produced CP4 EPSPS protein revealed a protein with a molecular weight of approximately 44 kDa, which was consistent with the *E. coli* produced protein.

This band was excised and N-terminal sequence analysis performed, the results of which indicated that the expected amino acid sequence of the mature CP4 EPSPS protein was present, with the exception of the initial methionine. As the DNA sequence demonstrated the presence of the methionine codon, the removal of the methionine in the purified plant-produced protein is likely due to cellular enzyme processing in the plant. This has been observed previously in canola, sugar beet, corn, cotton and soybean. The N-terminal sequence data confirms that the purified protein extracted from MON 89788 is the mature form of CP4 EPSPS and is consistent with the sequence of the *E. coli* produced reference standard.

MALDI-TOF mass spectrometry analysis identified 23 protein fragments that matched the expected mass of the trypsin-digested CP4 EPSPS protein. These covered 50.3% of the protein and identified it as the expected protein. A protein can usually be identified when 40% of the mass fragments are identified from the analysed protein. Immunoblot analysis with CP4 EPSPS specific antisera (goat antisera) also positively identified the approximately 44 kDa band as CP4 EPSPS and equivalent to the *E. coli* produced protein.

The functional activities of the plant-produced CP4 EPSPS protein and the *E. coli*-produced CP4 EPSPS reference standard were determined using a phosphate release assay. The specific activities of the MON 89788-produced CP4 EPSPS and *E. coli*-produced CP4 EPSPS proteins were 3.7 U/mg total protein and 4.4 U/mg total protein, respectively. Other studies have reported the average specific activity of the CP4 EPSPS protein to be between 3 and 6 U/mg. The enzyme assay demonstrated that the plant-produced CP4 EPSPS protein was as active as *E. coli*-produced CP4 EPSPS protein and thus the plant-produced protein is functionally equivalent to the *E. coli*-produced protein.

The isolated plant-produced CP4 EPSPS protein was analysed for post-translational modification through covalently bound carbohydrate moieties. After labelling with biotin, protein-bound carbohydrate moieties were detected with streptavidin-horseradish peroxidase and enhanced chemiluminescence. The *E. coli*-produced CP4 EPSPS protein was used as a non-glycosylated negative control and the transferrin protein as a positive control. There was a very faint band migrating at 44 kDa in both the plant and *E. coli* produced samples. This was considered to be non-specific reactivity as bacterial expression systems such as *E. coli* lack the ability to glycosylate proteins. As the markers are non-glycosylated proteins produced in *E. coli*, the presence of a faintly hybridising band at 20 kDa in the marker lane supports this conclusion. Therefore this analysis suggests that MON 89788-produced CP4 EPSPS is equivalent to the *E. coli* produced protein.

A combination of N-terminal sequence analysis, MALDI-TOF and Western blot have confirmed the identity of the plant-produced CP4 EPSPS protein. The characterisation of the *E. coli*-produced CP4 EPSPS protein indicates it is equivalent to the plant-produced CP4 EPSPS protein based on comparable electrophoretic mobility, enzyme activity, immunoreactivity and absence of detectable glycosylation. Based on the similarity of the results from the plant and microbial preparations, the MON 89788-produced protein is chemically and functionally equivalent to CP4 EPSPS protein expressed in *E. coli*.

4.4 Potential toxicity of novel proteins

Studies submitted:

McCoy, R.L. and A. Silvanovich (2003) Bioinformatics Analysis of the CP4 EPSPS Protein Utilizing the AD4, TOXIN5 and ALLPEPTIDES Databases. Unpublished Monsanto Report MSL-18752.

McCoy, R.L. and A. Silvanovich (2005) Updated Bioinformatics Evaluation of the CP4 EPSPS Protein Utilizing the AD5 Database. Monsanto Study Report MSL-19894.

Leach J.N., R.E. Hileman, J.J. Thorp, C. George and J. Astwood. (2002) Assessment of the *in vitro* digestibility of purified *E. coli*-produced CP4 EPSPS protein in simulated gastric fluid. Unpublished Monsanto Study Report MSL-17566.

The mature CP4 EPSPS protein in glyphosate-tolerant soybean MON 89788 is biochemically similar to the EPSPS proteins naturally present in a variety of food crops (e.g. soybean and corn), which have a history of safe consumption by humans (Padgett *et al.*, 1996; Harrison *et al.*, 1996). Also, the mature CP4 EPSPS protein in glyphosate-tolerant soybean MON 89788 is identical to, or shares greater than 99% sequence identity to, the amino acid sequence of the CP4 EPSPS protein produced in a number of other glyphosate-tolerant crops that have previously been approved for food use by FSANZ.

The CP4 EPSPS protein has previously undergone assessment by FSANZ when present in other GM (glyphosate-tolerant) crop varieties including soybean, cotton, canola, sugarbeet corn and lucerne. The data submitted for an assessment of potential toxicity have therefore been comprehensively appraised (see Final Assessment Reports for FSANZ Applications A338, A355, A362, A363, A378, A416, A525, A548, A553 and A575).

These assessments considered history of previous exposure to the protein through the diet, bioinformatic analysis of the primary and secondary structure of the CP4 EPSPS protein to examine any similarities with known protein toxins, biochemical tests (heat stability), and acute oral toxicity studies in animals. The previous assessments concluded that the CP4 EPSPS protein is not toxic and is therefore safe for human consumption.

Acute toxicity studies

To generate sufficient quantities of the CP4 EPSPS protein required for toxicity, and biochemical studies, it is necessary to produce the protein in bacterial expression systems. Prior to use, the bacterially produced protein is compared to the protein produced in the plant, to demonstrate their equivalence. The CP4 EPSPS used for further analyses was produced in the laboratory using recombinant *E. coli*. As outlined in the previous section, a range of biochemical methods was used to establish that *E. coli* -produced CP4 EPSPS protein is equivalent to the protein produced by glyphosate-tolerant soybean MON 89788.

The acute toxicity of the CP4 EPSPS protein has been previously tested by acute gavage exposure in mice and no deleterious effects were observed (Harrison *et al.*, 1996). The CP4 EPSPS protein was administered at levels 1000 fold higher than those anticipated in consumption of food products; the no effect level (NOEL) for oral toxicity in mice is 572 mg/kg body weight, and was the highest dose tested. Despite this high dose, there was no mortality or morbidity, and there were no significant differences in terminal body weights of animals in the treated and control groups. Upon necropsy, body cavities were opened and organs examined *in situ* and removed. There were no pathological findings attributable to the treatment with the CP4 EPSPS protein.

4.5 Potential allergenicity of novel proteins

The potential allergenicity of a novel protein is evaluated using an integrated, step-wise, case-by-case approach relying on various criteria used in combination, since no single criterion is sufficiently predictive of either allergenicity or non-allergenicity. The assessment focuses on:

- (i) the source of the novel protein,
- (ii) any significant amino acid sequence similarity of the novel protein with that of known allergens, and
- (iii) structural properties of the novel protein, including susceptibility to degradation in simulated digestion models.

In some cases, such as where the novel protein has sequence similarity to a known allergen, additional *in vitro* and *in vivo* immunological testing may be warranted. Applying such criteria systematically provides reasonable evidence on the potential of the novel protein to act as an allergen.

Source of protein

The CP4 EPSPS protein in soybean MON 89788 is derived from a naturally occurring, glyphosate-degrading bacterium, *Agrobacterium tumefaciens*, identified by the American Type Culture Collection. Species of *Agrobacterium* are not known human or animal pathogens, nor known to be allergenic.

Similarity to known allergens

Potential structural similarities between the CP4 EPSPS enzyme and proteins in the allergen databases (AD4 and AD5) were evaluated using the FASTA sequence alignment tool. Inspection of the results showed no significant similarities between the CP4 EPSPS protein and known allergens. The most significant alignment, to dust mite allergen Der f II, was only 30.5% identical over an 82 amino acid window requiring five gaps for alignment. This is less than the threshold for considering the possibility of cross-reactivity of 35% identity across 80 or more amino acids suggested by (Codex, 2004). This alignment produced an E score² of 0.66 and is not considered to indicate structural or functional homology between the CP4 EPSPS protein and the dust mite allergen Der f II. No immunologically relevant sequences (identity across eight contiguous amino acids) were detected when the CP4 EPSPS sequence was compared to the AD4 or AD5 sequence databases using a pair-wise comparison algorithm.

In vitro digestibility

Typically, food proteins that are allergenic tend to be stable to enzymes such as pepsin and the acidic conditions of the digestive system, exposing them to the intestinal mucosa and leading to an allergic response (Astwood and Fuchs, 1996; Metcalfe *et al.*, 1996; Kimber *et al.*, 1999).

² The E score reflects the degree of similarity between a pair of sequences and can be used to evaluate the significance of an alignment. The calculated E score depends on the overall length of joined (gapped) local sequence alignments, the quality (percent identity/similarity) of the overlap and the size of the database used for the FASTA search (Pearson and Lipman, 1988). For a pair of sequences, very small E score values may indicate a structurally relevant similarity. Conversely, large E score values are typically associated with poor alignments that do not represent a biologically relevant structural similarity.

Novel proteins are therefore investigated for their digestibility in simulated digestion models.

Previous assessment of the CP4 EPSPS protein found that it is rapidly degraded in simulated digestive fluids. The half-life of CP4 EPSPS was less than 15 seconds in the gastric system and less than 10 minutes in the intestinal system, based on Western blot analysis (Harrison *et al.*, 1996). Subsequent experiments to assess the *in vitro* digestibility of the CP4 EPSPS protein in simulated gastric fluid (SGF) showed that 95-98% of the CP4 EPSPS protein was digested within 15 seconds. Similarly, the EPSPS activity was reduced to <10% within 15 seconds of incubation in SGF.

4.6 Analysis of potential ORFs within the insert and at the junction regions

Studies Submitted:

McClain, J.S. and A. Silvanovich (2006) Bioinformatics Evaluation of DNA Sequences Flanking the 5' and 3' Junctions of the Inserted DNA in MON 89788 Soybean. Assessment of Putative Polypeptides. Monsanto Company unpublished report. MSL-20344.

As part of a comprehensive safety assessment, bioinformatics analyses were performed to assess the similarity to known allergens, protein toxins or pharmacologically active proteins of the putative polypeptides encoded by the DNA spanning the junctions between soybean genomic DNA and the 5' and 3' ends of the inserted DNA. Sequences spanning either the 5' or 3' junction region were translated from stop codon to stop codon in all six reading frames. As mentioned in Section 3.4, two of the novel open reading frames between stop codons were less than eight amino acids, so bioinformatics analysis of the other ten putative open reading frames was performed using the ALLPEPTIDES, TOXIN5 and AD6 (the allergen database) databases.

No alignments with any of the query sequences generated an E score of less than 1×10^{-5} . In addition to structural similarity, each putative polypeptide was screened for short polypeptide (eight amino acids) matches using a pair-wise comparison algorithm. No biologically relevant structural similarity to allergens, toxins, or bioactive proteins was observed for any of the potential polypeptides. A single eight amino acid alignment occurred between one of the sequences and an entry from the AD6 database, an unnamed protein from Indianmeal moth (*Plodia interpunctella*). However, as part of a recent review of all sequences in the AD6 database by an independent expert allergen panel, this protein sequence, along with 377 others, has been removed from subsequent versions of the database as there is insufficient evidence of allergenicity³. Excluding this result, there are no immunologically significant epitopes present in any of the reading frames at either DNA-insert junction.

The results of these bioinformatic analyses demonstrate that even in the unlikely event that the transgene junctions were transcribed, and further that any of the junction ORFs were translated, they would not share a sufficient degree of sequence similarity or identity to indicate that they would be potentially toxic, allergenic or have other health implications.

4.7 Conclusion

The CP4 EPSPS protein is expressed in MON 89788 soybean grain at a mean of 140 µg/g fresh weight.

³ <http://www.allergenonline.com/about.asp>

The characterisation of the CP4 EPSPS protein in MON 89788 indicates it is chemically and functionally equivalent to the *E. coli*-produced CP4 EPSPS protein based on comparable electrophoretic mobility, enzyme activity, immunoreactivity and absence of detectable glycosylation. These studies further indicate that the CP4 EPSPS protein is expressed in soybean MON 89788 as expected and does not appear to have undergone any unexpected post-translational modification. Therefore, previous studies of the acute toxicity carried out using *E. coli*-produced CP4 EPSPS protein are applicable to the protein produced by glyphosate-tolerant soybean MON 89788. No deleterious effects of CP4 EPSPS protein were observed in the toxicity study.

The CP4 EPSPS protein is structurally and biochemically similar to other EPSPS enzymes from various plant food sources that are currently part of the human diet and have been consumed over a long period of time without health concerns. The potential toxicity and allergenicity of the CP4 EPSPS protein has been assessed by FSANZ on numerous occasions and no adverse findings have been reported. Its use is approved in food derived from specific lines of soybean, sugarbeet, corn, cotton, canola and lucerne.

5. COMPOSITIONAL ANALYSES

A comparison of similarities and differences in composition between a GM plant and its conventional counterpart aids in the identification of potential safety and nutritional issues and is considered the most appropriate strategy for the safety and nutritional assessment of GM foods (WHO, 2000). Ideally, the comparator should be the near isogenic parental line grown under identical conditions. In this case, the transgene is the only genetic difference between the two tested varieties. The composition of glyphosate-tolerant soybean MON 89788 was compared to that of the A3244 control, the parent soybean line used for the initial transformation. In addition, twelve different conventional soybean varieties were included as additional comparators to establish reference ranges for compositional constituents. Any statistically significant differences between glyphosate-tolerant soybean MON 89788 and the control A3244 can be compared to the reference range to assess whether the differences are likely to be biologically relevant.

5.1 Key components

When determining similarities and differences in composition between a GM plant and its conventional counterpart, the critical components measured are determined by identifying key nutrients, key toxicants and anti-nutrients for the food source in question (FAO, 1996). The key nutrients and anti-nutrients are those components in a particular food that have a substantial impact in the overall diet. These can be major constituents (e.g., fats, proteins, carbohydrates) or minor components (e.g., minerals, vitamins). Key toxicants are those toxicologically significant compounds known to be inherently present in the plant, such as those compounds whose potency and level may be significant to health (e.g., increased levels of solanine in potatoes).

As a minimum, the key nutrients of soybean seed appropriate for a comparative study include the proximates (crude protein, fat, ash, acid detergent fibre and neutral detergent fibre), amino acids and fatty acids. In addition, international guidance suggests levels of the key anti-nutrients phytic acid, trypsin inhibitors, lectins and isoflavones should be determined for new varieties of soybean (OECD, 2001).

Phytic acid chelates mineral nutrients (including calcium, magnesium, potassium, iron and zinc) making them unavailable to monogastric animals, including humans. Protease inhibitors interfere with digestion of protein. Lectins are proteins that bind to carbohydrate-containing molecules. Both protease inhibitors and lectins can inhibit growth. The activity of protease inhibitors and lectins is heat-labile and they are inactivated during processing of soybean protein products and soybean meal so that the final edible soybean product should contain minimal levels of these anti-nutrients. Soybean contains a number of isoflavones reported to possess biochemical activity including estrogenic, anti-estrogenic and hypercholesterolaemic effects that have been implicated in adversely affecting animal reproduction (OECD, 2001). The three basic types of isoflavones in soybeans are daidzein, genistein and glycitein. Soybean also contains two low molecular weight carbohydrates, stachyose and raffinose, that are considered to be anti-nutrients due to the gas production and resulting flatulence caused by their consumption (OECD, 2001).

5.2 Levels of Key components

Study submitted:

Lundry, D.R., S.G. Riordan, M.L. Breeze and R. Sorbet (2006) Amended report for MSL-20163: Composition Analyses of Soybean Forage and Seed Collected from MON 89788 Grown in the United States during the 2005 Field Season. Unpublished Monsanto study report MSL-20300.

Compositional analysis

Compositional analyses of the soybean seed included proximates (protein, fat, ash and moisture and carbohydrates by calculation), acid detergent fibre (ADF), neutral detergent fibre (NDF), amino acid composition, fatty acid composition (C8-C22), vitamin E, the anti-nutrients stachyose, raffinose, trypsin inhibitor, phytic acid, lectin and isoflavones (daidzein, genistein and glycitein). In all, 56 analytical components of soybean grain were measured according to established protocols. Of the 56 components analysed, 14 minor fatty acids were excluded from the summary and analysis as more than half the observed values were below the assay's limit of quantitation.

Compositional analyses were conducted on soybean grown at five field sites across the United States during the 2005 growing season. Sites were located in York County (Nebraska), Clinton County (Illinois), Warren County (Illinois), Jackson County (Arkansas), and Fayette County (Ohio). Seed was planted in a randomised complete block design with three replicates of each test, control and reference substance. Plots containing glyphosate-tolerant soybean MON 89788 were treated with a commercial rate of glyphosate herbicide. One control seed sample and seven reference samples contained trace amounts of MON 89788 or control 40-3-2 ($\leq 3.05\%$). These levels of contamination are considered too low to have significantly affected the results of the compositional analyses.

Statistical analyses of the compositional data were conducted using a mixed model analysis of variance method. The five sites were analysed both separately and combined, giving six sets of comparisons. Statistical evaluation of the composition data compared the seed from the soybean test population to the non-transgenic control population. Statistically significant differences were determined at the 5% level of significance ($p < 0.05$). SAS® software was used to generate all summary statistics and perform all analyses.

Data from commercial varieties were not included in the final statistical analysis. The reference population data were used to develop population tolerance intervals. For each compositional component, 99% tolerance intervals were calculated that are expected to contain, with 95% confidence, 99% of the quantities expressed in the population of commercial lines.

In a study of this magnitude, a small percentage (approximately 5%) of statistically significant differences is expected to occur due to chance alone. For those comparisons in which the glyphosate-tolerant soybean test result was statistically different from the control, the test range was compared to the 99% tolerance interval derived from the commercial varieties. This determines whether the range of values for each test population is within the variance of a population of the commercial soybean varieties. Statistically significantly different values were also compared to literature ranges and ranges reported in the International Life Science Institute Crop Composition Database (ILSI, 2004).

Results and Discussion

The results of the combined site comparisons for grain are presented in Table 4. A summary of the statistically significant differences between glyphosate-tolerant soybean MON 89788 and the control line is presented in Table 5.

Results from the combined site analyses conducted on seed samples derived from glyphosate-tolerant soybean MON 89788 indicated that there were no statistically significant differences for 39 of the 42 analytes measured. There were three statistically significant differences observed between the test grain and non transgenic control: levels of the anti-nutrients daidzein and glycitein were lower in MON 89788 than in the control, and levels of vitamin E were higher in MON 89788 than the control.

For the means of the analytes that were statistically significantly different ($p < 0.05$) from the control, the values for MON 89788 were within the 99% tolerance interval developed from the conventional soybean varieties grown at the same locations (Table 5). The mean levels are also within the ILSI and literature ranges (Table 6). Hence, these differences are unlikely to be biologically meaningful.

Analytes were also examined for reproducibility and trends across sites. Statistically significant differences were observed in as many as two sites for only one component, raffinose. The levels of raffinose in MON 89788 were lower than the control at one site (AR) and higher than the control at the other (IL-2). As there is no consistent trend and the values are within the 99% tolerance interval and literature and ILSI ranges, they are unlikely to be biologically relevant (Table 5). For 16 analytes, statistically significant differences were observed at only one site. As these differences were not reproducible across sites and are within the 99% tolerance interval for conventional soybeans grown across sites and the ILSI and literature ranges, the differences are not considered to be biologically relevant (Table 5). In a study of this magnitude, a small percentage (approximately 5%) of statistically significant differences is expected to occur due to chance alone. Differences occurring in one of the field sites only which are not repeated at other sites, are not indicative of a pattern of change that could be attributed to the genetic changes and are more likely to be random occurrences. In this comparative study, changes in the levels of some analytes are in this category. Consequently, these differences, although statistically significant for the individual site, are not considered to be biologically meaningful.

The compositional data are consistent with the conclusion that grain from soybean MON 89788 is compositionally equivalent to grain produced by the control soybean variety and to conventional soybean varieties currently on the market.

Table 4: Statistical Summary of Combined-Site Soybean Grain Key Components for test MON 89788 vs. A3244

Analytical Component (Units) ¹	MON 89788 Mean (S.E.) [Range]	A3244 Mean (S.E.) [Range]	Difference (MON 89788 minus A3244)			Conventional (Range) [99% Tol. Int. ²]
			Mean (S.E.) [Range]	95% CI (Lower, Upper)	p-Value	
Amino Acid (% DW)						
Alanine (% DW)	1.77 (0.017) [1.56 - 1.87]	1.77 (0.018) [1.71 - 1.83]	-0.0035 (0.018) [-0.19 - 0.069]	-0.042, 0.035	0.845	(1.62 - 1.89) [1.51, 2.00]
Arginine (% DW)	3.06 (0.082) [2.73 - 3.31]	3.07 (0.083) [2.76 - 3.34]	-0.0095 (0.037) [-0.26 - 0.33]	-0.090, 0.071	0.801	(2.61 - 3.27) [2.27, 3.60]
Aspartic Acid (% DW)	4.73 (0.068) [4.20 - 5.08]	4.72 (0.070) [4.42 - 4.98]	0.0072 (0.045) [-0.41 - 0.33]	-0.090, 0.10	0.875	(4.21 - 5.02) [3.85, 5.44]
Cystine (% DW)	0.62 (0.0084) [0.58 - 0.67]	0.62 (0.0085) [0.59 - 0.65]	-0.00028 (0.0050) [-0.044 - 0.026]	-0.011, 0.010	0.955	(0.57 - 0.65) [0.55, 0.67]
Glutamic Acid (% DW)	7.53 (0.12) [6.69 - 8.20]	7.49 (0.13) [6.97 - 7.90]	0.035 (0.075) [-0.63 - 0.53]	-0.13, 0.20	0.647	(6.62 - 8.19) [5.86, 8.96]
Glycine (% DW)	1.78 (0.020) [1.58 - 1.88]	1.78 (0.021) [1.71 - 1.86]	0.0012 (0.018) [-0.18 - 0.11]	-0.037, 0.040	0.949	(1.62 - 1.90) [1.46, 2.05]
Histidine (% DW)	1.07 (0.014) [0.95 - 1.13]	1.07 (0.015) [1.02 - 1.13]	-0.0035 (0.0099) [-0.10 - 0.057]	-0.025, 0.018	0.729	(0.96 - 1.13) [0.90, 1.21]
Isoleucine (% DW)	1.83 (0.029) [1.65 - 1.97]	1.83 (0.031) [1.70 - 1.99]	-0.0092 (0.030) [-0.22 - 0.26]	-0.071, 0.053	0.760	(1.64 - 2.00) [1.44, 2.16]

Table 4 (continued): Statistical Summary of Combined-Site Soybean Grain Key Components for test MON 89788 vs. A3244

Analytical Component (Units) ¹	MON 89788 Mean (S.E.) [Range]	A3244 Mean (S.E.) [Range]	Difference (MON 89788 minus A3244)			Conventional (Range) [99% Tol. Int. ²]
			Mean (S.E.) [Range]	95% CI (Lower, Upper)	p-Value	
Amino Acid (% DW)						
Leucine (% DW)	3.18 (0.040) [2.81 - 3.39]	3.18 (0.042) [3.04 - 3.33]	-0.0024 (0.031) [-0.32 - 0.20]	-0.070, 0.065	0.940	(2.89 - 3.42) [2.62, 3.66]
Lysine (% DW)	2.62 (0.025) [2.33 - 2.76]	2.62 (0.026) [2.51 - 2.73]	-0.00003 (0.023) [-0.25 - 0.13]	-0.051, 0.050	0.998	(2.40 - 2.77) [2.22, 2.95]
Methionine (% DW)	0.52 (0.0059) [0.47 - 0.56]	0.53 (0.0062) [0.50 - 0.55]	-0.0081 (0.0060) [-0.040 - 0.032]	-0.021, 0.0049	0.200	(0.45 - 0.56) [0.42, 0.60]
Phenylalanine (% DW)	2.10 (0.030) [1.84 - 2.24]	2.10 (0.031) [2.00 - 2.19]	-0.0011 (0.021) [-0.21 - 0.14]	-0.047, 0.045	0.959	(1.90 - 2.29) [1.70, 2.45]
Proline (% DW)	2.05 (0.029) [1.81 - 2.21]	2.05 (0.029) [1.95 - 2.16]	0.0047 (0.020) [-0.18 - 0.12]	-0.039, 0.048	0.819	(1.86 - 2.23) [1.66, 2.38]
Serine (% DW)	2.23 (0.029) [1.93 - 2.42]	2.21 (0.030) [2.08 - 2.28]	0.019 (0.023) [-0.16 - 0.17]	-0.031, 0.069	0.432	(1.99 - 2.42) [1.84, 2.54]
Threonine (% DW)	1.58 (0.014) [1.42 - 1.68]	1.59 (0.015) [1.51 - 1.66]	-0.0073 (0.013) [-0.13 - 0.062]	-0.035, 0.020	0.573	(1.44 - 1.67) [1.38, 1.76]
Tryptophan (% DW)	0.39 (0.015) [0.34 - 0.44]	0.39 (0.015) [0.33 - 0.46]	-0.0025 (0.015) [-0.10 - 0.064]	-0.044, 0.039	0.875	(0.30 - 0.47) [0.25, 0.54]

Table 4 (continued): Statistical Summary of Combined-Site Soybean Grain Key Components for test MON 89788 vs. A3244

Analytical Component (Units) ¹	MON 89788 Mean (S.E.) [Range]	A3244 Mean (S.E.) [Range]	Difference (MON 89788 minus A3244)			Conventional (Range) [99% Tol. Int. ²]
			Mean (S.E.) [Range]	95% CI (Lower, Upper)	p-Value	
Amino Acid (% DW)						
Tyrosine (% DW)	1.41 (0.019) [1.25 - 1.48]	1.42 (0.020) [1.33 - 1.47]	-0.0091 (0.015) [-0.12 - 0.070]	-0.051, 0.033	0.582	(1.28 - 1.51) [1.18, 1.64]
Valine (% DW)	1.91 (0.035) [1.73 - 2.05]	1.93 (0.036) [1.77 - 2.11]	-0.017 (0.032) [-0.24 - 0.28]	-0.084, 0.051	0.615	(1.71 - 2.09) [1.51, 2.27]
Fatty Acid (% DW)						
16:0 Palmitic (% DW)	2.07 (0.094) [1.84 - 2.40]	2.07 (0.094) [1.71 - 2.46]	-0.0027 (0.052) [-0.21 - 0.24]	-0.14, 0.14	0.961	(1.66 - 2.35) [1.32, 2.64]
18:0 Stearic (% DW)	0.78 (0.027) [0.65 - 0.89]	0.77 (0.027) [0.61 - 0.86]	0.012 (0.018) [-0.053 - 0.14]	-0.036, 0.060	0.531	(0.63 - 1.07) [0.37, 1.28]
18:1 Oleic (% DW)	3.53 (0.14) [3.05 - 4.24]	3.54 (0.14) [2.92 - 4.09]	-0.015 (0.10) [-0.40 - 0.51]	-0.29, 0.26	0.890	(2.99 - 5.29) [2.06, 6.43]
18:2 Linoleic (% DW)	9.17 (0.47) [8.00 - 10.42]	9.25 (0.47) [7.42 - 11.29]	-0.079 (0.21) [-0.86 - 0.99]	-0.64, 0.48	0.720	(8.41 - 10.69) [7.75, 11.22]
18:3 Linolenic (% DW)	1.29 (0.063) [1.09 - 1.48]	1.30 (0.063) [1.09 - 1.60]	-0.0059 (0.028) [-0.13 - 0.15]	-0.082, 0.070	0.843	(1.02 - 1.55) [0.84, 1.69]
20:0 Arachidic (% DW)	0.061 (0.0026) [0.049 - 0.071]	0.060 (0.0026) [0.046 - 0.068]	0.0012 (0.0016) [-0.0048 - 0.012]	-0.0031, 0.0055	0.482	(0.046 - 0.076) [0.031, 0.094]

Table 4 (continued): Statistical Summary of Combined-Site Soybean Grain Key Components for test MON 89788 vs. A3244

Analytical Component (Units) ¹	MON 89788 Mean (S.E.) [Range]	A3244 Mean (S.E.) [Range]	Difference (MON 89788 minus A3244)			Conventional (Range) [99% Tol. Int. ²]
			Mean (S.E.) [Range]	95% CI (Lower, Upper)	p-Value	
Fatty Acid (% DW)						
20:1 Eicosenoic (% DW)	0.042 (0.0031) [0.032 - 0.050]	0.042 (0.0031) [0.029 - 0.053]	0.00036 (0.0013) [-0.0062 - 0.0073]	-0.0032, 0.0039	0.796	(0.030 - 0.057) [0.021, 0.065]
22:0 Behenic (% DW)	0.063 (0.0030) [0.050 - 0.072]	0.062 (0.0031) [0.046 - 0.071]	0.00094 (0.0014) [-0.0056 - 0.0096]	-0.0029, 0.0048	0.539	(0.046 - 0.073) [0.034, 0.091]
Fiber						
Acid Detergent Fiber (% DW)	18.01 (0.94) [14.64 - 23.94]	17.46 (0.95) [14.39 - 22.44]	0.54 (1.21) [-3.22 - 5.67]	-2.79, 3.88	0.676	(13.30 - 26.26) [9.62, 28.57]
Neutral Detergent Fiber (% DW)	18.18 (0.46) [16.38 - 20.49]	19.11 (0.48) [15.60 - 20.73]	-0.93 (0.60) [-3.35 - 2.77]	-2.34, 0.49	0.165	(14.41 - 23.90) [13.26, 26.33]
Isoflavones						
Daidzein (ug/g DW)	993.67 (114.34) [631.32 - 1571.41]	1073.57 (114.79) [747.53 - 1526.23]	-79.90 (30.47) [-272.18 - 106.63]	-146.14, -13.66	0.021	(274.88 - 1485.52) [0, 1925.63]
Genistein (ug/g DW)	797.90 (49.93) [565.26 - 996.66]	824.83 (50.35) [651.01 - 1003.02]	-26.93 (19.52) [-151.16 - 74.36]	-69.66, 15.81	0.193	(354.09 - 984.29) [0, 1387.95]
Glycitein (ug/g DW)	91.77 (9.88) [53.78 - 162.52]	102.61 (10.01) [72.93 - 148.31]	-10.84 (4.69) [-32.97 - 30.19]	-20.98, -0.70	0.037	(52.72 - 298.57) [0, 287.45]

Table 4 (continued): Statistical Summary of Combined-Site Soybean Grain Key Components for test MON 89788 vs. A3244

Analytical Component (Units) ¹	MON 89788 Mean (S.E.) [Range]	A3244 Mean (S.E.) [Range]	Difference (MON 89788 minus A3244)			Conventional (Range) [99% Tol. Int. ²]
			Mean (S.E.) [Range]	95% CI (Lower, Upper)	p-Value	
Proximate						
Ash (% DW)	5.04 (0.12) [4.66 - 5.60]	5.03 (0.12) [4.75 - 5.46]	0.0099 (0.073) [-0.81 - 0.42]	-0.14, 0.16	0.892	(4.61 - 5.57) [4.00, 6.08]
Carbohydrates (% DW)	37.07 (0.54) [35.01 - 40.24]	36.88 (0.56) [35.17 - 40.74]	0.20 (0.55) [-2.38 - 2.95]	-1.30, 1.69	0.738	(32.75 - 40.98) [27.86, 45.79]
Fat (% DW)	17.57 (0.74) [15.35 - 19.98]	17.72 (0.74) [14.40 - 20.91]	-0.15 (0.42) [-1.74 - 1.73]	-1.28, 0.99	0.745	(15.97 - 20.68) [15.38, 21.95]
Moisture (% FW)	7.76 (0.47) [6.41 - 9.35]	7.51 (0.47) [6.51 - 9.63]	0.25 (0.27) [-0.44 - 1.31]	-0.51, 1.01	0.417	(6.24 - 9.11) [4.64, 9.94]
Protein (% DW)	40.32 (0.72) [37.31 - 42.54]	40.38 (0.73) [36.96 - 42.44]	-0.069 (0.31) [-1.72 - 2.44]	-0.74, 0.60	0.828	(36.48 - 43.35) [31.50, 47.45]
Vitamin						
Vitamin E (mg/100g DW)	2.71 (0.22) [1.88 - 3.72]	2.52 (0.22) [1.58 - 3.07]	0.19 (0.065) [-0.23 - 0.66]	0.043, 0.33	0.015	(1.29 - 4.80) [0, 7.00]
Antinutrient						
Lectin (H.U./mg FW)	4.29 (0.97) [0.70 - 9.77]	4.55 (1.01) [1.44 - 10.87]	-0.26 (1.02) [-8.11 - 5.75]	-2.38, 1.86	0.800	(0.45 - 9.95) [0, 9.72]
Phytic Acid (% DW)	0.76 (0.035) [0.58 - 0.93]	0.75 (0.037) [0.51 - 1.07]	0.011 (0.044) [-0.24 - 0.30]	-0.084, 0.11	0.811	(0.41 - 0.96) [0.39, 1.07]

Table 4 (continued): Statistical Summary of Combined-Site Soybean Grain Key Components for test MON 89788 vs. A3244

Analytical Component (Units) ¹	MON 89788 Mean (S.E.) [Range]	A3244 Mean (S.E.) [Range]	Difference (MON 89788 minus A3244)			Conventional (Range) [99% Tol. Int. ²]
			Mean (S.E.) [Range]	95% CI (Lower, Upper)	p-Value	
Raffinose (% DW)	0.52 (0.063) [0.40 - 0.71]	0.54 (0.063) [0.31 - 0.83]	-0.014 (0.041) [-0.20 - 0.11]	-0.13, 0.099	0.751	(0.26 - 0.84) [0, 1.01]
Antinutrient						
Stachyose (% DW)	2.36 (0.070) [2.02 - 2.85]	2.50 (0.073) [2.12 - 3.04]	-0.15 (0.10) [-0.59 - 0.53]	-0.38, 0.085	0.183	(1.53 - 2.98) [1.19, 3.31]
Trypsin Inhibitor (TIU/mg DW)	33.69 (2.84) [24.59 - 53.85]	31.44 (2.88) [23.43 - 41.91]	2.25 (1.56) [-4.81 - 13.99]	-2.32, 6.81	0.231	(20.79 - 55.51) [5.15, 59.34]

¹DW = dry weight; FW = fresh weight; FA = fatty acid; S.E. = standard error; CI = Confidence Interval.

²With 95% confidence, interval contains 99% of the values expressed in the population of commercial varieties. Negative limits were set to zero.

Table 5: Summary of statistically significant differences comparing soybean MON 89788 to the Control A3244

Analytical Component (Units) ^a	Mean MON 89788 Test Event	Mean A3244 Control	Mean Diff. (% of A3244 Control Value)	Significance (p-Value)	MON 89788 Test Event (Range)	99% Tolerance Interval ^c
Statistical Differences Observed in Combined-Site Analyses						
Seed Daidzein (µg/g DW)	993.67	1073.57	-7.44	0.021	631.32 - 1571.41	0, 1925.63
Seed Glycitein (µg/g DW)	91.77	102.61	-10.56	0.037	53.78 - 162.52	0, 287.45
Seed Vitamin E (mg/100g DW)	2.71	2.52	7.41	0.015	1.88 - 3.72	0, 7.00
Statistical Differences Observed in More than One Site and Not in the Combined-Site						
Site AR ^b Seed Raffinose (% DW)	0.65	0.81	-20.02	0.024	0.58 - 0.71	0, 1.01
Site IL-2 ^b Seed Raffinose (% DW)	0.42	0.33	25.45	.035	0.40 - 0.43	0, 1.01
Statistical Differences Observed in One Site and Not in the Combined-Site						
Site AR Seed Phenylalanine (% DW)	2.00	2.01	-0.41	0.014	2.00 - 2.01	1.70, 2.45
Site AR Seed 16:0 Palmitic (% DW)	2.21	2.40	-7.73	0.004	2.17 - 2.25	1.32, 2.64
Site AR Seed 18:0 Stearic (% DW)	0.76	0.81	-5.43	0.024	0.75 - 0.77	0.37, 1.28
Site AR Seed 18:1 Oleic (% DW)	3.30	3.68	-10.31	0.001	3.24 - 3.36	2.06, 6.43
Site AR Seed 18:2 Linoleic (% DW)	10.27	11.02	-6.86	0.005	10.06 - 10.42	7.75, 11.22
Site AR Seed 18:3 Linolenic (% DW)	1.45	1.55	-6.16	0.029	1.41 - 1.48	0.84, 1.69
Site AR Seed 20:0 Arachidic (% DW)	0.060	0.064	-6.35	0.021	0.058 - 0.060	0.031, 0.094
Site AR Seed 20:1 Eicosenoic (%)	0.048	0.053	-8.60	0.032	0.047 - 0.049	0.021, 0.065
Site AR Seed 22:0 Behenic (% DW)	0.066	0.070	-5385	0.034	0.064 - 0.068	0.034, 0.091
Site AR Seed ADF (% DW)	21.17	16.10	31.47	0.003	19.28 - 23.94	9.62, 28.57
Site AR Seed Carbohydrates (% DW)	38.13	36.02	5.88	0.048	37.77 - 38.42	27.86, 45.79
Site AR Seed Fat (% DW)	18.82	20.41	-7.79	0.002	18.42 - 19.17	15.38, 21.95
Site AR Seed Stachyose (% DW)	2.32	2.83	-18.13	0.010	2.10 - 2.50	1.19, 3.31
Site IL-2 Seed Genistein (µg/g DW)	762.46	849.88	-10.29	0.032	721.05 - 797.84	0, 1387.95
Site IL-2 Seed Moisture (% FW)	8.54	7.48	14.04	0.045	8.19 - 9.13	4.64, 9.94
Site NE ^b Seed NDF (% DW)	17.42	19.91	-12.51	0.023	16.79 - 18.39	13.26, 26.33

^aDW = dry weight; FW = fresh weight. ^b AR = Arkansas Site; IL-2 = Warren county, Illinois Site; NE = Nebraska Site.

^cWith 95% confidence, interval contains 99% of the values expressed in the population of commercial lines. Negative limits were set to zero.

Table 6: Literature and ILSI Ranges for Components in Soybean Grain

Tissue/Component¹	Literature Range²	ILSI Range³
Proximates (% DW)		
Ash	4.61-5.94 ^b ; 4.29-5.88 ^a	3.885-6.542
Carbohydrates	29.3-41.3 ^a	29.6-50.2
Fat, total	198-277 ^c g/kg DW; 160-231 ^d g/kg DW	8.104-23.562
Moisture (% FW)	5.3-8.73 ^a , 5.18-14.3 ^b	5.1-14.9
Protein	329-436 ^c g/kg DW; 360-484 ^d g/kg DW	33.19-45.48
Fiber (% DW)		
Acid detergent fiber (ADF)	not available	7.81-18.61
Neutral detergent fiber (NDF)	not available	8.53-21.25
Crude fiber	5.74-7.89 ^a	4.12-10.93
Amino Acids (%DW)		
	% Dw^a	% DW^h
Alanine	1.60— 1.86	1.513-1.851
Arginine	2.56—3.46	2.285-3.358
Aspartic acid	4.18 —4.99	3.808-5.122
Cystine/Cysteine	0.54 — 0.66	0.370-0.808
Glutamic acid	6.64—8.16	5.843-8.093
Glycine	1.60 - 1.87	1.458-1.865
Histidine	0.98— 1.16	0.878-1.175
Isoleucine	1.65 — 1.95	1.563-2.043
Leucine	2.81 — 3.37	2.590-3.387
Lysine	2.47 — 2.84	2.285-2.839
Methionine	0.51 — 0.59	0.443-0.668
Phenylalanine	1.78 — 2.19	1.632-2.236
Proline	1.86—2.23	1.687-2.284
Serine	1.96—2.28	1.632-2.484
Threonine	1.51—1.73	1.251-1.618
Tryptophan	0.56 — 0.63	0.356-0.501
Tyrosine	1.35—1.59	1.016-1.559
Valine	1.71 — 2.02	1.627-2.204

Table 6 (continued): Literature and ILSI Ranges for Components in Soybean Grain

Tissue/Component¹	Literature Range²	ILSI Range³
Fatty Acids (% DW)		
12:0 Lauric	not available	not available
14:0 Myristic	not available	not available
16:0 Palmitic	1.44-2.31 ^f	not available
16:1 Palmitoleic	not available	not available
17:0 Heptadecanoic	not available	not available
17:1 Heptadecenoic	not available	not available
18:0 Stearic	0.54-0.91 ^f	not available
18:1 Oleic	3.15-8.82 ^f	not available
18:2 Linoleic	6.48-11.6 ^f	not available
18:3 Linolenic	0.72-2.16 ^f	not available
20:0 Arachidic	0.04-0.7 ^f	not available
20:1 Eicosenoic	not available	not available
20:2 Eicosadienoic	not available	not available
22:0 Behenic	not available	not available
Vitamins (mg/100 g)		
Vitamin E	FWⁱ 0.85g	DW 0.47-6.17
Anti-Nutrients		
Lectin (H.U./mg FW)	0.8-2.4 ^a	0.105-9.038
Trypsin Inhibitor (TIU/mg DW)	33.2-54.5 ^a	19.59-118.68
Raffinose	not available	0.212-0.661
Stachyose	not available	1.21-3.50
Isoflavones		
	mg/100 g FW	(mg/kg DW)
Daidzein	9.88-124.2 ^e	60.0-2453.5
Genistein	13-150.1 ^e	144.3-2837.2
Glycitein	4.22-20.4 ^e	15.3-310.4

¹FW=fresh weight; DW=dry weight;

²Literature range references: ^a(Padgette *et al.*, 1996). ^b(Taylor *et al.*, 1999).

^c(Maestri *et al.*, 1998). ^d(Hartwig and Kilen, 1991). ^e(USDA-ISU, 2002). ^f(OECD, 2001).

^g(USDA, 2005). ^hData converted from mg/g DW to g/100 g DW (% DW).

ⁱMoisture value = 8.54 g/100 g.

³ILSI Soybean Database, 2004 (ILSI 2004).

Conversions: % DW x 10⁴ = µg/g DW; mg/g DW x 10³ = mg/kg DW;
mg/100g DW X 10 = mg/kg DW; g/100g DW x 10 = mg/g DW

5.3 Assessment of endogenous allergenic potential

Studies Submitted:

Rice, E.A. and G.A. Bannon (2006) Assessment of Human IgE Binding to Glyphosate-Tolerant Second Generation Soybean MON 89788, Control, and Reference Soy Extracts. Monsanto Company unpublished report. MSL-20552.

Soybean naturally contains allergenic proteins and is one of a group of known allergenic foods including milk, eggs, fish, shellfish, wheat, peanuts, tree nuts and sesame. This group of foods accounts for approximately 90% of all food allergies. The presence of allergenic proteins in the diet of hypersensitive individuals can cause severe adverse reactions. The allergenic effect of soybeans is attributed to the globulin fraction of soybean proteins that comprise about 85% of total protein (OECD, 2001). Soybean-allergic individuals will also be allergic to MON 89788 soy.

In order to assess whether MON 89788 has altered endogenous allergenic potential, a study was conducted to determine binding levels of IgE antibody to protein extracts prepared from MON 89788 and the parental soybean A3244. Extracts from 24 commercial varieties of soybean were also measured to provide a reference range.

Sera from 26 clinically documented, soybean-allergic individuals and six non-allergic individuals were used to assess the range of IgE binding to each soybean extract. The soybean allergic patients all had a documented history of anaphylactic reactions to soybean and a positive Double-Blind Placebo Controlled Food Challenge (DBPCFC). Aqueous extracts were prepared from the ground seeds of MON 89788, A3244 and the reference varieties, and analysed with a validated enzyme linked immuno-sorbent assay (ELISA) for IgE binding. The tolerance interval of each serum was established by the IgE binding values of the 24 commercial soybean extracts. The tolerance interval represents the range of IgE binding to the commercial soybean varieties such that 99% of the IgE binding values are expected to fall within this range with 95% confidence.

Of the 26 sera from soy-allergic patients tested, 16 yielded positive IgE antibody binding values by ELISA for the majority of soy extracts. The lack of soy-specific IgE response in clinically confirmed soy allergic patients has been observed previously. None of the soybean varieties showed binding with the sera from non-allergic individuals.

For the 16 sera that yielded positive IgE values, the IgE-binding values of MON89788 and A3244 were compared to the calculated tolerance intervals. The results indicate that all MON 89788 and A3244 IgE binding values are within the established tolerance intervals for each serum, with the exception of one sample, where the IgE binding with A3244 was below the assay's limit of detection.

These data indicate that MON 89788 has similar IgE binding values to A3244 that are within the range established by the commercial soybean varieties. Thus, the levels of endogenous soybean allergens in MON 89788 and the control A3244 are comparable to the levels of endogenous allergens in commercially available soybean varieties.

5.4 Conclusion

Levels of key nutrients and key anti-nutrients in glyphosate-tolerant soybean MON 89788 were compared to levels in the non-transgenic parental line A3244 and to a range of conventional soybean varieties. The comparative analyses do not indicate any compositional differences of biological significance in the grain derived from glyphosate-tolerant soybean MON 89788 compared to the non-genetically modified control when grown in a range of geographical regions. With respect to both key nutrients and key anti-nutrients, soybean MON 89788 is compositionally equivalent to conventional soybean varieties. In addition, MON 89788 IgE binding to sera from soybean-allergic patients was within the tolerance interval established from 24 commercial soybean varieties and soybean MON 89788 is unlikely to have any greater allergenic potential than conventional soybean varieties.

6. NUTRITIONAL IMPACT

Establishing that a GM food is safe for human consumption is generally achieved through an understanding of the genetic modification and its direct consequences in the plant, together with an extensive compositional analysis of the food components derived from the GM plant and the non-GM counterpart.

To date, all approved GM plants with modified agronomic production traits (e.g. herbicide tolerance) have been shown to be compositionally equivalent to their conventional counterparts. Feeding studies in animals using feeds derived from the approved GM plants have shown equivalent nutritional performance to that observed with the non-GM feed. Thus the evidence to date is that where GM varieties have been shown to be compositionally equivalent to conventional varieties, feeding studies using target livestock species contribute minimally to a safety assessment.

For plants engineered with the intention of significantly changing their composition or nutrient bioavailability and thus their nutritional characteristics, however, it is recognised that suitable comparators may not be available for a nutritional assessment based solely on compositional analysis. In such cases, feeding trials with one or more target species may be useful to demonstrate wholesomeness in the test animals.

In the case of glyphosate-tolerant soybean MON 89788, the extent of the compositional and other available data is considered sufficient to establish the nutritional adequacy of the food. However, a 42 day feeding study in broiler chickens was submitted by the Applicant and was therefore evaluated by FSANZ as additional supporting information.

6.1 Feeding study in chickens (42-days)

Study submitted:

Davis, S.W. (2006) Comparison of Broiler Performance and Carcass Parameters When Fed Diets Containing Soybean Meal Produced from MON 89788, Control or Reference Soybeans. Unpublished Monsanto Study No. 06-01-30-12.

Study aim

To assess the nutritional wholesomeness of diets containing soybean meal produced from MON 89788 in comparison to conventional soybean meal.

Study conduct

Ross x Ross 308 male and female broilers were used in a 42-day study to compare the feeding value of soybean MON 89788 to the parental soybean A3244, and reference soybean varieties (A2804, A3559, A4324, ST3870, A2824 and A3469). 800 birds were used; 100 (50 male, 50 female) birds for each of eight treatments.

Diets were formulated to be isocaloric and contain the maximum amount of soybean meal possible while remaining nutritionally adequate (approximately 33% for starter diets and 30% for grower/finisher diets). Feed and water were available *ad libitum* throughout the study.

Broilers were weighed by pen on days 0 and 42, and individually at study termination (day 43, 44 or 45). Feed intake per pen was determined for the 42 day period, allowing calculation of feed efficiency by pen, based on total weight of surviving broilers in the pen or adjusted to include weight gain of any broilers that died or were culled during the study. At study termination, all surviving birds were processed to determine carcass yield and meat composition. Fat pad measurements were taken for each bird. One broiler per pen was randomly selected for breast and thigh meat quality assays.

Results

Chick mortality was very low (1% of 960 chicks started on day 0). Mortality averaged across male and female birds from day 7 to 42 was also low and ranged between 1 -5%. MON 89788 treated birds had an average mortality rate of 4%. The mortality was random, without any relationship to treatment and was comparable to the rate commonly observed in chicks in commercial feeding trials.

Performance measures were not different ($P > 0.05$) between the broilers fed diets containing MON 89788 and those fed control soybean meal with similar genetic background. These measurements included day 42 live bird weight, total feed intake, and unadjusted and adjusted feed conversion.

Likewise, carcass measurements were not different ($P > 0.05$) between birds fed MON 89788 diets and those on diets containing conventional soybean meal. These measurements included pre-processing live weight, chill weight, and weights of fat pad, breast, wing, drum and thigh parts. Moisture, protein and fat in the thigh and breast meat samples were similar between treatments.

For certain parameters, a significant ($P > 0.15$) difference was observed between male and female birds. In these cases, males and females were analysed separately. In all cases, the diet containing MON 89788 produced results similar to the control or reference diets.

Conclusion

No unexpected effects on bird performance or health were observed in the birds fed MON 89788 soybean meal. The MON 89788 soybean diet was comparable to conventional soybean meal diets in terms of performance and carcass measurements.

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Summary of first round of public consultation

Submitter	Option	Comments
Australian Food and Grocery Council	-	<ul style="list-style-type: none"> • Supports the Application, contingent upon satisfactory safety assessment by FSANZ. • Notes that an earlier version of glyphosate-tolerant soybean is already approved for food use and do not anticipate that there would be any health or safety concerns with this application.
Department of Human Services Victoria	-	<ul style="list-style-type: none"> • No objection to the Application progressing to Draft Assessment
Food Technology Association of Victoria Inc.	2	<ul style="list-style-type: none"> • No comment
New Zealand Food Safety Authority	-	<ul style="list-style-type: none"> • No comment at this stage. Will review the Draft Assessment Report
NSW Food Authority	-	<ul style="list-style-type: none"> • Supports the Application proceeding to Draft Assessment. • Notes that there are costs incurred in monitoring for the presence of GM Food. • Notes that The Director-General of the NSW Food Authority wrote to FSANZ on the cost impact of GM applications in April 2005. • Considers a national enforcement strategy surrounding GM food approvals should be developed.
Queensland Health	-	<ul style="list-style-type: none"> • No comment at this stage, but will review Draft Assessment Report when available