ANNEX 5

LITERATURE REVIEW

A literature review was conducted in January 2013 based on searching relevant STN databases. Executing the search profile given below hits were found in the following traditional bibliographic databases:

- Chemical Abstracts

  The Chemical Abstracts database covers all areas of biochemistry, chemistry and chemical engineering, and related sciences. CA contains records for documents reported in printed Chemical Abstracts (CA) from 19th century to the present

- Biosis

  The largest and most comprehensive life science database in the world, BIOSIS Previews® covers original research reports, reviews, and selected U.S. patents in biological and biomedical areas, with subject coverage ranging from aerospace biology to zoology.

- Caba

  The CAB Abstracts database covers worldwide literature from all areas of agriculture and related sciences including biotechnology, forestry, and veterinary medicine.

- CBNB

  Chemical Business NewsBase contains information about chemical markets and products worldwide, with special emphasis on Europe. CBNB covers legislation, environmental aspects of chemical business, merger information, markets, sales, new products, production, trading, and company results.

- Compendex

  The Computerized Engineering Index and EI Engineering Meetings (Ei COMPENDEX) database contains citations from worldwide engineering and technology journals and conference proceedings.

- Embase

  The Excerpta Medica database, covers worldwide literature in the biomedical and pharmaceutical fields, including biological science, biochemistry, human medicine, forensic science, pediatrics, pharmacy, pharmacology and drug therapy, pharmacoeconomics, psychiatry, public health, biomedical engineering and instrumentation, and environmental science.

- Medline

  MEDLINE contains information on every area of medicine. The MEDLINE database corresponds to Index Medicus, Index to Dental Literature, and International Nursing Index; OLDMEDLINE, with data from NLM's from the Cumulated Index Medicus (1960-1965) and Current List of Medical Literature (1958-1959); and, since August 2001, IN-PROCESS records, the latest documents before they have been completely indexed for inclusion on MEDLINE. Sources

The search profile was set as follows:

- Amflora

  or

- EH92-527-1 or “EH92 527 1” or eh925271

  or

- gbss or gbssi or “granule bound starch synthase”

  or

- (nptII or kanamycin resistance or neomycin phosphotransferase) and (potato or solanum)

  or

- (potato or solanum) and (amylopectin* or “amylo pectin*” or waxy starch or basf) and (gmo or transgen* or “genet* engine*)

Search performance:

- The focus was on scientific literature or news, patents were not included.
- All searches were done for the publication year 2012.
- All results were intellectually checked for relevance.

In the following all results from this literature review are listed including the abstracts.

Paper 1

BASF to concentrate plant biotechnology activities on main markets in N and S America.

Corporate Source
BASF

Source
BASF SE, D-67056 Ludwigshafen, Germany, tel: +49 (0) 621 600, website: http://www.basf.com

Abstract
Ludwigshafen , Germany - January 16, 2012 - BASF announced today that it is concentrating its plant biotechnology activities on the main markets in N and S America. The company will adjust the portfolio and site footprint of its subsidiary BASF Plant Science to reflect this change. The headquarters of BASF Plant Science will be moved from Limburgerhof, Germany, to Raleigh, NC. Research and development activities will be concentrated mainly in Raleigh, Ghent (Belgium) and Berlin (Germany). Development and commercialization of all products targeted solely at cultivation in the European market will be halted. Regulatory approval processes which have already started will be continued. Dr Stefan Marcinowski (member of the Board of Executive Directors of BASF, responsible for plant biotechnology) said BASF is convinced that plant biotechnology is a key technology. However, there is still a lack of acceptance for this technology in many parts of Europe - from the majority of consumers, farmers and politicians. Therefore, it does not make business sense to continue investing in products exclusively for cultivation in this market. BASF will therefore concentrate on the attractive markets for plant biotechnology in N and S America and the growth markets in Asia. Research Triangle Park near Raleigh, NC will become the new headquarters for BASF's activities in the area of plant biotechnology. It is planned that the current headquarters site in Limburgerhof, Germany, will retain 11 positions in some functions such as regulatory for Europe. The activities of BASF's Crop Protection division in Limburgerhof are not affected. Currently 157 employees work for BASF Plant Science in Limburgerhof. The company plans to close its sites in Gatersleben (Germany) and in Svalov (Sweden). Currently 57 people work in Gatersleben and six in Sweden. In total, it is planned to transfer 123 positions from Limburgerhof and Gatersleben to other BASF Plant Science sites (mainly Raleigh) and to reduce 78 positions over the next two years. Overall, this means that BASF is reducing 140 positions in Europe. BASF aims to offer the affected employees other positions within the BASF Group wherever possible. Consultations with the responsible employee representatives will start immediately. The company's research facilities at metanomics in Berlin and CropDesign in Ghent will be strengthened. BASF Plant Science will halt the development and commercialization of all products that are targeted solely for cultivation in the European markets (such as the genetically modified starch potatoes Amflora, Amadea and Modena; a potato resistant to the disease late blight called Fortuna as well as a late blight resistant starch potato and a wheat variety resistant to fungal disease. To maintain all options for the potato products, BASF Plant Science will continue the regulatory approval processes for the products already started. BASF Plant Science's product pipeline will continue its strong focus on the yield and stress projects in which crops are developed with higher yields and improved resistance to stress conditions like drought. This includes the collaboration with Monsanto for corn, soy, cotton, canola and wheat. At end 2011, the first product from this partnership, drought-tolerant corn, was approved for cultivation in the US. Cultivance soy beans, developed together with Embrapa, were approved for cultivation in Brazil at end 2009, and the approval process for key export markets is ongoing.

Paper 2

Scientific Opinion on the annual Post-Market Environmental Monitoring (PMEM) report from BASF Plant Science Company GmbH on the cultivation of genetically modified potato EH92-527-1 in 2010.

Corporate Source
European Food Safety Authority (EFSA), Parma, Italy.; EFSA Panel on Genetically Modified Organisms
EMAIL: gmo@efsa.europa.eu

Source
EFSA Journal (2012) Volume 10, Number 2, 2558 p., 24 refs. ISSN: 1831-4732 Published by: European Food Safety Authority, Parma

Abstract
Following a request from the European Commission, the Panel on Genetically Modified Organisms of the European Food Safety Authority (EFSA GMO Panel) assessed the monitoring report for the 2010 cultivation

season of GM potato EH92-527-1 (variety Amflora) provided by BASF. The EFSA GMO Panel assessed, in close collaboration with the EFSA Unit for Scientific Assessment Support, the methodology applied by the applicant for the four case-specific studies, the General Surveillance (GS) of potato EH92-527-1 and the field study to monitor potential adverse effects on potato-feeding organisms. From the overall dataset submitted by the applicant in its 2010 Amflora monitoring report, the EFSA GMO Panel does not identify adverse effects on the environment, human and animal health due to potato EH92-527-1 cultivation during the 2010 growing season. The outcomes of the 2010 Amflora monitoring report do not invalidate the previous EFSA GMO Panel's risk assessment conclusions on potato EH92-527-1. Nevertheless, the EFSA GMO Panel notes a number of weaknesses in the methodology for GS and therefore gives specific recommendations for improvement of the strategy, methodology and reporting for GS of potato EH92-527-1. Concerning the field study on potato-feeding organisms as required in the related Commission Decision, the EFSA GMO Panel makes recommendations in order to improve the study. However, the EFSA GMO Panel considers the GS framework as a more proportionate alternative for collecting relevant information on potato-feeding organisms.

Paper 3

13C pulse-labeling assessment of the community structure of active fungi in the rhizosphere of a genetically starch-modified potato (Solanum tuberosum) cultivar and its parental isoline.

Author(s)
Hannula, S. E.; Boschker, H. T. S.; Boer, W. de; Veen, J. A. van; de Boer, W.; van Veen, J. A.

Source
New Phytologist (2012) Volume 194, Number 3, pp. 784-799 ISSN: 0028-646X DOI: 10.1111/j.1469-8137.2012.04089.x Published by: Wiley-Blackwell, Oxford

Abstract
The aim of this study was to gain understanding of the carbon flow from the roots of a genetically modified (GM) amylopectin-accumulating potato (Solanum tuberosum) cultivar and its parental isoline to the soil fungal community using stable isotope probing (SIP). The microbes receiving 13C from the plant were assessed through RNA/phospholipid fatty acid analysis with stable isotope probing (PLFA-SIP) at three time-points (1, 5 and 12 d after the start of labeling). The communities of Ascomycota, Basidiomycota and Glomeromycota were analysed separately with RT-qPCR and terminal restriction fragment length polymorphism (T-RFLP). Ascomycetes and glomeromycetes received carbon from the plant as early as 1 and 5 d after labeling, while basidiomycetes were slower in accumulating the labeled carbon. The rate of carbon allocation in the GM variety differed from that in its parental variety, thereby affecting soil fungal communities. We conclude that both saprotrophic and mycorrhizal fungi rapidly metabolize organic substrates flowing from the root into the rhizosphere, that there are large differences in utilization of root-derived compounds at a lower phylogenetic level within investigated fungal phyla, and that active communities in the rhizosphere differ between the GM plant and its parental cultivar through effects of differential carbon flow from the plant.

Paper 4

A 3-year study reveals that plant growth stage, season and field site affect soil fungal communities while cultivar and GM-trait have minor effects.

Author(s)
Hannula, S. E.; Boer, W. de; Veen, J. van; de Boer, W.; van Veen, J.

Source
PLoS ONE (2012) Volume 7, Number 4, e33819 p., 53 refs. ISSN: 1932-6203 DOI: 10.1371/journal.pone.0033819 Published by: Public Library of Sciences (PLoS), San Francisco

Abstract
In this three year field study the impact of different potato (Solanum tuberosum L.) cultivars including a genetically modified (GM) amylopectin-accumulating potato line on rhizosphere fungal communities are investigated using molecular microbiological methods. The effects of growth stage of a plant, soil type and year on the rhizosphere fungi were included in this study. To compare the effects, one GM cultivar, the parental isoline, and four non-related cultivars were planted in the fields and analysed using T-RFLP on the

basis of fungal phylum specific primers combined with multivariate statistical methods. Additionally, fungal biomass and some extracellular fungal enzymes (laccases, Mn-peroxidases and cellulases) were quantified in order to gain insight into the function of the fungal communities. Plant growth stage and year (and agricultural management) had the strongest effect on both diversity and function of the fungal communities while the GM-trait studied was the least explanatory factor. The impact of cultivar and soil type was intermediate. Occasional differences between cultivars, the amylopectin-accumulating potato line, and its parental variety were detected, but these differences were mostly transient in nature and detected either only in one soil, one growth stage or one year.

Paper 5

Agrobacterium-mediated genetic transformation of potato (Solanum tuberosum L.) var. Cardinal and Heera.

Author(s)
Khatun, A.; Hasan, M. M.; Bachchu, M. A. A.; Moniruzzaman, M.; Nasiruddin, K. M.

Source
The Agriculturists (2012) Volume 10, Number 1, pp. 81-86, 10 refs. ISSN: 1729-5211 DOI: 10.3329/agric.v10i1.11068 Published by: Krishi Foundation, Mirpur

Abstract
Two potato varieties namely Cardinal and Heera were used in the Agrobacterium-mediated genetic transformation experiment to investigate the genetic transformation ability in the Biotechnology laboratory of the Department of Biotechnology, Bangladesh Agricultural University, Mymensingh, Bangladesh during 2006 to 2007. Agrobacterium tumefaciens strain LBA 4404 having a binary vector pB1121 of 14 KDa containing selectable marker gene npt II (neomycine phosphotransferase II) conferring kanamycin resistance, and the CIPK antisense gene encoding calcineurin B-like protein were used. Leaf and internodes were used as explants. Expression of the transgene (GUS) was confirmed by histochemical analysis. The variety Cardinal was found more suitable for expressing best GUS response (80% GUS positive) over Heera.

Paper 6

Standardization of protocol for Agrobacterium-mediated transformation in potato (Solanum tuberosum L.).

Author(s)
Molla, M. M. H.; Nasiruddin, K. M.; Al-Amin, M.; Haque, M. S.; Manir-uz-Zaman

Source
Bangladesh Journal of Agricultural Research (2012) Volume 37, Number 2, pp. 185-194, 14 refs. ISSN: 0258-7122 Published by: Bangladesh Agricultural Research Institute (BARI), Ghazipur

Abstract
The experiment was conducted at the Laboratory of Biotechnology, Biotechnology Division, Bangladesh Agricultural Research Institute, Gazipur-1701 during July 2007 to June 2008. An efficient and reproducible protocol for the production of transgenic potato plants was developed by inoculating internode explants of potato with Agrobacterium tumefaciens strain LBA4404 carrying a binary vector pBI121 having one reporter gene (gus) and selectable marker gene (nptII) resistant to Kanamycin. The transformation experiment was done by optimizing two important parameters names infection time and co-cultivation period. Most of the explants produced shoots within 21 days on 5 mg/l Zeatin riboside (ZR) and 50 mg/l Kanamycin supplemented MS medium without introducing callus. The infected explants produced 8.27 and 6.42 shoots in Asterix and Diamant varieties, respectively within 21 days. Transgenes were confirmed by molecular analysis. DNA from well established rooted plants confirmed nptII positive through PCR analysis. The transformation rates were 28.97 and 24.37% in Asterix and Diamant, respectively. Putative transformed plants of Diamant and Asterix varieties produced roots in 1/2MS medium supplemented with 50/mg Cefotaxim, 50 mg/l Kanamycin and 0.5 mg/l IBA.

Paper 7

An explosive innovation: Phylogenetic relationships of Solanum section Gonatotrichum (Solanaceae).

Author(s)
Stern, Stephen; Bohs, Lynn

Source
PhytoKeys, (2012) Vol. 8, pp. 83-98. http://www.pensoft.net/journals/phytokeys/. ISSN: 1314-2011. E-ISSN: 1314-2003.

Abstract
Solanum is one of the largest plant genera and exhibits a wide range of morphological diversity. Solanum section Gonatotrichum, the focus of this study, is unique within the genus because of its fruits that swell with turgor pressure and explosively dehisce to disperse the seeds. We infer phylogenetic relationships within section Gonatotrichum using DNA sequence data from two nuclear regions (ITS and the granule-bound starch synthase gene [GBSSI or waxy]) and the chloroplast region trnT-F. The resulting phylogenetic trees support the monophyly of the section with the inclusion of S. lignescens, a species not previously thought to belong to the group due to the presence of stellate hairs. This inclusion of this species in section Gonatotrichum suggests that the simple, often geniculate hairs of species in the group may represent reduced stellate hairs. The presence of heterantherous flowers appears to be derived in the section, but this character is largely lost in S. parcistrigosum.

Paper 8

Increased accumulation of anthocyanins in transgenic potato tubers by overexpressing the 3GT gene.

Author(s)
Wei, Qing; Wang, Quan-Yi; Feng, Zhi-Hang; Wang, Bing; Zhang, Yun-Feng; Yang, Qing

Source
Plant Biotechnology Reports, (JAN 2012) Vol. 6, No. 1, pp. 69-75. http://www.springerlink.com/content/120483/. ISSN: 1863-5466. E-ISSN: 1863-5474.

Abstract
In order to explore a biotechnological method for improving potato tuber color and creating plants with increased anthocyanin contents, a potato UDP-glucose: flavonoid-3-O-glucosyltransferase (3GT) gene was inserted behind the GBSSI promoter of pBin19, and this construct was introduced into Solanum tuberosum L. cultivar D,sir,e plants by Agrobacterium-mediated transformation. Six independent transgenic lines overexpressing the 3GT gene were identified by PCR and Southern blot analysis from 18 kanamycin-resistant plants. Due to the expression of 3GT gene, the tuber color and the anthocyanin content were enhanced noticeably in the transgenic plants compared to the wild-type control plants. This result suggests that the 3GT gene can potentially be used to improve potato color and enhance levels of antioxidants in the diet.

Paper 9

Statement on a request from the European Commission for the assessment of the scientific elements supporting the prohibition for the placing on the market of GM potato EH92-527-1 for cultivation purposes in Austria

Author(s)

Andersson, Hans Christer; Arpaia, Salvatore; Bartsch, Detlef; Casacuberta, Josep; Davies, Howard; du Jardin, Patrick; Flachowsky, Gerhard; Herman, Lieve; Jones, Huw; Karenlampi, Sirpa; Kiss, Jozsef; Kleter, Gijs; Kuiper, Harry; Messean, Antoine; Nielsen, Kaare Magne; Perry, Joe; Poting, Annette; Sweet, Jeremy; Tebbe, Christoph; von Wright, Atte Johannes; Wal, Jean-Michel; Andreoletti, Olivier; Budka, Herbert; Buncic, Sava; Collins, John D.; Griffin, John; Hald, Tine; Havelaar, Arie Hendric; Hope, James; Klein, Gunter; Koutsoumanis, Kostas; McLauchlin, James; Muller-Graf, Christine; Nguyen-The, Christophe; Noerrung, Birgit; Peixe, Luisa; Maradona, Miguel Prieto; Ricci, Antonia; Sofos, John; Threlfall, John; Vagsholm, Ivar; Vanopdenbosch, Emmanuel; Aguilera, Jaime; Gomes, Ana; Liebana, Ernesto; Mestdagh, Sylvie

Source

EFSA Journal (2012), 10(3), 2627, 13 pp. CODEN: EJFOA6

Abstract

A review. Austria notified to the European Commission its ordinance implementing a national safeguard measure prohibiting the placing on the market of GM potato EH92-527-1 for cultivation purposes in Austria, after which the European Commission asked the European Food Safety authority to assess the scientific elements supporting the prohibition. Having considered the information package provided by Austria and all relevant scientific publications, the GMO and BIOHAZ Panels concluded that: (i) no new data specific to the safety of the nptII gene have been provided; (ii) the risk posed by the formation of mosaic structures of aminoglycoside phosphotransferase genes could not be assessed without data documenting the existence of such structures among the existing gene variants and such data were not provided; (iii) the therapeutic relevance of kanamycin and neomycin was already addressed in the EFSA's opinion on ARM genes and as of yet there is no evidence to indicate that resistance to these antibiotics in clin.-relevant bacteria has developed as a result of acquisition of the nptII gene; (iv) the knowledge gaps and uncertainties highlighted in the Austrian document have already been considered in the EFSA's opinion on ARM genes. Austria did not provide any new or addnl. information on the mol. characterization or PMEM of potato EH92-527-1 after the date of consent for this GM event that would require the reassessment of existing information. The EFSA GMO Panel reiterates its scientific opinion on the 2010 monitoring report of GM potato EH92-527-1 in which it provides specific recommendations to improve the methodol. of the PMEM of the GM potato. Further, the EFSA GMO Panel concludes that no grounds exist to date that would lead to reconsideration of its opinion on GM potato EH92-527-1.

Paper 10

Transformation of PSAG12-ipt gomphosis gene into potato

Author(s)

Wu, Wangze; Peng, Xiaoli; Liu, Xiaoping

Source

Xibei Zhiwu Xuebao (2012), 32(5), 895-901 CODEN: XZXUEV; ISSN: 1000-4025

Abstract

A population of transgenic plants was produced by the transformation of internodal explants of potato using an Agrobacterium tumefaciens LBA4404-based vector contg. a gomphosis gene (PSAG12-ipt). The intermodal explants were more effective for transformation than leaf explants. The regeneration strategy utilized a three-step protocol, a 2 days pre-culture on the MS medium contg. 6-benzylaminopurine (6-BA) 0.25 mg/L, .alpha.-naphthaleneacetic acid (NAA) 0.25 mg/L, 2,4-dichlorophenoxyacetic acid (2,4-D) 0.25 mg/L, and supplemented 1% Na2SO3, followed the explants of pre-culture were incubated 8 min in Agrobacterium tumefaciens LBA4404 suspension (OD600 0.2-0.5), last, the explants were co-cultured 3 days on basal medium without supplemented any phytohormones. After 3 days co-cultivation, the explants of internode and leaf were transferred to basal medium supplemented phytohormones, 1% Na2SO3, 200 mg/L cefotaxime and 75 mg/L kanamycin until to regenerated plants. Transgenic plants were identified utilizing PSAG12 and ipt gene dual primer by PCR. The pos. transformation rate was 65.8%. Southern blotting anal. identification showed that most ipt gene were induced into potato genome only one copy.

Paper 11

Cloning of granule-bound starch synthase gene and construction of its RNAi vector in potato tuber

Author(s)
Liu, Yu-hui; Wang, Li; Yang, Hong-yu; Yu, Bin; Li, Yuan-ming; Zhang, Jun-lian; Wang, Di

Source
Zuowu Xuebao (2012), 38(7), 1187-1195 CODEN: TSHPA9; ISSN: 0496-3490

Abstract
There is about 17% starch in potato (Solarium tuberosum L.) tubers. Potato starch granules are composed of two polysaccharides, unbranched amylose (approx. 20% to 25%) and branched amylopectin (approx. 75% to 80%). To develop transgenic potato with high-amylopectin in tubers, a cDNA sequence of the potato GBSSI was got from the total RNA of potato tubers by RT-PCR using specific primers of conserved domain of GenBank Accession No. X58453 sequence. The GBSSI cDNA sequence shared 99.78% similarity with the GBSSI gene in GenBank (accession No. X58453). The full-length of cDNA was 1 824 bp, which contained 607 amino acids, three conserved domains and many important functional sites. The 3D structure of GBSSI was highly similar to that of the glycogen synthase, indicating that GBSSI has a function of starch synthesis. GBSSI similar gene obtained here was granule-bound starch synthase, and its sequence was submitted to GenBank, with the accession no. of EU403426. On the basis of a 542 bp RNAi target region from the CDS of GBSSI, the sense and antisense fragments were amplified and sepd. by a 237 bp intron to construct the RNA interference expression vector pBI121g-PgABI contg. 'sense gbssA-VP1-ABI3-like protein intron-antisense gbss B' regulated by Patatin promoter, which would lay a solid foundation for the study on synthesis of starch and breeding of transgenic potato with high amylopectin content or pure amylopectin.

Paper 12

Scientific opinion on a request from the European Commission for the assessment of the scientific elements put forward by Luxembourg to support the prohibition for the placing on the market of GM potato EH92-527-1 for cultivation purposes in Luxembourg

Author(s)
Arpaia, Salvatore; Birch, Andrew Nicholas Edmund; Chesson, Andrew; du Jardin, Patrick; Gathmann, Achim; Gropp, Jurgen; Herman, Lieve; Hoen-Sorteberg, Hilde-Gunn; Jones, Huw; Kiss, Jozsef; Kleter, Gijs; Lagiou, Pagona; Lovik, Martinus; Messean, Antoine; Naegeli, Hanspeter; Nielsen, Kaare Magne; Ovesna, Jaroslava; Perry, Joe; Rostoks, Nils; Tebbe, Christoph; Karenlampi, Sirpa; Gomes, Ana

Source
EFSA Journal (2012), 10(9), 2874, 8 pp. CODEN: EJFOA6

Abstract
Luxembourg notified to the European Commission its scientific arguments justifying the implementation of a national safeguard measure prohibiting the placing on the market of GM potato EH92-527-1 for cultivation purposes in Luxembourg, after which the European Commission asked the European Food Safety Authority (EFSA) to assess the scientific information supporting the prohibition. Having considered the information package provided by Luxembourg and all relevant scientific publications, the EFSA Panel on Genetically Modified Organisms (GMO Panel) concluded that: (i) no new data specific to the safety of the nptII gene have been provided; (ii) although bacterial DNA release and development of competence are expected to occur more efficiently in biofilms, the link between resistance in biofilms and cultivation/processing of GM potato EH92-527-1 was not established by Luxembourg and the main barriers, limiting the transformation frequency of bacterial cells with transgenic plant DNA, remain; (iii) the risk posed by the formation of mosaic structures of aminoglycoside phosphotransferase genes could not be assessed without data documenting the existence of such structures among the existing gene variants and such data were not provided; (iv) the knowledge gaps and uncertainties highlighted in the Luxembourgeois document and the therapeutic relevance of kanamycin and neomycin have already been considered in the previous EFSA opinion on antibiotic resistance marker genes and no new information on the safety of nptII gene as present in the GM potato EH92-527-1 has been identified in the scientific literature that would cause the GMO Panel to change its previous conclusions. Therefore, the EFSA GMO Panel concludes that no grounds exist to date that would lead to reconsideration of its opinion on GM potato EH92-527-1.

Paper 13

Identification of differentially expressed genes in potato associated with tuber dormancy release.

Author(s)
Liu, Bailin; Zhang, Ning; Wen, Yikai; Si, Huaijun; Wang, Di

Source
Molecular Biology Reports, (DEC 2012) Vol. 39, No. 12, pp. 11277-11287.
http://www.springerlink.com/content/100316/. CODEN: MLBRBU. ISSN: 0301-4851. E-ISSN: 1573-4978.

Abstract
Potato (Solanum tuberosum L.) tuber dormancy and sprouting is very important to potato cultivation and processing. In the present experiment, suppression subtractive hybridization was employed to identify differentially expressed genes in potato associated with tuber dormancy release. 576 random clones were selected from subtractive library and successfully sequenced. A total of 304 effective expressed sequence tags (ESTs) were obtained ultimately. The ESTs have been deposited in the EMBLnucleotide sequence data libraries under accession numbers from JK483901 to JK484204. GO annotation showed that 45, 34 and 3 % ESTs were associated with binding, catalytic activity and signaling respectively, some of which were confirmed to be involved in plant dormancy breaking, however, 14 % of the ESTs did not show significant homology to any database proteins. A real-time quantitative PCR (RT-qPCR) analysis of the expression patterns of 14 selectable transcripts showed that 13 selected candidate genes were significantly up-regulated in the development process of tuber from dormancy to sprouting. A full length cDNA of ADP-ribosylation factor (ARF) gene was cloned and found it belonged to potato ARF1 gene. Tissue specific expression analysis showed ARF1 expression level was the highest in tuber. RT-qPCR analysis of the expression profile of ARF1 gene from potato tuber dormancy to sprouting revealed that the ARF1 gene expression was significantly increased after tuber dormancy breaking, which suggested that it probably associated with tuber dormancy and sprouting.

Paper 14

Scientific Opinion on the annual Post-Market Environmental Monitoring (PMEM) report from BASF Plant Science Company GmbH on the cultivation of genetically modified potato EH92-527-1 in 2011.

Corporate Source
European Food Safety Authority (EFSA), Parma, Italy.; EFSA Panel on Genetically Modified Organisms
EMAIL: gmo@efsa.europa.eu

Source
EFSA Journal (2012) Volume 10, Number 12, 3015 p., 22 refs. ISSN: 1831-4732 Published by: European Food Safety Authority, Parma

Abstract
Following a request from the European Commission, the Panel on Genetically Modified Organisms of the European Food Safety Authority(EFSA GMO Panel) assessed the monitoring report for the 2011 growing season, provided by BASF, on the genetically modified (GM) potato EH92-527-1 (variety Amflora). On 26 January 2012, the EFSA GMO Panel had adopted a scientific opinion on the 2010 monitoring report on potato EH92-527-1. The EFSA GMO Panel followed the same approach as for the assessment of the 2010 monitoring report and assessed, in close collaboration with the EFSA Unit for Scientific Assessment Support, the methodology used by the applicant in 2011 for the case-specific studies, the general surveillance of potato EH92-527-1 and the field study to monitor potential adverse effects on potato-feeding organisms as required in the related Commission Decision. The EFSA GMO Panel notes similar shortcomings in the methodology for general surveillance and for the specific field study on potato-feeding organisms as were found in the 2010 monitoring report. Hence, the EFSA GMO Panel reiterates the same recommendations for improvement of the methodology for the post-market environmental monitoring of potato EH92-527-1 as it did in its scientific opinion on the 2010 monitoring report. The EFSA GMO Panel also assessed the methodology of a new study monitoring GM volunteers within and around fields cropped with potato EH92-527-1 in 2010. The EFSA GMO Panel identified flaws in that study and therefore makes recommendations to the applicant to improve the study design. However, from the overall dataset submitted by the applicant, the EFSA GMO Panel did not identify adverse effects on the environment or human and animal health due to potato EH92-527-1 cultivation. The outcomes of the 2011 monitoring report do not invalidate the conclusions of the EFSA GMO Panel's previous opinions on potato EH92-527-1.

Paper 15

Scientific Opinion on a request from the European Commission for the assessment of the scientific elements put forward by Hungary to support the prohibition for the placing on the market of GM potato EH92-527-1 for cultivation purposes in Hungary.

Corporate Source
European Food Safety Authority (EFSA), Parma, Italy.; EFSA Panel on Genetically Modified Organisms
EMAIL: gmo@efsa.europa.eu

Source
EFSA Journal (2012) Volume 10, Number 12, 3021 p., 24 refs. ISSN: 1831-4732 Published by: European Food Safety Authority, Parma

Abstract
Hungary notified to the European Commission its scientific arguments justifying the implementation of a national safeguard measure prohibiting the placing on the market of GM potato EH92-527-1 for cultivation purposes in Hungary, after which the European Commission asked the European Food Safety Authority (EFSA) to assess the scientific information supporting the prohibition. Having considered the information package provided by Hungary and all relevant scientific publications, the EFSA Panel on Genetically Modified Organisms (GMO Panel) concluded that (i) no new data specific to the safety of the nptII gene have been provided; (ii) the therapeutic relevance of kanamycin and neomycin was already addressed in the previous EFSA opinion on antibiotic resistance marker genes and kanamycin resistance in Mycobacterium tuberculosis results largely from chromosomal mutations and not from the transfer of aminoglycoside resistance genes such as nptII; (iii) the knowledge gaps and uncertainties highlighted in the Hungarian document have already been considered in the previous EFSA opinion on antibiotic resistance marker genes, and no new information on the safety of nptII gene as present in the GM potato EH92-527-1 has been identified in the scientific literature that would cause the GMO Panel to change its previous conclusions. Therefore, the EFSA GMO Panel concludes that no grounds exist to date that would lead to reconsideration of its opinion on GM potato EH92-527-1.

Paper 16

Various techniques for the modification of starch and the applications of its derivatives.

Author(s)
Kavlani, Neelam; Sharma, Vijay; Singh, Lalit

Source
International Research Journal of Pharmacy, (May 2012) Vol. 3, No. 5, pp. 25-31. Refs: 92 E-ISSN: 2230-8407

Abstract
Starch is a major carbohydrate easily extractable from various native sources, like potato, maize, corn, wheat, etc, which finds wide application in various food and non food industries. Since time immemorable various attempts are being made in order to modify this highly flexible polymer with an aim to enhance the positive attributes and eliminate the short comings of the native starches. Modifications are generally made by physical methods like osmotic-pressure treatment, deep-freezing and thrashing; chemical methods that primarily include derivatizations such as etherification, esterification and crosslinking, oxidation, cationization and grafting of starch; enzymatic degradation techniques and genetical modifications which involves the transgenic techniques targeting the various enzymes involved in starch biogenesis. All these techniques tends to produce a variety of derivatives with altered physicochemical properties and modified structural attributes of high technological value for instance carboxymethylated starch used as a binding and disintegrating agent. This review summarizes the various methods of starch modification that can be employed to produce a novel molecule with substantial applications in various industries including a large number of advances in pharmaceutical industry along with the future prospectives.