

Appendix 5.4 MON 810 literature review – List of all hits (June 2016-May 2017) -CABI CAB Abstracts® and Global Health® database

Record 1 of 50

Title: Phage-mediated immuno-PCR for ultrasensitive detection of Cry1Ac protein based on nanobody.

Author(s): (Liu YuanYuan); (Jiang DongJian); (Lu Xin); (Wang Wei); (Xu Yang); (He QingHua)

Source: Journal of Agricultural and Food Chemistry

Volume: 64

Issue: 41

Pages: 7882-7889

Published: 2016

Abstract: The widespread use of Cry proteins in transgenic plants for insect control has raised concerns about the environment and food safety in the public. An effective detection method for introduced Cry proteins is of significance for environmental risk assessment and product quality control. This paper describes a novel phage mediated immuno-PCR (iPCR) for the ultrasensitive determination of Cry proteins based on nanobodies. Three nanobodies against Cry1Ac protein were obtained from a naive phage displayed nanobody library without animal immunization process and were applied to the iPCR assay for Cry1Ac. The phage-mediated iPCR for Cry1Ac based on nanobodies showed a dynamic range of 0.001-100 ng/mL and a limit detection of 0.1 pg/mL. Specific measurement of this established method was performed by testing cross-reactivity of other Cry1Ac analogues, and the result showed negligible cross-reactivity with other test Cry proteins (Cry1Ab, Cry1F, Cry3B). Furthermore, the phage-mediated iPCR based on nanobody should be easily applicable to the detection of many other Cry proteins.

Accession Number: CABI:20163378578

ISSN: 0021-8561

Record 2 of 50

Title: Influences of genetically modified Bt maize on the serum biochemical parameters and enzyme activities in fattening Wuzhishan pigs.

Author(s): (Liu QuanWei); (Wei LiMin); (Wang Feng); (Zheng XinLi); (Huang LiLi); (Liu HaiLong); (Sun RuiPing); (Tan ShuYi)

Source: Swine Production

Issue: 1

Pages: 6-8

Published: 2016

Abstract: 32 6-month-old healthy fattening pigs with similar genetic backgrounds and an average initial weight of 29.831.67 kg were randomly divided into 2 treatments, 4 replicates of 4 pigs and the pigs were fed with diets containing genetically modified Bt maize (experimental group) or non-genetically modified maize (control) during the period of 60d, respectively, in order to study the effects of genetically modified Bt maize on biochemical parameters and enzyme activities of fattening Wuzhishan pigs. Blood was collected at 60d for sampling. Serum total protein, albumin, globin, glucose, urea nitrogen, glycerin trimyristate and total cholesterol concentrations in the experimental group were not significantly different from those of controls ($P>0.05$). There were no significant differences in serum alkaline phosphatase, aspartate aminotransferase, and alanine aminotransferase activities between the 2 groups ($P>0.05$). In conclusion, there were no adverse effects of genetically modified Bt maize on biochemical parameters and enzyme activities of fattening Wuzhishan pigs.

Accession Number: CABI:20163376422

ISSN: 1002-1957

Record 3 of 50

Title: Development of monoclonal antibody-based sensitive ELISA for the determination of Cry1Ie protein in transgenic plant.

Author(s): (Zhang YuWen); (Zhang Wei); (Liu Yan); (Wang JianHua); (Wang GuoYing); (Liu YunJun)

Source: Analytical and Bioanalytical Chemistry

Volume: 408

Issue: 28

Pages: 8231-8239

DOI: 10.1007/s00216-016-9938-5

Published: 2016

Abstract: Cry1Ie is a kind of *Bacillus thuringiensis* (Bt) toxin protein which has a different action model than the Cry1Ab and Cry1Ac protein. The transgenic maize expressing *Cry1Ie* might be commercially used in the near future and it is urgent to develop a method to detect Cry1Ie protein in transgenic plants and their products. To develop an ELISA method, Cry1Ie protein was expressed in *Escherichia coli* strain Transetta DE3, purified with the Ni-NTA spin columns, and then validated by sequencing. Bioassay results showed that the purified Cry1Ie protein was highly toxic to the Asian corn borer. The polyclonal antibody (pAb) and the specific monoclonal antibody (mAb) 1 G₄2D₆ were generated from rabbit and mice which were immunized with Cry1Ie protein, respectively. Western blotting of crude Cry1Ie protein extracts was established by employing mAb 1 G₄2D₆, whereas the mAb 1 G₄2D₆ negligibly recognized other Bt proteins. Sandwich ELISA against Cry1Ie protein was established by coating with pAb and detecting with mAb 1 G₄2D₆. The limit of detection (LOD), the limit of quantification (LOQ), and the quantification range of the assay in different matrices of maize plant were determined as 0.27-0.51, 0.29-0.78, and 0.45-15.71 ng/mL, respectively. Recoveries of Cry1Ie protein spiked in different maize tissues ranged from 75.1 to 99.5%. The established sandwich ELISA was verified using transgenic maize overexpressing *Cry1Ie*. The results in this study suggested that the established ELISA method is effective for detecting Cry1Ie protein in transgenic plants.

Accession Number: CABI:20163374808

ISSN: 1618-2642

Record 4 of 50

Title: Development of Bt rice and Bt maize in China and their efficacy in target pest control.

Author(s): (Liu QingSong); (Hallerman, E.); (Peng YuFa); (Li YunHe)

Source: International Journal of Molecular Sciences

Volume: 17

Issue: 10

Pages: 1561

Published: 2016

Abstract: Rice and maize are important cereal crops that serve as staple foods, feed, and industrial material in China. Multiple factors constrain the production of both crops, among which insect pests are an important one. Lepidopteran pests cause enormous yield losses for the crops annually. In order to control these pests, China plays an active role in development and application of genetic engineering (GE) to crops, and dozens of GE rice and GE maize lines expressing insecticidal proteins from the soil bacterium *Bacillus thuringiensis* (Bt) have been developed. Many lines have entered environmental release, field testing, and preproduction testing, and laboratory and field experiments have shown that most of the Bt rice and Bt maize lines developed in China exhibited effective control of major target lepidopteran pests on rice (*Chilo suppressalis*, *Scirpophaga incertulas*, and *Cnaphalocrocis medinalis*) and maize (*Ostrinia furnacalis*), demonstrating bright prospects for application. However, none of these Bt lines has yet been commercially planted through this writing in 2016. Challenges and perspectives for development and application of Bt rice and maize in China are discussed. This article provides a general context for colleagues to learn about research and development of Bt crops in China, and may shed light on future work in this field.

Accession Number: CABI:20163374903

ISSN: 1661-6596

Record 5 of 50

Title: Communities of endophytic microorganisms in different developmental stages from a local variety as well as transgenic and conventional isogenic hybrids of maize.

Author(s): (Silva, K. J. da); (Armas, R. D. de); (Soares, C. R. F. S.); (Ogliari, J. B.)

Source: World Journal of Microbiology & Biotechnology

Volume: 32

Issue: 11

Pages: 189

DOI: 10.1007/s11274-016-2149-6

Published: 2016

Abstract: The diversity of endophytic microorganisms may change due to the genotype of the host plant and its phenological stage. In this study we evaluated the effect of phenological stage, transgenes and genetic composition of maize on endophytic bacterial and fungal communities. The maize populations were composed of a local variety named Rosado (*RS*) and three isogenic hybrids. One isogenic hybrid was not genetically modified (*NGM*). Another hybrid (*Hx*) contained the transgenes *cry1F* and *pat* (T1507 event), which provide resistance to insects of the order *Lepidoptera* and tolerance to the glufosinate-ammonium herbicide, respectively. The third hybrid (*Hxrr*) contained the transgene *cp4 epsps* (NK603 event) combined with the transgenes *cry1F* and *pat* (T1507 event), which allow tolerance to the Roundup Ready herbicide, besides the characteristics of *Hx*. Evaluation of the foliar tissue was done through PCR-DGGE analysis, with specific primers for bacteria and fungi within four phenological stages of maize. The endophytic bacteria were only clustered by phenological stages; the structure of the fungal community was clustered by maize genotypes in each phenological stage. The fungal community from the local variety *RS* was different from the three hybrids (*NGM*, *Hx* and *Hxrr*) within the four evaluated stages. In the reproductive stage, the fungal community from the two transgenic hybrids (*Hx* and *Hxrr*) were separated, and the *Hxrr* was different from *NGM*, in the two field experiments. This research study showed that the genetic composition of the maize populations, especially the presence of transgenes, is the determining factor for the changes detected in the endophytic fungal community of maize leaves.

Accession Number: CABI:20163370419

ISSN: 0959-3993

Record 6 of 50

Title: Special Section: Pests and resistance.

Author(s): (Siegfried, B.); (Jurat-Fuentes, J. L.)

Edited by: Siegfried, B.; Jurat-Fuentes, J. L.

Source: Current Opinion in Insect Science

Volume: 15

Pages: iv-vi + 70-124, 131-143

DOI: 10.1016/j.cois.2016.05.001

Published: 2016

Abstract: This section contains 10 papers focusing on the progress on genomic approaches to uncover causal mutations in the European corn borer, *Ostrinia nubilalis* based on studies on the *Bacillus thuringiensis* toxin resistance mechanisms among Lepidoptera, *B. thuringiensis* resistance in Australian insect pest species, *B. thuringiensis* resistance in *Plutella* sp., susceptibility, mechanisms of response and resistance to *B. thuringiensis* toxins in *Spodoptera* spp., nutrition as a neglected factor in insect herbivore susceptibility to *Bt* toxins and intestinal regeneration as an insect resistance mechanism to entomopathogenic bacteria. Papers on the resistance to *Bt* maize by western corn rootworm, a model for the improved management of *Cry1F* resistance among lepidopteran pests, current situation of pests targeted by *Bt* crops in Latin America and the potential resistance management for the sustainable use of insect-resistant genetically modified maize and rice in China are also presented.

Accession Number: CABI:20163364194

ISSN: 2214-5745

Record 7 of 50

Title: *Bacillus thuringiensis* toxin resistance mechanisms among Lepidoptera: progress on genomic approaches to uncover causal mutations in the European corn borer, *Ostrinia nubilalis*.

Author(s): (Coates, B. S.)

Edited by: Siegfried, B.; Jurat-Fuentes, J. L.

Source: Current Opinion in Insect Science

Volume: 15

Pages: 70-77

DOI: 10.1016/j.cois.2016.04.003

Published: 2016

Abstract: Transgenic plants that express *Bacillus thuringiensis* (*Bt*) crystal (*Cry*) protein toxins (*Bt* crops) effectively control feeding by the European corn borer, *Ostrinia nubilalis*, although documented resistance evolution among a number of species in both the laboratory and field has heightened concerns about the durability of this technology. Research has provided major insights into the mutations that alter *Bt* toxin binding receptor structure and function within the midgut of Lepidoptera that directly impacts the efficacy of *Bt* toxins, and potentially leads to the evolution of resistance to *Bt* crops in the field. In this manuscript we provide an overview of available data on the identification of genes involved in high levels of resistance to *Cry* toxins, with emphasis on resistance described for *O. nubilalis* as the main target of *Bt* corn.

Accession Number: CABI:20163364195

ISSN: 2214-5745

Record 8 of 50

Title: Resistance to *Bt* maize by western corn rootworm: insights from the laboratory and the field.

Author(s): (Gassmann, A. J.)

Edited by: Siegfried, B.; Jurat-Fuentes, J. L.

Source: Current Opinion in Insect Science

Volume: 15

Pages: 111-115

DOI: 10.1016/j.cois.2016.04.001

Published: 2016

Abstract: Western corn rootworm is a serious pest of maize. Beginning in 2003, management of western corn rootworm included transgenic maize that produces insecticidal toxins derived from the bacterium *Bacillus thuringiensis* (*Bt*). The first *Bt* maize hybrids produced *Cry3Bb1*, but additional *Bt* toxins have since been introduced, including *eCry3.1Ab*, *mCry3A* and *Cry34/35Ab1*. Laboratory selection experiments found that western corn rootworm could develop resistance to all types of *Bt* maize following three to seven generations of selection. By 2009 cases of field-evolved resistance to *Cry3Bb1* maize had been identified, with populations also showing cross-resistance to *mCry3A* maize. Factors likely contributing to resistance were the lack of a high dose of *Bt* toxin for maize targeting rootworm and minimal fitness costs of resistance.

Accession Number: CABI:20163364201

ISSN: 2214-5745

Record 9 of 50

Title: *Cry1F* resistance among lepidopteran pests: a model for improved resistance management?

Author(s): (Velez, A. M.); (Vellichirammal, N. N.); (Jurat-Fuentes, J. L.); (Siegfried, B. D.)

Edited by: Siegfried, B.; Jurat-Fuentes, J. L.

Source: Current Opinion in Insect Science

Volume: 15

Pages: 116-124

DOI: 10.1016/j.cois.2016.04.010

Published: 2016

Abstract: The *Cry1Fa* protein from the bacterium *Bacillus thuringiensis* (*Bt*) is known for its potential to control lepidopteran pests, especially through transgenic expression in maize and cotton. The maize event TC1507 expressing the *cry1Fa* toxin gene became commercially available in the United States in 2003 for the management of key lepidopteran pests including the European corn borer, *Ostrinia nubilalis*, and the fall armyworm, *Spodoptera frugiperda*. A high-dose/refuge strategy has been widely adopted to delay evolution of resistance to event TC1507 and other transgenic *Bt* crops. Efficacy of this strategy depends on the crops expressing a high dose of the *Bt* toxin to targeted pests and adjacent refuges of non-*Bt* host plants serving as a source of abundant susceptible insects. While this strategy has proved effective in delaying

O. nubilalis resistance, field-evolved resistance to event TC1507 has been reported in *S. frugiperda* populations in Puerto Rico, Brazil, and the southeastern United States. This paper examines available information on resistance to Cry1Fa in *O. nubilalis* and *S. frugiperda* and discusses how this information identifies opportunities to refine resistance management recommendations for Bt maize.

Accession Number: CABI:20163364202

ISSN: 2214-5745

Record 10 of 50

Title: Current situation of pests targeted by Bt crops in Latin America.

Author(s): (Blanco, C. A.); (Chiaravalle, W.); (Dalla-Rizza, M.); (Farias, J. R.); (Garcia-Degano, M. F.); (Gastaminza, G.); (Mota-Sanchez, D.); (Murua, M. G.); (Omoto, C.); (Pieralisi, B. K.); (Rodriguez, J.); (Rodriguez-Maciel, J. C.); (Teran-Santofimio, H.); (Teran-Vargas, A. P.); (Valencia, S. J.); (Willink, E.)

Edited by: Siegfried, B.; Jurat-Fuentes, J. L.

Source: Current Opinion in Insect Science

Volume: 15

Pages: 131-138

DOI: 10.1016/j.cois.2016.04.012

Published: 2016

Abstract: Transgenic crops producing *Bacillus thuringiensis*- (*Bt*) insecticidal proteins (*Bt* crops) have provided useful pest management tools to growers for the past 20 years. Planting *Bt* crops has reduced the use of synthetic insecticides on cotton, maize and soybean fields in 11 countries throughout Latin America. One of the threats that could jeopardize the sustainability of *Bt* crops is the development of resistance by targeted pests. Governments of many countries require vigilance in measuring changes in *Bt*-susceptibility in order to proactively implement corrective measures before *Bt*-resistance is widespread, thus prolonging the usefulness of *Bt* crops. A pragmatic approach to obtain information on the effectiveness of *Bt*-crops is directly asking growers, crop consultants and academics about *Bt*-resistance problems in agricultural fields, first-hand information that not necessarily relies on susceptibility screens performed in laboratories. This type of information is presented in this report. Problematic pests of cotton and soybeans in five Latin American countries currently are effectively controlled by *Bt* crops. Growers that plant conventional (non-*Bt*) cotton or soybeans have to spray synthetic insecticides against multiple pests that otherwise are controlled by these *Bt* crops. A similar situation has been observed in six Latin American countries where *Bt* maize is planted. No synthetic insecticide applications are used to control corn pests because they are controlled by *Bt* maize, with the exception of *Spodoptera frugiperda*. While this insect in some countries is still effectively controlled by *Bt* maize, in others resistance has evolved and necessitates supplemental insecticide applications and/or the use of *Bt* maize cultivars that express multiple *Bt* proteins. Partial control of *S. frugiperda* in certain countries is due to its natural tolerance to the *Bt* bacterium. Of the 31 pests targeted and controlled by *Bt* crops in Latin America, only *S. frugiperda* has shown tolerance to certain *Bt* proteins in growers' fields, the most reliable indication of the status of *Bt*-susceptibility in most of the American continent.

Accession Number: CABI:20163364203

Author Identifiers:

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Omoto, Celso	D-9794-2012	0000-0002-6432-830X

ISSN: 2214-5745

Record 11 of 50

Title: Integrating insect, resistance, and floral resource management in weed control decision-making.

Author(s): (DiTommaso, A.); (Averill, K. M.); (Hoffmann, M. P.); (Fuchsberg, J. R.); (Losey, J. E.)

Source: Weed Science

Volume: 64

Issue: 4

Pages: 743-756

DOI: 10.1614/WS-D-16-00052.1

Published: 2016

Abstract: Managing agricultural pests with an incomplete understanding of the impacts that tactics have on crops, pests, and other organisms poses risks for loss of short-term profits and longer-term negative impacts, such as evolved resistance and nontarget effects. This is especially relevant for the management of weeds that are viewed almost exclusively as major impediments to crop production. Seldom considered in weed management are the benefits weeds provide in agroecosystems, which should be considered for optimal decision-making. Integration of weed costs and benefits will become increasingly important as management for pests transitions away from nearly complete reliance on herbicides and transgenic crop traits as the predominant approach for control. Here, we introduce a weed-management decision framework that accounts for weed benefits and exemplify how in-crop weed occurrence can increase crop yields in which a highly damaging insect also occurs. We highlight a case study showing how management decision-making for common milkweed, which is currently controlled primarily with glyphosate in herbicide-tolerant corn, can be improved by integrating management of the European corn borer (ECB), which is currently controlled primarily by the transgenic toxin Cry1 in *Bacillus thuringiensis* corn. Our data reveal that milkweed plants harboring aphids provide a food source (honeydew) for parasitoid wasps, which attack ECB eggs. Especially at high ECB population densities (>1 egg mass leaf⁻¹), maintaining low milkweed densities (<1 stem m⁻²), effectively helps to minimize yield losses from ECB and to increase the economic injury level of this aggressive perennial weed. In addition, milkweed is the host for the monarch butterfly, so breeding-ground occurrences of the plant, including crop fields, may help sustain populations of this iconic insect. Using a more-holistic approach to integrate the management of multiple crop pests has the capacity to improve decision-making at the field scale, which can improve outcomes at the landscape scale.

Accession Number: CABI:20163361016

ISSN: 0043-1745

Record 12 of 50

Title: One-year oral toxicity study on a genetically modified maize MON810 variety in Wistar Han RCC rats (EU 7th Framework Programme project GRACE).

Author(s): (Zeljnkova, D.); (Alacova, R.); (Ondrejko, J.); (Ambrusova, K.); (Bartusova, M.); (Kebis, A.); (Kovriznych, J.); (Rollerova, E.); (Szabova, E.); (Wimmerova, S.); (Cernak, M.); (Krivosikova, Z.); (Kuricova, M.); (Liskova, A.); (Spustova, V.); (Tulinska, J.); (Levkut, M.); (Revajova, V.); (Sevcikova, Z.); (Schmidt, K.); (Schmidtko, J.); (Schmidt, P.); (Paz, J. L. la); (Corujo, M.); (Pla, M.); (Kleter, G. A. (et al))

Source: Archives of Toxicology

Volume: 90

Issue: 10

Pages: 2531-2562

DOI: 10.1007/s00204-016-1798-4

Published: 2016

Abstract: The GRACE (GMO Risk Assessment and Communication of Evidence; www.grace-fp7.eu) project was funded by the European Commission within the 7th Framework Programme. A key objective of GRACE was to conduct 90-day animal feeding trials, animal studies with an extended time frame as well as analytical, in vitro and in silico studies on genetically modified (GM) maize in order to comparatively evaluate their use in GM plant risk assessment. In the present study, the results of a 1-year feeding trial with a GM maize MON810 variety, its near-isogenic non-GM comparator and an additional conventional maize variety are presented. The feeding trials were performed by taking into account the guidance for such studies published by the EFSA Scientific Committee in 2011 and the OECD Test Guideline 452. The results obtained show that the MON810 maize at a level of up to 33% in the diet did not induce adverse effects in male and female Wistar Han RCC rats after a chronic exposure.

Accession Number: CABI:20163354623

ISSN: 0340-5761

Record 13 of 50

Title: Three toxins, two receptors, one mechanism: mode of action of Cry1A toxins from *Bacillus thuringiensis* in *Heliothis virescens*.

Author(s): (Bretschneider, A.); (Heckel, D. G.); (Pauchet, Y.)

Source: Insect Biochemistry and Molecular Biology

Volume: 76

Pages: 109-117**DOI:** 10.1016/j.ibmb.2016.07.008**Published:** 2016

Abstract: Insecticidal crystal (Cry) proteins from *Bacillus thuringiensis* (Bt) are highly active against Lepidoptera. However, field-evolved resistance to Bt toxins is on the rise. The 12-cadherin domain protein HevCaLP and the ABC transporter HevABCC2 are both genetically linked to Cry toxin resistance in *Heliothis virescens*. We investigated their interaction using stably expressing non-lytic clonal *Sf9* cell lines expressing either protein or both together. Untransfected *Sf9* cells are innately sensitive to Cry1Ca toxin, but not to Cry1A toxins; and quantitative PCR revealed negligible expression of genes involved in Cry1A toxicity such as cadherin, ABCC2, alkaline phosphatase (ALP) and aminopeptidase N (APN). Cry1Aa, Cry1Ab or Cry1Ac caused swelling of *Sf9* cells expressing HevABCC2, and caused faster swelling, lysis and up to 86% mortality in cells expressing both proteins. No such effect was observed in control *Sf9* cells or in cells expressing only HevCaLP. The results of a mixing experiment demonstrated that both proteins need to be expressed within the same cell for high cytotoxicity, and suggest a novel role for HevCaLP. Binding assays showed that the toxin-receptor interaction is specific. Our findings confirm that HevABCC2 is the central target in Cry1A toxin mode of action, and that HevCaLP plays a supporting role in increasing Cry1A toxicity.

Accession Number: CABI:20163357648**ISSN:** 0965-1748**Record 14 of 50****Title:** Genetic basis of Cry1F-resistance in a laboratory selected Asian corn borer strain and its cross-resistance to other *Bacillus thuringiensis* toxins.**Author(s):** (Wang YueQin); (Wang YiDong); (Wang ZhenYing); (Bravo, A.); (Soberon, M.); (He KangLai)**Source:** PLoS ONE**Volume:** 11**Issue:** 8**Pages:** e0161189**Published:** 2016

Abstract: The Asian corn borer (ACB), *Ostrinia furnacalis* (Guenee) (Lepidoptera: Crambidae), is the most destructive insect pest of corn in China. Susceptibility to the Cry1F toxin derived from *Bacillus thuringiensis* has been demonstrated for ACB, suggesting the potential for Cry1F inclusion as part of an insect pest management program. Insects can develop resistance to Cry toxins, which threatens the development and use of Bt formulations and Bt crops in the field. To determine possible resistance mechanisms to Cry1F, a Cry1F-resistant colony of ACB (ACB-FR) that exhibited more than 1700-fold resistance was established through selection experiments after 49 generations of selection under laboratory conditions. The ACB-FR strain showed moderate cross-resistance to Cry1Ab and Cry1Ac of 22.8- and 26.9-fold, respectively, marginally cross-resistance to Cry1Ah (3.7-fold), and no cross-resistance to Cry1Ie (0.6-fold). The bioassay responses of progeny from reciprocal F₁ crosses to different Cry1 toxin concentrations indicated that the resistance trait to Cry1Ab, Cry1Ac and Cry1F has autosomal inheritance with no maternal effect or sex linked. The effective dominance (*h*) of F₁ offspring was calculated at different concentrations of Cry1F, showing that *h* decreased as concentration of Cry1F increased. Finally, the analysis of actual and expected mortality of the progeny from a backcross (F₁ * resistant strain) indicated that the inheritance of the resistance to Cry1F in ACB-FR was due to more than one locus. The present study provides an understanding of the genetic basis of Cry1F resistance in ACB-FR and also shows that pyramiding Cry1F with Cry1Ah or Cry1Ie could be used as a strategy to delay the development of ACB resistance to Bt proteins.

Accession Number: CABI:20163358395**ISSN:** 1932-6203**Record 15 of 50****Title:** Larval development of *Spodoptera eridania* and *Spodoptera frugiperda* fed on fresh ear of field corn expressing the Bt proteins (Cry1F and Cry1F+Cry1A.105+Cry2Ab2).**Author(s):** (Bortolotto, O. C.); (Bueno, A. de F.); (Queiroz, A. P. de); (Silva, G. V.)**Source:** Ciencia Rural**Volume:** 46**Issue:** 11**Pages:** 1898-1901**Published:** 2016

Abstract: The objective of this study was to evaluate extent of larval period, larval survival (%), food consumption, and pupal biomass of *Spodoptera eridania* and *Spodoptera frugiperda* (Lepidoptera: Noctuidae) fed on fresh ears of field corn expressing Bt proteins (Cry1F and Cry1F+Cry1A.105+Cry2Ab2). Larvae of *Spodoptera* spp. survived less than two days when they consumed Bt corn cobs and showed 100% mortality. *Spodoptera eridania* reared on non-Bt corn cobs showed higher larval development (21.6 days) than *S. frugiperda* (18.4 days) and lower viability (56.4% and 80.2% for *S. eridania* and *S. frugiperda*, respectively). A higher amount of corn grains was consumed by *S. eridania* (5.4 g) than by *S. frugiperda* (3.9 g). In summary, this study demonstrated that the toxins Cry1F and Cry1F+Cry1A.105+Cry2Ab2 expressed in fresh corn cobs contributed to protect ears of corn against *S. frugiperda* and the non-target pest *S. eridania*. However, it is important to monitor non-Bt cornfields because of the potential of both species to cause damage to ear of corn.

Accession Number: CABI:20163346428**ISSN:** 0103-8478**Record 16 of 50****Title:** Detection of transgenic maize Bt11 with insect resistance and herbicide tolerance based on MPCR.**Author(s):** (Li Yi); (Yin Quan)**Source:** Guizhou Agricultural Sciences**Volume:** 44**Issue:** 6**Pages:** 48-52**Published:** 2016

Abstract: The MPCR detection system was established by optimization of reaction conditions and test of specificity and sensitivity according to the molecular characteristics of transgenic maize Bt11 with insect resistance and herbicide tolerance, referring to the specificity primer sequence in national relevant standards and selecting an endogenous reference gene (*zSSIb*) and four exogenous genes (Cry1Ab, P-CaMV 35S, T-NOS and PAT) as MPCR detection genes to establish the multiplex PCR detection method of transgenic maize Bt11 with insect resistance and herbicide tolerance. Results: The system including 56°C annealing temperature, template concentration ≥200 bp and primer ratio of 0.1 zSSIb: 0.2 Cry1 Ab: 0.2 P-CaMV 35S: 0.2 T-NOS: 0.2 PAT is verified by using the known samples. 5 genes of zSSIb, Cry1Ab, P-CaMV 35S, T-NOS and PAT are simultaneously detected from transgenic maize Bt11 with insect resistance and herbicide tolerance but 5 genes of zSSIb, Cry1Ab, P-CaMV 35S, T-NOS and PAT are not detected from other samples simultaneously. In conclusion, the established MPCR detection system can be used in detection of transgenic maize Bt11 with insect resistance and herbicide tolerance.

Accession Number: CABI:20163346745**ISSN:** 1001-3601**Record 17 of 50****Title:** Resistance of Bt-maize (MON810) against the stem borers *Busseola fusca* (Fuller) and *Chilo partellus* (Swinhoe) and its yield performance in Kenya.**Author(s):** (Tefera, T.); (Mugo, S.); (Mwimali, M.); (Anani, B.); (Tende, R.); (Beyene, Y.); (Gichuki, S.); (Oikeh, S. O.); (Nang'ayo, F.); (Okeno, J.); (Njeru, E.); (Pillay, K.); (Meisel, B.); (Prasanna, B. M.)**Source:** Crop Protection**Volume:** 89**Pages:** 202-208**DOI:** 10.1016/j.cropro.2016.07.023**Published:** 2016

Abstract: A study was conducted to assess the performance of maize hybrids with Bt event MON810 (Bt-hybrids) against the maize stem borer *Busseola fusca* (Fuller) in a biosafety greenhouse (BGH) and against the spotted stem borer *Chilo partellus* (Swinhoe) under confined field trials (CFT) in Kenya for three seasons during 2013-2014. The study comprised 14 non-commercialized hybrids (seven pairs of near-isogenic Bt and non-Bt hybrids) and four non-Bt commercial hybrids. Each plant was artificially

infested twice with 10 first instar larvae. In CFT, plants were infested with *C. partellus* 14 and 24 days after planting; in BGH, plants were infested with *B. fusca* 21 and 31 days after planting. In CFT, the seven *Bt* hybrids significantly differed from their non-*Bt* counterparts for leaf damage, number of exit holes, percent tunnel length, and grain yield. When averaged over three seasons, *Bt*-hybrids gave the highest grain yield (9.7 t ha⁻¹), followed by non-*Bt* hybrids (6.9 t ha⁻¹) and commercial checks (6 t ha⁻¹). *Bt*-hybrids had the least number of exit holes and percent tunnel length in all the seasons as compared to the non-*Bt* hybrids and commercial checks. In BGH trials, *Bt*-hybrids consistently suffered less leaf damage than their non-*Bt* near isolines. The study demonstrated that MON810 was effective in controlling *B. fusca* and *C. partellus*. *Bt*-maize, therefore, has great potential to reduce the risk of maize grain losses in Africa due to stem borers, and will enable the smallholder farmers to produce high-quality grain with increased yield, reduced insecticide inputs, and improved food security.

Accession Number: CABI:20163341489

ISSN: 0261-2194

Record 18 of 50

Title: Reproductive isolation between two populations of *Diatraea saccharalis* (F.) (Lepidoptera: Crambidae) from different host plant species and regions in Argentina.

Author(s): (Fogliata, S. V.); (Vera, A.); (Gastaminza, G.); (Cuenya, M. I.); (Zucchi, M. I.); (Willink, E.); (Castagnaro, A. P.); (Murua, M. G.)

Source: Bulletin of Entomological Research

Volume: 106

Issue: 5

Pages: 591-597

DOI: 10.1017/S0007485316000249

Published: 2016

Abstract: The sugarcane borer, *Diatraea saccharalis* (F.), has a widespread distribution throughout the Western Hemisphere and is a pest of many crop plants including sugarcane, corn, sorghum and rice. The use of *Bacillus thuringiensis* (*Bt*) corn has been the primary tool for managing this species in corn fields. Sugarcane borer control has been recently threatened by observations of susceptibility and/or resistance to certain varieties of *Bt* corn and the protein used in many newer varieties. This has led to increased interest in understanding sugarcane borer genetic diversity and gene flow within and among its populations and the consequent exchange of alleles between geographically distant populations. The objective of this study was to examine reproductive compatibility between host-associated geographic populations of *D. saccharalis* in Argentina and to determine whether this pest represents a complex of host-associated cryptic species rather than a wide ranging generalist species. Intra and inter-population crosses revealed that *D. saccharalis* populations from the northwestern and Pampas regions presented evidence of prezygotic and postzygotic incompatibility. Such a result is likely to be the product of an interruption of gene flow produced by either geographic or host plant associated isolation, suggesting that Tucuman (northwestern) and Buenos Aires (Pampas) populations of *D. saccharalis* are a distinct genotype and possibly an incipient species.

Accession Number: CABI:20163329357

Author Identifiers:

Author	ResearcherID Number	ORCID Number
Zucchi, Maria	D-2637-2012	

ISSN: 0007-4853

Record 19 of 50

Title: People's reliance on the affect heuristic may result in a biased perception of gene technology.

Author(s): (Siegrist, M.); (Sutterlin, B.)

Source: Food Quality and Preference

Volume: 54

Pages: 137-140

DOI: 10.1016/j.foodqual.2016.07.012

Published: 2016

Abstract: In an experiment, we demonstrated that the same outcome of a new corn variety was evaluated less positively if it was from gene technology (GT) compared with conventional breeding technology (CT). The participants (N=205) were randomly assigned to one of two experimental conditions-GT or CT. In the first step, the participants' affect associated with GT or CT plants was measured. Then, the participants read a hypothetical scenario about a new genetically modified (GT condition) or conventionally produced (CT condition) corn variety that was more resistant to the corn borer. They were presented with a matrix in which 1976 black (50%) and white (50%) cells were randomly scattered. The participants were informed that each cell represented a test plot and that the corn plants in the white test plots were not damaged by the corn borer. The participants were then asked to estimate the percentage of the plots infested by the corn borer and how effective they perceived the new corn variety was in resisting the pest. The results indicated that the participants assigned to the GT condition perceived the new corn variety as significantly less effective compared with the participants assigned to the CT condition. No significant difference was observed for estimated percentages. The results suggest that the difference in perceived effectiveness between genetically modified and conventionally bred corn can be explained by people's reliance on the affect heuristic.

Accession Number: CABI:20163331556

Author Identifiers:

Author	ResearcherID Number	ORCID Number
Siegrist, Michael	A-1032-2008	0000-0002-6139-7190

ISSN: 0950-3293

Record 20 of 50

Title: Field application and feasibility of genetically modified dipstick.

Author(s): (He Jing); (Li Hui); (Cai Jun); (Ou JingKun); (Huang HeZhou); (Zeng XiangRong)

Source: Journal of Food Safety and Quality

Volume: 7

Issue: 7

Pages: 2775-2780

Published: 2016

Abstract: Objective: To evaluate the performance of the field application and design of experimental scheme of rapid, sensitive transgenic dipstick. Methods: In this study, the detection performance of the transgenic dipsticks from 3 companies were evaluated with transgenic rice Cry1Ab/Cry1Ac *Bt* protein, such as sensitivity and cross reactivity, and 5 different samples were detected by the transgenic dipsticks and real time PCR. Results: The results showed that the minimum limit of detection was up to 0.25% and there was no cross reactivity. The results of the detection of 5 different samples with the transgenic dipsticks were consistent with the real-time PCR method. In addition, transgenic dipsticks had a good performance in field operation. Conclusion: The transgenic dipstick shows a good practical application performance. When used for actual application testing, it should be designed corresponding experimental scheme to achieve accurate detection, according to the testing purpose and target protein antigens. Therefore, the transgenic dipstick will have a good market prospect.

Accession Number: CABI:20163331074

ISSN: 2095-0381

Record 21 of 50

Title: Development of *Helicoverpa* spp. in *Bt* maize expressing different proteins.

Title: Desenvolvimento de *Helicoverpa* spp. em milho *Bt* com expressao de diferentes proteinas.

Author(s): (Santos, C. A. dos); (Marucci, R. C.); (Barbosa, T. A. N.); (Araujo, O. G.); (Waquil, J. M.); (Dias, A. S.); (Hebach, F. C.); (Mendes, S. M.)

Source: Pesquisa Agropecuaria Brasileira

Volume: 51

Issue: 5

Pages: 537-544

DOI: 10.1590/S0100-204X2016000500014**Published:** 2016

Abstract: The objective of this work was to evaluate the biological responses of *Helicoverpa zea* and *Helicoverpa armigera* (Lepidoptera: Noctuidae) in maize hybrids expressing different proteins. The Cry1F, Cry1A(b), Cry1A.105+Cry2Ab2, and Vip3A proteins and their isogenic conventional counterparts were evaluated. Larvae were fed on spikelets of Bt and conventional maize, which were changed every two days. The variables evaluated were: survival 48 hours after hatching, larval survival, larval and pupal weight, larval development period, and pre-imaginal period. There was a significant interaction between Bt maize event and *Helicoverpa* species for all evaluated biological variables. *Helicoverpa armigera* larvae showed higher survival 48 hours after hatching on maize expressing the Cry1F and Vip3 proteins when compared to *H. zea*. Lethal period was greater for *H. armigera* than for *H. zea*, but, in maize expressing Cry1A(b) protein, it was four times lower. There were no survivals for both *Helicoverpa* species in the evaluated Bt hybrids. In isogenic conventional counterparts, the adaptation index of *H. armigera* was higher than that of *H. zea*, which indicates greater ease of adaptation to the environment of that species.

Accession Number: CABI:20163334323**ISSN:** 0100-204X**Record 22 of 50****Title:** Fitness index and lethal time of fall armyworm on Bt corn.**Title:** Índice de adaptacao e tempo letal da lagarta-do-cartucho em milho Bt.**Author(s):** (Waquil, M. S.); (Pereira, E. J. G.); (Carvalho, S. S. de S.); (Pitta, R. M.); (Waquil, J. M.); (Mendes, S. M.)**Source:** Pesquisa Agropecuaria Brasileira**Volume:** 51**Issue:** 5**Pages:** 563-570**DOI:** 10.1590/S0100-204X2016000500017**Published:** 2016

Abstract: The objective of this work was to evaluate the fitness index and lethal time of fall armyworm [*Spodoptera frugiperda* (Lepidoptera: Noctuidae)] populations on Bt corn expressing the Cry1Ab, Cry1F, Cry1A.105/Cry2Ab2, and Vip3Aa20 proteins. Three bioassays were conducted with larvae collected at the municipality of Inhauma, in the state of Minas Gerais, and at the municipality of Sinop, in the state of Mato Grosso, Brazil. Larvae from these populations were fed with leaves of non-Bt and Bt corn. The following variables were evaluated: larval survival, pupae mass, and larval development period. Then, the fitness indexes and lethal time of these populations were calculated. For lethal time analysis, mortality data of a population collected from Cry1F Bt corn in the municipality of Piumhi, in the state of Minas Gerais, were also used. The Cry1Ab Bt corn showed a limited but durable efficiency. The Cry1A.105/Cry2Ab2 and Vip3Aa20 Bt corn reduced *S. frugiperda* performance, respectively, to less than 5 and 0%, regardless of the origin of the colony. The population from Sinop showed high larval performance in Cry1F Bt corn, showing its resistance to this protein and a certain level of fitness cost. The lethal time can be a variable that indicates evolution of resistance, since it is greater for populations with greater fitness.

Accession Number: CABI:20163334326**ISSN:** 0100-204X**Record 23 of 50****Title:** Selection and application of broad-specificity human domain antibody for simultaneous detection of Bt Cry toxins.**Author(s):** (Xu ChongXin); (Zhang Xiao); (Liu XiaoQin); (Liu Yuan); (Hu XiaoDan); (Zhong JianFeng); (Zhang CunZheng); (Liu XianJin)**Source:** Analytical Biochemistry**Volume:** 512**Pages:** 70-77**Published:** 2016

Abstract: Bt Cry toxin is a kind of bio-toxins that used for genetically modified crops (GMC) transformation widely. In this study, total 15 positive clones could bind the Bt Cry toxins which isolated from a human domain antibody library by 5 rounds affinity selection. According to analyzing of PCR amplification and enzyme-linked immunosorbent assay (ELISA), the most positive phage domain antibody (named F5) gene was cloned into the pET26b vector and expressed in *E. coli* BL21. The purified antibody was used to develop an indirect competitive ELISA (IC-ELISA) for Cry1Ab, Cry1Ac, Cry1B, Cry1C and Cry1F toxins, respectively. The working range of detection for standard curves in IC-ELISA were 0.258-1.407 g/mL, the medium inhibition concentration (IC₅₀) were 0.727-0.892 g/mL and detection limit (IC₁₀) were 0.029-0.074 g/mL for those Bt Cry toxins. The affinity of F5 domain antibody with Cry1Ab, Cry1Ac, Cry1B, Cry1C and Cry1F toxins were 1.21-5.94*10⁷ M⁻¹. The average recoveries of the 5 kinds of Bt Cry toxins from spiked wheat samples were ranged from 81.2%-100.8% with a CV at 2.5%-9.4%. The results showed that we successfully obtained the broad-specificity human domain antibody for simultaneous detection of Bt Cry toxins in agricultural product samples.

Accession Number: CABI:20163323017**ISSN:** 0003-2697**Record 24 of 50****Title:** Cry1Ab-expressing rice did not influence expression of fecundity-related genes in the wolf spider *Pardosa pseudoannulata*.**Author(s):** (Wang Juan); (Peng YuanDe); (He Chao); (Wei BaoYang); (Liang YunShan); (Yang HuiLin); (Wang Zhi); (Stanley, D.); (Song QiSheng)**Source:** Gene**Volume:** 592**Issue:** 1**Pages:** 1-7**Published:** 2016

Abstract: The impact of *Bacillus thuringiensis* (Bt) toxin proteins on non-target predatory arthropods is not well understood at the cellular and molecular levels. Here, we investigated the potential effects of Cry1Ab expressing rice on fecundity of the wolf spider, *Pardosa pseudoannulata*, and some of the underlying molecular mechanisms. The results indicated that brown planthoppers (BPHs) reared on Cry1Ab-expressing rice accumulated the Cry toxin and that reproductive parameters (pre-oviposition period, post-oviposition stage, number of eggs, and egg hatching rate) of the spiders that consumed BPHs reared on Bt rice were not different from those that consumed BPHs reared on the non-Bt control rice. The accumulated Cry1Ab did not influence several vitellin (Vt) parameters, including stored energy and amino acid composition, during one generation. We considered the possibility that the Cry toxins exert their influence on beneficial predators via more subtle effects detectable at the molecular level in terms of gene expression. This led us to transcriptome analysis to detect differentially expressed genes in the ovaries of spiders exposed to dietary Cry1Ab and their counterpart control spiders. Eight genes, associated with vitellogenesis, vitellogenin receptor activity, and vitellin membrane formation were not differentially expressed between ovaries from the treated and control spiders, confirmed by qPCR analysis. We infer that dietary Cry1Ab expressing rice does not influence fecundity, nor expression levels of Vt-associated genes in *P. pseudoannulata*.

Accession Number: CABI:20163322977**ISSN:** 0378-1119**Record 25 of 50****Title:** A 52-week safety study in cynomolgus macaques for genetically modified rice expressing Cry1Ab/1Ac protein.**Author(s):** (Mao Jie); (Sun Xing); (Cheng JianHua); (Shi YongJie); (Wang XinZheng); (Qin JunJie); (Sang ZhiHong); (He Kun); (Xia Qing)**Source:** Food and Chemical Toxicology**Volume:** 95**Pages:** 1-11**Published:** 2016

Abstract: A 52-week feeding study in cynomolgus macaques was carried out to evaluate the safety of Bt rice Huahui 1 (HH1), a transgenic rice line expressing Cry1Ab/1Ac protein. Monkeys were fed a diet with 20% or 60% HH1 rice, 20% or 60% parental rice (Minghui 63, MH63), normal diet, normal diet spiked with purified recombinant Cry1Ab/1Ac fusion protein or bovine serum albumin (BSA) respectively. During the feeding trial, clinical observations were conducted daily, and multiple parameters, including body weight, body temperature, electrocardiogram, hematology, blood biochemistry, serum metabolome and gut microbiome were examined at regular intervals. Upon sacrifice, the organs were weighted, and the macroscopic, microscopic and electron microscopic examinations were performed. The results show no

adverse or toxic effects of Bt rice HH1 or Cry1Ab/1Ac fusion protein on monkeys. Therefore, the present 52-week primate feeding study suggests that the transgenic rice containing Cry 1Ab/1Ac is equivalent to its parental rice line MH63.

Accession Number: CABI:20163317074

ISSN: 0278-6915

Record 26 of 50

Title: Functional dominance of different aged larvae of Bt-resistant *Spodoptera frugiperda* (Lepidoptera: Noctuidae) on transgenic maize expressing Vip3Aa20 protein.

Author(s): (Miraldo, L. L.); (Bernardi, O.); (Horikoshi, R. J.); (A. e Amaral, F. S.); (Bernardi, D.); (Omoto, C.)

Source: Crop Protection

Volume: 88

Pages: 65-71

DOI: 10.1016/j.cropro.2016.06.004

Published: 2016

Abstract: Fall armyworm (FAW), *Spodoptera frugiperda* (J. E. Smith), is the main target pest of transgenic maize expressing insecticidal proteins from *Bacillus thuringiensis* Berliner (Bt) in Brazil. To optimize resistance management strategies, we evaluated the functional dominance of different aged larvae of Bt-resistant FAW on Vip3Aa20 maize. We measured the survival and development of Vip3Aa20-resistant, -heterozygote, and -susceptible strains on MIR162 (expressing Vip3Aa20) and Bt11* MIR162* GA21 (expressing Vip3Aa20 and Cry1Ab) maize. The resistant strain, from neonate to sixth instar, showed more than 72% survival on Vip3Aa20 maize. From surviving larvae, more than 64 and 54% developed to pupae and adults, respectively. In contrast, heterozygote and susceptible strains showed no larval survival up to fourth instar, and less than 25% larval survival in the fifth and sixth instar on Vip3Aa20 maize. These larvae produced less than 21% of pupae and adults. The development time of FAW strains from neonate-to-adult exposed to Vip3Aa20 maize was similar; however, the resistant strain showed an increase of ~2 d when compared to those fed only non-Bt maize. In summary, the resistance of *S. frugiperda* to Vip3Aa20 maize is functionally recessive from neonate up to fourth instar larvae. However, high larval survival of resistant strain and some survival of heterozygote larvae in advanced instars on Vip3Aa20 maize were observed. These results will be important for designing insect resistance management to Bt maize plants expressing Vip3Aa20 protein in Brazil.

Accession Number: CABI:20163306879

Author Identifiers:

Author	ResearcherID Number	ORCID Number
Omoto, Celso	D-9794-2012	0000-0002-6432-830X

ISSN: 0261-2194

Record 27 of 50

Title: Performance of Cry1A.105-selected fall armyworm (Lepidoptera: Noctuidae) on transgenic maize plants containing single or pyramided Bt genes.

Author(s): (Niu Ying); (Head, G. P.); (Price, P. A.); (Huang FangNeng)

Source: Crop Protection

Volume: 88

Pages: 79-87

Published: 2016

Abstract: Cry1A.105 is a Cry protein expressed in some transgenic *Bacillus thuringiensis* (Bt) maize products. In this study, performance of five populations of fall armyworm, *Spodoptera frugiperda* (J.E. Smith), were evaluated on four non-Bt and eight commercial and experimental Bt maize hybrids/lines (hereafter referred as maize products). The five insect populations included one Cry1A.105-susceptible strain, two Cry1A.105-resistant strains, and two F₁ heterozygous genotypes. The eight Bt maize hybrids/lines consisted of five single-gene Bt maize products containing Cry1A.105, Cry2Ab2, Cry1F, or Cry1Ab protein, and three pyramided Bt maize products expressing Cry1A.105/Cry2Ab2, Cry1A.105/Cry2Ab2/Cry1F, or Cry1Ab/Vip3A for targeting aboveground lepidopteran maize pests. In the study, neonates of each population were tested on leaf tissues in the laboratory and whole plants in the greenhouse. Cry1A.105 and Cry1F maize killed 92.2-100% susceptible larvae in both test methods, while resistant larvae survived well on these two maize products. Performance of the two F₁ populations on Cry1A.105 and Cry1F maize varied between the two test methods. In leaf tissue bioassay, Cry1Ab maize was marginally effective against the susceptible population. In contrast, few live larvae and little leaf injury from any of the five populations were observed on Cry2Ab2 and the three pyramided Bt maize products. The results of this study showed evidence of cross resistance of the Cry1A.105-resistant *S. frugiperda* to Cry1F and Cry1Ab maize, but not to the Bt maize products containing Cry2Ab2 or Vip3A. Data generated from this study will be useful in developing resistance management strategies for the sustainable use of Bt maize technology.

Accession Number: CABI:20163306881

ISSN: 0261-2194

Record 28 of 50

Title: Effect of genetically modified Bt maize in an artificial diet on the survival of *Cydia pomonella* (Lepidoptera: Tortricidae).

Author(s): (Stenekamp, D.); (Pringle, K.); (Addison, M.)

Source: Florida Entomologist

Volume: 99

Issue: Special Issue 1

Pages: 200-205

Published: 2016

Abstract: Genetically modified maize contains an insecticidal gene from the soil bacterium *Bacillus thuringiensis* (Bt), which is an important component in integrated pest management strategies against lepidopteran pests of maize. A project is being implemented in the Western Cape of South Africa against the codling moth, *Cydia pomonella* (L.) (Lepidoptera: Tortricidae), a pome fruit pest, using an area-wide integrated pest management approach with a sterile insect technique component. The project requires rearing of large numbers of the target pest for which an artificial diet that contains maize meal as the main ingredient is used. Most of the maize produced in South Africa is Bt maize, which is known to be toxic to codling moth. The aim of this study was to assess the impact of Bt maize in the diet of codling moth on its production parameters. Codling moths were reared for a period of 44 d on artificial diets that contained 5 different concentrations of Bt maize meal and a control using non-Bt maize. The use of Bt maize in the larval diet resulted in larval mortality, delayed larval development and larvae leaving the diet prematurely. Delayed larval development seemed to be the response with most negative consequences. Since optimal rearing of codling moth is not feasible using meal from genetically modified maize with insecticidal properties, another nutritious meal lacking an insecticidal component must be substituted in the artificial diet.

Accession Number: CABI:20163289942

ISSN: 0015-4040

Record 29 of 50

Title: Effect of feeding transgenic *cry1Ab/cry1Ac* rice on indices of immune function in broilers.

Author(s): (Liu RanRan); (Zhao GuiPing); (Zheng MaiQing); (Liu Jie); (Zhang JingJing); (Li Peng); (Li QingHe); (Feng JingHai); (Zhang MinHong); (Wen Jie)

Source: Journal of Integrative Agriculture

Volume: 15

Issue: 6

Pages: 1355-1363

Published: 2016

Abstract: The safety of feeding transgenic *cry1Ab/cry1Ac* rice (a genetically modified (GM) rice variety) to broilers was examined from an immunological perspective. Hatching Arbor Acres chickens (240) were assigned to two dietary treatments (diets containing GM or non-GM rice) with 12 replicates per group and 10 birds per replicate. Traits were measured on one randomly selected bird from each replicate at d 21 and 42. The 42-d feeding trial revealed that *cry1Ab/cry1Ac* rice had no significant effect relative to non-GM rice on body weight and the immune organ indices. No significant pathological lesion in the spleen and bursa of Fabricius was found in the GM rice group. There were no significant differences in serum concentrations of immunoglobulin Y (IgY), IgM, interleukin 4 (IL-4) and IL-6 between the two groups at d 21 or 42, except for IL-6 being higher ($P < 0.05$) in the GM-fed chickens at d 42. There were no differences in the T and B lymphocyte transformation rate and CD4⁺/CD8⁺ ratio between the two groups at d 42. Additionally, there was no significant difference between the two diets in expression of relevant genes *viz.* the major

histocompatibility complex class II β chain (*BLB2*), interferon β 1 (*IFNbeta*), tumour necrosis factor alpha-like (*TNFalpha*) and toll-like receptor 4 (*TLR4*) in the spleen and bursa of Fabricius. All the data demonstrated that transgenic *cryIAb/cryIAc* rice had no adverse effect on these aspects of immune function of broilers during 42-d feeding trial. Transgenic rice was therefore indistinguishable from non-GM rice in terms of short-term feeding in chickens.

Accession Number: CABI:20163287291

ISSN: 2095-3119

Record 30 of 50

Title: Expression of *cryIAb* gene from a novel *Bacillus thuringiensis* strain SY49-1 active on pest insects.

Author(s): (Azizoglu, U.); (Ayvaz, A.); (Yilmaz, S.); (Karaborklu, S.); (Temizgul, R.)

Source: Brazilian Journal of Microbiology

Volume: 47

Issue: 3

Pages: 597-602

DOI: 10.1016/j.bjm.2016.04.011

Published: 2016

Abstract: In this study, the *cryIAb* gene of previously characterized and Lepidoptera-, Diptera-, and Coleoptera-active *Bacillus thuringiensis* SY49-1 strain was cloned, expressed and individually tested on *Ephesia kuehniella* (Lepidoptera: Pyralidae) and *Plodia interpunctella* (Lepidoptera: Pyralidae) larvae. pET-*cryIAb* plasmids were constructed by ligating the *cryIAb* into pET28a (+) expression vector. Constructed plasmids were transferred to an *Escherichia coli* BL21 (DE3) strain rendered competent with CaCl₂. Isopropyl beta-D-1-thiogalactopyranoside was used to induce the expression of *cryIAb* in *E. coli* BL21(DE3), and consequently, ~130 kDa of Cry1Ab was obtained. Bioassay results indicated that recombinant Cry1Ab at a dose of 1000 g g⁻¹ caused 40% and 64% mortality on *P. interpunctella* and *E. kuehniella* larvae, respectively. However, the mortality rates of *Bt* SY49-1 strains' spore-crystal mixture at the same dose were observed to be 70% on *P. interpunctella* and 90% on *E. kuehniella* larvae. The results indicated that *cryIAb* may be considered as a good candidate in transgenic crop production and as an alternative biocontrol agent in controlling stored product moths.

Accession Number: CABI:20163278239

ISSN: 1517-8382

Record 31 of 50

Title: Long-term toxicity study on genetically modified corn with *cryIAC* gene in a Wuzhishan miniature pig model.

Author(s): (Chen Liang); (Sun Zhe); (Liu QuanWei); (Zhong RuQing); (Tan ShuYi); (Yang XiaoGuang); (Zhang HongFu)

Source: Journal of the Science of Food and Agriculture

Volume: 96

Issue: 12

Pages: 4207-4214

DOI: 10.1002/jfsa.7624

Published: 2016

Abstract: BACKGROUND: The objective of the present study was to investigate the chronic effect of transgenic maize lines by the insertion of the *cryIAC* gene from *Bacillus thuringiensis* (Bt) on the growth performance, immune response and health using a Wuzhishan miniature pig model through a 196-day feeding study. RESULTS: Based on the gender and weight, 72 Wuzhishan miniature pigs were randomly assigned one of the diets containing 65% non-transgenic isogenic corn or Bt corn at three stages of growth (day 0-69, 70-134 and 135-196). The potential toxicological effects of transgenic corn on pigs were explored. No difference between the diet treatments for growth performance and haematology parameters at any stages of growth. Although subtle differences in serum content of alanine aminotransferase, relative kidney weight and some immune response were observed between the Bt group and isogenic group, they were not considered as diet treatment-related. CONCLUSION: Long-term feeding Bt corn carrying *cryIAC* genes to Wuzhishan miniature pigs did not indicate adverse effects on the growth, immune response and health indicators at any stages of growth.

Accession Number: CABI:20163272611

ISSN: 0022-5142

Record 32 of 50

Title: Field-evolved resistance to Cry1Ab maize by *Spodoptera frugiperda* in Brazil.

Author(s): (Omoto, C.); (Bernardi, O.); (Salmeron, E.); (Sorgatto, R. J.); (Dourado, P. M.); (Crivellari, A.); (Carvalho, R. A.); (Willse, A.); (Martinelli, S.); (Head, G. P.)

Source: Pest Management Science

Volume: 72

Issue: 9

Pages: 1727-1736

DOI: 10.1002/ps.4201

Published: 2016

Abstract: BACKGROUND: The first *Bt* maize in Brazil was launched in 2008 and contained the MON 810 event, which expresses Cry1Ab protein. Although the Cry1Ab dose in MON 810 is not high against fall armyworm (FAW), *Spodoptera frugiperda* (J.E. Smith), MON 810 provided commercial levels of control. To support insect resistance management in Brazil, the baseline and ongoing susceptibility of FAW was examined using protein bioassays, and the level of control and life history parameters of FAW were evaluated on MON 810 maize. RESULTS: Baseline diet overlay assays with Cry1Ab (16 g cm⁻²) caused 76.3% mortality to field FAW populations sampled in 2009. Moderate mortality (48.8%) and significant growth inhibition (88.4%) were verified in leaf-disc bioassays. In greenhouse trials, MON 810 had significantly less damage than non-*Bt* maize. The surviving FAW larvae on MON 810 (22.4%) had a 5.5 day increase in life cycle time and a 24% reduction in population growth rate. Resistance monitoring (2010-2015) showed a significant reduction in Cry1Ab susceptibility of FAW over time. Additionally, a significant reduction in the field efficacy of MON 810 maize against FAW was observed in different regions from crop season 2009 to 2013. CONCLUSIONS: The decrease in susceptibility to Cry1Ab was expected, but the specific contributions to this resistance by MON 810 maize cannot be distinguished from cross-resistance to Cry1Ab caused by exposure to Cry1F maize. Technologies combining multiple novel insecticidal traits with no cross-resistance to the current Cry1 proteins and high activity against the same target pests should be pursued in Brazil and similar environments.

Accession Number: CABI:20163267034

Author Identifiers:

Author	ResearcherID Number	ORCID Number
Omoto, Celso	D-9794-2012	0000-0002-6432-830X
Bernardi, Oderlei	D-3580-2013	0000-0001-9320-1642

ISSN: 1526-498X

Record 33 of 50

Title: Selection and characterization of resistance to the Vip3Aa20 protein from *Bacillus thuringiensis* in *Spodoptera frugiperda*.

Author(s): (Bernardi, O.); (Bernardi, D.); (Horikoshi, R. J.); (Okuma, D. M.); (Miraldo, L. L.); (Fatoreto, J.); (Medeiros, F. C. L.); (Burd, T.); (Omoto, C.)

Source: Pest Management Science

Volume: 72

Issue: 9

Pages: 1794-1802

DOI: 10.1002/ps.4223

Published: 2016

Abstract: BACKGROUND: *Spodoptera frugiperda* is one the main target pests of maize events expressing Vip3Aa20 protein from *Bacillus thuringiensis* (*Bt*) in Brazil. In

this study, we selected a resistant strain of *S. frugiperda* on Bt maize expressing Vip3Aa20 protein and characterized the inheritance and fitness costs of the resistance. RESULTS: The resistance ratio of the Vip3Aa20-resistant strain of *S. frugiperda* was >3200-fold. Neonates of the Vip3Aa20-resistant strain were able to survive and emerge as fertile adults on Vip3Aa20 maize, while larvae from susceptible and heterozygous strains did not survive. The inheritance of Vip3Aa20 resistance was autosomal recessive and monogenic. Life history studies to investigate fitness cost revealed an 11% reduction in the survival rate until adult stage and a ~50% lower reproductive rate of the Vip3Aa20-resistant strain compared with susceptible and heterozygous strains. CONCLUSION: This is the first characterization of *S. frugiperda* resistance to Vip3Aa protein. Our results provide useful information for resistance management programs designed to prevent or delay resistance evolution to Vip3Aa proteins in *S. frugiperda*.

Accession Number: CABI:20163267043

Author Identifiers:

Author	ResearcherID Number	ORCID Number
Omoto, Celso	D-9794-2012	0000-0002-6432-830X

ISSN: 1526-498X

Record 34 of 50

Title: Spiders from multiple functional guilds are exposed to Bt-endotoxins in transgenic corn fields via prey and pollen consumption.

Author(s): (Peterson, J. A.); (Obrycki, J. J.); (Harwood, J. D.)

Source: Biocontrol Science and Technology

Volume: 26

Issue: 9

Pages: 1230-1248

DOI: 10.1080/09583157.2016.1193591

Published: 2016

Abstract: A comprehensive assessment of risk to natural enemies from Bt-endotoxins from bioengineered crops must evaluate potential harm, as well as exposure pathways in non-target arthropod food webs. Despite being abundant generalist predators in agricultural fields, spiders (Araneae) have often been overlooked in the context of Bt crop risk assessment. Spiders and their prey were collected from transgenic corn fields expressing lepidopteran-specific Cry1Ab, coleopteran-specific Cry3Bb1, both proteins, and a non-transgenic near isolate. Spiders and prey were screened for Cry1Ab and Cry3Bb1 using qualitative enzyme-linked immunosorbent assay. Spiders from the three most common functional guilds, wandering sheet-tangle weavers, orb-weavers, and ground runners, tested positive for Cry1Ab and Cry3Bb1 proteins, with the highest per cent positive (8.0% and 8.3%) during and after anthesis. Laboratory feeding trials revealed that Bt-endotoxins were detectable in the *Pardosa* sp. (Lycosidae)-immature cricket-Bt corn pathway, but not in the *Tennesseellum formica* (Linyphiidae)-Collembola-Bt corn pathway. Additionally, direct consumption of transgenic corn pollen by *Pardosa* sp., *T. formica*, and *Cyclosa turbinata* (Araneidae) resulted in transfer of both Cry1Ab and Cry3Bb1 endotoxins. This study demonstrates that Bt-endotoxins are taken up by diverse members of a spider community via pollen and prey consumption and should be factored into future risk assessment.

Accession Number: CABI:20163255118

ISSN: 0958-3157

Record 35 of 50

Title: Genetically modified rice Bt-ShanYou63 expressing Cry1Ab/c protein does not harm *Daphnia magna*.

Author(s): (Zhang Li); (Guo RuQing); (Fang ZhiXiang); (Liu Biao)

Source: Ecotoxicology and Environmental Safety

Volume: 132

Pages: 196-201

DOI: 10.1016/j.ecoenv.2016.06.011

Published: 2016

Abstract: The genetically modified (GM) rice Bt-ShanYou63 (Bt-SY63) received an official biosafety certificate while its safety remained in dispute. In a lifelong study, *Daphnia magna* were experimentally fed a basal diet of rice flours from Bt-SY63 or its parental rice ShanYou63 (SY63) at concentrations of 0.2 mg, 0.3 mg, or 0.4 mg C (per individual per day). Overall the survival, body size, and reproduction of the animals were comparable between Bt-SY63 and ShanYou63. The results showed that no significant differences were observed in growth and reproduction parameters between *D. magna* fed GM and non-GM flour and no dose-related changes occurred in all the values. Based on the different parameters assessed, the GM rice Bt-SY63 is a safe food source for *D. magna* that does not differ in quality from non-GM rice.

Accession Number: CABI:20163260998

ISSN: 0147-6513

Record 36 of 50

Title: Toxicity of *Bacillus thuringiensis* crystal proteins against eri silkworm, *Samia cynthia ricini* (Lepidoptera: Saturniidae).

Author(s): (Kumar, D. S.); (Muddanuru Tarakeswari); (Maddukuri Lakshminarayana); (Mulpuri Sujatha)

Source: Journal of Invertebrate Pathology

Volume: 138

Pages: 116-119

DOI: 10.1016/j.jip.

Published: 2016

Abstract: Ten purified crystal proteins of *Bacillus thuringiensis* (Bt) were tested at concentrations ranging from 2.93 to 3000 ng/cm² for their toxicity to eri silkworm through protein paint bioassays using castor leaves. Based on LC₅₀ values, Cry1Aa (2.6 ng/cm²) was highly toxic followed by Cry1Ac (29.3 ng/cm²) and Cry1Ab (68.7 ng/cm²). The Cry1Ca and Cry1Ea proteins were moderately toxic to eri silkworm larvae and resulted in 23% and 28% mortality, respectively at the highest concentration tested (3000 ng/cm²). Only reduction in larval weight was observed with Cry2Aa, Cry1Da and Cry9Aa proteins while Cry3Aa and Cry1Ba proteins were found to be nontoxic.

Accession Number: CABI:20163258516

ISSN: 0022-2011

Record 37 of 50

Title: Heritability of wing size and shape of the rice and corn strains of *Spodoptera frugiperda* (J.E. Smith) (Lepidoptera: Noctuidae).

Author(s): (Canas-Hoyos, N.); (Marquez, E. J.); (Saldamando-Benjumea, C. I.)

Source: Neotropical Entomology

Volume: 45

Issue: 4

Pages: 411-419

DOI: 10.1007/s13744-016-0393-y

Published: 2016

Abstract: *Spodoptera frugiperda* (J.E. Smith) (Lepidoptera: Noctuidae) represents a pest of economic importance in all Western Hemisphere. This polyphagous species has diverged into two populations that have been mainly recognized with various mitochondrial and nuclear molecular markers and named "the rice" and "the corn" strains. In Colombia, both strains have evolved prezygotic and postzygotic isolation. They differ in tolerance to *Bacillus thuringiensis* (Cry1Ac and Cry1Ab endotoxins) and the insecticides lambda-cyhalothrin and methomyl. In 2014, a wing morphometric analysis made in 159 individuals from a colony showed that both strains significantly differ in wing shape. The species also exhibits sexual dimorphism in the rice strain as in females wing size is larger than in males. Here, we continued this work with another wing morphometric approach in laboratory-reared strains to calculate wing size and shape heritabilities using a full-sib design and in wild populations to determine if this method distinguishes these strains. Our results show that male heritabilities of both traits were higher than female ones. Wild populations were significantly different in wing shape and size. These results suggest that wing morphometrics can be used as an alternative method to molecular markers to differentiate adults from laboratory-reared populations and wild populations of this pest, particularly in males of this species. Finally, Q_{ST} values obtained for wing size and shape further demonstrated that both strains are genetically differentiated in nature.

Accession Number: CABI:20163262604

ISSN: 1519-566X

Record 38 of 50

Title: Gut microbiota of *Busseola fusca* (Lepidoptera: Noctuidae).

Author(s): (Snyman, M.); (Gupta, A. K.); (Bezuidenhout, C. C.); (Claassens, S.); (Berg, J. van den)

Source: World Journal of Microbiology & Biotechnology

Volume: 32

Issue: 7

Pages: 115

DOI: 10.1007/s11274-016-2066-8

Published: 2016

Abstract: *Busseola fusca* (Fuller) (Lepidoptera: Noctuidae) is a stemborer pest that attacks maize (*Zea mays*) throughout sub-Saharan Africa. Genetically modified maize has been shown to be effective against *B. fusca*. However, resistance of *B. fusca* against Bt-maize has developed and spread throughout South Africa. Previous studies suggested that gut microbiota contribute to mortality across a range of Lepidoptera. To fully assess the role of microbiota within the gut, it is essential to understand the microbiota harboured by natural *B. fusca* populations. This study aimed to identify the gut-associated bacteria by 16S rRNA gene sequencing. A total of 78 bacterial strains were characterised from the midgut of *B. fusca* larvae that were collected from 30 sites across the maize producing region of South Africa. Molecular phylogenetic analyses revealed bacteria affiliated to *Proteobacteria*, *Actinobacteria*, and *Firmicutes*. Taxonomic distribution placed these isolates into 15 different genera representing 20 species. The majority of bacteria identified belong to the genera *Bacillus*, *Enterococcus*, and *Klebsiella*. The *B. fusca* gut represents an intriguing and unexplored niche for analysing microbial ecology. The study could provide opportunities for developing new targets for pest management and contribute to understanding the phenomenon of resistance evolution of this species.

Accession Number: CABI:20163262645

Author Identifiers:

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Claassens, Sarina	F-8944-2010	0000-0003-3955-4361

ISSN: 0959-3993

Record 39 of 50

Title: Life-history traits of *Spodoptera frugiperda* populations exposed to low-dose Bt maize.

Author(s): (Sousa, F. F.); (Mendes, S. M.); (Santos-Amaya, O. F.); (Araujo, O. G.); (Oliveira, E. E.); (Pereira, E. J. G.)

Source: PLoS ONE

Volume: 11

Issue: 5

Pages: e0156608

DOI: 10.1371/journal.pone.0156608

Published: 2016

Abstract: Exposure to *Bacillus thuringiensis* (Bt) toxins in low- and moderate-dose transgenic crops may induce sublethal effects and increase the rate of Bt resistance evolution, potentially compromising control efficacy against target pests. We tested this hypothesis using the fall armyworm *Spodoptera frugiperda*, a major polyphagous lepidopteran pest relatively tolerant to Bt notorious for evolving field-relevant resistance to single-gene Bt maize. Late-instar larvae were collected from Bt Cry1Ab and non-Bt maize fields in five locations in Brazil, and their offspring was compared for survival, development, and population growth in rearing environment without and with Cry1Ab throughout larval development. Larval survival on Cry1Ab maize leaves varied from 20 to 80% among the populations. Larvae reared on Cry1Ab maize had seven-day delay in development time in relation to control larvae, and such delay was shorter in offspring of armyworms from Cry1Ab maize. Population growth rates were 50-70% lower for insects continuously exposed to Cry1Ab maize relative to controls, showing the population-level effect of Cry1Ab, which varied among the populations and prior exposure to Cry1Ab maize in the field. In three out of five populations, armyworms derived from Bt maize reared on Cry1Ab maize showed higher larval weight, faster larval development and better reproductive performance than the armyworms derived from non-Bt maize, and one of these populations showed better performance on both Cry1Ab and control diets, indicating no fitness cost of the resistance trait. Altogether, these results indicate that offspring of armyworms that developed on field-grown, single-gene Bt Cry1Ab maize had reduced performance on Cry1Ab maize foliage in two populations studied, but in other three populations, these offspring had better overall performance on the Bt maize foliage than that of the armyworms from non-Bt maize fields, possibly because of Cry1Ab resistance alleles in these populations. Implications of these findings for resistance management of *S. frugiperda* in Bt crops are discussed.

Accession Number: CABI:2016325127

Author Identifiers:

Author	ResearcherID Number	ORCID Number
Pereira, Eliseu	C-5365-2015	0000-0002-8957-6465

ISSN: 1932-6203

Record 40 of 50

Title: Health status and potential uptake of transgenic DNA by Japanese quail fed diets containing genetically modified plant ingredients over 10 generations.

Author(s): (Korwin-Kossakowska, A.); (Sartowska, K.); (Tomczyk, G.); (Prusak, B.); (Sender, G.)

Source: British Poultry Science

Volume: 57

Issue: 3

Pages: 415-423

DOI: 10.1080/00071668.2016.1162281

Published: 2016

Abstract: The hypothesis assumes that feed containing GMOs affects animal health and results in the transgene product accumulating in the body. Therefore, the objective of the study was to evaluate the impact of genetically modified (GM) ingredients used in poultry diets on aspects of bird health status and accumulation of transgenic DNA in eggs, breast muscle and internal organs. A total of 10 generations of Japanese quail were fed three types of diets: group A - containing GM soya (Roundup Ready) and non-GM maize, group B - containing GM maize (MON810) and non-GM soya, and group C - containing non-GM soya and maize. Bird performance traits were monitored throughout the trial. In 17-week-old animals of each generation, health examination took place on birds from each group including *post-mortem* necropsy and histological organ evaluation. For the purpose of transgenic DNA detection, samples of selected important tissues were taken. A molecular screening method of PCR amplification was used. The analysis of the sectional examination of birds used in the current experiment did not indicate the existence of the pathological changes caused by pathogens, nutritional factors or of environmental nature. The histopathological changes occurred in all three dietary groups and there were no statistically significant differences between the groups. There was no transgene amplification - neither *CaMV35S* promoter sequence nor *nos* terminator sequence, in the samples derived from breast muscle, selected tissues and germinal discs (eggs). According to the obtained results, it was concluded that there was no negative effect of the use of GM soya or maize with regard to bird health status or to the presence of transgenic DNA in the final consumable product.

Accession Number: CABI:20163239871

ISSN: 0007-1668

Record 41 of 50

Title: Development of a model system approach for generating fragments of the Cry1Ab protein.

Author(s): (Albright, V. C.); (Hellmich, R. L.); (Coats, J. R.)

Source: Journal of AOAC International

Volume: 99

Issue: 3**Pages:** 792-805**DOI:** 10.5740/jaoacint.15-0229**Published:** 2016

Abstract: The use of transgenic crops expressing one or more crystal (Cry) proteins for insect management has grown dramatically since their introduction nearly 2 decades ago. However, many questions surrounding the environmental fate of these proteins still persist. One area of particular interest is the possible detection of Cry protein fragments by the antibodies used in ELISA kits. A model system approach is used to generate environmentally relevant fragments by simulating conditions and digestive enzymes that are known to exist in environments in which Cry proteins may be present. Seven different types of model systems were screened for their ability to generate fragments of the Cry1Ab protein; five of these model systems reliably generated Cry1Ab fragments. These fragments were analyzed in a subsequent study to determine whether the fragments were still detectable by ELISA and whether they retained any bioactivity.

Accession Number: CABI:20163231159**ISSN:** 1060-3271**Record 42 of 50****Title:** Bacterial vegetative insecticidal proteins (Vip) from entomopathogenic bacteria.**Author(s):** (Maissa Chakroun); (Banyuls, N.); (Bel, Y.); (Escriche, B.); (Ferre, J.)**Source:** Microbiology and Molecular Biology Reviews**Volume:** 80**Issue:** 2**Pages:** 329-350**DOI:** 10.1128/MMBR.00060-15**Published:** 2016

Abstract: Entomopathogenic bacteria produce insecticidal proteins that accumulate in inclusion bodies or parasporal crystals (such as the Cry and Cyt proteins) as well as insecticidal proteins that are secreted into the culture medium. Among the latter are the Vip proteins, which are divided into four families according to their amino acid identity. The Vip1 and Vip2 proteins act as binary toxins and are toxic to some members of the Coleoptera and Hemiptera. The Vip1 component is thought to bind to receptors in the membrane of the insect midgut, and the Vip2 component enters the cell, where it displays its ADP-ribosyltransferase activity against actin, preventing microfilament formation. Vip3 has no sequence similarity to Vip1 or Vip2 and is toxic to a wide variety of members of the Lepidoptera. Its mode of action has been shown to resemble that of the Cry proteins in terms of proteolytic activation, binding to the midgut epithelial membrane, and pore formation, although Vip3A proteins do not share binding sites with Cry proteins. The latter property makes them good candidates to be combined with Cry proteins in transgenic plants (*Bacillus thuringiensis*-treated crops [Bt crops]) to prevent or delay insect resistance and to broaden the insecticidal spectrum. There are commercially grown varieties of Bt cotton and Bt maize that express the Vip3Aa protein in combination with Cry proteins. For the most recently reported Vip4 family, no target insects have been found yet.

Accession Number: CABI:20163231250**ISSN:** 1092-2172**Record 43 of 50****Title:** Detection of transgenic proteins in maize flour marketed in Bogota, Colombia.**Title:** Deteccion de proteinas transgenicas en harinas de maiz comercializadas en Bogota, Colombia.**Author(s):** (Tabima-Cubillos, L. Y.); (Chaparro-Giraldo, A.); (Trujillo-Guiza, M. L.)**Source:** Revista de Salud Publica**Volume:** 18**Issue:** 3**Pages:** 470-483**Published:** 2016

Abstract: Objective: To detect the presence or absence of transgenic proteins derived from GM crops in maize flour marketed in Bogota D.C., Colombia. Methods: 11 extraction protocols for total protein were evaluated in 17 precooked flour, two uncooked and three positive controls. Subsequently, the presence of 7 transgenic proteins (CP4-EPSPS, Cry1Ab, Cry1Ac, Cry1F, Cry2A, Cry34Ab1 and Cry3Bb1) using commercial ELISA kits was determined. Results It was determined that the best protocol for total protein extraction was buffer with Triton X-100, which allowed obtaining protein concentrations greater than 0.5 mg per gram of flour and does not generate interference with the ELISA technique. Four transgenic proteins were detected: CP4EPSPS, Cry1F, Cry1Ab and Cry34Ab1 in precooked and uncooked flour with percentages varying between 20 and 100%. Conclusion Seven of the 19 maize flours contain traces of transgenic protein (B2, B8, A3, O3, O1, C1 and C2) that provide resistance to lepidopterans and coleopterans, and tolerance to glyphosate herbicide, (CP4EPSPS - Cry1Ab, Cry1F, Cry34Ab1 and Cry3Bb1). All detected events are approved for human consumption in Colombia, according to the Ministry of Health and Social Protection.

Accession Number: CABI:20163236956**ISSN:** 0124-0064**Record 44 of 50****Title:** Transgenic *Bt* (*Cry1Ab/Ac*) rice lines with different genetic backgrounds exhibit superior field performance under pesticide-free environment.**Author(s):** (Jiang Yang); (Ling Lin); (Zhang LingLi); (Wang KangXu); (Cai MingLi); (Zhan Ming); (Li ChengFang); (Wang JinPing); (Chen Xuan); (Lin YongJun); (Cao CouGui)**Source:** Field Crops Research**Volume:** 193**Pages:** 117-122**DOI:** 10.1016/j.fcr.2016.03.014**Published:** 2016

Abstract: Transgenic rice with *Cry Bacillus thuringiensis* (*Bt*) genes have been developed in the last few decades. The performance of transgenic rice, especially the yield and resistance, must be meticulously evaluated prior to commercial production. In this study, yield and resistance performance of newly bred transgenic *Bt* (*Cry1Ab/Ac*) rice lines with different genetic backgrounds were first investigated under pesticide-free field environment. Transgenic *Bt* (*Cry1Ab/Ac*) rice lines showed high insect resistances and superior agronomic traits, resulting in obvious yield advantages ranging from 9.1% to 38.0% over their respective non-*Bt* control lines. *Bt* protein content (BTC) was similar among the *Bt* (*Cry1Ab/Ac*) rice lines in different years, while it was much higher in leaves than in stems of the *Bt* (*Cry1Ab/Ac*) rice lines. Different genetic backgrounds of *Bt* (*Cry1Ab/Ac*) rice lines affected the yield advantage but had no influence on the resistance and BTC. The results suggested that *Bt* (*Cry1Ab/Ac*) rice lines have gained obvious yield advantages and high resistances regardless of genetic background under pesticide-free environment.

Accession Number: CABI:20163230120**ISSN:** 0378-4290**Record 45 of 50****Title:** Evaluation of foliar damage by *Spodoptera frugiperda* (Lepidoptera: Noctuidae) to genetically modified corn (Poales: Poaceae) in Mexico.**Author(s):** (Aguirre, L. A.); (Hernandez-Juarez, A.); (Flores, M.); (Cerna, E.); (Landeros, J.); (Frias, G. A.); (Harris, M. K.)**Source:** Florida Entomologist**Volume:** 99**Issue:** 2**Pages:** 276-280**DOI:** 10.1653/024.099.0218**Published:** 2016

Abstract: The fall armyworm, *Spodoptera frugiperda* Smith & Abbot (Lepidoptera: Noctuidae), is a key pest of corn, *Zea mays* L. (Poales: Poaceae), in Mexico. The development of genetically modified (GM) corn hybrids for resistance to this insect, with the inclusion of several genes coding for proteins Cry1Ab, Vip3Aa20, and mCry3A of *Bacillus thuringiensis* Berliner (Bacillales: Bacillaceae) (*Bt*), offer an alternative to conventional insecticides to control this pest. Resistance to fall armyworms of the GM corn hybrids Agrisure 3000 GT, Agrisure Viptera 3110, and Agrisure Viptera 3111 was evaluated in 4 locations at Sinaloa for a 3 yr period. Damage evaluation

showed that the maize hybrids with the *Bt* gene insertion were not affected by the fall armyworm as compared with their respective isolines, which were seriously damaged. The results reaffirm the insect control benefits provided by this technology and provide a baseline for resistance management.

Accession Number: CABI:20163222408

Author Identifiers:

Author	ResearcherID Number	ORCID Number
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ISSN: 0015-4040

Record 46 of 50

Title: Frequency of Cry1F non-recessive resistance alleles in North Carolina field populations of *Spodoptera frugiperda* (Lepidoptera: Noctuidae).

Author(s): (Li GuoPing); (Reisig, D.); (Miao Jin); (Gould, F.); (Huang FangNeng); (Feng HongQiang)

Source: PLoS ONE

Volume: 11

Issue: 4

Pages: e0154492

Published: 2016

Abstract: Fall armyworm, *Spodoptera frugiperda* (J.E. Smith) (Lepidoptera: Noctuidae), is a target species of transgenic corn (*Zea mays* L.) that expresses single and pyramided *Bacillus thuringiensis* (*Bt*) toxin. In 2014, *S. frugiperda* were collected from a light trap in North Carolina, and a total of 212 F₁/F₂ isofemale lines of *S. frugiperda* were screened for resistance to *Bt* and non-*Bt* corn. All of the 212 isolines were susceptible to corn tissue expressing Cry1A.105 + Cry2Ab, Cry1F + Cry1A.105 + Cry2Ab, and Cry1F + Cry1Ab + Vip3Aa20. Growth rate bioassays were performed to isolate non-recessive *Bt* resistance alleles. Seven individuals out of the 212 isofemale lines carried major non-recessive alleles conferring resistance to Cry1F. A pooled colony was created from the seven individuals. This colony was 151.21 times more resistant to Cry1F than a known-susceptible population and was also resistant to Cry1A.105, but was not resistant to Cry2Ab and Vip3Aa20. The results demonstrate that field populations of *S. frugiperda* collected from North Carolina are generally susceptible to Cry1F, but that some individuals carry resistant alleles. The data generated in this study can be used as baseline data for resistance monitoring.

Accession Number: CABI:20163219454

ISSN: 1932-6203

Record 47 of 50

Title: Effects of remaining *Bt*-transgenic rice straws on benthos communities in fields.

Author(s): (Liu Fang); (Jiang WanXiang); (Li JunSheng); (Liang YuYong); (Liu YongBo)

Source: Research of Environmental Sciences

Volume: 29

Issue: 4

Pages: 522-528

Published: 2016

Abstract: To detect the potential effects of *Bt*-transgenic rice straws remaining in fields on benthos communities, transgenic *Cry1Ab/Ac* rice "Huahui-1" and its non-transgenic parent rice "Minghui-63" were buried in paddy fields for seven weeks. We analyzed the differences of biodiversity indices of benthos communities and decomposition rate between *Bt*-transgenic and non-transgenic rice straws. The concentration of *Bt* (*Cry1Ab/Ac*) protein in transgenic rice straws was measured using a quantified ELISA method. (1) In total, 223 benthos were found on all *Bt*-transgenic and non-transgenic rice straws, and the benthic species belonged to nine families. Seven families were found on *Bt* rice straws and on non-fit rice straws. (2) Neither the rice straw type nor the harvest time had an effect on benthos abundance and species number, the Shannon-Wiener index, Simpson diversity index or Pielou evenness of benthos communities. (3) The percentage of residual straws decreased with buried time, and was not significantly different between *Bt*-transgenic and non-transgenic rice straws; both *Bt*-transgenic and non-transgenic rice straws remained at 44.0% of dry weight after being buried seven weeks in the field. (4) The average concentration of *Bt* protein in transgenic rice straws varied between 1.99-3.04 g/g during the bury period; the *Bt* protein content in transgenic rice straws had no significant difference among five harvesting times and was 2.04 g/g after being buried seven weeks. These results showed that *Bt*-transgenic rice had no obvious effect on the biodiversity of benthos communities.

Accession Number: CABI:20163228710

ISSN: 1001-6929

Record 48 of 50

Title: Accumulation and variability of maize pollen deposition on leaves of European Lepidoptera host plants and relation to release rates and deposition determined by standardised technical sampling.

Author(s): (Hofmann, F.); (Kruse-Plass, M.); (Kuhn, U.); (Otto, M.); (Schlechtriemen, U.); (Schroder, B.); (Vogel, R.); (Wosniok, W.)

Source: Environmental Sciences Europe

Volume: 28

Issue: 14

Pages: (26 April 2016)

Published: 2016

Abstract: Background: Risk assessment for GMOs such as *Bt* maize requires detailed data concerning pollen deposition onto non-target host-plant leaves. A field study of pollen on lepidopteran host-plant leaves was therefore undertaken in 2009-2012 in Germany. During the maize flowering period, we used in situ microscopy at a spatial resolution adequate to monitor the feeding behaviour of butterfly larvae. The plant-specific pollen deposition data were supplemented with standardised measurements of pollen release rates and deposition obtained by volumetric pollen monitors and passive samplers. Results: In 2010, we made 5377 measurements of maize pollen deposited onto leaves of maize, nettle, goosefoot, sorrel and blackberry. Overall mean leaf deposition during the flowering period ranged from 54 to 478 n/cm² (grains/cm²) depending on plant species and site, while daily mean leaf deposition values were as high as 2710 n/cm². Maximum single leaf-deposition values reached up to 103,000 n/cm², with a 95% confidence-limit upper boundary of 11,716 n/cm². Conclusions: Daily means and variation of single values uncovered by our detailed measurements are considerably higher than previously assumed. The recorded levels are more than a single degree of magnitude larger than actual EU expert risk assessment assumptions. Because variation and total aggregation of deposited pollen on leaves have been previously underestimated, lepidopteran larvae have actually been subjected to higher and more variable exposure. Higher risks to these organisms must consequently be assumed. Our results imply that risk assessments related to the effects of *Bt* maize exposure under both realistic cultivation conditions and worst-case scenarios must be revised. Under common cultivation conditions, isolation buffer distances in the kilometre range are recommended rather than the 20-30 m distance defined by the EFSA.

Accession Number: CABI:20163209786

ISSN: 2190-4715

Record 49 of 50

Title: Monitoring the prevalence of genetically modified maize in commercial animal feeds and food products in Turkey.

Author(s): (Turkec, A.); (Lucas, S. J.); (Karlik, E.)

Source: Journal of the Science of Food and Agriculture

Volume: 96

Issue: 9

Pages: 3173-3179

DOI: 10.1002/jsfa.7496

Published: 2016

Abstract: BACKGROUND: EU legislation strictly controls use of genetically modified (GM) crops in food and feed products, and requires them to be labelled if the total GM content is greater than 9 g kg⁻¹ (for approved GM crops). We screened maize-containing food and feed products from Turkey to assess the prevalence of GM material. RESULTS: With this aim, 83 food and feed products - none labelled as containing GM material - were screened using multiplex real-time polymerase chain reaction (PCR)

for four common GM elements (35 S/NOS/bar/FMV). Of these, 18.2% of feeds and 6% of food samples tested positive for one or more of these elements, and were subjected to event-specific PCR to identify which GM organisms they contained. Most samples were negative for the approved GM events tested, suggesting that they may contain adventitious GM contaminants. One sample was shown to contain an unapproved GM event (MON810, along with GA21) at a concentration well above the statutory labelling requirement. CONCLUSION: Current legislation has restricted the penetration of GM maize into the Turkish food industry but not eliminated it, and the proliferation of different GM events is making monitoring increasingly complex. Our results indicate that labelling requirements are not being followed in some cases.

Accession Number: CABI:20163204913

ISSN: 0022-5142

Record 50 of 50

Title: The impact of *Bacillus thuringiensis* technology on the occurrence of fumonisins and other mycotoxins in maize.

Author(s): (Diaz-Gomez, J.); (Marin, S.); (Capell, T.); (Sanchis, V.); (Ramos, A. J.)

Source: World Mycotoxin Journal

Volume: 9

Issue: 3

Pages: 475-486

DOI: 10.3920/WMJ2015.1960

Published: 2016

Abstract: In many developing countries, maize is both a staple food crop and a widely-used animal feed. However, adventitious colonisation or damage caused by insect pests allows fungi to penetrate the vegetative parts of the plant and the kernels, the latter resulting in mycotoxin contamination. Maize seeds contaminated with fumonisins and other mycotoxins pose a serious threat to both humans and livestock. However, numerous studies have reported a significant reduction in pest damage, disease symptoms and fumonisin levels in maize hybrids expressing the *Bacillus thuringiensis* (Bt) gene *cry1Ab*, particularly in areas where the European corn borer is prevalent. When other pests are also present, the *cry1Ab* gene alone offers insufficient protection, and combinations of insecticidal genes are required to reduce damage to plants caused by insects. The combination of Cry1Ab protein with other Cry proteins (such as Cry1F) or Vip proteins has reduced the incidence of pests and, indirectly, mycotoxin levels. Maize hybrids expressing multiple Bt genes, such as SmartStax, are less susceptible to damage by insects, but mycotoxin levels are not routinely and consistently compared in these crops. Bt maize has a greater economic impact on *Fusarium* toxins than aflatoxins. The main factors that determine the effectiveness of Bt hybrids are the type of pest and the environmental conditions, but the different fungal infection pathways must also be considered. An alternative strategy to reduce mycotoxin levels in crops is the development of transgenic plants expressing genes that protect against fungal infection or reduce mycotoxin levels by *in situ* detoxification. In this review article, we summarise what is known about the relationship between the cultivation of Bt maize hybrids and contamination levels with different types of mycotoxins.

Accession Number: CABI:20163204357

ISSN: 1875-0710

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Title: Investigations of immunogenic, allergenic and adjuvant properties of Cry1Ab protein after intragastric exposure in a food allergy model in mice.

Author(s): (Andreassen, M.); (Bohn, T.); (Wikmark, O. G.); (Bodin, J.); (Traavik, T.); (Lovik, M.); (Nygaard, U. C.)

Source: BMC Immunology

Volume: 17

Issue: 10

Pages: (4 May 2016)

Published: 2016

Abstract: Background: In genetically modified (GM) crops there is a risk that the inserted genes may introduce new allergens and/or adjuvants into the food and feed chain. The MON810 maize, expressing the insecticidal Cry1Ab toxin, is grown in many countries worldwide. In animal models, intranasal and intraperitoneal immunisations with the purified Cry1Ab proteins have induced immune responses, and feeding trials with Cry1Ab-containing feed have revealed some altered immune responses. Previous investigations have primarily measured antibody responses to the protein, while investigations of clinical food allergy symptoms, or allergy promotion (adjuvant effect) associated with the Cry1Ab protein are largely missing. We aimed to investigate immunogenic, allergenic and adjuvant properties of purified Cry1Ab toxin (trypCry1Ab, i.e., trypsin activated Cry1Ab) in a mouse model of food allergy. Method: Female C3H/HeJ mice were immunized by intragastric gavage of 10 g purified, trypsin activated Cry1Ab toxin (trypCry1Ab) alone or together with the food allergen lupin. Cholera toxin was added as a positive control for adjuvant effect to break oral tolerance. Clinical symptoms (anaphylaxis) as well as humoral and cellular responses were assessed. Results: In contrast to results from previous airway investigations, we observed no indication of immunogenic properties of trypCry1Ab protein after repeated intragastric exposures to one dose, with or without CT as adjuvant. Moreover, the results indicated that trypCry1Ab given by the intragastric route was not able to promote allergic responses or anaphylactic reactions against the co-administered allergen lupin at the given dose. Conclusion: The study suggests no immunogenic, allergenic or adjuvant capacity of the given dose of trypCry1Ab protein after intragastric exposure of prime aged mice.

Accession Number: CABI:20163199384

ISSN: 1471-2172

Record 2 of 42

Title: Diversity of Coccinellidae in Ecological Compensation Areas of Italy and overlap with maize pollen shedding period.

Author(s): (Lami, F.); (Masetti, A.); (Neri, U.); (Lener, M.); (Staiano, G.); (Arpaia, S.); (Burgio, G.)

Source: Bulletin of Insectology

Volume: 69

Issue: 1

Pages: 49-57

Published: 2016

Abstract: Ladybird beetles (Coleoptera Coccinellidae) are important predators of aphids and other crop pests, and there is great interest in their conservation in agroecosystems. Bt-maize, genetically engineered to express insecticidal Cry proteins, is regarded as a taxon-specific way of controlling pests, but some concerns have been raised about the possibility of unintended negative effects on non-target organisms, including coccinellids. One of the possible routes of exposure of ladybird beetles to Cry toxins is by feeding on maize pollen, as for many species pollen is an important integrative food source. In this study, coccinellid adults were sampled by sweep netting in Ecological Compensation Areas (ECAs) in three sites of Northern and Central Italy, where conventional maize cultivars are grown (Bt-maize is currently forbidden for commercial cultivation in Italy). The coccinellid communities were sampled during and around the typical flowering periods of maize in order to check their diversity and their overlap with pollen shedding. A total of 11 species were recorded. *Hippodamia variegata* (Goeze), *Coccinella septempunctata* L. and the exotic *Harmonia axyridis* (Pallas) were the most abundant species in Northern Italy, whereas *Tythaspis sedecimpunctata* (L.) and *Coccinula quatuordecimpustulata* (L.) were dominant in Central Italy. The potential exposure to maize pollen was different in the two areas, since in Northern Italy the maize flowering coincided with a period of high coccinellid activity in the field, whereas in Central Italy the ladybird population peaks occurred roughly one month earlier than the anthesis. The collected data might be useful for exposure characterization of ladybird beetles in a possible future scenario of Bt-maize cropping in the studied areas.

Accession Number: CABI:20163201994

ISSN: 1721-8861

Record 3 of 42

Title: Tissue culture independent *Agrobacterium tumefaciens* mediated *in planta* transformation method for tropical maize (*Zea mays* L.).

Author(s): (Alok Abhishek); (Rita Kumari); (Karjagi, C. G.); (Pradyumn Kumar); (Bhupender Kumar); (Sain Dass); (Kumar, R. S.); (Ramteke, P. W.)

Source: Proceedings of the National Academy of Sciences India. Section B, Biological Sciences

Volume: 86

Issue: 2

Pages: 375-384

DOI: 10.1007/s40011-014-0454-0

Published: 2016

Abstract: Tropical maize is recalcitrant to tissue culture regeneration because of its poor response to *in vitro* regeneration after transformation. In this context, the present study has developed the tissue culture independent *in planta* transformation protocol for tropical maize by transferring plasmid meristem cells of germinating seeds of tropical maize genotype through *Agrobacterium tumefaciens* infection. The protocol was developed by using *Agrobacterium* strain EHA105 containing vector pCambia3301 carrying *cry1Ab*, *gus* and *bar* genes. The expression of transgene *gus* in T₀ plants was confirmed by measuring the hydrolysis rate of the fluorescent substrate 4-methylumbelliferyl-beta-D-glucuronide (MUG) assay whereas the presence of *cry1Ab* gene was confirmed by polymerase chain reaction and T₀ plants were allowed to grow in glass house into whole plant until maturity and were selfed to produce seeds of T₁ generation. The presence of transgene and its segregation was studied in T₁ generation through Southern and enzyme-linked immunosorbent assay confirming the presence of transgene and its expression respectively. The developed protocol is cost-effective, efficient and genotype independent without involvement of any tissue culture procedure and can generate a relatively large number of transgenic plants in approximately 75-90 days.

Accession Number: CABI:20163202186

ISSN: 0369-8211

Record 4 of 42

Title: Screening of new isolates of *Bacillus thuringiensis* for *cryI* genes and testing of toxicity against *Dichocrocis punctiferalis* (Family: *Pyrilidae*, order: *Lepidoptera*).

Author(s): (Manikandan, R.); (Muthukumar, C.); (Ramalakshmi, A.); (Balasubramani, V.); (Udayasuriyan, V.)

Source: Microbiology (Moscow)

Volume: 85

Issue: 2

Pages: 191-197

DOI: 10.1134/S0026261716020144

Published: 2016

Abstract: In order to identify the more toxic novel *cry* gene, the *cryI* gene was screened in six indigenous isolates of Bt by PCR with degenerate primers showed amplification in all the Bt isolates. Subsequent screening of *cryI* subfamily gene(s) by gene specific primer showed amplification of *cryIA* gene in the five Bt isolates, three out of the six *cryI* positive isolates showed the presence of *cryIAa* gene. One of the six Bt isolates showed the presence of *cryIAb* gene. Five Bt isolates showed amplification for *cryIAc* gene and a variation in size of amplification was observed in one of the Bt isolates Bt, T27. Further, SDS-PAGE analysis of a spore crystal mixture isolated from new isolates of Bt, T27 showed a single band of ~135 kDa indicating presence of *cryIAc* gene. The toxicity analysis of Bt strain T27 against *Dichocrocis punctiferalis* showed 100 per cent mortality on the fifth day after treatment. The varied ~925 bp amplicon of *cryIAc* gene of Bt, T27 was amplified and cloned

in a T/A vector. Comparison of nucleotide sequence data generated from the *cry1Ac* (~925 bp) gene showed 99 percent homology and two amino acid variation when comparison with its holotype sequence of Cry1Ac1.

Accession Number: CABI:20163194380

ISSN: 0026-2617

Record 5 of 42

Title: Change in the diversity of bacterial community in larval midguts of the striped stem borer, *Chilo suppressalis* (Lepidoptera: Crambidae), after treatment with *Bacillus thuringiensis* insecticidal proteins.

Author(s): (Li Zhen); (Han LanZhi); (Liu YuDi); (Hou MaoLin)

Source: Acta Entomologica Sinica

Volume: 59

Issue: 3

Pages: 292-300

Published: 2016

Abstract: Aim: To clarify the change in the bacterial community in larval midguts of the striped stem borer, *Chilo suppressalis* (Lepidoptera: Crambidae) after treatment with *Bacillus thuringiensis* insecticidal proteins. Methods: Midguts were dissected from *C. suppressalis* larvae that were collected from Beijing (BJ) and Fuzhou (FZ) of China and successively reared with artificial diets without Bt insecticidal proteins and with Bt insecticidal proteins (Cry1Ab, Cry1Ac and Cry1Ca), respectively. Degeneration gradient gel electrophoresis (DGGE) and Illumina MiSeq platform were employed to detect the bacterial community in these midguts and to compare its difference among different treatments (BJCK, BJCry1Ab, BJCry1Ac, FZCK and FZ1Ca) of the two populations. Results: The DGGE profiles demonstrated that there was difference in bacterial abundance in larval midguts of *C. suppressalis* among different treatments. Analyses on DNA sequence of 16S rDNA libraries indicated that among the midgut bacteria *Enterococcus* bacteria of Firmicutes was the most dominant, followed by bacteria of *Lactobacillus* and *Bacillus* (Firmicutes), Proteobacteria, Chloroflexi, and Bacteroidetes. The proportions of the dominant *Enterococcus* bacteria in the larvae treated with Bt insecticidal proteins (BJCry1Ab, BJCry1Ac and FZ1Ca) were higher than those in the larvae without treatment with Bt (BJCK and FZCK), but the proportions of *Lactobacillus* bacteria were lower in the larvae treated with Bt insecticidal proteins. The bacterial abundance also differed between BJCK and FZCK. Conclusion: The results suggest that the bacterial abundance in larval midguts of *C. suppressalis* changes after treatment with Bt insecticidal proteins, which may be related to the difference in Bt insecticidal proteins, geographical sites and successive rearing time.

Accession Number: CABI:20163181593

ISSN: 0454-6296

Record 6 of 42

Title: *Daphnia magna* negatively affected by chronic exposure to purified Cry-toxins.

Author(s): (Bohn, T.); (Rover, C. M.); (Semenchuk, P. R.)

Source: Food and Chemical Toxicology

Volume: 91

Pages: 130-140

DOI: 10.1016/j.fct.2016.03.009

Published: 2016

Abstract: Cry-toxin genes originating from *Bacillus thuringiensis* are inserted into genetically modified (GM) plants, often called Bt-plants, to provide insect resistance to pests. Significant amounts of Bt-plant residues, and thus Cry-toxins, will be shed to soil and aquatic environments. We exposed *Daphnia magna* to purified Cry1Ab and Cry2Aa toxins for the full life-span of the animals. We used single toxins in different doses and combinations of toxins and Roundup, another potential stressor on the rise in agricultural ecosystems. Animals exposed to 4.5 mg/L (ppm) of Cry1Ab, Cry2Aa and the combination of both showed markedly higher mortality, smaller body size and very low juvenile production compared to controls. Animals exposed to 0.75 mg/L also showed a tendency towards increased mortality but with increased early fecundity compared to the controls. Roundup stimulated animals to strong early reproductive output at the cost of later rapid mortality. We conclude that (i) purified Cry-toxins in high concentrations are toxic to *D. magna*, indicating alternative modes-of-action for these Cry-toxins; (ii) Cry-toxins act in combination, indicating that 'stacked events' may have stronger effects on non-target organisms; (iii) further studies need to be done on combinatorial effects of multiple Cry-toxins and herbicides that co-occur in the environment.

Accession Number: CABI:20163183942

ISSN: 0278-6915

Record 7 of 42

Title: Challenges in conducting transgenic R&D in developing countries: the Philippine experience.

Author(s): (Mendoza, E. M. T.)

Edited by: Muleo, R.; Chagne, D.

Source: Acta Horticulturae

Issue: 1110

Pages: 185-195

Published: 2016

Abstract: The Philippines is the first Asian country to establish a biosafety regulatory system in 1990 and to commercialize a genetically modified (GM) food crop (Bt corn) in 2003. After ten years, GM corn (insect-protected or Bt, herbicide tolerant or HT and stacked with both traits) is planted to more than 800,000 ha. However, the success that GM corn enjoys in the country has not yet been transferred to the home-grown GM or transgenic crops. Presently, four GM crops: Bt cotton, Bt eggplant, Golden Rice and long shelf-life papaya are being field tested in The Philippines. Among the challenges confronting the conduct of R&D and commercialization of these transgenic crops are as follows: (a) access to technology and/or lack of know-how; (b) funding constraints; (c) strict regulation; and (d) acceptance and activism. We have addressed these challenges in various ways. Lack of technology and know-how is addressed by technology acquisition as well as extensive training of personnel. Funds for projects come from government agencies (Philippines' Department of Science and Technology and the Department of Agriculture) and international funding agencies. Modern biotech products are regulated under the National Committee on Biosafety of the Philippines (EO 490) of 1990 and the National Biosafety Framework (EO 514) of 2006 and regulation is widely perceived by researchers as strict and very slow. However, it is also the strict and science-based regulation, which has allowed the commercialization of Bt corn. Lastly, similar to the experience in other countries, strong and persistent anti-biotech groups exist in The Philippines. To address this, continuous dissemination of science-based information is undertaken by both public and private agencies for better understanding and appreciation of modern biotechnology by the general public and all concerned sectors.

Accession Number: CABI:20163163336

Conference: XXIX International Horticultural Congress on Horticulture: Sustaining Lives, Livelihoods and Landscapes (IHC2014): International Symposium on Molecular Biology in Horticulture, Brisbane, Australia.

ISSN: 0567-7572

ISBN: 978-94-62611-04-7

Record 8 of 42

Title: Annual post-market environmental monitoring (PMEM) report on the cultivation of genetically modified maize MON 810 in 2014 from Monsanto Europe S.A.

Group Author(s): Panel on Genetically Modified Organisms

Source: EFSA Journal

Volume: 14

Issue: 4

Pages: 4446

Published: 2016

Abstract: Following a request from the European Commission, the Panel on Genetically Modified Organisms of the European Food Safety Authority (GMO Panel) assessed the annual post-market environmental monitoring (PMEM) report for the 2014 growing season of maize MON 810 provided by Monsanto Europe S.A. The GMO Panel concludes that the insect resistance monitoring data do not indicate a decrease in susceptibility of field Iberian populations of corn borers to the Cry1Ab protein over the 2014 season. However, as the methodology for insect resistance monitoring remained unchanged compared to previous PMEM reports, the GMO Panel reiterates its

previous recommendations for improvement of the insect resistance management plan. The GMO Panel considers that the farmer alert system to report complaints regarding product performance could complement the information obtained from the laboratory bioassays, but encourages the consent holder to provide more information in order to be in a position to appraise its usefulness. The data on general surveillance activities do not indicate any unanticipated adverse effects on human and animal health or the environment arising from the cultivation of maize MON 810 cultivation in 2014. The GMO Panel reiterates its previous recommendations to improve the methodology for the analysis of farmer questionnaires and conduct of the literature review in future annual PMEM reports on maize MON 810. The GMO Panel urges the consent holder to consider how to make best use of the information recorded in national registers to optimise sampling for farmer questionnaires, and requests to continue reviewing and discussing relevant scientific publications on possible adverse effects of maize MON 810 on rove beetles. Also, the GMO Panel encourages relevant parties to continue developing a methodological framework to use existing networks in the broader context of environmental monitoring.

Accession Number: CABI:20163166358

ISSN: 1831-4732

Record 9 of 42

Title: Comparative survival and development of spotted bollworm, *Earias vittella* (Fabricius) on *Bt* and isogenic non *Bt* cotton genotypes under field cage conditions.

Author(s): (Sera, P. S.); (Ramesh Arora)

Source: Journal of Cotton Research and Development

Volume: 30

Issue: 1

Pages: 97-103

Published: 2016

Abstract: Survival and development of *Earias vittella* (Fabricius) was studied on four *Bt* cotton hybrids, one each from four different events, viz., MRC 6301 *Bt* (*cry1Ac* gene), JKCH 1947 *Bt* (modified *cry1Ac* gene), NCEH 6R *Bt* (fusion *cry1Ac/cry1Ab* gene) and MRC 7017 BG II (*cry1Ac* and *cry2Ab* genes) along with their isogenic non-*Bt* genotypes at different crop ages under field cage conditions at the Cotton Research Farm, Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana. Four plants per genotype were tagged and covered with portable screen cages in the field. Fifty neonates from the stock culture were placed gently using soft camel hair brush and were evenly distributed on each tagged plant with in cages each time on 90, 120 and 150 days old crop. The observations were recorded on larval survival, larval period, larval growth index, pupal survival, pupal period and survival index. All *Bt* cotton hybrids showed zero survival index indicating strong in-built resistance against *E. vittella* as compared to the isogenic non-*Bt* genotypes under field conditions. None of the neonates could manage to complete the larval period and reach pupal stage at any of the selected crop ages (90, 120 and 150 days old crop) signifying that toxin content was still sufficient to cause 100 per cent mortality of neonates even when released at later crop stages. Conversely, larval survival varied from 56.5 to 63.0 per cent on non-*Bt* genotypes. Among non-*Bt* genotypes, the survival index was higher on JKCH 1947 followed by NCEH 6R, MRC 7017 and MRC 6301.

Accession Number: CABI:20163167846

ISSN: 0972-8619

Record 10 of 42

Title: Comparison of susceptibility of *Chilo suppressalis* and *Bombyx mori* to five *Bacillus thuringiensis* proteins.

Author(s): (Jiao YaoYu); (Yang Yan); (Meissle, M.); (Peng YuFa); (Li YunHe)

Source: Journal of Invertebrate Pathology

Volume: 136

Pages: 95-99

Published: 2016

Abstract: Transformation of rice with genes encoding insecticidal Cry proteins from *Bacillus thuringiensis* (*Bt*) should confer high resistance to target lepidopteran pests, such as *Chilo suppressalis*, and low toxicity to non-target organisms, such as silkworm *Bombyx mori*. Five purified Cry proteins that have been used for plant transformation were tested using dietary exposure assays. The susceptibility of *C. suppressalis* larvae to the five insecticidal proteins in the decreasing order was: Cry1Ca > Cry1Ab > Cry1Ac > Cry2Aa > Cry1Fa. However, the toxicities of the Cry proteins to *B. mori* were in the order: Cry1Fa > Cry1Ca > Cry2Aa > Cry1Ab > Cry1Ac. The Cry1Ca, Cry1Ab and Cry1Ac proteins exhibited relatively high toxicity to *C. suppressalis* larvae, with EC₅₀ values of 16.4, 45.8 and 89.6 ng/g, respectively. The toxicities of the three Cry proteins to *B. mori* larvae were 8, 14, and 22 times lower, with EC₅₀ values of 138.3, 628.4 and 1939.2 ng/g, respectively. The Cry1Fa and Cry2Aa proteins showed high toxicity to *B. mori* larvae, with EC₅₀ values of 135.7 and 373.9 ng/g, respectively, but low toxicity to *C. suppressalis* larvae, with EC₅₀ values of 6092.1 and 1208.5 ng/g, respectively. We thus conclude that Cry1Ab, Cry1Ac and Cry1Ca are appropriate for transforming rice to control lepidopteran rice pests. In contrast, Cry1Fa and Cry2Aa are not appropriate due to their high toxicity to silkworm larvae and low activity against the target pest.

Accession Number: CABI:20163163993

ISSN: 0022-2011

Record 11 of 42

Title: Biological activity of Bt proteins expressed in different structures of transgenic corn against *Spodoptera frugiperda*.

Author(s): (Bernardi, D.); (Bernardi, O.); (Horikoshi, R. J.); (Salmeron, E.); (Okuma, D. M.); (Omoto, C.)

Source: Ciencia Rural

Volume: 46

Issue: 6

Pages: 1019-1024

DOI: 10.1590/0103-8478cr20150047

Published: 2016

Abstract: *Spodoptera frugiperda* (J. E. Smith) is the main target pest of Bt corn technologies, such as YieldGard VT PRO(tm) (Cry1A.105/Cry2Ab2) and PowerCore(tm) (Cry1A.105/Cry2Ab2/Cry1F). In this study, it was evaluated the biological activity of Bt proteins expressed in different plant structures of YieldGard VT PRO(tm) and PowerCore(tm) corn against *S. frugiperda*. Complete mortality of *S. frugiperda* neonates was observed on leaf-disc of both Bt corn technologies. However, the mortality in silks and grains was lower than 50 and 6%, respectively. In addition, more than 49% of the surviving larvae in silks and grains completed the biological cycle. However, all life table parameters were negatively affected in insects that developed in silks and grains of both Bt corn events. In summary, the low biological activity of Bt proteins expressed on silks and grains of YieldGard VT PRO(tm) and PowerCore(tm) corn can contribute to the resistance evolution in *S. frugiperda* populations.

Accession Number: CABI:20163150699

Author Identifiers:

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ISSN: 0103-8478

Record 12 of 42

Title: Effect of Cry1F maize on the behavior of susceptible and resistant *Spodoptera frugiperda* and *Ostrinia nubilalis*.

Author(s): (Velez, A. M.); (Alves, A. P.); (Blankenship, E. E.); (Siegfried, B. D.)

Source: Entomologia Experimentalis et Applicata

Volume: 159

Issue: 1

Pages: 37-45

DOI: 10.1111/eea.12409

Published: 2016

Abstract: Understanding the behavior of pests targeted with *Bacillus thuringiensis* Berliner (Bt) crops is important to define resistance management strategies. Particularly the study of larval movement between plants is important to determine the feasibility of refuge configurations. Exposure to Bt maize, *Zea mays* L. (Poaceae), has been suggested to increase larval movement in lepidopteran species but few studies have examined the potential for resistance to interact with behavioral responses to Bt toxins. Choice and no-choice experiments were conducted with *Spodoptera frugiperda* (JE Smith) (Lepidoptera: Noctuidae) and *Ostrinia nubilalis* (Hubner) (Lepidoptera:

Crambidae) to determine whether Cry1F resistance influences neonate movement. Leaf discs of Cry1F maize and the corresponding isolate were used to characterize behavioral responses. In both experiments, the location (on or off of plant tissues) and mortality of susceptible and Cry1F resistant neonates was recorded for 5 days, but the analysis of larvae location was performed until 7 h. Our results indicated no strong difference between resistant and susceptible phenotypes in *S. frugiperda* and *O. nubilalis*, although a small percentage of susceptible neonates in both species abandoned maize tissue expressing Cry1F. However, significant behavioral differences were observed between species. *Ostrinia nubilalis* exhibited increased movement between leaf discs, whereas *S. frugiperda* selected plant tissue within the first 30 min and remained on the chosen plant regardless of the presence of Cry1F. *Spodoptera frugiperda* reduced larval movement may have implications to refuge configuration. This study represents the first step toward understanding the effects of Cry1F resistance on Lepidoptera larval behavior. Information regarding behavioral differences between species could aid in developing better and more flexible resistance management strategies.

Accession Number: CABI:20163137911

ISSN: 0013-8703

Record 13 of 42

Title: Farm-level GM coexistence policies in the EU: context, concepts and developments.

Author(s): (Schenkelaars, P.); (Wesseler, J.)

Edited by: Wesseler, J.; Punt, M.

Source: Eurochoices

Volume: 15

Issue: 1

Pages: 5-11

DOI: 10.1111/1746-692X.12112

Published: 2016

Abstract: Many EU MS have implemented coexistence policies to govern the cultivation of GM crops on their territory but only one GM crop, the Bt maize event MON810, is currently cultivated in the EU. From a practical point of view, a combination of paper traceability and implementation of isolation distances between GM and non-GM maize are considered as being the most effective way of segregating both types of materials. In general, infringements will however only become apparent after harvesting the crops. Liability issues will then be invoked late in the process restricting or at least limiting flexibility in the marketing of the materials in an appropriate way. Nevertheless, following the general guidelines for coexistence developed by the European Commission, EU Member States are progressively regulating coexistence at the national level. The policies in the EU governing coexistence can be differentiated into *ex-ante* regulations and *ex-post* liability rules. This differentiation is useful as the economic implications between the two differ. With regard to maize, studies show that the costs of complying with the given threshold values for GM content at farm level range from zero to 2 per cent of the total growing costs for both conventional and organic production.

Accession Number: CABI:20163148849

ISSN: 1478-0917

Record 14 of 42

Title: A comprehensive assessment of the effects of transgenic Cry1Ac/Cry1Ab rice Huahui 1 on adult *Micraspis discolor* (Fabricius) (Coleoptera: Coccinellidae).

Author(s): (Zhou Xia); (Guo YunLing); (Kong Hua); (Zuo Jiao); (Huang QiXing); (Jia RuiZong); (Guo AnPing); (Xu Lin)

Source: PLoS ONE

Volume: 11

Issue: 2

Pages: e0142714

DOI: 10.1371/journal.pone.0142714

Published: 2016

Abstract: *Micraspis discolor* (Fabricius) (Coleoptera: Coccinellidae) is a widely distributed coleoptera predator in southern Asia in rice ecosystem, and adult *M. discolor* feed on both rice pollen and soft-bodied arthropods. Biotrophic bioassay and tritrophic bioassay were conducted to evaluate the potential impact of Cry1Ac/Cry1Ab-expressing rice Huahui 1 and its non-transgenic counterpart Minghui 63 on fitness parameters of adult *M. discolor*. The results showed that the survival, and fecundity of this beetle adults were not different when they fed on Bt rice or non-Bt rice pollen or *Nilaparvata lugens* (Stal) reared on Bt rice or non-Bt rice. Toxicity assessment to ensure *M. discolor* adults were not sensitive to Cry1Ab or Cry1Ac protein independent from the pollen background, *M. discolor* adults were fed with an artificial diet containing Cry1Ac, Cry1Ab or both protein approximately 10 times higher concentration than in Huahui 1 rice pollen. No difference was detected for any of the life-table parameters tested between Cry protein-containing and pure diet. Artificial diet containing E-64 (N-(trans-Epoxysuccinyl)-L-leucine 4-guanidinobutylamide) was included as a positive control. In contrast, the pre-oviposition and fecundity of *M. discolor* were significantly adversely affected by feeding on E-64-containing diet. In both bioassays, the uptakes of Cry protein by adult *M. discolor* were tested by ELISA measurements. These results indicated that adults of *M. discolor* are not affected by Cry1Ab- or Cry1Ac-expressing rice pollen and are not sensitive to Cry protein at concentrations exceeding the levels in rice pollen in Huahui1. This suggests that *M. discolor* adults would not be harmed by Cry1Ac/Cry1Ab rice if Bt rice Huahui 1 were commercialized.

Accession Number: CABI:20163140868

ISSN: 1932-6203

Record 15 of 42

Title: Single amino acid insertions in extracellular loop 2 of *Bombyx mori* ABCC2 disrupt its receptor function for *Bacillus thuringiensis* Cry1Ab and Cry1Ac but not Cry1Aa toxins.

Author(s): (Tanaka, S.); (Miyamoto, K.); (Noda, H.); (Endo, H.); (Kikuta, S.); (Sato, R.)

Source: Peptides

Volume: 78

Pages: 99-108

DOI: 10.1016/j.peptides.2016.01.006

Published: 2016

Abstract: In a previous report, seven Cry1Ab-resistant strains were identified in the silkworm, *Bombyx mori*; these strains were shown to have a tyrosine insertion at position 234 in extracellular loop 2 of the ABC transporter C2 (BmABCC2). This insertion was confirmed to destroy the receptor function of BmABCC2 and confer the strains resistance against Cry1Ab and Cry1Ac. However, these strains were susceptible to Cry1Aa. In this report, we examined the mechanisms of the loss of receptor function of the transporter by expressing mutations in Sf9 cells. After replacement of one or two of the five amino acid residues in loop 2 of the susceptible BmABCC2 gene [BmABCC2_S] with alanine, cells still showed susceptibility, retaining the receptor function. Five mutants with single amino acid insertions at position 234 in BmABCC2 were also generated, resulting in loop 2 having six amino acids, which corresponds to replacing the tyrosine insertion in the resistant BmABCC2 gene [BmABCC2_R(+234Y)] with another amino acid. All five mutants exhibited loss of function against Cry1Ab and Cry1Ac. These results suggest that the amino acid sequence in loop 2 is less important than the loop size (five vs. six amino acids) or loop structure for Cry1Ab and Cry1Ac activity. Several domain-swapped mutant toxins were then generated among Cry1Aa, Cry1Ab, and Cry1Ac, which are composed of three domains. Swapped mutants containing domain II of Cry1Ab or Cry1Ac did not kill Sf9 cells expressing BmABCC2_R(+234Y), suggesting that domain II of the Cry toxin is related to the interaction with the receptor function of BmABCC2. This also suggests that different reactions against Bt-toxins in some *B. mori* strains, that is, Cry1Ab resistance or Cry1Aa susceptibility, are attributable to structural differences in domain II of Cry1A toxins.

Accession Number: CABI:20163132494

Author Identifiers:

Author	ResearcherID Number	ORCID Number
Sato, Ryoichi	G-1074-2013	

ISSN: 0196-9781

Record 16 of 42

Title: Can pyramids and seed mixtures delay resistance to Bt crops?

Author(s): (Carriere, Y.); (Fabrick, J. A.); (Tabashnik, B. E.)

Source: Trends in Biotechnology
Volume: 34
Issue: 4
Pages: 291-302
DOI: 10.1016/j.tibtech.2015.12.011
Published: 2016

Abstract: The primary strategy for delaying the evolution of pest resistance to transgenic crops that produce insecticidal proteins from *Bacillus thuringiensis* (Bt) entails refuges of plants that do not produce Bt toxins and thus allow survival of susceptible pests. Recent advances include using refuges together with Bt crop 'pyramids' that make two or more Bt toxins effective against the same pest, and planting seed mixtures yielding random distributions of pyramided Bt and non-Bt corn plants within fields. We conclude that conditions often deviate from those favoring the success of pyramids and seed mixtures, particularly against pests with low inherent susceptibility to Bt toxins. For these problematic pests, promising approaches include using larger refuges and integrating Bt crops with other pest management tactics.

Accession Number: CABI:20163133070
ISSN: 0167-7799

Record 17 of 42

Title: Frequency of *Bacillus thuringiensis* Cry1A.105 resistance alleles in field populations of the fall armyworm, *Spodoptera frugiperda*, in Louisiana and Florida.
Author(s): (Huang FangNeng); (Qureshi, J. A.); (Head, G. P.); (Price, P. A.); (Levy, R.); (Yang Fei); (Niu Ying)

Source: Crop Protection
Volume: 83
Pages: 83-89
DOI: 10.1016/j.cropro.2016.01.019
Published: 2016

Abstract: Fall armyworm, *Spodoptera frugiperda* (J.E. Smith), is a major pest of many crops and a cross-crop target of transgenic maize, cotton, and soybean containing *Bacillus thuringiensis* (Bt) genes. Some of the current Bt maize products for controlling lepidopteran species contain the Bt event MON 89034. The objective of this study was to determine the frequency of resistance alleles in field populations of *S. frugiperda* collected from Louisiana and Florida, U.S. to Cry1A.105, one of the two Bt genes in MON 89034. A total of 150 F₂ two-parent families of *S. frugiperda* were established using single-pair mating of field-collected individuals in 2011, which included 79 families from two locations in Louisiana and 71 families from one location in Florida. F₂ screen was conducted to detect resistance alleles in these families to Cry1A.105 protein in maize plants. Four out of the 79 Louisiana and 14 out of the 71 Florida families were identified to possess resistance alleles to the Cry1A.105 maize plants. Thus, the corresponding frequency of resistance alleles to Cry1A.105 maize was estimated to be 0.0158 with a 95% credibility interval (CI) of 0.0052-0.0323 for the Louisiana populations and 0.0559 with a 95% CI of 0.0319-0.0868 for the Florida populations. The resistant families survived on whole Cry1A.105 maize plants and demonstrated a significant level (>116-fold) of resistance to the Cry1A.105 protein in a diet-incorporated bioassay. These findings suggest that resistance allele frequency in *S. frugiperda* to single-gene Cry1A.105 maize in the U.S. southeast region apparently is not rare, most likely due to the selection of Cry1F resistance and its cross-resistance to Cry1A.105.

Accession Number: CABI:20163122805
Author Identifiers:

Author	ResearcherID Number	ORCID Number
Yang, Fei	Q-6498-2016	

ISSN: 0261-2194

Record 18 of 42

Title: Sequential sampling plan for assessing corn rootworm (Coleoptera: Chrysomelidae) larval injury to Bt maize.
Author(s): (Hong, B.); (Nowatzki, T. M.); (Sult, T. S.); (Owens, E. D.); (Pilcher, C. D.)

Source: Crop Protection
Volume: 82
Pages: 36-44
DOI: 10.1016/j.cropro.2016.01.001
Published: 2016

Abstract: In-field product performance assessments are an essential component of corn rootworm (*Diabrotica* spp.; CRW) resistance management plans for transgenic maize (*Zea mays* L.) products expressing proteins derived from the bacterium *Bacillus thuringiensis* (Bt). The goal of a successful field sampling program is to accurately characterize in-field product performance while also minimizing resource demand, as collection of maize root samples to evaluate CRW injury can present resource challenges such as labor intensiveness, potential safety issues, and a limited time window available for sampling. A resource-efficient sequential sampling plan was developed that utilizes data-driven root injury threshold values derived from benchmark product performance data for both single and pyramided Bt maize traits for CRW control. This sequential sampling methodology incorporates unbiased sampling and controlled false positive and false negative error rates, enabling accurate assessment decisions to be made with efficient resource use. Our proposed approach enables systematic and effective classification of in-field Bt maize product performance, with applications to other CRW control technologies besides Bt maize products.

Accession Number: CABI:20163122788
ISSN: 0261-2194

Record 19 of 42

Title: Field studies show no significant effect of a Cry1Ab/Ac producing transgenic cotton on the fungal community structure in rhizosphere soil.
Author(s): (Xie Ming); (Zhang YanJun); (Peng DeLiang); (Wu Gang); (Xu Peng); (Zhao JinJin); (Zhang ZhaoRong)

Source: European Journal of Soil Biology
Volume: 73
Pages: 69-76
Published: 2016

Abstract: Transgenic cotton GK 12 expressing insecticidal Cry1Ab/1Ac gene can effectively control the lepidopteran pests in agriculture, however it may have unintended side-effects on soil fungal communities. Therefore, the fungal community size and structure in rhizosphere soil of Bt and non-Bt cottons were analyzed by real-time polymerase chain reaction (qPCR) and denaturing gradient gel electrophoresis (DGGE) at growth stages and three annual replications in an intensive conventional cultivation system. The Cry1Ab/1Ac protein was undetectable or occasionally detectable at a low level (<0.1 ng/g soil) at seedling and senescence, and that the concentration of Cry1Ab/Ac protein in soil extracts did not increase over time or repeated cultivations. No significant differences in fungal population size and structure in rhizosphere soil were found between Bt-cotton GK 12 and its near-isogenic comparator at all growth stages, but they were different between Bt-cotton GK 12 and conventional cotton DP 5415 at some growth stages. The fungal population size and structure was significantly influenced by variation in years and plant growth stages. Sequencing results from DGGE bands showed that the dominant fungi were not different between Bt-cotton GK 12 and its near-isogenic comparator. Thus, the data of this study do not indicate any significant effect of Bt-cotton GK 12 on the fungal community size and structure in rhizosphere soil during these three continuous years.

Accession Number: CABI:20163121123
ISSN: 1164-5563

Record 20 of 42

Title: Dominance of Cry1F resistance in *Spodoptera frugiperda* (Lepidoptera: Noctuidae) on TC1507 Bt maize in Brazil.
Author(s): (Farias, J. R.); (Andow, D. A.); (Horikoshi, R. J.); (Sorgatto, R. J.); (Santos, A. C. dos); (Omoto, C.)

Source: Pest Management Science
Volume: 72
Issue: 5
Pages: 974-979
DOI: 10.1002/ps.4077

Published: 2016

Abstract: BACKGROUND: Dominance of resistance has been one of the major parameters affecting the rate of evolution of resistance to *Bt* crops. High dose is the capacity of *Bt* crops to kill heterozygous insects and has been an essential component of the most successful strategy to manage resistance to these crops. Experiments were conducted to evaluate directly and indirectly whether the TC1507 event is high dose to *Spodoptera frugiperda* (JE Smith). RESULTS: About 8% of heterozygote neonate larvae were able to survive, complete larval development and emerge as normal adults on TC1507 leaves, while susceptible larvae could not survive for 5 days. The estimated dominance of resistance was 0.150.09 and significantly higher than zero; therefore, the resistance to Cry1F expressed in TC1507 was not completely recessive. A 25-fold dilution of TC1507 maize leaf tissue in an artificial diet was able to cause a maximum mortality of only 37%, with growth inhibition of 82% at 7 days after larval infestation. CONCLUSION: Resistance to Cry1F in TC1507 maize is incompletely recessive in *S. frugiperda*. TC1507 maize is not high dose for *S. frugiperda*. Additional or alternative resistance management strategies, such as the replacement of single-trait *Bt* maize with pyramided *Bt* maize, which produces multiple proteins targeting the same insect pests, should be implemented wherever this technology is in use and *S. frugiperda* is the major pest.

Accession Number: CABI:20163126064

Author Identifiers:

Author	ResearcherID Number	ORCID Number
Omoto, Celso	D-9794-2012	0000-0002-6432-830X

ISSN: 1526-498X

Record 21 of 42

Title: Rapid selection and characterization of Cry1F resistance in a Brazilian strain of fall armyworm.

Author(s): (Leite, N. A.); (Mendes, S. M.); (Santos-Amaya, O. F.); (Santos, C. A.); (Teixeira, T. P. M.); (Guedes, R. N. C.); (Pereira, E. J. G.)

Source: Entomologia Experimentalis et Applicata

Volume: 158

Issue: 3

Pages: 236-247

DOI: 10.1111/eea.12399

Published: 2016

Abstract: Transgenic maize (*Zea mays* L., Poaceae) event TC1507, producing the Cry1F protein of *Bacillus thuringiensis* Berliner, has been used for management of the fall armyworm, *Spodoptera frugiperda* (JE Smith) (Lepidoptera: Noctuidae), in Brazil since 2009. A strain of *S. frugiperda*, obtained from field collections of larvae in TC1507 maize in Minas Gerais state in 2010, was selected in the laboratory for resistance to Cry1F using leaves of TC1507 maize in two selection regimes. Continuous exposure of larvae to Cry1F was more effective than exposure for 6, 8, and 10 days in the selection of resistant *S. frugiperda* individuals. With only four generations of laboratory selection, a strain with high levels of resistance to Cry1F was obtained, as indicated by the survival of insects reared on leaves of TC1507 maize plants and by the more than 300-fold resistance level measured in bioassays with the purified Cry1F protein. Importantly, reciprocal crosses between control and the Cry1F-selected strains revealed that the resistance is autosomal and incompletely recessive, and the response obtained in the backcross of the F₁ generation with the resistant strain was consistent with simple monogenic inheritance. Additionally, there were no apparent fitness costs associated with resistance either for survival or larval growth on non-Bt maize leaves. Our findings provide experimental evidence for rapid evolution of Cry1F resistance in *S. frugiperda* in the laboratory and further reinforce the potential of this species to evolve field resistance to the TC1507 maize as previously reported. The resistant strain isolated in this study provides an opportunity to estimate the resistance allele frequency in the field and to determine the biochemical and molecular basis of the resistance, which should provide further information to assist in the resistance management of *S. frugiperda* on transgenic maize producing *B. thuringiensis* proteins.

Accession Number: CABI:20163112002

Author Identifiers:

Author	ResearcherID Number	ORCID Number
Pereira, Eliseu	C-5365-2015	0000-0002-8957-6465

ISSN: 0013-8703

Record 22 of 42

Title: Effects of three-year cultivation of Cry1Ab-expressing Bt maize on soil microarthropod communities.

Author(s): (Arias-Martin, M.); (Garcia, M.); (Lucianez, M. J.); (Ortego, F.); (Castanera, P.); (Farinos, G. P.)

Source: Agriculture, Ecosystems & Environment

Volume: 220

Pages: 125-134

DOI: 10.1016/j.agee.2015.09.007

Published: 2016

Abstract: The impact of Cry1Ab-expressing Bt maize (event MON810) on non-target fauna has been a major concern since its deployment in Europe. In this paper, we have assessed the levels of Cry1Ab in rhizosphere soil samples from a Bt maize crop and evaluated the potential effects of Bt maize on soil microarthropods by a three-year trial in an experimental farm-scale field in Central Spain. The Cry1Ab toxin was detected in decaying soil organic matter (OM) from Bt maize plots up to three months after harvest, with values ranging between 0.10 and 0.18 ng Cry1Ab/mg OM, but it showed low insecticidal activity. The study focused on Acari and Collembola, the two major components of the soil microarthropod community. They accounted for 88% of the total specimens collected, and they were identified at the suborder and species level, respectively. Interestingly, Cry1Ab was detected for the first time in field collected collembolans, *Entomobrya* spp., demonstrating their exposure to the toxin. The abundance of mites and collembolans and the frequency of occurrence of the main collembolan species did not rely on the type of maize except for *Parisotoma notabilis*, more abundant and frequent in Bt maize plots. However, significant differences among years were common in both groups. Noticeably, we found higher values of species richness and diversity of collembolans in Cry1Ab-expressing Bt maize than in non-Bt plots, which could be explained under different scenarios. Our results suggest that continuous cultivation of Bt maize does not negatively affect soil microarthropods, indicating that Bt maize could be compatible with this community.

Accession Number: CABI:20163106076

Author Identifiers:

Author	ResearcherID Number	ORCID Number
Ortego, Felix	F-9402-2011	
Partearroyo, CIB-Biblioteca	L-3262-2014	0000-0002-1692-4481
FARINOS, GEMA	D-9849-2015	0000-0002-4952-5372

ISSN: 0167-8809

Record 23 of 42

Title: *FUM* gene expression profile and fumonisin production by *Fusarium verticillioides* inoculated in Bt and non-Bt maize.

Author(s): (Rocha, L. O.); (Barroso, V. M.); (Andrade, L. J.); (Pereira, G. H. A.); (Ferreira-Castro, F. L.); (Duarte, A. P.); (Michelotto, M. D.); (Correa, B.)

Source: Frontiers in Microbiology

Volume: 7

Issue: January

Pages: 01503

Published: 2016

Abstract: This study aimed to determine the levels of fumonisins produced by *Fusarium verticillioides* and *FUM* gene expression on Bt (*Bacillus thuringiensis*) and non-Bt maize, post harvest, during different periods of incubation. Transgenic hybrids 30F35 YG, 2B710 Hx and their isogenic (30F35 and 2B710) were collected from the field and a subset of 30 samples selected for the experiments. Maize samples were sterilized by gamma radiation at a dose of 20 kGy. Samples were then inoculated with *F. verticillioides* and analyzed under controlled conditions of temperature and relative humidity for fumonisin B₁ and B₂ (FB₁ and FB₂) production and *FUM1*, *FUM3*,

FUM6, *FUM7*, *FUM8*, *FUM13*, *FUM14*, *FUM15*, and *FUM19* expression. 2B710 Hx and 30F35 YG kernel samples were virtually intact when compared to the non-*Bt* hybrids that came from the field. Statistical analysis showed that FB₁ production was significantly lower in 30F35 YG and 2B710 Hx than in the 30F35 and 2B710 hybrids ($P < 0.05$). However, there was no statistical difference for FB₂ production ($P > 0.05$). The kernel injuries observed in the non-*Bt* samples have possibly facilitated *F. verticillioides* penetration and promoted FB₁ production under controlled conditions. *FUM* genes were expressed by *F. verticillioides* in all of the samples. However, there was indication of lower expression of a few *FUM* genes in the *Bt* hybrids; and a weak association between FB₁ production and the relative expression of some of the *FUM* genes were observed in the 30F35 YG hybrid.

Accession Number: CABI:20163106740

ISSN: 1664-302X

Record 24 of 42

Title: Testing dose-dependent effects of stacked Bt maize pollen on in vitro-reared honey bee larvae.

Author(s): (Steijven, K.); (Steffan-Dewenter, I.); (Hartel, S.)

Source: Apidologie

Volume: 47

Issue: 2

Pages: 216-226

Published: 2016

Abstract: In agricultural landscapes all over the world, honey bees are exposed to genetically modified (GM) pollen. Stacked Bt-maize varieties combine multiple Bt proteins against different insect taxa with herbicide resistance. To test for potential effects on non-target organisms, we conducted an in vitro larvae-rearing experiment where we fed increasing amounts of stacked Bt pollen to honey bee larvae. Bt pollen was equally well digested as two control maize varieties. No dose-dependent effects of Bt maize were detected in terms of survival and developmental delay. However, for prepupal weight we did find a dose-dependent response, suggesting a pleiotropic effect. Comparing this finding with the literature we conclude that the found effect is not likely to occur in a field situation. We could however show that dose-dependent effects are detectable. Our results underline the importance of testing dose-dependent effects of GM plant material in an environmental risk assessment (ERA).

Accession Number: CABI:20163096774

ISSN: 0044-8435

Record 25 of 42

Title: Field-evolved mode 1 resistance of the fall armyworm to transgenic Cry1Fa-expressing corn associated with reduced Cry1Fa toxin binding and midgut alkaline phosphatase expression.

Author(s): (Jakka, S. R. K.); (Gong Liang); (Hasler, J.); (Rahul Banerjee); (Sheets, J. J.); (Narva, K.); (Blanco, C. A.); (Jurat-Fuentes, J. L.)

Source: Applied and Environmental Microbiology

Volume: 82

Issue: 4

Pages: 1023-1034

DOI: 10.1128/AEM.02871-15

Published: 2016

Abstract: Insecticidal protein genes from the bacterium *Bacillus thuringiensis* (Bt) are expressed by transgenic Bt crops (Bt crops) for effective and environmentally safe pest control. The development of resistance to these insecticidal proteins is considered the most serious threat to the sustainability of Bt crops. Resistance in fall armyworm (*Spodoptera frugiperda*) populations from Puerto Rico to transgenic corn producing the Cry1Fa insecticidal protein resulted, for the first time in the United States, in practical resistance, and Bt corn was withdrawn from the local market. In this study, we used a field-collected Cry1Fa corn-resistant strain (456) of *S. frugiperda* to identify the mechanism responsible for field-evolved resistance. Binding assays detected reduced Cry1Fa, Cry1Ab, and Cry1Ac but not Cry1Ca toxin binding to midgut brush border membrane vesicles (BBMV) from the larvae of strain 456 compared to that from the larvae of a susceptible (Ben) strain. This binding phenotype is descriptive of the mode 1 type of resistance to Bt toxins. A comparison of the transcript levels for putative Cry1 toxin receptor genes identified a significant downregulation (>90%) of a membrane-bound alkaline phosphatase (ALP), which translated to reduced ALP protein levels and a 75% reduction in ALP activity in BBMV from 456 compared to that of Ben larvae. We cloned and heterologously expressed this ALP from susceptible *S. frugiperda* larvae and demonstrated that it specifically binds with Cry1Fa toxin. This study provides a thorough mechanistic description of field-evolved resistance to a transgenic Bt crop and supports an association between resistance and reduced Cry1Fa toxin binding and levels of a putative Cry1Fa toxin receptor, ALP, in the midguts of *S. frugiperda* larvae.

Accession Number: CABI:20163101472

ISSN: 0099-2240

Record 26 of 42

Title: Evaluation of European corn borer *Ostrinia nubilalis* (Lepidoptera: Crambidae) larval movement and survival in structured and seed blend refuge plantings.

Author(s): (Oyediran, I.); (Dively, G.); (Huang, F.); (Burd, T.)

Source: Crop Protection

Volume: 81

Pages: 145-153

DOI: 10.1016/j.cropro.2015.12.008

Published: 2016

Abstract: Blending *Bacillus thuringiensis* (Bt) corn and non-Bt corn seeds in the same bag is a convenient and easier compliance solution to satisfy refuge regulations. However, there has been considerable debate and concern about larval movement of the target insects in a seed blend because of its potential effect on the development of resistance. Reported here are studies to determine the larval movement of European corn borers, *Ostrinia nubilalis* (Hubner), in a seed blend compared to a structured refuge and their effects on survival, feeding injury and larval fitness. Also evaluated is the relative performance of a purple-seeded corn hybrid as a surrogate host plant for tracking gene flow. Seed blend and structured refuge arrangements of Agrisure GT/CB/LL Bt corn expressing Cry1Ab and isoline plants were evaluated at two locations in 2013 and 2014 by manually infesting refuge plants with first and second generation corn borer larvae. The majority of leaf and stalk injury was recorded on the refuge plant, which amounted to 66-83% of the total tunnel length. In both refuge arrangements, plant injury and the number of larvae recovered significantly decreased on neighboring plants with increasing distance away from the refuge plant in the same row. The relative decline in injury was much more pronounced in the seed blend, with neighbor Bt plants experiencing very minor tunneling or no injury at all due to the high dose trait. Eighty-nine percent fewer live larvae were also found on neighbor Bt plants in the seed blend compared to those found in the structured refuge plots. Larvae that moved to Bt plants as well as older instars that were manually placed on Bt plants failed to complete development. Comparison of the number of tunnels and larvae recovered per refuge plant indicated that the seed blend may not produce as many susceptible individuals as those produced in a structured refuge arrangement. Although the purple-seeded hybrid showed lower levels of ear and stalk injury, it could serve as an appropriate surrogate refuge plant to track gene flow.

Accession Number: CABI:20163099767

ISSN: 0261-2194

Record 27 of 42

Title: Genetic basis of Cry1F resistance in two Brazilian populations of fall armyworm, *Spodoptera frugiperda*.

Author(s): (Santos-Amaya, O. F.); (Tavares, C. S.); (Monteiro, H. M.); (Teixeira, T. P. M.); (Guedes, R. N. C.); (Alves, A. P.); (Pereira, E. J. G.)

Source: Crop Protection

Volume: 81

Pages: 154-162

DOI: 10.1016/j.cropro.2015.12.014

Published: 2016

Abstract: Large-scale adoption of transgenic crops expressing genes from *Bacillus thuringiensis* (Bt) imposes high selection pressure for evolution of field-relevant resistance that can reduce pest control efficacy, such as reported for Cry1F maize (*Zea mays* L.) in populations of fall armyworm, *Spodoptera frugiperda* (J. E. Smith) (Lepidoptera: Noctuidae), of Puerto Rico, Brazil, and the United States. As part of our effort to improve fall armyworm resistance management to Bt crops, here we determined the genetic basis of Cry1F resistance in two *S. frugiperda* strains originated from field collections in different regions of Brazil and further selected in the laboratory for high levels of resistance to Cry1F maize. Continuous exposure to the TC1507 event for 11 generations resulted in more than 183-fold resistance to Cry1F in

the two strains studied, and such a high resistance level enabled the insects to complete larval development on the Bt maize plants. Genetic analyses using concentration-response bioassays with progenies from reciprocal crosses between resistant and susceptible insects indicated that the inheritance of the resistance is autosomal, recessive and without maternal effects. Backcross of the F₁ progeny with the parental resistant strains revealed that the resistance in the two selected strains is conferred by a single locus or set of tightly linked loci. These results support some of the assumptions of the strategy in use for fall armyworm resistance management to Bt Cry1F maize, but survival rates of heterozygotes on the Bt plants were higher than 5%, showing that the Cry1F maize does not produce a high dose of the insecticidal protein for *S. frugiperda*. Additionally, we detected a delay in larval development time that may favor assortative mating of individuals carrying resistance alleles. These findings are consistent with the rapid evolution of Cry1F resistance in certain field populations of fall armyworm. Implications for resistance management of *S. frugiperda* to Bt maize are discussed.

Accession Number: CABI:20163099768

Author Identifiers:

Author	ResearcherID Number	ORCID Number
Pereira, Eliseu	C-5365-2015	0000-0002-8957-6465

ISSN: 0261-2194

Record 28 of 42

Title: The synergic and antagonistic activity of Cry1Ab and Cry2Aa proteins against lepidopteran pests.

Author(s): (Azizoglu, U.); (Ayvaz, A.); (Yilmaz, S.); (Temizgul, R.)

Source: Journal of Applied Entomology

Volume: 140

Issue: 3

Pages: 223-227

DOI: 10.1111/jen.12241

Published: 2016

Abstract: Cry1Ab and Cry2Aa were overexpressed in *Escherichia coli* BL21(DE3), and their proportions were determined for evaluating their synergic and antagonistic interactions on *Ephesia kuehniella* and *Plodia interpunctella*. Results indicated antagonistic interaction on both lepidopteran pests, and it was concluded that 1:1 combination of Cry1Ab:Cry2Aa should be avoided in control programmes for these larvae.

Accession Number: CABI:20163096193

ISSN: 0931-2048

Record 29 of 42

Title: Nitrogen and phosphorus nutrition and stoichiometry in the response of maize to various N rates under different rotation systems.

Author(s): (Ma, B. L.); (Zheng, Z. M.); (Morrison, M. J.); (Gregorich, E. G.)

Source: Nutrient Cycling in Agroecosystems

Volume: 104

Issue: 1

Pages: 93-105

DOI: 10.1007/s10705-016-9761-6

Published: 2016

Abstract: Better understanding of plant nutrition and nutrient interactions is of critical importance for developing best management practices in crop production. A three-year study was conducted to examine N and P nutrition and their association in maize as affected by rotation system, N application rate and hybrid maize. Rotation by N treatments were composed of maize-alfalfa (MA), maize-soybean (MS) and continuous maize (MM), fertilized in maize year at 0, 50, 100 and 150 kg N ha⁻¹, respectively. The two maize varieties were glyphosate-resistant (RR) non-Bt (non-Bt) and stacked RR+Bt near-isoline (Bt) hybrids. Our data showed that grain yield, stover, and total aboveground (or shoot) dry matter, N and P uptake (except for stover P) in amounts followed the order MA > MS > MM and were well responsive to N rates. Grain and shoot N and P contents of Bt maize was greater ($P < 0.05$) than those of non-Bt hybrid in MM. The N:P ratio was positively correlated with N application rates, and was greater in rotational maize than in MM. Both hybrids attained their maximum yields at approximately 201 kg ha⁻¹ of grain N and 255 kg ha⁻¹ of shoot N, corresponding to 36 and 43 kg P ha⁻¹ in grain and shoot. Nitrogen harvest index, P harvest index and nutrient internal efficiency were responsive to N rates but were not different between the hybrids. This study revealed that the critical grain and shoot N content achieving maximum yield appeared to concomitantly result in high P contents.

Accession Number: CABI:20163088534

ISSN: 1385-1314

Record 30 of 42

Title: A high-throughput, in-vitro assay for *Bacillus thuringiensis* insecticidal proteins.

Author(s): (Willcoxon, M. I.); (Dennis, J. R.); (Lau, S. I.); (Xie WeiPing); (You You); (Leng Song); (Fong, R. C.); (Yamamoto, T.)

Source: Journal of Biotechnology

Volume: 217

Pages: 72-81

Published: 2016

Abstract: A high-throughput, in-vitro assay for *Bacillus thuringiensis* (Bt) insecticidal proteins designated as Cry was developed and evaluated for screening a large number of Cry protein variants produced by DNA shuffling. This automation-amenable assay exploits an insect cell line expressing a single receptor of Bt Cry proteins. The Cry toxin used to develop this assay is a variant of the Cry1Ab protein called IP1-88, which was produced previously by DNA shuffling. Cell mortality caused by the activated Bt Cry toxin was determined by chemical cell viability assay in 96/384-well microtiter plates utilizing CellTiter 96 obtained from Promega. A widely-accepted mode-of-action theory of certain Bt Cry proteins suggests that the activated toxin binds to one or more receptors and forms a pore through the insect gut epithelial cell apical membrane. A number of insect proteins such as cadherin-like protein (Cad), aminopeptidase-N (APN), alkaline phosphatase (ALP) and ABC transporter (ABCC) have been identified as the receptors of Bt Cry toxins. In this study, Bt Cry toxin receptors *Ostrinia nubilalis* (European corn borer) cadherin-like protein (On-Cad) and aminopeptidase-N 1 and 3 (On-APN1, On-APN3) and *Spodoptera frugiperda* (fall armyworm) cadherin-like protein (Sf-Cad) were cloned in an insect cell line, Sf21, and a mammalian cell line, Expi293F. It was observed by ligand blotting and immunofluorescence microscopy that trypsin-activated IP1-88 bound to On-Cad and On-APN1, but not Sf-Cad or On-APN3. In contrast, IP1-88 bound only to APN1 in BBMV (Brush Border Membrane Vesicles) prepared from the third and fourth-instar *O. nubilalis* larval midgut. The sensitivity of the recombinant cells to the toxin was then tested. IP1-88 showed no toxicity to non-recombinant Sf21 and Expi293F. Toxicity was observed only when the On-Cad gene was cloned and expressed. Sf-Cad and On-APN1 were not able to make those cells sensitive to the toxin. Since the expression of On-Cad alone was sufficient to make both insect and mammalian cells sensitive to the IP1-88 toxin, it is not likely that a secondary receptor, which may exist specifically in the Sf21 insect cell but not in the Expi293F cell, is involved in the cytotoxicity of IP1-88.

Accession Number: CABI:20163080318

ISSN: 0168-1656

Record 31 of 42

Title: Survival and development of spotted bollworm, *Earias vittella* (Fabricius) (Lepidoptera: Nolidae) on different transgenic Bt and isogenic non-Bt cotton genotypes.

Author(s): (Shera, P. S.); (Ramesh Arora)

Source: Phytoparasitica

Volume: 44

Issue: 1

Pages: 99-113

DOI: 10.1007/s12600-016-0505-6

Published: 2016

Abstract: Four Bt cotton hybrids, each with one of four different events, viz., MRC 6301 Bt (*cry1Ac* gene), JKCH 1947 Bt (modified *cry1Ac* gene), NCEH 6R Bt (fusion *cry1Ac/cry1Ab* gene) and MRC 7017 Bollgard II (*cry1Ac* and *cry2Ab* genes) were compared for survival and development of *Earias vittella* (Fabricius) along with their

isogenic non-Bt genotypes. None of the neonates were able to complete the larval period and reach pupal stage on squares of 90, 120 and 150 days old crop of all Bt hybrids. Likewise, on bolls also, zero per cent larval survival was observed in all Bt hybrids except JKCH 1947 Bt where 0.67 per cent larvae could manage to reach pre-pupal stage at 120 and 150 days old crop but failed to form cocoon and enter pupal stage. The surviving larva took more development time (3.7 to 5.4 days) as compared to larvae fed on bolls of JKCH 1947 non-Bt. The average survival period (ASP) of larvae was in order of 150 > 120 > 90 days old crop among the crop ages; JKCH 1947 Bt > MRC 6301 Bt > NCEH 6 R Bt > MRC 7017 Bollgard II among Bt hybrids; and bolls > squares between fruiting bodies. However, reverse was true for speed index of toxic effect. The concentration of Cry toxin varied significantly in squares and bolls and also among the crop ages. The amount of Cry toxin in squares and bolls had significant negative correlation with ASP of the *E. vittella* larvae.

Accession Number: CABI:20163084441

ISSN: 0334-2123

Record 32 of 42

Title: The interaction of two-spotted spider mites, *Tetranychus urticae* Koch, with Cry protein production and predation by *Amblyseius andersoni* (Chant) in Cry1Ac/Cry2Ab cotton and Cry1F maize.

Author(s): (Guo YanYan); (Tian JunCe); (Shi WangPeng); (Dong XueHui); (Romeis, J.); (Naranjo, S. E.); (Hellmich, R. L.); (Shelton, A. M.)

Source: Transgenic Research

Volume: 25

Issue: 1

Pages: 33-44

Published: 2016

Abstract: Crops producing insecticidal crystal (Cry) proteins from the bacterium, *Bacillus thuringiensis* (Bt), are an important tool for managing lepidopteran pests on cotton and maize. However, the effects of these Bt crops on non-target organisms, especially natural enemies that provide biological control services, are required to be addressed in an environmental risk assessment. *Amblyseius andersoni* (Acari: Phytoseiidae) is a cosmopolitan predator of the two-spotted spider mite, *Tetranychus urticae* (Acari: Tetranychidae), a significant pest of cotton and maize. Tri-trophic studies were conducted to assess the potential effects of Cry1Ac/Cry2Ab cotton and Cry1F maize on life history parameters (survival rate, development time, fecundity and egg hatching rate) of *A. andersoni*. We confirmed that these Bt crops have no effects on the biology of *T. urticae* and, in turn, that there were no differences in any of the life history parameters of *A. andersoni* when it fed on *T. urticae* feeding on Cry1Ac/Cry2Ab or non-Bt cotton and Cry1F or non-Bt maize. Use of a susceptible insect assay demonstrated that *T. urticae* contained biologically active Cry proteins. Cry protein concentrations declined greatly as they moved from plants to herbivores to predators and protein concentration did not appear to be related to mite density. Free-choice experiments revealed that *A. andersoni* had no preference for Cry1Ac/Cry2Ab cotton or Cry1F maize-reared *T. urticae* compared with those reared on non-Bt cotton or maize. Collectively these results provide strong evidence that these crops can complement other integrated pest management tactics including biological control.

Accession Number: CABI:20163077149

ISSN: 0962-8819

Record 33 of 42

Title: Corn stover ethanol yield as affected by grain yield, Bt trait, and environment.

Author(s): (Tumbalam, P.); (Thelen, K. D.); (Adkins, A.); (Dale, B.); (Balan, V.); (Gunawan, C.); (Gao, J.)

Source: Biomass and Bioenergy

Volume: 85

Pages: 119-125

DOI: 10.1016/j.biombioe.2015.12.004

Published: 2016

Abstract: Literature values for glucose release from corn stover are highly variable which would likely result in tremendous variability in bio-refinery ethanol yield from corn stover feedstock. A relatively recent change in United States corn genetics is the inclusion of the *Bacillus thuringiensis* (Bt) trait, which now accounts for three-fourths of all US planted corn acreage. The objective of this study was to evaluate the effect of corn grain yield, inclusion of the Bt trait, and location environment on corn stover quality for subsequent ethanol conversion. Two hybrid pairs (each having a Bt and non-Bt near-isoline) were analyzed giving a total of 4 hybrids. In 2010 and 2011, field plots were located in Michigan at four latitudinal differing locations in four replicated plots at each location. Stover composition and enzymatic digestibility was analyzed and estimated ethanol yield (g g^{-1}) was calculated based on hydrolyzable glucon and xylan levels. Analysis showed that there were no significant differences in total glucose or xylose levels nor in enzymatically hydrolyzable glucon and xylan concentrations between Bt corn stover and the non-Bt stover isolines. Regression analyses between corn grain yield (Mg ha^{-1}) and corn stover ethanol yield (g g^{-1}) showed an inverse relationship indicative of a photosynthate source-sink relationship. Nevertheless, the quantity of stover produced was found to be more critical than the quality of stover produced in maximizing potential stover ethanol yield on a land area basis.

Accession Number: CABI:20163069703

ISSN: 0961-9534

Record 34 of 42

Title: Investigating transgenic corn hybrids as a method for mycotoxin control.

Author(s): (Abbas, H. K.); (Bellaloui, N.); (Bruns, H. A.)

Source: Food and Nutrition Sciences

Volume: 7

Issue: 1

Pages: 44-54

DOI: 10.4236/fns.2016.71006

Published: 2016

Abstract: Transgenic Bt corn hybrids have been available for more than 10 years and are known to control specific insects. More recently, so-called "stacked-gene" hybrids, have been released with multiple insect resistance genes and genes for herbicide resistance, resulting in up to 6 traits per plant. Because insect damage can lead to increased levels of mycotoxins, such as aflatoxins and fumonisin, we designed a study to compare ten commercially available corn hybrids, two non-transgenic, four with both herbicide and insect tolerance (stacked-gene) and four with glyphosate tolerance only to determine if any hybrid class had the advantage of reduced mycotoxin contamination. The experiment was carried out in the Mississippi State University Delta Research Extension fields in Stoneville, MS for two years in fine sandy loam and clay soil. Rows were either inoculated at the V10 stage of growth with toxigenic *Aspergillus flavus* K54 (NRRL 58987, isolated from corn kernels in Mississippi), grown on wheat, and applied at a rate of 22.42 kg/ha or allowed to become naturally infected with disease-producing fungi, including various *Fusarium* and other *Aspergillus* spp. Mycotoxin production differed according to the soil type with lower levels detected in the hybrids planted in clay soil vs. sandy soil. However, no significant differences in mycotoxin production were found amongst the hybrid classes. More research is needed to identify conditions under which transgenic hybrids might produce higher yields and lower mycotoxin levels. Presently, selection of transgenic hybrids will not replace integrated strategies of biocontrol, host plant resistance, or good crop management practices for achieving adequate mycotoxin control in corn.

Accession Number: CABI:20163068687

ISSN: 2157-944X

Record 35 of 42

Title: Comparison of three transgenic Bt rice lines for insecticidal protein expression and resistance against a target pest, *Chilo suppressalis* (Lepidoptera: Crambidae).

Author(s): (Wang YaNan); (Ke KaiQie); (Li YunHe); (Han LanZhi); (Liu YanMin); (Hua HongXia); (Peng YuFa)

Source: Insect Science

Volume: 23

Issue: 1

Pages: 78-87

DOI: 10.1111/1744-7917.12178

Published: 2016

Abstract: Two transgenic rice lines (T2A-1 and T1C-19b) expressing *cry2A* and *cry1C* genes, respectively, were developed in China, targeting lepidopteran pests including *Chilo suppressalis* (Walker) (Lepidoptera: Crambidae). The seasonal expression of Cry proteins in different tissues of the rice lines and their resistance to *C. suppressalis* were assessed in comparison to a Bt rice line expressing a *cry1Ab/Ac* fusion gene, Huahui 1, which has been granted a biosafety certificate. In general, levels of Cry

proteins were T2A-1 > Huahui 1 > T1C-19b among rice lines, and leaf > stem > root among rice tissues. The expression patterns of Cry protein in the rice line plants were similar: higher level at early stages than at later stages with an exception that high Cry1C level in T1C-19b stems at the maturing stage. The bioassay results revealed that the three transgenic rice lines exhibited significantly high resistance against *C. suppressalis* larvae throughout the rice growing season. According to Cry protein levels in rice tissues, the raw and corrected mortalities of *C. suppressalis* caused by each *Bt* rice line were the highest in the seedling and declined through the jointing stage with an exception for T1C-19b providing an excellent performance at the maturing stage. By comparison, T1C-19b exhibited more stable and greater resistance to *C. suppressalis* larvae than T2A-1, being close to Huahui 1. The results suggest *cry1C* is an ideal *Bt* gene for plant transformation for lepidopteran pest control, and T1C-19b is a promising *Bt* rice line for commercial use for tolerating lepidopteran rice pests.

Accession Number: CABI:20163075200

ISSN: 1672-9609

Record 36 of 42

Title: A rapid loop-mediated isothermal amplification method for detection of the modified GM *cryIA* gene in transgenic insect-resistant cotton and rice.

Author(s): (Shen PeiLi); (Geng FengZhen); (Yu Yan); (Zhang YunZhe); (Wang ZhiXin); (Li ZhiHui); (Zhang Wei); (Shu ChangLong); (Zhang YongJun); (Tan JianXin)

Source: Food Control

Volume: 62

Pages: 357-364

DOI: 10.1016/j.foodcont.2015.10.035

Published: 2016

Abstract: Among the commercial genetically modified (GM) crops, the insect-resistant GM crops are the major cultivars that *cry* gene is introduced into. A *cryIAb/IAc* GM fusion gene (GFM *cryIA*) and a GM truncated *cryIAC* gene (*cryIAC*-Mon) is the key foreign gene employed for construction of GM crops by China researchers and Monsanto Technology LLC respectively. Here these two genes are entitled "GM *cryIA*" gene and a rapid visual loop-mediated isothermal amplification (LAMP) assay method for detection of GM *cryIA* in transgenic insect-resistant crops was established. The LAMP assay was performed at an optimal temperature of 65°C for 60 min in the presence of a set of four specific primers recognized six distinct sequences of the GM *cryIA* gene. The rough detection limit to the GM *cryIA* in samples is as low as 0.01% (a weight ratio of transgenic insect-resistant rice/cotton to non-transgenic rice/cotton). Comparatively, the sensitivity of this LAMP method is 10 times over that of the conventional PCR method. Fifteen cultivars/events and five *Bt* strains with or without *cryIA* gene were analyzed using the LAMP method as well as PCR method. The results demonstrate that this LAMP method shows a distinct specificity to the GM *cryIA* gene comparing with PCR analysis. Therefore, this LAMP method will be a potential effective tool for screening the GM *cryIA* gene in GM crops which are widely plant in China and other developing countries.

Accession Number: CABI:20163052844

ISSN: 0956-7135

Record 37 of 42

Title: Comparative study on oviposition and larval preference of spotted bollworm, *Earias vittella* on Bt and non-Bt cotton.

Author(s): (Shera, P. S.); (Ramesh Arora)

Source: Journal of Environmental Biology

Volume: 37

Issue: 1

Pages: 121-127

Published: 2016

Abstract: Oviposition and larval preference of spotted bollworm, *Earias vittella* (Fabricius) was assessed on four transgenic Bt cotton hybrids, viz. MRC 6304 Bt (*cryIAC* gene), JKCH 1947 Bt (modified *cryIAC* gene), NCEH 6R Bt (*cryIAb/cryIAC* fused gene) and MRC 7017 BG II (*cryIAC* and *cry2Ab* genes) in comparison to the respective isogenic cotton. The results showed that Bt toxin did not deter oviposition preference of *E. vittella* moths as there was no significant difference in the number of eggs laid on squares/bolls of Bt and non-Bt cotton hybrids, across different crop growth stages. There was also no behavioral change in larval preference with respect to selecting non-Bt cotton in comparison to Bt cotton. Floral bodies from Bt and the respective isogenic cotton genotypes were equally preferred by both first and third instar larvae after 24 hrs indicating that initial selection was independent of susceptibility to Bt toxin. However, *E. vittella* larvae showed significant difference in preference for different cotton genotypes. Studies on the relative preference indicated that third instar larvae had greater preference for bolls (7.29-7.50%) than for the squares (5.0-5.21%) and reverse was true for the first instar larvae which showed greater preference for squares (7.08-7.29%) than for the bolls (5.21-5.42%), in a multiple-choice test. It may be concluded that oviposition and larval preference of *E. vittella* did not differ significantly between Bt and isogenic non-Bt cotton genotypes.

Accession Number: CABI:20163056907

ISSN: 0254-8704

Record 38 of 42

Title: Evaluation of soil-applied insecticides with Bt maize for managing corn rootworm larval injury.

Author(s): (Estes, R. E.); (Tinsley, N. A.); (Gray, M. E.)

Source: Journal of Applied Entomology

Volume: 140

Issue: 1/2

Pages: 19-27

Published: 2016

Abstract: The western corn rootworm, *Diabrotica virgifera virgifera* LeConte, is considered one of the most significant insect pests of maize in North America. Larvae of other secondary subterranean pests such as grape colaspis, *Colaspis brunnea* (F.), and Japanese beetle, *Popillia japonica* Newman, can also injure maize seedlings and cause yield loss. In the past decade, maize hybrids containing Bt proteins have been used to manage the western corn rootworm; additionally, seeds are commonly treated with a neonicotinoid and fungicide combination to control secondary pests. Recently, soil-applied insecticides have been used in conjunction with rootworm Bt hybrids (and seed-applied insecticides) in areas with perceived risk for increased rootworm larval or secondary pest damage. We conducted a series of trials from 2009 to 2011 that examined multiple rootworm Bt hybrids and their near-isolines, along with two soil-applied insecticides, to determine whether the Bt plus insecticide combination resulted in an increased level of efficacy or yield. We also sampled for Japanese beetle and grape colaspis larvae to determine their potential for reducing yield. Densities of secondary pests in our trials were low and likely had no effect on maize yield. The addition of a soil-applied insecticide to rootworm Bt hybrids improved efficacy only once across 17 location-years, when overall corn rootworm injury was highest; an improvement in yield was never observed. Our results suggest that the use of a soil-applied insecticide with a rootworm Bt hybrid should only be considered in scenarios with potentially significant rootworm larval populations. However, potential negative consequences related to trait durability when soil insecticides are used with rootworm Bt maize should be considered.

Accession Number: CABI:20163032656

ISSN: 0931-2048

Record 39 of 42

Title: Cryopreservation for retaining morphology, genetic integrity, and foreign genes in transgenic plants of *Torenia fourmieri*.

Author(s): (Li JingWei); (Li HouHua); (Wang RenRui); (Gao XiaoXia); (Wang QiaoChun)

Source: Acta Physiologiae Plantarum

Volume: 38

Issue: 1

Pages: 8

Published: 2016

Abstract: *Torenia fourmieri*, a popular potted flower crop, is frequently used as a model plant in genetic transformation studies, and transgenic plants expressing various foreign genes have been obtained in this plant. A safe and long-term conservation of the transgenic plants is necessary. In this study, shoot tips of transgenic plants of *T. fourmieri* were successfully cryopreserved by droplet-vitrification. Growth patterns, and morphologies of leaves and flowers were identical between the plantlets recovered from cryopreservation and the in vitro stock cultures (control). No polymorphic bands and no alternations at ploidy level assessed by ISSR and FCM, respectively, were found in the transgenic plantlets recovered from cryopreservation in comparison with the in vitro stock cultures. The transgene *Cry IAb* analyzed by PCR was maintained, and its expression levels measured by qRT-PCR did not change in the cryo-derived transgenic plantlets. Therefore, cryopreservation can be considered a promising strategy for safe and long-term conservation of the transgenes.

Accession Number: CABI:20163024674**ISSN:** 0137-5881**Record 40 of 42****Title:** Rove beetles (Coleoptera Staphylinidae) - their abundance and competition with other predatory groups in Bt maize expressing Cry34Ab1, Cry35Ab1, Cry1F and CP4 EPSPS proteins.**Author(s):** (Palinkas, Z.); (Zalai, M.); (Szenasi, A.); (Kadar, F.); (Dorner, Z.); (Balog, A.)**Source:** Crop Protection**Volume:** 80**Pages:** 87-93**Published:** 2016**Abstract:** This study investigated the effects of different GM maize crops on the abundances of rove beetles. It also investigated competition between rove beetles and other epigeic arthropod predatory groups (ground beetles and spiders). Altogether a total of 5926 rove beetle individuals belonging to 25 species were collected. Whilst the average number of rove beetle individuals per replicate per sampling date varied and, moreover, decreased each year, there were no observed differences in rove beetle abundance when compared between isogenic and GM maize plots within the study period. Furthermore, no clear trends on positive correlations between weed coverage and rove beetle abundances were detected. Altogether a total number of 76,070 ground beetle individuals and 11,126 spiders (including all Araneae) were collected with pitfall traps. Analyses revealed a strong negative relationship between rove beetles and the other two groups in each treatment and year. According to the results the effect of interspecific competition on rove beetle abundance in GM maize is much higher than the effects of treatments including both Bt toxins and extra glyphosate applications.**Accession Number:** CABI:20163025173**ISSN:** 0261-2194**Record 41 of 42****Title:** Effects of refuges on the evolution of resistance to transgenic corn by the western corn rootworm, *Diabrotica virgifera virgifera* LeConte.**Author(s):** (Deitloff, J.); (Dunbar, M. W.); (Ingber, D. A.); (Hibbard, B. E.); (Gassmann, A. J.)**Source:** Pest Management Science**Volume:** 72**Issue:** 1**Pages:** 190-198**DOI:** 10.1002/ps.3988**Published:** 2016**Abstract:** BACKGROUND: *Diabrotica virgifera virgifera* LeConte is a major pest of corn and causes over a billion dollars of economic loss annually through yield reductions and management costs. Corn producing toxins derived from *Bacillus thuringiensis* (*Bt*) has been developed to help manage *D. v. virgifera*. However, previous studies have demonstrated the ability of this species to evolve resistance to *Bt* toxins in both laboratory and field settings. RESULTS: We used an experimental evolution approach to test the refuge strategies for delaying resistance of *D. v. virgifera* to corn producing *Bt* toxin Cry34/35Ab1. In the absence of refuges, *D. v. virgifera* developed resistance to *Bt* corn after three generations of selection. In some cases, non-*Bt* refuges reduced the level of resistance compared with the strain selected in the absence of refuges, but refuge strains did show reduced susceptibility to *Bt* corn compared with the unselected strain. CONCLUSIONS: In this study, non-*Bt* refuges delayed resistance to *Bt* corn by *D. v. virgifera* in some cases but not others. Combining the refuge strategy with pyramids of multiple *Bt* toxins and applying other pest management strategies will likely be necessary to delay resistance of *D. v. virgifera* to *Bt* corn.**Accession Number:** CABI:20163022223**ISSN:** 1526-498X**Record 42 of 42****Title:** The fate of fusion Cry1Ab/1Ac proteins from *Bt*-transgenic rice in soil and water.**Author(s):** (Liu YongBo); (Li JunSheng); (Luo ZunLan); (Wang HuaRu); (Liu Fang)**Source:** Ecotoxicology and Environmental Safety**Volume:** 124**Pages:** 455-459**Published:** 2016**Abstract:** Toxin proteins from transgenic crops entering into the environment are likely affect non-target organisms. To investigate the entry route and fate of fusion Cry1Ab/1Ac proteins from transgenic rice expressing insecticide toxins from *Bacillus thuringiensis* (*Bt*) in soil and water, we conducted greenhouse and field experiments in 2013 and 2014. Cry1Ab/1Ac proteins from *Bt*-transgenic rice in soil was found within a horizontal range of 25 cm, where most of plant roots distributed. Concentration of Cry1Ab/1Ac proteins was lower in water than in soil in the greenhouse experiment, and no Cry1Ab/1Ac protein was detected in field water. Cry1Ab/1Ac concentration from rice straws was higher in ditch water than in distilled water due to the existence of aquatic organisms in ditch water. *Bt* proteins from transgenic crops enter into soil ecosystems mainly through root exudates and into aquatic ecosystems through plant residues, which determines *Bt* fate in the environment.**Accession Number:** CABI:20153446166**ISSN:** 0147-6513

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Publication Type: J

*Record 1 of 7. Search terms matched: CRY1AB(2)

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Accession Number: CABI:20163396153

Document Type: Journal article

Author(s): Zhang YanJun; Xie Ming; Li Qian; Zhang XiaoLin; Zhang ZhaoRong

Title: Monitoring changes in the actinobacterial field communities present in the rhizosphere soil of a transgenic cotton producing Cry1Ab/Ac proteins.

Source: Crop Protection, 91 1-7; 2017

Language: English

Abstract: Transgenic cotton GK 12 producing Cry1Ab/Ac proteins can effectively control lepidopteran pests in agriculture. However, there are concerns that GK 12 has unintended side-effects on actinobacterial communities in the soil. Actinobacterial communities in the rhizosphere soil of cottons were analyzed by real-time PCR (qPCR) and denaturing gradient gel electrophoresis (DGGE) at different growth stages in three annual replications under field conditions. Population sizes and community structures of Actinobacteria were markedly affected by natural variations in years, growth stages and cultivars. No significant differences were found in population sizes (excepting at budding in 2009), community structures, and Shannon indices of Actinobacteria (excepting at budding in 2010) between the GK 12 and its non-transgenic parent Simian 3, although there were differences between the GK 12 and the conventional cotton DP 5415. Phylogenetic analysis of DGGE band sequences indicated that *Cellulosimicrobium* sp. and *Rhodococcus* sp. only occurred in the GK 12 and the Simian 3. The dominant Actinobacteria did not differ between the GK 12 and the Simian 3. In conclusion, the overall impacts of the GK 12 on actinobacterial communities in the rhizosphere soil, based on qPCR and DGGE, were not significant during three continuous years in northern China.

Publication Type: J

*Record 2 of 7. Search terms matched: BT(4); CORN(1); MAIZE(6); ZEA MAYS(1)

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*Order Full Text []

Accession Number: CABI:20163376422

Document Type: Journal article

Author(s): Liu QuanWei; Wei LiMin; Wang Feng; Zheng XinLi; Huang LiLi; Liu HaiLong; Sun RuiPing; Tan ShuYi

Title: Influences of genetically modified Bt maize on the serum biochemical parameters and enzyme activities in fattening Wuzhishan pigs.

Source: Swine Production, (1):6-8; 2016

Language: Chinese

Language of Summary: English

Abstract: 32 6-month-old healthy fattening pigs with similar genetic backgrounds and an average initial weight of 29.831.67 kg were randomly divided into 2 treatments, 4 replicates of

4 pigs and the pigs were fed with diets containing genetically modified Bt maize (experimental group) or non-genetically modified maize (control) during the period of 60d, respectively, in order to study the effects of genetically modified Bt maize on biochemical parameters and enzyme activities of fattening Wuzhishan pigs. Blood was collected at 60d for sampling. Serum total protein, albumin, globin, glucose, urea nitrogen, glycerin trimyristate and total cholesterol concentrations in the experimental group were not significantly different from those of controls ($P>0.05$). There were no significant differences in serum alkaline phosphatase, aspartate aminotransferase, and alanine aminotransferase activities between the 2 groups ($P>0.05$). In conclusion, there were no adverse effects of genetically modified Bt maize on biochemical parameters and enzyme activities of fattening Wuzhishan pigs.

Publication Type: J

*Record 3 of 7. Search terms matched: CRY1AB(1)

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Accession Number: CABI:20163378578

Document Type: Journal article

Author(s): Liu YuanYuan; Jiang DongJian; Lu Xin; Wang Wei; Xu Yang; He QingHua

Title: Phage-mediated immuno-PCR for ultrasensitive detection of Cry1Ac protein based on nanobody.

Source: Journal of Agricultural and Food Chemistry, 64 (41):7882-7889; 2016

Language: English

Abstract: The widespread use of Cry proteins in transgenic plants for insect control has raised concerns about the environment and food safety in the public. An effective detection method for introduced Cry proteins is of significance for environmental risk assessment and product quality control. This paper describes a novel phage mediated immuno-PCR (iPCR) for the ultrasensitive determination of Cry proteins based on nanobodies. Three nanobodies against Cry1Ac protein were obtained from a naive phage displayed nanobody library without animal immunization process and were applied to the iPCR assay for Cry1Ac. The phage-mediated iPCR for Cry1Ac based on nanobodies showed a dynamic range of 0.001-100 ng/mL and a limit detection of 0.1 pg/mL. Specific measurement of this established method was performed by testing cross-reactivity of other Cry1Ac analogues, and the result showed negligible cross-reactivity with other test Cry proteins (Cry1Ab, Cry1F, Cry3B). Furthermore, the phage-mediated iPCR based on nanobody should be easily applicable to the detection of many other Cry proteins.

Publication Type: J

*Record 4 of 7. Search terms matched: BT(4); CORN(1); MAIZE(5); ZEA MAYS(1)

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Accession Number: CABI:20163390548

Document Type: Journal article

Author(s): Morse, S.

Title: What you see is news: press reporting of Bt maize and Bt cotton between 1996 and 2015.

Source: Outlook on Agriculture, 45 (3):206-214; 2016

Language: English

Abstract: This article uses the Nexis database to explore the global media reporting of Bt maize and Bt cotton between 1996 and 2015 in terms of trends over time and how this relates to region (North America, Europe and Asia) and topic (six in total) of focus. While Bt cotton and Bt maize are 'genetically modified' (GM), there are differences between them in terms of the extent and pattern of media reporting. An apparent spike in media reporting of Bt maize between 1998 and 2001 is largely linked to the North America and Europe regions, and covers the period just after the first commercial release of that variety. For Bt cotton, the broad trend in media reporting mirrors the increase in Bt cotton area, and a sharp rise in press reporting as of 2008/2009 in Asia follows a rapid increase in the area of Bt cotton in India since that time. For both crops, the count of articles classified as 'Environment and natural resources' was significantly higher than for the other topics and for both crops, the topic 'Safety, accidents and disasters' had the lowest count. The media picks up on many signals within the GM crop arena, and may have a significant influence given that the public may rely heavily upon the media for its information regarding GM.

DOI: [10.1177/0030727016666237](https://doi.org/10.1177/0030727016666237)

Publication Type: J

***Record 5 of 7.** Search terms matched: BORER(1); BT(1); CORN(2); CRY1AB(3); LEPIDOPTERA(1); MAIZE(2); OSTRINIA(5); RESISTANT(2); ZEA MAYS(1)

*[Click Here to View Full Record](#)

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Accession Number: CABI:20163394671

Document Type: Journal article

Author(s): Xu LiNa; Ling YingHui; Wang YueQin; Wang ZhenYing; Hu BenJin; Zhou ZiYan; Hu Fei; He KangLai

Title: Identification of differentially expressed microRNAs between *Bacillus thuringiensis* Cry1Ab-resistant and -susceptible strains of *Ostrinia furnacalis*.

Source: Scientific Reports, 5 (15461):srep15461; 2015

Language: English

Abstract: The Asian corn borer (ACB), *Ostrinia furnacalis* (Guenee), can develop strong resistance to Cry1Ab, the most widely commercialized Cry toxin for Bt maize worldwide. It is essential to understand the mechanism of resistance for management of this species, but information on the post-transcriptional regulation of Bt resistance in this target insect is limited. In the present study, RNA was extracted from the ACB in various larval stages (1-5 instar) from Cry1Ab-sensitive (ACB-BtS) and -resistant (ACB-AbR) strains, each of which included two biological replicates. Using Illumina sequencing, a total of 23,809,890 high-quality reads were collected from the four ACB libraries. The numbers of known microRNAs (miRNAs) were 302 and 395 for ACB-BtS and 268 and 287 for ACB-AbR. Using Mireap software, we identified 32 and 16 potential novel miRNAs for ACB-BtS and 18 and 22 for ACB-AbR. Among them, 21 known and 1 novel miRNAs had significantly different expression between ACB-BtS and

ACB-AbR. Several miRNAs were observed to target potential Bt receptor genes, such as aminopeptidase N and cadherin-like protein. The glycosylphosphatidylinositol-anchor biosynthetic process and ABC transporters pathway were identified through Gene Ontology and KEGG pathway analysis of target genes of the differentially expressed miRNAs.

Publication Type: B

***Record 6 of 7.** Search terms matched: AB(1); CORN(2); CRY1(1); MAIZE(2); MON810(1); ZEA MAYS(1)

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*Order Full Text []

Accession Number: CABI:20163365638

Document Type: Conference paper

Author(s): Rondini, C.; Torricelli, M.; Pierboni, E.; Tovo, G. R.

Title: Real-time PCR and lateral flow test, two different approaches to detect and to quantify respectively DNA transgenic maize MON810 and CRY1_{AB} encoded protein in corn grain samples.

Source: Joint meeting, LXIX Convegno SISVet, XV Convegno SICV, XIII Convegno SIRA, XII Convegno AIPVet, XI Convegno SoFiVet, II Convegno RNIV, Perugia, Italia 15-17 giugno 2015. Atti 2015, 298; 2015

Conference: Joint meeting, LXIX Convegno SISVet, XV Convegno SICV, XIII Convegno SIRA, XII Convegno AIPVet, XI Convegno SoFiVet, II Convegno RNIV, Perugia, Italia 15-17 giugno 2015. Atti 2015.

Language: English

ISBN: 978-88-909002-0-7

Publication Type: J

***Record 7 of 7.** Search terms matched: BORER(1); CORN(2); MAIZE(6); RESISTANT(4); ZEA MAYS(1)

*[Click Here to View Full Record](#)

*Order Full Text []

Accession Number: CABI:20163392369

Document Type: Journal article

Author(s): Xie ShuZhang; Lei KaiRong; Yang XiaoYan; Hu MingYu; Lin Qing; Wu Hong

Title: Study on insect-resistant gene of *GmCry1F* transformation in maize by agrobacterium-mediated.

Source: Southwest China Journal of Agricultural Sciences, 28 (3):962-966; 2015

Language: Chinese

Language of Summary: English

Abstract: The cultivation of transgenic insect-resistant maize is one of the effective ways to reduce the damage caused by corn borer. A new insect-resistant gene GmCry1F was obtained by optimizing and modifying the coding regions of wild *Bacillus thuringiensis* Cry1F gene in this study. Then it introduced target gene into maize Hi-II via *Agrobacterium*-mediated, finally

identified the experimental results by PCR and immuno strip test. The results showed that the plant express vector CUB-ubi::GmCry1F-35s::bar has been constructed successfully. Twenty-five transgenic plants were obtained through light differentiation culture in which seventeen transgenic plants were positive by PCR and immuno strip test. It was demonstrated that gene GmCry1F had been integrated into the maize genome. This result provided some good research materials and reference to the transgenic insect-resistant maize breeding.

Publication Type: J

***Record 1 of 17.** Search terms matched: 1AB(1); CRY(1); LEPIDOPTERA(3); MAIZE(1); YIELD(1)

*[Click Here to View Full Record](#)

*Order Full Text []

Accession Number: CABI:20173018948

Document Type: Journal article

Author(s): Cerqueira, F. B.; Alves, G. B.; Correa, R. F. T.; Martins, E. S.; Barbosa, L. C. B.; Nascimento, I. R. do; Monnerat, R. G.; Ribeiro, B. M.; Aguiar, R. W. de S.

Title: Selection and characterization of *Bacillus thuringiensis* isolates with a high insecticidal activity against *Spodoptera frugiperda* (Lepidoptera: Noctuidae).

Source: Bioscience Journal, 32 (6):1522-1536; 2016

Language: English

Language of Summary: Portuguese

Abstract: *Spodoptera frugiperda* (SMITH, 1797) (Lepidoptera: Noctuidae) affects diverse crops of great economic interest, for instance, it can cause severe yield losses in maize, rice and sorghum. In this study, a selection and characterization of *Bacillus thuringiensis* (BERLINER, 1911) isolates with a high insecticidal activity against *S. frugiperda* was performed. Fifty-two crystal-forming *B. thuringiensis* isolates that were identified from 3384 *Bacillus*-like colonies were examined and screened by PCR for the presence cry genes (cry1, cry1Aa, cry1Ab, cry1Ac, cry1D, cry2 and cry2Ab). Four isolates that showed high toxicity towards *S. frugiperda* were shown to harbor cry2 genes. The crystals were analyzed by electron microscopy and showed bipyramidal and cuboidal shapes. Furthermore, these four isolates had lethal concentration (LC50) values of 44.5 ng/cm² (SUFT01), 74.0 ng/cm² (SUFT02), 89.0 ng/cm² (SUFT03) and 108 ng/cm² (SUFT 04) to neonate *S. frugiperda* larvae. An ultrastructural analysis of midgut cells from *S. frugiperda* incubated with the SUFT01 spore-crystal complex showed disruptions in cellular integrity and in the microvilli of the midgut columnar cells. The isolates characterized in this work are good candidates for the control of *S. frugiperda*, and could be used for the formulation of new bioinsecticides.

Publication Type: J

***Record 2 of 17.** Search terms matched: BT(6); CORN(1); MAIZE(14); ZEA MAYS(1)

*[Click Here to View Full Record](#)

*Order Full Text []

Accession Number: CABI:20173001681

Document Type: Journal article

Author(s): Guo JingFei; He KangLai; Bai ShuXiong; Zhang TianTao; Liu YunJun; Wang FuXin; Wang ZhenYing

Title: Effects of transgenic *cryIle* maize on non-lepidopteran pest abundance, diversity and community composition.

Source: Transgenic Research, 25 (6):761-772; 2016

Language: English

Abstract: Non-lepidopteran pests are exposed to, and may be influenced by, Bt toxins when feeding on Bt maize that express insecticidal Cry proteins derived from *Bacillus thuringiensis* (Bt). In order to assess the potential effects of transgenic cryIle maize on non-lepidopteran pest species and ecological communities, a 2-year field study was conducted to compare the non-lepidopteran pest abundance, diversity and community composition between transgenic cryIle maize (Event IE09S034, Bt maize) and its near isoline (Zong 31, non-Bt maize) by whole plant inspections. Results showed that Bt maize had no effects on non-lepidopteran pest abundance and diversity (Shannon-Wiener diversity index, Simpson's diversity index, species richness, and Pielou's index). There was a significant effect of year and sampling time on those indices analyzed. Redundancy analysis indicated maize type, sampling time and year totally explained 20.43% of the variance in the non-lepidopteran pest community composition, but no association was presented between maize type (Bt maize and non-Bt maize) and the variance. Nonmetric multidimensional scaling analysis showed that sampling time and year, rather than maize type had close relationship with the non-lepidopteran pest community composition. These results corroborated the hypothesis that, at least in the short-term, the transgenic cryIle maize had negligible effects on the non-lepidopteran pest abundance, diversity and community composition.

Publication Type: J

***Record 3 of 17.** Search terms matched: BT(3); CORN(2); LEPIDOPTERA(1); MAIZE(7); OSTRINIA(3); ZEA MAYS(1)

*[Click Here to View Full Record](#)

*Order Full Text []

Accession Number: CABI:20173019536

Document Type: Journal article

Author(s): Chen HongXing; Yang Rui; Yang Wang; Zhang Liu; Camara, I.; Dong XueHui; Liu YiQing; Shi WangPeng

Title: Efficacy of Bt maize producing the Cry1Ac protein against two important pests of corn in China.

Source: Environmental Science and Pollution Research, 23 (21):21511-21516; 2016

Language: English

Abstract: *Ostrinia furnacalis* (Guenee) and *Helicoverpa armigera* (Hubner) are the most important pests of maize in China. A laboratory study and a 2-year field study on the efficacy of transgenic maize expressing the Cry1Ac protein BT38 against *O. furnacalis* and *H. armigera* were performed. We found that the husks, kernels, and silks of BT38 showed significant efficacy against larvae of *O. furnacalis* and *H. armigera*. In the field, when neonate larvae of *O.*

furnacalis and *H. armigera* were on plants at different growth stages and when levels of leaf-damage or number of damaged silks were used to score efficacy, we found that BT38 showed significant insecticidal efficacy against *O. furnacalis* and *H. armigera*, but the non-Bt maize did not show significant efficacy against either pest. These results suggest that the insecticidal efficacy of Bt maize expressing the Cry1Ac protein could be useful in the integrated pest management of these key maize pests.

DOI: [10.1007/s11356-016-7340-7](https://doi.org/10.1007/s11356-016-7340-7)

Publication Type: J

***Record 4 of 17.** Search terms matched: BORER(1); BT(4); CORN(1); CRY1AB(2); LEPIDOPTERA(3); MAIZE(6); RESISTANT(1); ZEA MAYS(1)

*[Click Here to View Full Record](#)

*Order Full Text []

Accession Number: CABI:20173025875

Document Type: Journal article

Author(s): Erasmus, A.; Marais, J.; Berg, J. van den

Title: Movement and survival of *Busseola fusca* (Lepidoptera: Noctuidae) larvae within maize plantings with different ratios of non-Bt and Bt seed.

Source: Pest Management Science, 72 (12):2287-2294; 2016

Language: English

Abstract: BACKGROUND: Products of plant biotechnology, for example genetically modified Bt maize, provide useful tools for pest management. The benefits provided by insect-resistant plants are, however, threatened by the evolution of resistance by target pest species. The high-dose/refuge insect resistance management strategy (IRM) as well as seed mixtures are globally used as IRM strategies. *Busseola fusca* (Lepidoptera: Noctuidae), the target stem borer of Bt maize in Africa, evolved resistance to Bt maize expressing Cry1Ab protein in South Africa. Owing to high larval mobility and subsequent sublethal exposure of larvae moving between non-Bt and Bt plants, more rapid resistance evolution has been proposed as a possibility with deployment of seed mixture strategies. RESULTS: Laboratory and field studies were conducted to study *B. fusca* larval mobility. In the laboratory, different scenarios of *B. fusca* larval movement between single-gene (Cry1Ab) and stacked-trait (Cry1A.105 and Cry2Ab2) Bt maize were studied. Data on larval survival and mass over time indicated that Cry proteins do not kill larvae above certain developmental stages. A 2 year field study with the single gene and the stacked event was conducted using seed mixtures containing 5, 10, 15 and 20% non-Bt seed as well as a control treatment (non-Bt seed only). CONCLUSION: Larval movement continued for 5 weeks and resulted in a significant incidence of Bt and non-Bt damaged plants, indicating that the movement behaviour of *B. fusca* is of such a nature that seed mixtures as an IRM strategy may not be effective to delay resistance evolution.

Publication Type: J

***Record 5 of 17.** Search terms matched: BT(6); CORN(1); CRY1AB(7); MAIZE(8); ZEA MAYS(1)

*[Click Here to View Full Record](#)

*Order Full Text []

Accession Number: CABI:20173026192

Document Type: Journal article

Author(s): Andow, D. A.; Zwahlen, C.

Title: Ground beetle acquisition of Cry1Ab from plant- and residue-based food webs.

Source: Biological Control, 103 204-209; 2016

Language: English

Abstract: Ground beetles are significant predators in agricultural habitats. While many studies have characterized effects of Bt maize on various carabid species, few have examined the potential acquisition of Cry toxins from live plants versus plant residue. In this study, we examined how live Bt maize and Bt maize residue affect acquisition of Cry1Ab in six species. Adult beetles were collected live from fields with either current-year Bt maize, one-year-old Bt maize residue, two-year-old Bt maize residue, or fields without any Bt crops or residue for the past two years, and specimens were analyzed using ELISA. Observed Cry1Ab concentrations in the beetles were similar to that reported in previously published studies. Only one specimen of *Cyclotrachelus iowensis* acquired Cry1Ab from two-year-old maize residue. Three species acquired Cry1Ab from fields with either live plants or plant residue (*Cyclotrachelus iowensis*, *Poecilus lucublandus*, *Poecilus chalcites*), implying participation in both live-plant and residue-based food webs. Two species acquired toxin from fields with live plants, but not from fields with residue (*Bembidion quadrimaculatum*, *Elaphropus incurvus*), suggesting participation only in live plant-based food webs. One species did not acquire Cry1Ab from either live-plant or residue (*Scarites quadriceps*), suggesting that its food sources might not contain significant amounts of Cry1Ab. These results revealed significant differentiation among carabid species in their associations with live-plant and residue-based food webs in agricultural fields.

Publication Type: J

*Record 6 of 17. Search terms matched: CRY1AB(4)

*[Click Here to View Full Record](#)

*Order Full Text []

Accession Number: CABI:20173004591

Document Type: Journal article

Author(s): Raen, A. Z.; Dang Cong; Wang Fang; Peng YuFa; Ye GongYin

Title: Thrips-mediated impacts from transgenic rice expressing Cry1Ab on ecological fitness of non-target predator *Orius tantilus* (Hemiptera: Anthocoridae).

Source: Journal of Integrative Agriculture, 15 (9):2059-2069; 2016

Language: English

Abstract: Various rice lines have been genetically modified with genes from *Bacillus thuringiensis* (Bt) to continuously produce Bt insecticidal proteins against lepidopteran larvae. The Bt insecticidal protein constantly expresses in the plants to create an opportunity for non-target herbivores to acquire and convey the protein to their predators or parasitoids across trophic levels. This paper evaluates the effects of Bt rice (namely, Kemindao 1 (KMD1) and Kemindao 2 (KMD2)) expressing Cry1Ab as compared to its non-Bt control line, Xiushui 11 on non-target predator *Orius tantilus* (a generalist predatory anthocorid of thrips) under laboratory and field conditions. To measure several biological parameters such as total nymphal duration

and fecundity of this bug, it was reared on thrips and pollens of KMD1 and KMD2 as compared to their control under laboratory conditions. By comparison with the control, Bt rice did not significantly affect main life-history characteristics (total nymphal duration, female adult longevity, oviposition period and fecundity) of this anthocorid preying on Bt rice-fed thrips along with Bt rice pollens, except that the fecundity of this predator for KMD1 was distinctly lower as compared with KMD2 or the control. Enzyme-linked immunosorbent assay (ELISA) results showed that no Cry1Ab protein was detected in this predator fed on thrips or rice pollen from Bt rice but was in Bt rice pollens. With the beat plate, plastic bag and color trap sampling methods, two-year field monitoring of *O. tantilus* abundance demonstrated that Bt rice had no significant detrimental effects on the population dynamics and seasonal average densities of this predatory anthocorid as compared with the control. Thus, it is suggested that growing our tested Bt rice (KMD1 and KMD2) producing Cry1Ab will pose a negligible risk to the anthocorid, *O. tantilus*.

DOI: [10.1016/S2095-3119\(16\)61414-4](https://doi.org/10.1016/S2095-3119(16)61414-4)

Publication Type: J

***Record 7 of 17.** Search terms matched: BT(1); CORN(8); MAIZE(1); RESISTANT(2); ZEA MAYS(1)

*[Click Here to View Full Record](#)

*Order Full Text []

Accession Number: CABI:20173014526

Document Type: Journal article

Author(s): Martinez, J. C.; Caprio, M. A.

Title: IPM use with the deployment of a non-high dose Bt pyramid and mitigation of resistance for western corn rootworm (*Diabrotica virgifera virgifera*).

Source: Environmental Entomology, 45 (3):747-761; 2016

Language: English

Abstract: Recent detection of western corn rootworm resistance to Bt (*Bacillus thuringiensis*) corn prompted recommendations for the use of integrated pest management (IPM) with planting refuges to prolong the durability of Bt technologies. We conducted a simulation experiment exploring the effectiveness of various IPM tools at extending durability of pyramided Bt traits. Results indicate that some IPM practices have greater merits than others. Crop rotation was the most effective strategy, followed by increasing the non-Bt refuge size from 5 to 20%. Soil-applied insecticide use for Bt corn did not increase the durability compared with planting Bt with refuges alone, and both projected lower durabilities. When IPM participation with randomly selected management tools was increased at the time of Bt commercialization, durability of pyramided traits increased as well. When non-corn rootworm expressing corn was incorporated as an IPM option, the durability further increased. For corn rootworm, a local resistance phenomenon appeared immediately surrounding the resistant field (hotspot) and spread throughout the local neighborhood in six generations in absence of mitigation. Hotspot mitigation with random selection of strategies was ineffective at slowing resistance, unless crop rotation occurred immediately; regional mitigation was superior to random mitigation in the hotspot and reduced observed resistance allele frequencies in the neighborhood. As resistance alleles of mobile pests can escape hotspots, the scope of mitigation should extend beyond

resistant sites. In the case of widespread resistance, regional mitigation was less effective at prolonging the life of the pyramid than IPM with Bt deployment at the time of commercialization.

Publication Type: J

***Record 8 of 17.** Search terms matched: BT(2); CORN(2); LEPIDOPTERA(2); MAIZE(7); ZEA MAYS(1)

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*Order Full Text []

Accession Number: CABI:20173014554

Document Type: Journal article

Author(s): Bentivenha, J. P. F.; Baldin, E. L. L.; Hunt, T. E.; Paula-Moraes, S. V.; Blankenship, E. E.

Title: Intraguild competition of three noctuid maize pests.

Source: Environmental Entomology, 45 (4):999-1008; 2016

Language: English

Abstract: The western bean cutworm *Striacosta albicosta* (Smith), the fall armyworm *Spodoptera frugiperda* (J. E. Smith), and the corn earworm *Helicoverpa zea* (Boddie) (Lepidoptera: Noctuidae) are among the major lepidopteran pests of maize in the United States, belonging to the same guild and injuring the reproductive tissues of this crop. Here, intraguild competition of these lepidopterans on non-Bt maize was evaluated through survival analysis of each species under laboratory and field conditions. Competition scenarios were carried out in arenas containing maize silk or ear tissue, using larvae on different stadium of development. Fitness cost competition studies were conducted to examine the influence of intraguild competition and cannibalism and predation rates on larval development. The survival of *S. albicosta* competing with the other species was significantly lower than in intraspecific competition, even when the larvae were more developed than the competitor. For *S. frugiperda*, survival remained high in the different competition scenarios, except when competing in a smaller stadium with *H. zea*. Larvae of *H. zea* had a high rate of cannibalism, higher survival when competing against *S. albicosta* than *S. frugiperda*, and reduced survival when the *H. zea* larvae were at the same development stadium or smaller than the competitors. Based on fitness cost results, the absence of a competitor for the feeding source may confer an advantage to the larval development of *S. frugiperda* and *H. zea*. Our data suggest that *S. frugiperda* has a competitive advantage against the other species, while *S. albicosta* has the disadvantage in the intraguild competition on non-Bt maize.

DOI: [10.1093/ee/nvw068](https://doi.org/10.1093/ee/nvw068)

Publication Type: J

***Record 9 of 17.** Search terms matched: CRY1AB(2)

*[Click Here to View Full Record](#)

*Order Full Text []

Accession Number: CABI:20173014565

Document Type: Journal article

Author(s): Ren ShaoPeng; Yang Fan; Gao MingQing; Pu DeQiang; Shi Min; Ye GongYin; Shen ZhiCheng; Chen XueXin

Title: Effects of transgenic Bt rice on nontarget *Rhopalosiphum maidis* (Homoptera: Aphididae).

Source: Environmental Entomology, 45 (4):1090-1096; 2016

Language: English

Abstract: The effects of three transgenic *Bacillus thuringiensis* (Bt) rice lines, KMD1, KMD2, and G8-7, on biological parameters and population dynamics of nontarget insect, *Rhopalosiphum maidis* (Fitch) (Homoptera: Aphididae), were investigated in the laboratory and field. No significant differences were found between Bt and non-Bt rice lines for aphid survival. The developmental time of *R. maidis* that fed on KMD1 and KMD2 did not differ significantly from those of the individuals feeding on the parental variety Xiushui11, but significantly prolonged developmental time was observed on G8-7 as compared with its parental variety Xiushui10. Aphid fecundity was significantly higher on Bt than on parental rice. A 2-yr field survey indicated that Bt rice did not significantly affect the population dynamics of *R. maidis* in comparison with non-Bt rice. Additionally, guttation droplets of Bt rice and aphids feeding on Bt rice were analyzed for presence of Cry1Ab using ELISA. No Cry1Ab protein was found in aphid adults feeding on Bt rice lines both in the laboratory and field. By using the guttation droplets from the top of rice seedlings, we designed a novel method to collect phloem sap, and found that relatively low concentrations were detected in the guttation droplets from Bt rice lines. In conclusion, although the Bt rice lines tested in this study stimulate the fecundity of *R. maidis*, the aphid population density did not increase in Bt rice fields.

Publication Type: J

***Record 10 of 17.** Search terms matched: BT(1); CORN(5); MAIZE(4); RESISTANT(3); ZEA MAYS(1)

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Accession Number: CABI:20173017758

Document Type: Journal article

Author(s): Zhao JianZhou; O Neal, M. A.; Richtman, N. M.; Thompson, S. D.; Cowart, M. C.; Nelson, M. E.; Pan ZaiQi; Alves, A. P.; Yamamoto, T.

Title: mCry3A-selected western corn rootworm (Coleoptera: Chrysomelidae) colony exhibits high resistance and has reduced binding of mCry3A to midgut tissue.

Source: Journal of Economic Entomology, 109 (3):1369-1377; 2016

Language: English

Abstract: Several Bt maize events expressing various insecticidal Cry protein genes have been commercialized for management of western corn rootworm, *Diabrotica virgifera virgifera* LeConte (Coleoptera: Chrysomelidae). We used high efficacy (>99.7%) experimental maize events that express mCry3A for selections under laboratory conditions to develop a western corn rootworm colony resistant to mCry3A at higher levels than published results. The resistance ratio (RR) to mCry3A was >97-fold based on LC50 values in diet-based bioassays after six generations of selections when compared to that of an unselected Control colony. Using a sublethal seedling assay (SSA) method, we confirmed that the colony had no cross-

resistance to maize event DAS-59122-7, which expresses Cry34/35Ab. Reciprocal crosses between the mCry3A-resistant colony and the susceptible colony were performed to test the inheritance of resistance. Larval survival and development evaluated by the SSA method indicated that resistance to mCry3A was inherited autosomally and was incompletely recessive (h1/40.23-0.25). Specific binding of mCry3A to brush border membrane vesicles of midgut tissue revealed reduced binding in the resistant colony when compared to binding in the susceptible colony. This is the first report where resistance in western corn rootworm has been shown to involve reduced binding of a Cry3-class protein in midgut tissue.

DOI: [10.1093/jee/tow049](https://doi.org/10.1093/jee/tow049)

Publication Type: J

***Record 11 of 17.** Search terms matched: BT(3); CORN(23); MAIZE(1); RESISTANT(2); ZEA MAYS(1)

*[Click Here to View Full Record](#)

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Accession Number: CABI:20173017761

Document Type: Journal article

Author(s): Shrestha, R. B.; Jakka, S. R. K.; French, B. W.; Gassmann, A. J.

Title: Field-based assessment of resistance to Bt corn by western corn rootworm (Coleoptera: Chrysomelidae).

Source: Journal of Economic Entomology, 109 (3):1399-1409; 2016

Language: English

Abstract: Western corn rootworm, *Diabrotica virgifera virgifera* LeConte, is a serious pest of corn and is managed with corn that produces insecticidal toxins derived from the bacterium *Bacillus thuringiensis* (Bt). Beginning in 2009, resistance to Cry3Bb1 corn, and severe injury to Cry3Bb1 corn in the field, was observed in Iowa. However, few data exist on how Cry3Bb1-resistant western corn rootworm interact with various management practices in the field. Using a field experiment, we measured adult emergence and feeding injury to corn roots for both Cry3Bb1-resistant and Cry3Bb1-susceptible populations of western corn rootworm when tested against various Bt corn hybrids and a soil-applied insecticide. Between 2012 and 2013, we evaluated five fields that were associated with greater than one node of feeding injury to Cry3Bb1 corn by western corn rootworm (i.e., problem-field populations), and a laboratory strain that had never been exposed to Bt corn (i.e., control population). Adult emergence for western corn rootworm and root injury to corn were significantly higher in problem-field populations than control populations for both Cry3Bb1 corn and mCry3A corn. By contrast, corn with Cry34/35Ab1, either alone or pyramided with Cry3Bb1, significantly reduced adult emergence and root injury in both problem fields and control fields. In problem fields, application of the soil-applied insecticide to Cry3Bb1 corn significantly reduced root injury, but not adult emergence. Our results are discussed in terms of developing strategies for managing western corn rootworm with resistance to Cry3Bb1 and mCry3A, and delaying the additional evolution of Bt resistance by this pest.

DOI: [10.1093/jee/tow087](https://doi.org/10.1093/jee/tow087)

Publication Type: J

*Record 12 of 17. Search terms matched: CRY1AB(7)

[*Click Here to View Full Record](#)

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Accession Number: CABI:20173014499

Document Type: Journal article

Author(s): Lu Zengbin; Dang Cong; Han NaiShun; Shen ZhiCheng; Peng YuFa; Stanley, D.; Ye GongYin

Title: The new transgenic *Cry1Ab/Vip3H* rice poses no unexpected ecological risks to arthropod communities in rice agroecosystems.

Source: Environmental Entomology, 45 (2):518-525; 2016

Language: English

Abstract: The ecological risks to nontarget organisms should be rigorously assessed before Bt crops are released. Here, the impacts of a new Cry1Ab/Vip3H rice line on arthropod communities in rice agroecosystems were evaluated across 3yr. Arthropods collected via vacuum were sorted into five guilds. The abundance and proportion of each guild as well as community-level parameters were determined in Cry1Ab/Vip3H and control rice fields. Changes in arthropod species assemblage over sampling dates were investigated by principal response curves (PRCs). Cry1Ab/Vip3H rice did not exert significant impacts on the seasonal density and proportion of each guild, except parasitoids. Detritivore seasonal density, but not its relative abundance, was significantly affected by Cry1Ab/Vip3H rice. Four community indices (species richness S, Shannon-Wiener index H', Simpson index D, and evenness index J') were similar between rice types. PRCs revealed a slight community difference between rice types in the past two tested years, with rice types accounting for 1.0-3.5% of the variance among arthropod communities. However, sampling dates explain 32.1-67.6% for these community differences. Of the 46 taxa with higher species weights, 26.1% of the taxa were significantly different, including seven taxa with higher abundance and five with lower density in Cry1Ab/Vip3H rice fields. These differences may be attributed to change in abundance of prey or hosts but not to direct effects of Bt proteins. We infer that this new Cry1Ab/Vip3H rice line poses no unintended ecological risks to the arthropod community.

Publication Type: J

*Record 13 of 17. Search terms matched: BT(2); CORN(10); LEPIDOPTERA(4); MAIZE(1); ZEA MAYS(1)

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Accession Number: CABI:20173017684

Document Type: Journal article

Author(s): Pan ZaiQi; Onstad, D.; Crain, P.; Crespo, A.; Hutchison, W.; Buntin, D.; Porter, P.; Catchot, A.; Cook, D.; Pilcher, C.; Flexner, L.; Higgins, L.

Title: Evolution of resistance by *Helicoverpa zea* (Lepidoptera: Noctuidae) infesting insecticidal crops in the Southern United States.

Source: Journal of Economic Entomology, 109 (2):821-831; 2016

Language: English

Abstract: We created a deterministic, frequency-based model of the evolution of resistance by corn earworm, *Helicoverpa zea* (Boddie) (Lepidoptera: Noctuidae), to insecticidal traits expressed in crops planted in the heterogeneous landscapes of the southern United States. The model accounts for four generations of selection by insecticidal traits each year. We used the model results to investigate the influence of three factors on insect resistance management (IRM): (1) how does adding a third insecticidal trait to both corn and cotton affect durability of the products, (2) how does unstructured corn refuge influence IRM, and (3) how do block refuges (50% compliance) and blended refuges compare with regard to IRM? When Bt cotton expresses the same number of insecticidal traits, Bt corn with three insecticidal traits provides longer durability than Bt corn with two pyramided traits. Blended refuge provides similar durability for corn products compared with the same level of required block refuge when the rate of refuge compliance by farmers is 50%. Results for Mississippi and Texas are similar, but durabilities for corn traits are surprisingly lower in Georgia, where unstructured corn refuge is the highest of the three states, but refuge for Bt cotton is the lowest of the three states. Thus, unstructured corn refuge can be valuable for IRM but its influence is determined by selection for resistance by Bt cotton.

Publication Type: J

***Record 14 of 17.** Search terms matched: BT(3); CORN(9); LEPIDOPTERA(2); MAIZE(1); ZEA MAYS(2)

*[Click Here to View Full Record](#)

*Order Full Text []

Accession Number: CABI:20173017689

Document Type: Journal article

Author(s): Kanel, M. B. von; Gore, J.; Catchot, A.; Cook, D.; Musser, F.; Caprio, M.

Title: Influence of dual-Bt protein corn on bollworm, *Helicoverpa zea* (Boddie), survivorship on Bollgard II cotton.

Source: Journal of Economic Entomology, 109 (2):860-864; 2016

Language: English

Abstract: Similar Cry proteins are expressed in both Bt corn, *Zea mays* L., and cotton, *Gossypium hirsutum* (L.), commercial production systems. At least one generation of corn earworm, *Helicoverpa zea* (Boddie), completes development on field corn in the Mid-South before dispersing across the landscape into other crop hosts like cotton. A concern is that Bt corn hybrids may result in selection for *H. zea* populations with a higher probability of causing damage to Bt cotton. The objective of this study was to determine the susceptibility of *H. zea* offspring from moths that developed on non-Bt and VT Triple Pro (VT3 PRO) field corn to lyophilized Bollgard II cotton tissue expressing Cry1Ac and Cry2Ab. Offspring of individuals reared on VT3 PRO expressing Cry1A.105 and Cry2Ab had a significantly higher LC50 two out of the three years this study was conducted. Excess larvae were placed on artificial diet and allowed to pupate to determine if there were any inheritable fitness costs associated with parental development on VT3 PRO corn. Offspring resulting from males collected from VT3 PRO had significantly lower pupal weight and longer pupal duration compared with offspring of individuals collected from non-Bt corn. However, offspring from females collected from VT3 PRO were not different from non-Bt offspring. Paternal influence on offspring in insects is

not commonly observed, but illustrates the side effects of development on a transgenic plant expressing less than a high dose, 25 times the concentration needed to kill susceptible larvae.

DOI: [10.1093/jee/tov401](https://doi.org/10.1093/jee/tov401)

Publication Type: J

*Record 15 of 17. Search terms matched: BT(1); CORN(3); LEPIDOPTERA(3); MAIZE(1); ZEA MAYS(1)

*[Click Here to View Full Record](#)

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Accession Number: CABI:20173017617

Document Type: Journal article

Author(s): Caprio, M. A.; Martinez, J. C.; Porter, P. A.; Bynum, E.

Title: The impact of inter-kernel movement in the evolution of resistance to dual-toxin Bt-corn varieties in *Helicoverpa zea* (Lepidoptera: Noctuidae).

Source: Journal of Economic Entomology, 109 (1):307-319; 2016

Language: English

Abstract: Seeds or kernels on hybrid plants are primarily F2 tissue and will segregate for heterozygous alleles present in the parental F1 hybrids. In the case of plants expressing Bt-toxins, the F2 tissue in the kernels will express toxins as they would segregate in any F2 tissue. In the case of plants expressing two unlinked toxins, the kernels on a Bt plant fertilized by another Bt plant would express anywhere from 0 to 2 toxins. Larvae of corn earworm [*Helicoverpa zea* (Boddie)] feed on a number of kernels during development and would therefore be exposed to local habitats (kernels) that varied in their toxin expression. Three models were developed for plants expressing two Bt-toxins, one where the traits are unlinked, a second where the traits were linked and a third model assuming that maternal traits were expressed in all kernels as well as paternally inherited traits. Results suggest that increasing larval movement rates off of expressing kernels tended to increase durability while increasing movement rates off of nonexpressing kernels always decreased durability. An ideal block refuge (no pollen flow between blocks and refuges) was more durable than a seed blend because the refuge expressed no toxins, while pollen contamination from plants expressing toxins in a seed blend reduced durability. A linked-trait model in an ideal refuge model predicted the longest durability. The results suggest that using a seed-blend strategy for a kernel feeding insect on a hybrid crop could dramatically reduce durability through the loss of refuge due to extensive cross-pollination.

DOI: [10.1093/jee/tov295](https://doi.org/10.1093/jee/tov295)

Publication Type: J

*Record 16 of 17. Search terms matched: BT(2); CORN(2); LEPIDOPTERA(4); MAIZE(5); MON810(1); RESISTANT(1); ZEA MAYS(2)

*[Click Here to View Full Record](#)

*Order Full Text []

Accession Number: CABI:20173017615

Document Type: Journal article

Author(s): Crespo, A. L. B.; Alves, A. P.; Wang YiWei; Hong, B.; Flexner, J. L.; Catchot, A.; Buntin, D.; Cook, D.

Title: Survival of corn earworm (Lepidoptera: Noctuidae) on Bt maize and cross-pollinated refuge ears from seed blends.

Source: Journal of Economic Entomology, 109 (1):288-298; 2016

Language: English

Abstract: Refuge is mandated in the United States where genetically modified maize (*Zea mays* L.) expressing insecticidal proteins derived from *Bacillus thuringiensis* Berliner (Bt) are cultivated. Currently, refuge is deployed in different ways including blocks, field strips, or seed blends containing Bt and non-Bt maize. Seed blends provide practical advantages for refuge implementation. However, concerns related to the movement of insect larvae, potential differential survival of heterozygous resistant larvae, reduction in insect production, and cross-pollination of ears resulting in sublethal selection, have delayed seed blend use for Lepidoptera in the southern United States, where maize plantings are used as refuge for *Helicoverpa zea* (Boddie). In this study, we evaluated the relative survival of *H. zea* in Bt events and in seed blends compared with pure stand refuge and the relative survival of *H. zea* on the individual components of the pyramid 1507xMON810xMIR162. The results showed variation on the production of *H. zea* in refuge plants from seed blends compared with pure stand refuge plants. The relative survival of *H. zea* on the events 1507, MON810, MIR162, and 1507xMON810xMIR162 ranked similarly across the three locations tested. These results can be used in computer simulation modeling efforts to evaluate the feasibility of seed blends as a refuge deployment strategy with the pyramid 1507xMON810xMIR162. Because the reduction on survival of *H. zea* due to blending was variable, a sensitivity analysis that includes all possible scenarios of reduction in survival should be considered.

DOI: [10.1093/jee/tov272](https://doi.org/10.1093/jee/tov272)

Publication Type: J

*Record 17 of 17. Search terms matched: BT(6); CORN(6); MAIZE(7); ZEA MAYS(1)

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Accession Number: CABI:20173017577

Document Type: Journal article

Author(s): Andow, D. A.; Pueppke, S. G.; Schaafsma, A. W.; Gassmann, A. J.; Sappington, T. W.; Meinke, L. J.; Mitchell, P. D.; Hurley, T. M.; Hellmich, R. L.; Porter, R. P.

Title: Early detection and mitigation of resistance to *Bt* maize by western corn rootworm (Coleoptera: Chrysomelidae).

Source: Journal of Economic Entomology, 109 (1):1-12; 2016

Language: English

Abstract: Transgenic Bt maize that produces less than a high-dose has been widely adopted and presents considerable insect resistance management (IRM) challenges. Western corn rootworm, *Diabrotica virgifera virgifera* LeConte, has rapidly evolved resistance to Bt maize in the field, leading to local loss of efficacy for some corn rootworm Bt maize events. Documenting and responding to this resistance has been complicated by a lack of rapid diagnostic bioassays and

by regulatory triggers that hinder timely and effective management responses. These failures are of great concern to the scientific and agricultural community. Specific challenges posed by western corn rootworm resistance to Bt maize, and more general concerns around Bt crops that produce less than a high-dose of Bt toxin, have caused uncertainty around current IRM protocols. More than 15 years of experience with IRM has shown that high-dose and refuge-based IRM is not applicable to Bt crops that produce less than a high-dose. Adaptive IRM approaches and pro-active, integrated IRM-pest management strategies are needed and should be in place before release of new technologies that produce less than a high-dose. We suggest changes in IRM strategies to preserve the utility of corn rootworm Bt maize by (1) targeting local resistance management earlier in the sequence of responses to resistance and (2) developing area-wide criteria to address widespread economic losses. We also favor consideration of policies and programs to counteract economic forces that are contributing to rapid resistance evolution.

DOI: [10.1093/jee/tov238](https://doi.org/10.1093/jee/tov238)

Publication Type: J

***Record 1 of 19.** Search terms matched: CRY1AB(3)

*[Click Here to View Full Record](#)

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Accession Number: CABI:20173046221

Document Type: Journal article

Author(s): Wang Juan; Peng YuanDe; Xiao KaiFu; Wei BaoYang; Hu JiLin; Wang Zhi; Song QiSheng; Zhou XuGuo

Title: Transcriptomic response of wolf spider, *Pardosa pseudoannulata*, to transgenic rice expressing *Bacillus thuringiensis* Cry1Ab protein.

Source: BMC Biotechnology, 17 (7):(18 January 2017); 2017

Language: English

Abstract: Background: *Bacillus thuringiensis* (Bt) toxin produced in Cry1-expressing genetically modified rice (Bt rice) is highly effective to control lepidopteran pests, which reduces the needs for synthetic insecticides. Non-target organisms can be exposed to Bt toxins through direct feeding or trophic interactions in the field. The wolf spider *Pardosa pseudoannulata*, one of the dominant predators in South China, plays a crucial role in the rice agroecosystem. In this study, we investigated transcriptome responses of the 5th instar spiders fed on preys maintained on Bt- and non-Bt rice. Results: Comparative transcriptome analysis resulted in 136 differentially expressed genes (DEGs) between spiderlings preying upon *N. lugens* fed on Bt- and non-Bt rice (Bt- and non-Bt spiderlings). Functional analysis indicated a potential impact of Bt toxin on the formation of new cuticles during molting. GO and KEGG enrichment analyses suggested that GO terms associated with chitin or cuticle, including "chitin binding", "chitin metabolic process", "chitin synthase activity", "cuticle chitin biosynthetic process", "cuticle hydrocarbon biosynthetic process", and "structural constituent of cuticle", and an array of amino acid metabolic pathways, including "alanine, aspartate and glutamate

metabolism", "glycine, serine and theronine metabolism", "cysteine and methionine metabolism", "tyrosine metabolism", "phenylalanine metabolism and phenylalanine", and "tyrosine and tryptophan biosynthesis" were significantly influenced in response to Cry1Ab. Conclusions: The Cry1Ab may have a negative impact on the formation of new cuticles during molting, which is contributed to the delayed development of spiderlings. To validate these transcriptomic responses, further examination at the translational level will be warranted.

Publication Type: J

***Record 2 of 19.** Search terms matched: CRY1AB(5); LEPIDOPTERA(1)

*[Click Here to View Full Record](#)

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Accession Number: CABI:20173051648

Document Type: Journal article

Author(s): Portugal, L.; Munoz-Garay, C.; Martinez de Castro, D. L.; Soberon, M.; Bravo, A.

Title: Toxicity of Cry1A toxins from *Bacillus thuringiensis* to CF1 cells does not involve activation of adenylate cyclase/PKA signaling pathway.

Source: Insect Biochemistry and Molecular Biology, 80 21-31; 2017

Language: English

Abstract: Bacillus thuringiensis (Bt) bacteria produce Cry toxins that are able to kill insect pests. Different models explaining the mode of action of these toxins have been proposed. The pore formation model proposes that the toxin creates pores in the membrane of the larval midgut cells after interaction with different receptors such as cadherin, aminopeptidase N and alkaline phosphatase and that this pore formation activity is responsible for the toxicity of these proteins. The alternative model proposes that interaction with cadherin receptor triggers an intracellular cascade response involving protein G, adenylate cyclase (AC) and protein kinase A (PKA). In addition, it was shown that Cry toxins induce a defense response in the larvae involving the activation of mitogen-activated kinases such as MAPK p38 in different insect orders. Here we analyzed the mechanism of action of Cry1Ab and Cry1Ac toxins and a collection of mutants from these toxins in the insect cell line CF1 from *Choristoneura fumiferana*, that is naturally sensitive to these toxins. Our results show that both toxins induced permeability of K⁺ ions into the cells. The initial response after intoxication with Cry1Ab and Cry1Ac toxins involves the activation of a defense response that involves the phosphorylation of MAPK p38. Analysis of activation of PKA and AC activities indicated that the signal transduction involving PKA, AC and cAMP was not activated during Cry1Ab or Cry1Ac intoxication. In contrast we show that Cry1Ab and Cry1Ac activate apoptosis. These data indicate that Cry toxins can induce an apoptotic death response not related with AC/PKA activation. Since Cry1Ab and Cry1Ac toxins affected K⁺ ion permeability into the cells, and that mutant toxins affected in pore formation are not toxic to CF1, we propose that pore formation activity of the toxins is responsible of triggering cell death response in CF1 cells.

DOI: [10.1016/j.ibmb.2016.11.004](https://doi.org/10.1016/j.ibmb.2016.11.004)

Publication Type: J

***Record 3 of 19.** Search terms matched: CORN(2); CRY1AB(1); MAIZE(1); RESISTANT(1); ZEA MAYS(1)

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[*Order Full Text \[\]](#)

Accession Number: CABI:20173031688

Document Type: Journal article

Author(s): Xu ChongXin; Liu XiaoQin; Zhang CunZheng; Zhang Xiao; Zhong JianFeng; Liu Yuan; Hu XiaoDan; Lin ManMan; Liu XianJin

Title: Establishment of a sensitive time-resolved fluoroimmunoassay for detection of *Bacillus thuringiensis* CryIIe toxin based nanobody from a phage display library.

Source: Analytical Biochemistry, 518 53-59; 2017

Language: English

Abstract: CryIIe toxin was an insect-resistant protein used in genetically modified crops (GMC). In this study, a large human VH gene nanobodies phage displayed library was employed to select anti-CryIIe toxin antibody by affinity panning. After 5 rounds of panning, total 12 positive monoclonal phage particles were obtained. One of the identified positive phage nanobody was expressed in *E. coli* BL21 and the purified protein was indicated as a molecular mass of approximately 20 kDa by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE). Then a sensitive indirect competitive time-resolved fluoroimmunoassay (IC-TRFIA) was established for detection of CryIIe toxin by the purified protein. The working range of detection for CryIIe toxin standards in the IC-TRFIA were 0.08-6.44 ng mL⁻¹ and the medium inhibition of control (IC₅₀) was 0.73 ng mL⁻¹. It showed a weak cross-reactivity with CryIAb toxin (at 5.6%), but did not recognize CryIB, CryIC, CryIF, and Cry2A toxins (were <0.1%). The average recoveries of CryIIe toxin from respectively spiked in rice, corn and soil samples were in the range of 83.5%-96.6% and with a coefficient of variation (CV) among 2.0%-8.6%. These results showed the IC-TRFIA was promising for detection of CryIIe toxin in agricultural and environmental samples.

Publication Type: J

***Record 4 of 19.** Search terms matched: CORN(1); MAIZE(12); MON810(5); PROTECTION(1); TOLERANCE(2); ZEA MAYS(1)

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Accession Number: CABI:20173058322

Document Type: Journal article

Group Author(s): European Food Safety Authority

Title: Relevance of new scientific evidence on the occurrence of teosinte in maize fields in Spain and France for previous environmental risk assessment conclusions and risk management recommendations on the cultivation of maize events MON810, Bt11, 1507 and GA21.

Source: EFSA Supporting Publications, 13 (9):EN-1094; 2016

Language: English

Abstract: Following a request of the European Commission, the European Food Safety Authority (EFSA) assessed the available scientific information on teosinte for its relevance for the environmental risk assessment (ERA) of genetically modified (GM) maize MON810, Bt11, 1507 and GA21 for cultivation. The presence of teosinte in the European Union (EU) has been

reported in maize fields in Spain and France. Since teosinte is not indigenous to the EU, it does not represent an environmental entity of concern requiring protection. Instead, it is considered a weed that can compete with cultivated maize, and is subject to control and/or eradication measures. Pathways to harm from the cultivation of maize MON810, Bt11, 1507 and GA21 were hypothesised for situations where GM maize and teosinte would grow sympatrically. For each of these pathways it is unlikely that environmental harm will be realised. The growth habits of teosinte species and subspecies, and maize * teosinte hybrids are such that the acquisition of insect resistance and/or herbicide tolerance through vertical gene flow is unlikely to change their relative invasive characteristics under EU conditions. The impact of insect resistance and/or herbicide tolerance in maize * teosinte hybrids on other organisms, the abiotic environment or biogeochemical cycles is likely to be very low, provided that measures are employed to control and/or eradicate teosinte and its progeny in infested agricultural areas. EFSA concludes that there are no data that indicate the necessity to revise the previous ERA conclusions and risk management recommendations for maize MON810, Bt11, 1507 and GA21 made by the GMO Panel. Therefore, the previous GMO Panel risk assessment conclusions and risk management recommendations on maize MON810, Bt11, 1507 and GA21 for cultivation remain valid and applicable.

Publication Type: J

***Record 5 of 19.** Search terms matched: BT(2); CORN(1); CRY1AB(5); MAIZE(5); MON810(4); ZEA MAYS(1)

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Accession Number: CABI:20173058307

Document Type: Journal article

Group Author(s): European Food Safety Authority

Title: Relevance of a new scientific publication (Bohn et al., 2016) for previous environmental risk assessment conclusions on the cultivation of Bt-maize events MON810 and Bt11.

Source: EFSA Supporting Publications, 13 (7):EN-1073; 2016

Language: English

Abstract: Following a request from the European Commission, the European Food Safety Authority (EFSA) assessed the scientific publication by Bohn et al. (2016), including its relevance for the environmental risk assessment of Bt-maize events MON810 and Bt11 for cultivation. In their publication, Bohn et al. (2016) reported that the purified Cry1Ab protein is toxic to the non-target aquatic crustacean *Daphnia magna* (Cladocera: Daphniidae) at concentrations exceeding expected environmental concentrations under field conditions, and thus suggesting cross-order activity of the Cry1Ab protein against *D. magna*. EFSA acknowledges that the study reported in the publication by Bohn et al. (2016) addresses an objective relevant for the environmental risk assessment of Bt-plants expressing the Cry1Ab protein for cultivation, as the data can inform environmental risk assessments by determining the activity spectrum of the Cry1Ab protein, and corroborating or rejecting the risk hypothesis of no harm to *D. magna*. However, owing to limitations associated with the design and reporting of the study, EFSA considers that several uncertainties remain, which do not allow a proper interpretation of the effects observed by Bohn et al. (2016). In addition, EFSA notes that the

observed differences were seen at Cry1Ab protein concentrations above expected environmental concentrations under field conditions, and that the authors did not bring their study results in the context of expected exposure levels in the field. As the evidence reported in Bohn et al. (2016) is insufficient to indicate the necessity to revise the environmental risk assessment conclusions for maize MON810 and Bt11, EFSA considers that the risk assessment conclusions on maize MON810 and Bt11 for cultivation made by the Panel on Genetically Modified Organisms remain valid and applicable.

Publication Type: J

***Record 6 of 19.** Search terms matched: BT(4); CORN(1); LEPIDOPTERA(2); MAIZE(9); MON810(3); ZEA MAYS(1)

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Accession Number: CABI:20173058305

Document Type: Journal article

Group Author(s): European Food Safety Authority

Title: Relevance of a new scientific publication (Hofmann et al., 2016) for previous environmental risk assessment conclusions and risk management recommendations on the cultivation of *Bt*-maize events MON810, Bt11 and 1507.

Source: EFSA Supporting Publications, 13 (7):EN-1070; 2016

Language: English

Abstract: Following a request from the European Commission, the European Food Safety Authority (EFSA) assessed the relevance of the Hofmann et al. (2016) publication for the environmental risk assessment and risk management of the Bt-maize events MON810, Bt11 and 1507 for cultivation. Hofmann et al. (2016) reported data on pollen deposition on maize and weed species in maize fields obtained from a 3 year study in Germany. Data on pollen deposition on host plant leaves in relation to distance from the nearest maize field are informative, as they can be used to develop mathematical models applied to estimate the risk to non-target Lepidoptera associated with the ingestion of Bt-maize pollen deposited on their host plants. EFSA considers that there are no data in Hofmann et al. (2016) that indicate the necessity to revise the previous environmental risk assessment conclusions and risk management recommendations for Bt-maize made in EFSA (2015). EFSA is of the opinion that the publication provides new data that confirm the robustness of exposure factors estimated by EFSA (2015), and give reassurance that the 'Most Realistic' scenario proposed by EFSA (2015) is a reliable basis for risk management recommendations based on the sensitivities of the notional species modelled. Therefore, EFSA considers that the previous risk assessment conclusions and risk management recommendations on maize MON810, Bt11 and 1507 for cultivation made by the Panel on Genetically Modified Organisms remain valid and applicable.

Publication Type: J

***Record 7 of 19.** Search terms matched: BORER(1); CORN(2); CRY1AB(5); LEPIDOPTERA(1); MAIZE(3); MON 810(1); OSTRINIA(4); PROTECTION(1); ZEA MAYS(1)

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Accession Number: CABI:20173051182

Document Type: Journal article, Conference paper

Author(s): Buuk, C.; Gloyna, K.; Thieme, T.

Edited by: Meissle M.

Title: Is there any change in susceptibility of European corn borer (*Ostrinia nubilalis*) to Cry1Ab protein?

Source: IOBC/WPRS Bulletin, 114 1-6; 2016

Conference: Proceedings of the IOBC/WPRS Working Group "GMOs in Integrated Plant Production", Sofia, Bulgaria, 1-3 June 2015.

Language: English

Abstract: In accordance with the EuropaBio Harmonised IRM plan (September, 2012) the baseline susceptibility of *Ostrinia nubilalis* (ECB) to the Cry1Ab protein needs to be established after which subsequent routine monitoring for changes in susceptibility should be carried out. The objective is to detect, in a timely manner, shifts relative to baseline susceptibility that could result in inadequate protection against the target species. This program will enable early detection of potential development of resistance in *O. nubilalis* if it occurs, and this will allow the proposal and implementation of additional risk mitigation measures. During 2005-2014, 14 areas with 140 samples of ECB were analysed. Thus far, susceptibility to Cry1Ab have been assessed for one laboratory colony and ECB collected in maize fields in Czech Republic, France, Germany, Italy, Hungary, Slovakia, Poland, Portugal, Romania, and Spain. ECB larvae were exposed to artificial diet treated with increasing Cry1Ab concentrations, and mortality and growth inhibition were evaluated after 7 days. Variation in Cry1Ab susceptibility (MIC50) of field samples was up to 13.1-fold. A smaller variability was found for ECB pooled according to geographic and climatic conditions (up to 6.6-fold). It was planned that all *O. nubilalis* larvae from field collections that survived the bioassay at the highest dose should be transferred to plastic boxes in groups of approximately 50 larvae, provided with newly detached MON 810 maize leaves, and fed ad libitum to record any survivors. As for the seasons reported here no surviving larvae were found after 10 days and thus confirmatory experiments were not conducted.

Publication Type: J

***Record 8 of 19.** Search terms matched: BT(2); CORN(1); LEPIDOPTERA(2); MAIZE(6); ZEA MAYS(1)

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Accession Number: CABI:20173051191

Document Type: Journal article, Conference paper

Author(s): Svobodova, Z.; Romeis, J.; Habustova, O. S.; Meissle, M.

Edited by: Meissle M.

Title: Susceptibility of *Spodoptera littoralis* (Boisd.) to lepidopteran active Cry proteins in stacked *Bt* maize.

Source: IOBC/WPRS Bulletin, 114 65-70; 2016

Conference: Proceedings of the IOBC/WPRS Working Group "GMOs in Integrated Plant Production", Sofia, Bulgaria, 1-3 June 2015.

Language: English

Abstract: *Spodoptera littoralis* (Boisd.) (Lepidoptera: Noctuidae) is an important polyphagous pest in the Mediterranean area. However, insecticidal proteins produced by genetically modified (GM) plants have sublethal effects on their caterpillars. We used stacked GM maize expressing lepidopteran active Cry1F, Cry1A.105, and Cry2Ab2 proteins from *Bacillus thuringiensis* (Bt) to explore the synergic effect on *S. littoralis*. We designed 48-hour long bitrophic study to assess the effect of three lepidopteran active Cry proteins on mortality of *S. littoralis* caterpillars. The second aim of our study was to investigate whether the different Cry proteins dilute differently when they are transferred from the plant to *S. littoralis*. More than 98% mortality was observed for first, second, and third *S. littoralis* instars. All Cry proteins were diluted when transferred from maize to *S. littoralis*. Cry1A.105 was the least reduced Cry protein detected in *S. littoralis* while Cry2Ab2 was the most diluted Cry protein despite the fact that it was the most expressed Cry protein in leaves. We conclude that stacking of three lepidopteran active Cry proteins cause high mortality to *S. littoralis* in contrast to only sublethal effects reported in the literature for GM maize expressing single Cry proteins. *Spodoptera* species have been often used in trophic experiments as a source of Cry proteins to natural enemies. However, high mortality of *S. littoralis* caterpillars fed stacked Bt maize prevents the use of this species as a source of Cry proteins in feeding bioassays with natural enemies.

Publication Type: J

*Record 9 of 19. Search terms matched: MAIZE(1); PROTECTION(1); YIELD(13); YIELDGAP(1)

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Accession Number: CABI:20173049997

Document Type: Bulletin article, Conference paper

Author(s): Itteisum, M. K. van; Vries, S. C. de; Oort, P. A. J. van; Grassini, P.

Title: Estimation of global yield gaps and implications from their analysis.

Source: Proceedings - International Fertiliser Society, (795):1-20; 2016

Conference: Proceedings of the International Fertiliser Society 795, Cambridge, UK, 9th December, 2016.

Language: English

Abstract: Yield gap analysis has become popular to assess how much and where food production can be increased on existing land. It is also helpful in identifying an acceptable compromise between yield, resource use efficiency and local emissions of nutrients or crop protection agents, as resource use efficiencies tend to decrease once yields exceed a certain percentage of potential yields (e.g. 80%). The literature provides many examples of global and regional studies with yield gap analyses. The global ones are appealing because of their consistent use of one method and global databases, but they lack local or even regional agronomic rigour. Regional studies use a range of different methodologies and are therefore

hard to compare mutually. In the Global Yield Gap Atlas (www.yieldgap.org) yield gaps of all key agricultural commodities are estimated for all food producing countries, using a global protocol. The protocol is always applied with local data on weather, soils, cropping systems and actual farm yields, and the results are evaluated with local experts. This paper presents results for an initial 35 countries covering, respectively, c.60%, 58%, and 35% of global rice, maize, and wheat production. It then demonstrates how results can be used to explore options for future self-sufficiency in cereal production in sub-Saharan Africa, the sub-continent with the fastest increase in cereal demand until 2050. Next, the paper presents a method that enables yield gap analysis to be used for the prioritisation of research and development investments. Once yield gaps have been assessed, a key follow up question is why yield gaps exist: what are their underlying biophysical and socio-economic causes? To this end it is helpful to decompose yield gaps into efficiency, resource and technology gaps. Finally, yield gaps can be usefully translated into nutrient (uptake and application) gaps. These indicate by how much the balanced nutrition of crops should increase to realise a certain percentage of yield gap closure.

Publication Type: J

***Record 10 of 19.** Search terms matched: CORN(1); LEPIDOPTERA(2); MAIZE(2); MON 810(1); ZEA MAYS(1)

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Accession Number: CABI:20173046770

Document Type: Journal article

Group Author(s): European Food Safety Authority

Title: Annual report of the EFSA Scientific Network for Risk Assessment of GMOs for 2015.

Source: EFSA Supporting Publications, 13 (2):EN-1002; 2016

Language: English

Abstract: The EFSA Scientific Network for Risk Assessment of GMOs (the GMO Network) was established in accordance with EFSA's strategy for cooperation and networking with Member States. The goals of the GMO Network are to improve dialogue among members, build mutual understanding of risk assessment principles, enhance knowledge and confidence in the scientific assessment carried out in the EU, and increase the transparency of the process among Member States and EFSA. The annual reports of the GMO Network inform the public and the EFSA Advisory Forum about the specific activities and achievements of the network. During its meeting in 2015, the GMO Network discussed the following documents and topics: the draft guidance document on the agronomic and phenotypic characterisation of GM plants; the draft guidance document for the risk assessment of the renewal of GM plant products authorised under Regulation (EC) No 1829/2003; the use of EFSA Comprehensive European Food Consumption Database for estimating dietary exposure to GM foods; EFSA's self-task to supplement its previous risk mitigation measures reducing exposure of non-target Lepidoptera to maize MON 810, Bt11 or 1507 pollen; new plant breeding techniques including synthetic biology; second generation GMOs; and the use of negative segregants in the comparative assessment. In 2015, GMO Network members attended EFSA scientific meetings relevant for the risk assessment of GMOs.

Publication Type: J

***Record 11 of 19.** Search terms matched: BT(1); CORN(1); LEPIDOPTERA(1); MAIZE(5); OSTRINIA(3); PROTECT(1); PROTECTION(1); SESAMIA(1); ZEA MAYS(1)

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Accession Number: CABI:20173040057

Document Type: Journal article

Author(s): Priesnitz, K. U.; Vaasen, A.; Gathmann, A.

Title: Baseline susceptibility of different European lepidopteran and coleopteran pests to *Bt* proteins expressed in *Bt* maize: a systematic review.

Source: Environmental Evidence, 5 (27):(12 December 2016); 2016

Language: English

Abstract: Background: Lepidopteran and coleopteran species are the most important pests in maize. They can be controlled using genetically modified (GM) crops expressing insecticidal *Bacillus thuringiensis* (*Bt*) proteins. The long-term success of this technology demands a pest resistance management. Important information for the successful management of resistance is the baseline susceptibility of the different target pests to the different *Bt* proteins. The data on baseline susceptibility should enable risk assessors and managers to assess whether a GM maize produces a *Bt* protein in a high-dose to specific target organisms and resistance has evolved during the commercial cultivation of this GM maize events. Methods: Our systematic search followed an a priori protocol including the database platforms Web of Science, Scopus, CAB abstracts, Science Direct and JSTOR. We additionally conducted a Google scholar search. We collated all search results and screened all retrieved articles using predetermined inclusion criteria. We identified 30 studies, which fulfilled the criteria of including a relevant *Bt* protein, a relevant species, an appropriate endpoint, and field-derived pest generations reared in the laboratory no longer than three generations. We then made a quality assessment to discover if the studies considered the dose response curves with confidence intervals, described the protein source, tested the protein concentration and the protein activity via positive controls, use more than ten larvae per concentration, more than two replications, and more than five protein concentrations. Since no quantitative synthesis was possible the synthesis of the results was done in a narrative form. Results: Seventy percent of the studies fulfilled five or more criteria and 17% fulfilled four of the seven criteria. Six *Bt* proteins were tested on one or more of the four species *Ostrinia nubilalis*, *Helicoverpa armigera*, *Sesamia nonagrioides*, and *Diabrotica virgifera virgifera*. We extracted the baseline susceptibility for the given protein-species-combinations and the test method with the *Bt* protein applied either on the surface of the diet or incorporated. Although, the data displays a high heterogeneity and are thus hard to compare, they give an overview of the baseline susceptibility of lepidopteran/coleopteran pests to *Bt* proteins. Conclusion: Our systematic review illustrates the heterogeneity of the data and indicates the necessity of standard protocols for testing susceptibility of insect pests, which provide comparable data. The cultivation of *Bt* crops, as with any other plant protection measure, is likely to result in resistance evolution in the target pests. Industry, policy makers, and research should combine knowledge to protect the benefits of this technology.

Publication Type: J

***Record 12 of 19.** Search terms matched: BT(4); CORN(12); MAIZE(13); YIELD(2); ZEA MAYS(1)

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Accession Number: CABI:20173036408

Document Type: Journal article

Author(s): Ordosch, D.; Narem, R.; Szczepaniec, A.

Title: Effectiveness of Bt maize against corn rootworm (Coleoptera: Chrysomelidae) and species composition in South Dakota ten years following the introduction of transgenic maize.

Source: Journal of Agricultural and Urban Entomology, 32 (1):59-70; 2016

Language: English

Abstract: Corn rootworms, *Diabrotica* spp. (Coleoptera: Chrysomelidae), are the most economically important pest of maize in the United States. The larvae consume maize roots, contributing to poor nutrient uptake, lodging of the plants, and severe yield loss. Transgenic maize expressing toxins from the bacterium *Bacillus thuringiensis* (Bt) have been employed to combat the pest. However, corn rootworm resistance to Bt maize has recently been reported and spurred research on the effectiveness of Bt toxins against corn rootworm across the Corn Belt. Thus, our objectives were twofold. First, we quantified the efficacy of Bt maize hybrids against corn rootworm in South Dakota. Second, we surveyed populations of *Diabrotica* species in areas where Bt maize had been grown since its commercialization in 2003. Maize hybrids expressing Cry3Bb1, Cry34/35Ab1, and mCry3A were evaluated at two locations with previous corn rootworm infestations or in fields that were in continuous maize for three or more consecutive years. We reported damage to maize expressing Cry3Bb1 and mCry3A toxins. We also observed significantly higher numbers of western corn rootworm than northern corn rootworm in our *Diabrotica* species surveys, suggesting that western corn rootworm are the dominant species in the region. This research has implications for maize production and sustainable corn rootworm management in South Dakota and the Northern Plains, and will advance our knowledge of the incidence of resistance to Bt toxins and long-term impact of Bt hybrids on species diversity of *Diabrotica*.

DOI: [10.3954/1523-5475-32.1.59](https://doi.org/10.3954/1523-5475-32.1.59)

Publication Type: J

***Record 13 of 19.** Search terms matched: BT(1); CORN(1); CRY1AB(1); LEPIDOPTERA(1); MAIZE(2); OSTRINIA(4); RESISTANT(1); ZEA MAYS(1)

*[Click Here to View Full Record](#)

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Accession Number: CABI:20173060932

Document Type: Journal article

Author(s): Dai PingLi; Jia HuiRu; Jack, C. J.; Geng LiLi; Liu Feng; Hou ChunSheng; Diao QingYun; Ellis, J. D.

Title: Bt Cry1Ie toxin does not impact the survival and pollen consumption of Chinese honey bees, *Apis cerana cerana* (Hymenoptera, Apidae).

Source: Journal of Economic Entomology, 109 (6):2259-2263; 2016

Language: English

Abstract: The cryIIe gene may be a good candidate for the development of Bt maize because over-expression of CryIIe is highly toxic to Lepidopteran pests such as *Heliothis armigera* Hubner and *Ostrinia furnacalis* Guenee. The Bt cryIIe gene also has no cross resistance with other insecticidal proteins such as CryIAb, CryIAc, CryIAh, or CryIF. Chinese honey bees (*Apis cerana cerana*) are potentially exposed to insect-resistant genetically modified (IRGM) crops expressing CryIIe toxin via the collection of IRGM crop pollen. In this study, we tested whether Chinese honey bee workers are negatively affected by sugar syrup containing 20, 200, or 20,000 ng/ml CryIIe toxin and 48 ng/ml imidacloprid under controlled laboratory conditions. Our results demonstrated that the CryIIe toxin does not adversely impact survival and pollen consumption of Chinese honey bees. However, imidacloprid decreases Chinese honey bee survival and the total pollen consumption on the 5th, 6th, and 18th d of exposure. The described bioassay is suitable to assess the effects of GM expressed toxins against honey bee.

Publication Type: J

***Record 14 of 19.** Search terms matched: CRY1AB(1); LEPIDOPTERA(3)

*[Click Here to View Full Record](#)

*Order Full Text []

Accession Number: CABI:20173042212

Document Type: Journal article

Author(s): Shera, P. S.; Ramesh Arora

Title: Impact of transgenic Bt cotton on nutritional indices of spotted bollworm, *Earias vittella* (Fabricius) (Lepidoptera: Nolidae).

Source: *Phytoparasitica*, 44 (4):447-457; 2016

Language: English

Abstract: The quality of food consumed by the insect is the key factor determining the utilization of food, thus having great impact on its survival, development, and longevity. Genetically modified plants with genes from soil inhabiting spore forming bacterium, *Bacillus thuringiensis* Berliner produces delta-endotoxin, which target the gut of insect, so food intake and its utilization are likely to be affected. Four Bt cotton hybrids, each with one of four events, viz. MRC 6301 Bt (cryIAc gene), JKCH 1947 Bt (modified cryIAc gene), NCEH 6R Bt (cryIAb/cryIAc fused gene) and MRC 7017 BG II (cryIAc and cry2Ab genes) were compared for nutritional indices of spotted bollworm, *Earias vittella* (Fabricius) (Lepidoptera: Nolidae) along their isogenic non-Bt genotypes. Various consumption and utilization indices, viz. consumption index (CI), relative growth rate (RGR), efficiency of conversion of ingested food (ECI) and efficiency of conversion of digested food (ECD) were worked out. The data show that all the Bt hybrids significantly reduced CI, RGR, ECI and ECD of 4th instar *E. vittella* larvae as compared to their isogenic non-Bt genotypes when fed on squares and bolls of 90, 120 and 150 days crop age. Further, the Bollgard II genotype MRC 7017 BG II was found to be more lethal and recorded significantly lower values for all the above given indices. Despite the fact that, the differences between Bt and their isogenic non-Bt genotypes decreased with increasing age of the crop but still Bt cotton hybrids were significantly inferior as insect food as compared to the non-Bt ones even at the later stages of the crop growth. The amount of CryIAc toxin in squares and bolls of Bt cotton had a significant negative correlation with food

consumption and utilization indices of *E. vittella* larvae. The studies thus indicated that Bt toxin has a substantial impact on the nutritional performance of *E. vittella*.

DOI: [10.1007/s12600-016-0540-3](https://doi.org/10.1007/s12600-016-0540-3)

Publication Type: J

*Record 15 of 19. Search terms matched: BORER(2); BT(3); CORN(15); LEPIDOPTERA(3); MAIZE(1); OSTRINIA(5); ZEA MAYS(1)

[*Click Here to View Full Record](#)

*Order Full Text []

Accession Number: CABI:20173037366

Document Type: Journal article

Author(s): Schmidt-Jeffris, R. A.; Huseth, A. S.; Nault, B. A.

Title: Estimating *E*-race European corn borer (Lepidoptera: Crambidae) adult activity in snap bean fields based on corn planting intensity and their activity in corn in New York agroecosystems.

Source: Journal of Economic Entomology, 109 (5):2210-2214; 2016

Language: English

Abstract: European corn borer, *Ostrinia nubilalis* (Hubner), is a major pest of processing snap bean because larvae are contaminants in pods. The incidence of *O. nubilalis* -contaminated beans has become uncommon in New York, possibly because widespread adoption of Bt field corn has suppressed populations. Snap bean fields located where Bt corn has been intensively grown in space and time may be at lower risk for *O. nubilalis* than fields located where Bt corn is not common. To manage *O. nubilalis* infestation risk, growers determine insecticide application frequency in snap bean based on pheromone-trapping information in nearby sweet corn fields; adult activity is presumed equivalent in both crops. Our goal was to determine if corn planting intensity and adult activity in sweet corn could be used to estimate *O. nubilalis* populations in snap bean in New York in 2014-2015. Numbers of *O. nubilalis* adults captured in pheromone-baited traps located in snap bean fields where corn was and was not intensively grown were similar, suggesting that *O. nubilalis* does not respond to local levels of Bt corn in the landscape. Numbers of *Ostrinia nubilalis* captured in pheromone-baited traps placed by snap bean fields and proximal sweet corn fields were not related, indicating that snap bean growers should no longer make control decisions based on adult activity in sweet corn. Our results also suggest that the risk of *O. nubilalis* infestations in snap bean is low (~80% of the traps caught zero moths) and insecticide applications targeting this pest should be reduced or eliminated.

Publication Type: J

*Record 16 of 19. Search terms matched: BT(3); CORN(11); CORNFIELDS(3); MAIZE(1); ZEA MAYS(2)

[*Click Here to View Full Record](#)

*Order Full Text []

Accession Number: CABI:20173037352

Document Type: Journal article

Author(s): Dunbar, M. W.; O'Neal, M. E.; Gassmann, A. J.

Title: Effects of field history on corn root injury and adult abundance of northern and western corn rootworm (Coleoptera: Chrysomelidae).

Source: Journal of Economic Entomology, 109 (5):2096-2104; 2016

Language: English

Abstract: Western corn rootworm, *Diabrotica virgifera virgifera* LeConte (Coleoptera: Chrysomelidae), and northern corn rootworm, *Diabrotica barberi* Smith & Lawrence, are major pests of corn (*Zea mays* L.). Corn producing *Bacillus thuringiensis* (Bt) toxins are widely used to manage *Diabrotica* spp.; however, Bt resistance by *D. v. virgifera* has led to high levels of feeding injury in the field. We tested whether field history affected root injury and abundance of adult *Diabrotica* spp. In 2013 and 2014, four types of cornfields were sampled: (1) recently rotated fields, (2) continuous cornfields, (3) fields with a history of injury to Bt corn (past problem fields), and (4) fields with greater than one node of injury to Bt corn at the time of sampling (current problem fields). Data were collected on field history, root injury, and the abundance of adult *Diabrotica* spp. from each field. Root injury and the abundance of *D. v. virgifera* were significantly greater in current problem fields compared to the other field types, while *D. barberi* were significantly more abundant in recently rotated fields. Root injury and the abundance of *D. v. virgifera* did not differ among recently rotated fields, continuous cornfields, and past problem fields. Analysis of field history showed that recently rotated fields were characterized by significantly less Bt corn, soil-applied insecticides, and years planted to corn continuously. These results suggest that greater cropping practice diversity can reduce management inputs for *Diabrotica* spp.; however, its effects on resistance evolution remain undetermined.

DOI: [10.1093/jee/tow163](https://doi.org/10.1093/jee/tow163)

Publication Type: J

*Record 17 of 19. Search terms matched: CRY1AB(1); LEPIDOPTERA(1)

*[Click Here to View Full Record](#)

*Order Full Text []

Accession Number: CABI:20173060561

Document Type: Journal article

Author(s): Zhang YaKun; Zhao Dan; Guo Wei; Wang Wei; Lu XiuJun; Li RuiJun

Title: Screening of *Bacillus thuringiensis* strains with high toxicity against *Spodoptera exigua* and identification of a new *cry2Ah5* gene.

Source: Chinese Journal of Biological Control, 32 (3):414-420; 2016

Language: Chinese

Language of Summary: English

Abstract: According to the results of bioassay, five *Bacillus thuringiensis* strains with high toxicity against *Spodoptera exigua* were obtained. The median lethal concentrations (LC50) of these strains ranged from 0.556 to 0.914 mg/mL spores and crystals mixture, and the strain GS3 had the highest toxicity with a LC50 of 0.556 mg/mL. These strains contained *cry1Aa*, *cry1Ab*, *cry1La*, *cry1Ia*, *cry1Ib*, *cry2Ab*, *cry2Ad*, *cry2Ah*, *cry7Ab* and *cry9Ba* genes, forming globular or bipyramidal in different sizes crystals. All of them expressed 60 kD and 130-150 kD proteins, and two of them also lowly expressed 80 kD proteins. A new *cry2A* gene identified

from the strain GS3 with an accession number of KT692984 was designated cry2Ah5 by the International Nomenclature Committee of Bt delta-endotoxin genes. Sequence analysis showed that cry2Ah5 contained a 1899 bp open reading frame, which encoded a 70.8 kD protein composing of 632 amino acids. The pI of this protein was 8.18. The Cry2Ah5 protein showed 97%-99% sequence identity with other Cry2Ah. The cry2Ah5 gene expressed a 70 kD protein in Escherichia coli BL21 (DE3) corresponding to the predict molecular weight. Our research provided more strains and genetic resources for the biological control of *S. exigua*.

Publication Type: J

***Record 18 of 19.** Search terms matched: BORER(1); BT(1); CORN(13); CRY1AB(6); LEPIDOPTERA(6); MAIZE(1); YIELD(4); ZEA MAYS(1)

*[Click Here to View Full Record](#)

*Order Full Text []

Accession Number: CABI:20173037322

Document Type: Journal article

Author(s): Reay-Jones, F. P. F.; Bessin, R. T.; Brewer, M. J.; Buntin, D. G.; Catchot, A. L.; Cook, D. R.; Flanders, K. L.; Kerns, D. L.; Porter, R. P.; Reisig, D. D.; Stewart, S. D.; Rice, M. E.

Title: Impact of Lepidoptera (Crambidae, Noctuidae, and Pyralidae) pests on corn containing pyramided Bt traits and a blended refuge in the southern United States.

Source: Journal of Economic Entomology, 109 (4):1859-1871; 2016

Language: English

Abstract: Blended refuge for transgenic plants expressing *Bacillus thuringiensis* (Bt) toxins has been approved in the northern United States as a resistance management strategy alternative to a structured refuge. A three-year study (2012-2014) was conducted with 54 trials across nine states in the southern United States to evaluate plant injury from lepidopteran pests of corn and yield in a corn hybrid expressing Cry1F * Cry1Ab * Vip3Aa20 (Pioneer Brand Optimum Leptra) planted as a pure stand and in refuge blends of 5, 10, and 20% in both early and late plantings. Injury by corn earworm, *Helicoverpa zea* Boddie (Lepidoptera: Noctuidae), and fall armyworm, *Spodoptera frugiperda* (J. E. Smith) (Lepidoptera: Noctuidae), was generally proportional to the percentage of non-Bt corn within each refuge blend. Across locations, ear injury in plots with 100% Cry1F * Cry1Ab * Vip3Aa20 (Optimum Leptra) corn ranged from no injury to a maximum of 0.42 cm² per ear in Mississippi in 2013. Leaf injury ratings in 100% non-Bt plots in early and late planted trials in 2014 were 86- and 70-fold greater than in 100% Cry1F * Cry1Ab * Vip3Aa20 (Optimum Leptra) plots. Plants in plots with blended refuges had significantly greater leaf injury in 2012 (5, 10, and 20% refuge blends), in the early-planted corn in 2013 (10 and 20% only), and in both early- and late-planted corn in 2014 (20% only) as compared with leaf injury in a pure stand of Cry1F * Cry1Ab * Vip3Aa20 (Optimum Leptra) seen during these years. Corn ears in plots with blended refuges also had significantly greater area of kernels injured in 2012 (5, 10, and 20%), in early- and late-planted corn in 2013 (5, 10, and 20%), and in early (10 and 20% only)- and late-planted corn (5, 10, and 20%) in 2014 as compared with ear injury in a pure stand of Cry1F * Cry1Ab * Vip3Aa20 (Optimum Leptra) seen during these years. Infestations of southwestern corn borer, *Diatraea grandiosella* Dyar (Lepidoptera: Crambidae), were also significantly reduced by Cry1F * Cry1Ab * Vip3Aa20

(Optimum Leptra). Despite these differences in injury, yield averaged across locations varied among refuge blends only in the late-planted trials in 2013, with greater yields in the 0% refuge blend than in the 20% blend; however, when examining yield separately by location, only two of nine locations had higher yields in the 100% Bt plots than in any of the blended refuge plots. As a complement to studying the contribution of blended refuge to delaying resistance, quantifying injury and yield in a range of refuge blends is a necessary step to provide management information on the range of lepidopteran pests that occur in the southern United States.

DOI: [10.1093/jee/tow109](https://doi.org/10.1093/jee/tow109)

Publication Type: J

***Record 19 of 19.** Search terms matched: BT(5); CORN(29); MAIZE(1); ZEA MAYS(1)

*[Click Here to View Full Record](#)

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Accession Number: CABI:20173037323

Document Type: Journal article

Author(s): Gassmann, A. J.; Shrestha, R. B.; Jakka, S. R. K.; Dunbar, M. W.; Clifton, E. H.; Paolino, A. R.; Ingber, D. A.; French, B. W.; Masloski, K. E.; Dounda, J. W.; St. Clair, C. R.

Title: Evidence of resistance to Cry34/35Ab1 corn by western corn rootworm (Coleoptera: Chrysomelidae): root injury in the field and larval survival in plant-based bioassays.

Source: Journal of Economic Entomology, 109 (4):1872-1880; 2016

Language: English

Abstract: Western corn rootworm, *Diabrotica virgifera virgifera* LeConte (Coleoptera: Chrysomelidae), is a serious pest of corn in the United States, and recent management of western corn rootworm has included planting of Bt corn. Beginning in 2009, western corn rootworm populations with resistance to Cry3Bb1 corn and mCry3A corn were found in Iowa and elsewhere. To date, western corn rootworm populations have remained susceptible to corn producing Bt toxin Cry34/35Ab1. In this study, we used single-plant bioassays to test field populations of western corn rootworm for resistance to Cry34/35Ab1 corn, Cry3Bb1 corn, and mCry3A corn. Bioassays included nine rootworm populations collected from fields where severe injury to Bt corn had been observed and six control populations that had never been exposed to Bt corn. We found incomplete resistance to Cry34/35Ab1 corn among field populations collected from fields where severe injury to corn producing Cry34/35Ab1, either singly or as a pyramid, had been observed. Additionally, resistance to Cry3Bb1 corn and mCry3A corn was found among the majority of populations tested. These first cases of resistance to Cry34/35Ab1 corn, and the presence of resistance to multiple Bt toxins by western corn rootworm, highlight the potential vulnerability of Bt corn to the evolution of resistance by western corn rootworm. The use of more diversified management practices, in addition to insect resistance management, likely will be essential to sustain the viability of Bt corn for management of western corn rootworm.

DOI: [10.1093/jee/tow110](https://doi.org/10.1093/jee/tow110)

Publication Type: J

***Record 1 of 9.** Search terms matched: BT(2); CORN(1); LEPIDOPTERA(2); MAIZE(11); RESISTANT(1); ZEA MAYS(1)

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Accession Number: CABI:20173068227

Document Type: Journal article

Author(s): Bernardi, D.; Bernardi, O.; Horikoshi, R. J.; Salmeron, E.; Okuma, D. M.; Farias, J. R.; Nascimento, A. R. B. do; Omoto, C.

Title: Selection and characterization of *Spodoptera frugiperda* (Lepidoptera: Noctuidae) resistance to MON 89034 * TC1507 * NK603 maize technology.

Source: Crop Protection, 94 64-68; 2017

Language: English

Abstract: The transgenic maize MON 89034 * TC1507 * NK603 expressing Cry1A.105, Cry1F and Cry2Ab2 proteins has been used for controlling fall armyworm (FAW), *Spodoptera frugiperda* (J. E. Smith), in Brazil since 2010. To design resistance management strategies, we selected and characterized the resistance to MON89034 * TC1507 * NK603 maize in a field-derived strain of FAW and investigated fitness costs associated with resistance. In greenhouse assays, more than 64% of neonates from resistant strain (RR) survived on MON 89034 * TC1507 * NK603 maize plants and produced fertile adults. In contrast, neonates from susceptible (SS) and heterozygous strains did not survive on MON 89034 * TC1507 * NK603 maize plants, indicating that resistance is functionally recessive. In laboratory assays, individuals from the RR strain fed on MON 89034 * TC1507 * NK603 maize presented similar life table parameters of those fed on non-Bt maize. However, life history studies with non-Bt maize to investigate fitness costs revealed that the RR strain had a ~4 d longer egg-to-adult period, 9% reduction in the survival rate until adult stage, and ~35% lower reproductive rate than SS and heterozygous strains. In summary, our results showed that the resistance of FAW to MON 89034 * TC1507 * NK603 maize is functionally recessive and associated with relevant fitness costs. Therefore, the adoption of refuge areas as a resistance management strategy can prolong the lifetime of MON 89034 * TC1507 * NK603 maize in Brazil.

Publication Type: J

***Record 2 of 9.** Search terms matched: CORN(1); MAIZE(3); MON810(1); ZEA MAYS(1)

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Accession Number: CABI:20173086770

Document Type: Journal article

Author(s): Gatto, F.; Bassani, N.; Rosa, S. F.; Lievens, A.; Brustio, R.; Kreysa, J.; Querci, M.

Title: Semi-quantification of GM maize using ready-to-use RTi-PCR plates.

Source: Food Analytical Methods, 10 (2):549-558; 2017

Language: English

Abstract: European Union (EU) legislation foresees that food and feed are labelled for their genetically modified organism (GMO) content when the ingredients contain authorised GMOs in a proportion higher than 0.9%. Non-authorised GMOs are not allowed on the EU market.

Exception is made for feed materials containing traces of GM events lawfully placed on the market in non-EU countries and for which an authorisation is pending in the EU or expired: in these cases, a minimum required performance limit (MRPL) of 0.1% is applied. Considering that the number of GMOs placed on the EU market is constantly growing, laboratories need to expand their capacity accordingly to be able to identify and, if necessary, quantify any GM material. To this purpose, our laboratory had previously developed a multi-target ready-to-use system, also known as a pre-spotted plate (PSP), which allows the qualitative detection of up to 44 GM events in one single real-time (RTi) PCR experiment. Should any event be detected, the laboratory would proceed with its quantification. This study evaluates the possibility to use the data generated by the PSP system in a semi-quantitative manner, allowing a categorisation of the GM quantity in the sample. DeltaCq values were calculated and modelled via linear regression to estimate limits indicating whether the GM content is (1) above, (2) below or (3) near a defined quantity and thus requires further quantification. Identifying the GM events present in a sample and simultaneously discriminating whether it needs or not further quantification would offer to testing laboratories a valuable gain in time and resources. Six maize GM events frequently found in food and feed were selected for this evaluation (Bt11, MON810, MON88017, MON89034, NK603 and TC1507). The feasibility of the approach was successfully verified in-house using spiked and proficiency test samples.

DOI: [10.1007/s12161-016-0609-0](https://doi.org/10.1007/s12161-016-0609-0)

Publication Type: B

***Record 3 of 9.** Search terms matched: BORER(1); BT(3); CORN(5); CRY1AB(1); LEPIDOPTERA(2); MAIZE(1); SESAMIA(4); ZEA MAYS(1)

*[Click Here to View Full Record](#)

*Order Full Text []

Accession Number: CABI:20173053871

Document Type: Conference paper

Author(s): Dahi, H. F.; Aly, M. Z. Y.; Soliman, M. M. M.; Salem, S. A. R.

Edited by: Kovacevic D.

Title: The efficiency of *Bt* corn expressing entomocidal protein Cry1Ab on biochemical parameters of *Sesamia cretica* (Lederer)(Lepidoptera: Noctuidae).

Source: VII International Scientific Agriculture Symposium, "Agrosym 2016", 6-9 October 2016, Jahorina, Bosnia and Herzegovina. Proceedings, 1675-1681; 2016

Conference: VII International Scientific Agriculture Symposium, "Agrosym 2016", 6-9 October 2016, Jahorina, Bosnia and Herzegovina. Proceedings.

Language: English

Abstract: The present investigation aims to throw a light on the efficiency of Bt corn on biochemical parameters of 4th larval instar of pink corn borer *Sesamia cretica* (Led.) under laboratory conditions. The results showed that 24 h post feeding on Bt corn, caused a 36.05% increase in the larval protein content than their value in the control. Although, total carbohydrates was decreased by 49.13% in larvae than their value in the control. The disturbance in the carbohydrate level was expressed by impairment in the activity of carbohydrate enzymes in treated 4th instar larvae. In treated instar larvae there was a significant increase in the enzyme activity of alpha and beta esterase as well as in acetyl choline esterase.

Also, a significant increase in the enzyme activities of both Glutamic pyruvic transaminase and glutathione S-transferase was recorded in treated larvae the values were 24.68% and 69.78% respectively. Meanwhile there was no significant in Glutamic oxaloacetic transaminase level in treated larvae.

ISBN: 978-99976-632-7-6

Publication Type: B

***Record 4 of 9.** Search terms matched: BORER(3); BT(1); CORN(5); LEPIDOPTERA(2); MAIZE(3); SESAMIA(4); ZEA MAYS(1)

*[Click Here to View Full Record](#)

*Order Full Text []

Accession Number: CABI:20173053701

Document Type: Conference paper

Author(s): Yanar, D.; Yanar, Y.; Atay, T.; Yalcin, M.; Beldek, O.

Edited by: Kovacevic D.

Title: Effects of 18 local *Beauvaria bassiana* (Balsamo) vuillemin entomopathogen fungi isolates on pink corn borer *Sesamia cretica* Led. under laboratory conditions.

Source: VII International Scientific Agriculture Symposium, "Agrosym 2016", 6-9 October 2016, Jahorina, Bosnia and Herzegovina. Proceedings, 699-703; 2016

Conference: VII International Scientific Agriculture Symposium, "Agrosym 2016", 6-9 October 2016, Jahorina, Bosnia and Herzegovina. Proceedings.

Language: English

Abstract: The spread of silage maize production in Turkey caused significant increase at population level of corn borer, *Sesamia cretica* Led. (Lepidoptera: Noctuidae) In the management of this pest general insecticides, such as organic phosphates and synthetic pyrethroids are used. Its damage still occurs in corn fields, in spite of the use of biological control agents, such as entomopathogenic fungi, nematodes or bacteria and egg-larval-pupa parasitoids, as well as Bt-maize, as a popular application for management of *S. cretica*. In order to detect more effective microbial control agents against this pest and contribute to the integrated pest management studies of corn borer, a study of insecticidal effect of 18 different isolates of entomopathogenic fungi *Beauvaria bassiana* obtained from soil collected from different fields crop production areas in Tokat Province in 2015. The isolates consist of *B. bassiana* isolates (GOPT-19(2)-1, GOPT-41-1, GOPT-64, GOPT-107, GOPT-114, GOPT-122, GOPT-127, GOPT-144, GOPT-167, GOPT-221, GOPT-284, GOPT-294, GOPT-302, GOPT-355, GOPT-440, GOPT-453, GOPT-458, GOPT-465). Pathogenicity of tested isolates to *S. cretica* was evaluated by dipping larvae (fourth instar) to spore suspension from each isolate. Within 9 days, all fungal isolates caused significant mortality against larva of *S. cretica*. *B. bassiana* isolates GOPT-144 was found to be the most virulent with 90.83% mortality among investigated fungal isolates, followed by GOPT-64 (75.42% mortality) and GOPT-107 (63.75% mortality) against the *S. cretica*. These results indicated that isolates with high virulence could be used for biological control and integrated management of *S. cretica*.

ISBN: 978-99976-632-7-6

Publication Type: J

*Record 5 of 9. Search terms matched: CRY1AB(6)

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*Order Full Text []

Accession Number: CABI:20173080328

Document Type: Journal article

Author(s): Liu Hua; Chang XiaoLei; Jiang Wei; Bai Lan; Zheng ShuFeng; Wang JinBin; Wang Wei; Pan AiHu; Wang RongTan; Tang XueMing

Title: Effect of Cry1Ab/c protein residues from *Bt* cotton-producing areas in regions with marginal water in three provinces in eastern China.

Source: Biodiversity Science, 24 (12):1373-1380; 2016

Language: Chinese

Language of Summary: English

Abstract: To investigate Cry1Ab/c protein residues in marginal water regions of transgenic cotton-producing areas, this study focused on 15 sampling points from three provinces of eastern China using random sampling. We sampled three consecutive years during the flowering and harvesting of cotton, respectively, purified Cry1Ab/c proteins in these samples were detected using the ELISA (enzyme-linked immunosorbent assay) method. Results showed that: (1) The highest concentration of Cry1Ab/c protein in marginal water reached 0.4 ppb at one sampling point. At the other four monitoring points, the residual concentration of Cry1Ab/c protein was less than 0.04 ppb. (2) The closer the cotton field, the higher the positive detection rate, and the positive rate was 13.3% in the cotton field canals. (3) The positive protein detection rate was 12.4% in planting fields that had been planted for more than 7 years. We also found that during the harvest season the positive protein detection rate was easier to detect than during the flowering period. Our findings indicated that the Bt cotton-producing areas should be properly monitored during the harvest season, in order to reduce the potential impacts of Cry1Ab/c protein on the marginal water sources in transgenic cotton producing areas.

DOI: [10.17520/biods.2016142](https://doi.org/10.17520/biods.2016142)

Publication Type: J

*Record 6 of 9. Search terms matched: BT(4); CORN(1); CRY1AB(8); LEPIDOPTERA(1); MAIZE(13); RESISTANT(1); ZEA MAYS(1)

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*Order Full Text []

Accession Number: CABI:20173074440

Document Type: Journal article

Author(s): Chang Xue; Wang Wei; Shen ZhiCheng; Ye GongYin

Title: Evaluation of transgenic *cry1Ab/cry2Aj* and *cry1Ab/vip3DA* maize events for their resistance to *Helicoverpa armigera*, *Spodoptera exigua* and *Prodenia litura*.

Source: Acta Phytophylacica Sinica, 43 (6):951-957; 2016

Language: Chinese

Language of Summary: English

Abstract: In order to evaluate the resistance of transgenic cry1Ab/cry2Aj maize and cry1Ab/vip3DA maize to *Helicoverpa armigera* (Hubner), *Spodoptera exigua* (Hubner) and *Prodenia litura* (Fabricius), the survival and development of the larvae of the three insect pests treated with three transgenic cry1Ab/cry2Aj maize events and one transgenic cry1Ab/vip3DA maize event were conducted through laboratory bioassay, and the insecticidal activity and control efficacy of different tissues and organs of these Bt events were investigated. The results showed that the mortalities of *H. armigera* neonate larvae were 87.50%-90.00% when fed on leaves of Bt maize events at 96 h after infestation, and most larvae fed on silks and ear of Bt maize events died at 96 h after infestation. The mortalities of *S. exigua* neonate larvae fed on leaves, silks and ear of Bt maize events were 22.50%-68.33% at 168 h after infestation, while the larval development was inhibited severely and the weight inhibition rate ranged from 85.00% to 95.00%. The mortalities of *P. litura* neonate larvae fed on leaves, silks and ear of Bt maize events were significantly higher than that of the control at 96 h after infestation, and more than 90.00% larvae were killed at 168 h after infestation. The results indicated that these transgenic cry1Ab/cry2Aj and cry1Ab/vip3DA maize events provided efficient resistance against *H. armigera* and *P. litura* neonate larvae, and could serve as breeding sources for the development of insect-resistant pyramided transgenic maize.

Publication Type: J

***Record 7 of 9.** Search terms matched: BT(5); CORN(12); MAIZE(1); PROTECTION(1); ZEA MAYS(1)

*[Click Here to View Full Record](#)

*Order Full Text []

Accession Number: CABI:20173068194

Document Type: Journal article

Author(s): Lit, I. L., Jr.; Caasi-Lit, M. T.; Abenis, K. O.; Manalo, N. A. Q.; Larona, A. R.; Eusebio, O. L.; Benigno, E. A.

Title: Non-target organisms on Bt corn hybrids MON89034 and MON89034/NK603: Part 3. Functional guilds of arthropods in regulated field trial sites during the wet season in Luzon and Mindanao, Philippines.

Source: Philippine Entomologist, 30 (1):29-51; 2016

Language: English

Abstract: Regulated field experiments were conducted in Ilagan, Isabela and Tupi, South Cotabato to assess the effects of two new Bt corn hybrids (MON89034 expressing two insecticidal proteins, Cry1A.105 and Cry2Ab2 and MON89034/NK603 that additionally expresses glyphosate resistance) on non-target organisms (NTOs) specifically arthropods. Effects were assessed in comparison with two non-Bt corn hybrids (DK818 isogenic conventional corn and NK603 with glyphosate resistance trait) with no chemical protection. Arthropods were sampled using sweep net and vacuum, pitfall trapping, sugar- and protein-baiting and visual counting. A total of 15,970 and 31,699 individuals were collected in Isabela and South Cotabato, respectively. These arthropods are spread in 18 insect orders with 113 families for Isabela and 20 insect orders with 127 families for South Cotabato. The functional guilds (predators, parasitoids, pollinators, neutrals, non-target corn herbivores) appeared unhampered by the corn type as to their respective roles in the corn agroecosystem. The overall

trend indicates that the mean number of arthropods was highest at the reproductive stage of the corn plant. The addition of NK603 in the wet season trial had no effect on the arthropod populations. In summary, the combined analysis showed that the arthropod populations were not significantly different among treatments and the levels of arthropod populations in non-Bt and Bt-corn fields did not show any significant difference. Data generated from both dry and wet season trials support the hypothesis that MON89034 and MON89034/NK603 have no effects on non-target arthropods in the corn ecosystem and suggest that there are no significant seasonal variations in the effects of Bt corn hybrids on NTOs.

Publication Type: J

***Record 8 of 9.** Search terms matched: BORER(2); BT(6); CORN(9); LEPIDOPTERA(1); MAIZE(1); OSTRINIA(4); PROTECT(1); RESISTANT(2); ZEA MAYS(1)

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*Order Full Text []

Accession Number: CABI:20173065333

Document Type: Journal article

Author(s): Jiang Fan; Zhang TianTao; Bai ShuXiong; Wang ZhenYing; He KangLai

Title: Evaluation of Bt corn with pyramided genes on efficacy and insect resistance management for the Asian corn borer in China.

Source: PLoS ONE, 11 (12):e0168442; 2016

Language: English

Abstract: A Bt corn hybrid (AcIe) with two Bt genes (cry1Ie and cry1Ac) was derived by breeding stack from line expressing Cry1Ie and a line expressing Cry1Ac. Efficacy of this pyramided Bt corn hybrid against the Asian corn borer (ACB), *Ostrinia furnacalis*, was evaluated. We conducted laboratory bioassays using susceptible and resistant ACB strains fed on artificial diet or fresh plant tissues. We also conducted field trials with artificial infestations of ACB neonates at the V6 and silk stages. The toxin-diet bioassay data indicated that mixtures of Cry1Ac and Cry1Ie proteins had synergistic insecticidal efficacy. The plant tissue bioassay data indicated that Bt corn hybrids expressing either a single toxin (Cry1Ac or Cry1Ie) or two toxins had high efficacy against susceptible ACB. Damage ratings in the field trials indicated that the Bt corn hybrids could effectively protect against 1st and the 2nd generation ACB in China. The hybrid line with two Bt genes showed a higher efficacy against ACB larvae resistant to Cry1Ac or Cry1Ie than the hybrid containing one Bt gene, and the two gene hybrid would have increased potential for managing or delaying the evolution of ACB resistance to Bt corn plants.

Publication Type: J

***Record 9 of 9.** Search terms matched: BT(1); CORN(9); CRY1AB(5); LEPIDOPTERA(1); MAIZE(1); TOLERANT(1); ZEA MAYS(1)

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*Order Full Text []

Accession Number: CABI:20173065639

Document Type: Journal article

Author(s): Dively, G. P.; Venugopal, P. D.; Finkenbinder, C.

Title: Field-evolved resistance in corn earworm to Cry proteins expressed by transgenic sweet corn.

Source: PLoS ONE, 11 (12):e0169115; 2016

Language: English

Abstract: Background: Transgenic corn engineered with genes expressing insecticidal toxins from the bacterium *Bacillus thuringiensis* (Berliner) (Bt) are now a major tool in insect pest management. With its widespread use, insect resistance is a major threat to the sustainability of the Bt transgenic technology. For all Bt corn expressing Cry toxins, the high dose requirement for resistance management is not achieved for corn earworm, *Helicoverpa zea* (Boddie), which is more tolerant to the Bt toxins. Methodology/Major Findings: We present field monitoring data using Cry1Ab (1996-2016) and Cry1A.105+Cry2Ab2 (2010-2016) expressing sweet corn hybrids as in-field screens to measure changes in field efficacy and Cry toxin susceptibility to *H. zea*. Larvae successfully damaged an increasing proportion of ears, consumed more kernel area, and reached later developmental stages (4th-6th instars) in both types of Bt hybrids (Cry1Ab-event Bt11, and Cry1A.105+Cry2Ab2-event MON89034) since their commercial introduction. Yearly patterns of *H. zea* population abundance were unrelated to reductions in control efficacy. There was no evidence of field efficacy or tissue toxicity differences among different Cry1Ab hybrids that could contribute to the decline in control efficacy. Supportive data from laboratory bioassays demonstrate significant differences in weight gain and fitness characteristics between the Maryland *H. zea* strain and a susceptible strain. In bioassays with Cry1Ab expressing green leaf tissue, Maryland *H. zea* strain gained more weight than the susceptible strain at all concentrations tested. Fitness of the Maryland *H. zea* strain was significantly lower than that of the susceptible strain as indicated by lower hatch rate, longer time to adult eclosion, lower pupal weight, and reduced survival to adulthood.

Conclusions/Significance: After ruling out possible contributing factors, the rapid change in field efficacy in recent years and decreased susceptibility of *H. zea* to Bt sweet corn provide strong evidence of field-evolved resistance in *H. zea* populations to multiple Cry toxins. The high adoption rate of Bt field corn and cotton, along with the moderate dose expression of Cry1Ab and related Cry toxins in these crops, and decreasing refuge compliance probably contributed to the evolution of resistance. Our results have important implications for resistance monitoring, refuge requirements and other regulatory policies, cross-resistance issues, and the sustainability of the pyramided Bt technology.

Publication Type: J

*Record 1 of 13. Search terms matched: BT(1); CORN(5); MAIZE(1); PROTECT(1); YIELD(1); ZEA MAYS(1)

*[Click Here to View Full Record](#)

*Order Full Text []

Accession Number: CABI:20173106571

Document Type: Journal article

Author(s): Andow, D. A.; Wright, R. J.; Hodgson, E. W.; Hunt, T. E.; Ostlie, K. R.

Title: Farmers' perspectives on resistance in western corn rootworm to CRW-Bt corn in Midwest USA.

Source: Journal of Agricultural Extension and Rural Development, 9 (3):27-38; 2017

Language: English

Abstract: Resistance in western corn rootworm to transgenic corn hybrids was first confirmed in 2011 in Midwestern USA, and threatens their continued use. Farmers are often the first line of resistance detection, so their understanding and attitudes toward this issue are critical for improving resistance management. We conducted telephone focus groups during 2013 with farmers who had experienced rootworm resistance. There were four stages in dealing with unexpected rootworm injury: Awareness of a problem, diagnosis, confirmation, and recommendations. Most farmers discovered the problem themselves, but this usually happened too late in the growing season to limit yield loss. Once aware of a problem, farmers first sought help diagnosing the problem from their seed dealer, chemical rep, and/or crop consultant. They considered the problem to be a significant one, both because of its severity and suddenness, and were concerned about their difficulty in obtaining a correct diagnosis. They eventually used extension entomology specialists to confirm the diagnosis. Farmers gathered recommendations from independent consultants, input suppliers, and extension and indicated that they would aggressively deal with the problem, because they were not sure of what would work to protect their crop. They recommended that public extension put more emphasis on increasing awareness of the problem, assessing the extent of the problem and being an unbiased source of information. However, farmers were unlikely to report rootworm injury if the perceived barriers to reporting outweighed the perceived incentives. These barriers were emotional ones, including being unsure who to trust, fear that reporting will be time-consuming, and shame that they did something wrong. The incentive was access to credible advice. They did not automatically acknowledge the broader social benefits of reporting. Thus, extension probably needs to be explicit about these broader benefits to obtain information about the extent of the problem. With the conflicting demands and multiple information sources, it will be a challenge for extension to involve farmers to improve resistance monitoring and management.

Publication Type: J

*Record 2 of 13. Search terms matched: CORN(1); MAIZE(5); MON810(2); ZEA MAYS(1)

*[Click Here to View Full Record](#)

*Order Full Text []

Accession Number: CABI:20173126193

Document Type: Journal article

Author(s): Schmidt, K.; Schmidtke, J.; Schmidt, P.; Kohl, C.; Wilhelm, R.; Schiemann, J.; Voet, H. van der; Steinberg, P.

Title: Variability of control data and relevance of observed group differences in five oral toxicity studies with genetically modified maize MON810 in rats.

Source: Archives of Toxicology, 91 (4):1977-2006; 2017

Language: English

Abstract: The data of four 90-day feeding trials and a 1-year feeding trial with the genetically modified (GM) maize MON810 in Wistar Han RCC rats performed in the frame of EU-funded project GRACE were analysed. Firstly, the data obtained from the groups having been fed the

non-GM maize diets were combined to establish a historical control data set for Wistar Han RCC rats at the animal housing facility (Slovak Medical University, Bratislava, Slovakia). The variability of all parameters is described, and the reference values and ranges have been derived. Secondly, the consistency of statistically significant differences found in the five studies was analysed. In order to do so, the body weight development, organ weight, haematology and clinical biochemistry data were compared between the studies. Based on the historical control data, equivalence ranges for these parameters were defined, and the values measured in the GM maize-fed groups were compared with these equivalence ranges. Thirdly, the (statistical) power of these feeding studies with whole food/feed was assessed and detectable toxicologically relevant group differences were derived. Linear mixed models (LMM) were applied, and standardized effect sizes (SES) were calculated in order to compare different parameters as well as to provide an overall picture of group and study differences at a glance. The comparison of the five feeding trials showed a clear study effect in the control data. It also showed inconsistency both in the frequency of statistically significant differences and in the difference values between control and test groups.

DOI: [10.1007/s00204-016-1857-x](https://doi.org/10.1007/s00204-016-1857-x)

Publication Type: J

*Record 3 of 13. Search terms matched: BORER(2); BT(1); CORN(3); LEPIDOPTERA(1); MAIZE(6); OSTRINIA(3); RESISTANT(4); ZEA MAYS(1)

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Accession Number: CABI:20173106360

Document Type: Journal article

Author(s): Petzold-Maxwell, J. L.; Siegfried, B. D.; Hellmich, R. L.; Abel, C. A.; Coates, B. S.; Spencer, T. A.; Horikoshi, R. J.; Gassmann, A. J.

Title: Fitness costs associated with Cry1F resistance in the European corn borer.

Source: Journal of Applied Entomology, 141 (1/2):67-79; 2017

Language: English

Abstract: Crops producing insecticidal toxins derived from the bacterium *Bacillus thuringiensis* (Bt) are widely planted to manage insect pests. Bt crops can provide an effective tool for pest management; however, the evolution of Bt resistance can diminish this benefit. The European corn borer, *Ostrinia nubilalis* Hubner, is a significant pest of maize and is widely managed with Bt maize in the Midwest of the United States. When Bt crops are grown in conjunction with non-Bt refuges, fitness costs of Bt resistance can delay the evolution of resistance. Importantly, fitness costs often vary with ecological factors, including host-plant genotype and diapause. In this study, we examined fitness costs associated with Cry1F resistance in *O. nubilalis* when insects were reared on three maize lines. Fitness costs were tested in two experiments. One experiment assessed the fitness costs when Cry1F-resistant and Cry1F-susceptible insects were reared on plants as larvae and experienced diapause. The second experiment tested resistant, susceptible and F1 heterozygotes that were reared on plants but did not experience diapause. Despite some evidence of greater adult longevity for Cry1F-resistant insects, these insects produced fewer fertile eggs than Cry1F-susceptible insects, and this occurred independent of diapause. Reduced fecundity was not detected among heterozygous individuals, which indicated

that this fitness cost was recessive. Additionally, maize lines did not affect the magnitude of this fitness cost. The lower fitness of Cry1F-resistant *O. nubilalis* may contribute to the maintenance of Cry1F susceptibility in field populations more than a decade after Cry1F maize was commercialized.

Publication Type: J

***Record 4 of 13.** Search terms matched: BT(2); CORN(3); MAIZE(6); PROTECTION(1); RESISTANT(3); ZEA MAYS(1)

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Accession Number: CABI:20173106357

Document Type: Journal article

Author(s): Schrader, P. M.; Estes, R. E.; Tinsley, N. A.; Gassmann, A. J.; Gray, M. E.

Title: Evaluation of adult emergence and larval root injury for Cry3Bb1-resistant populations of the western corn rootworm.

Source: Journal of Applied Entomology, 141 (1/2):41-52; 2017

Language: English

Abstract: The transgenic maize (*Zea mays* L.) event MON 88017 produces the *Bacillus thuringiensis* Berliner (Bt) toxin Cry3Bb1 to provide protection from western corn rootworm (*Diabrotica virgifera virgifera* LeConte) larval feeding. In response to reports of reduced performance of Cry3Bb1-expressing maize at two locations in Illinois, we conducted a two-year experiment at these sites to characterize suspected resistance, as well as to evaluate root injury and adult emergence. Single-plant bioassays were performed on larvae from each population that was suspected to be resistant. Results indicate that these populations had reduced mortality on Cry3Bb1-expressing maize relative to susceptible control populations. No evidence of cross-resistance between Cry3Bb1 and Cry34/35Ab1 was documented for the Cry3Bb1-resistant populations. Field studies were conducted that included treatments with commercially available rootworm Bt hybrids and their corresponding non-Bt near-isolines. When compared with their near-isolines, larval root injury and adult emergence were typically reduced for hybrids expressing Cry34/35Ab1 either alone or in a pyramid. In many instances, larval root injury and adult emergence were not significantly different for hybrids expressing mCry3A or Cry3Bb1 alone when compared with their non-Bt near-isolines. These findings suggest that Cry34/35Ab1-expressing Bt maize may represent a valuable option for maize growers where Cry3Bb1 resistance is either confirmed or suspected. Consistent trends in adult size (head capsule width and dry mass) for individuals recovered from emergence cages were not detected during either year of this experiment. Because of the global importance of transgenic crops for managing insect pests, these results suggest that improved decision-making for insect resistance management is needed to ensure the durability of Bt maize.

Publication Type: J

***Record 5 of 13.** Search terms matched: BORER(2); BT(1); CORN(2); LEPIDOPTERA(1); MAIZE(3); RESISTANT(2); ZEA MAYS(1)

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Accession Number: CABI:20173118359

Document Type: Journal article

Author(s): Campagne, P.; Capdevielle-Dulac, C.; Pasquet, R.; Cornell, S. J.; Kruger, M.; Silvain, J. F.; LeRu, B.; Berg, J. van den

Title: Genetic hitchhiking and resistance evolution to transgenic *Bt* toxins: insights from the African stalk borer *Busseola fusca* (Noctuidae).

Source: Heredity, 118 (4):330-339; 2017

Language: English

Abstract: Since transgenic crops expressing *Bacillus thuringiensis* (Bt) toxins were first released, resistance evolution leading to failure in control of pests populations has been observed in a number of species. Field resistance of the moth *Busseola fusca* was acknowledged 8 years after Bt maize was introduced in South Africa. Since then, field resistance of this corn borer has been observed at several locations, raising questions about the nature, distribution and dynamics of the resistance trait. Using genetic markers, our study identified four outlier loci clearly associated with resistance. In addition, genetic structure at neutral loci reflected extensive gene flow among populations. A realistically parameterised model suggests that resistance could travel in space at speed of several kilometres a year. Markers at outlier loci delineated a geographic region associated with resistance spread. This was an area of approximately 100 km radius, including the location where resistance was first reported. Controlled crosses corroborated these findings and showed significant differences of progeny survival on Bt plants depending on the origin of the resistant parent. Last, our study suggests diverse resistance mutations, which would explain the widespread occurrence of resistant larvae in Bt fields across the main area of maize production in South Africa.

DOI: [10.1038/hdy.2016.104](https://doi.org/10.1038/hdy.2016.104)

Publication Type: J

***Record 6 of 13.** Search terms matched: CORN(3); MAIZE(1); MON810(1); ZEA MAYS(1)

*[Click Here to View Full Record](#)

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Accession Number: CABI:20173123121

Document Type: Journal article

Author(s): Castan, M.; Ali, S. E. B.; Hochegger, R.; Ruppitsch, W.; Haslberger, A. G.; Brandes, C.

Title: Analysis of the genetic stability of event NK603 in stacked corn varieties using high-resolution melting (HRM) analysis and Sanger sequencing.

Source: European Food Research and Technology, 243 (3):353-365; 2017

Language: English

Abstract: The examination of transgenic loci is an integral part of biosafety legislation in the European Union (EU). The EU directive 2001/18/EC requires any genetically modified (GM) event to be stable. Mutations in the nucleotide sequence of GM events must be avoided in the production and use of seeds. In the present work, an F1 and an F2 generation of the corn event NK603 were studied in stacked varieties (NK603 * MON810). The central aspect of this work was to utilize high-resolution melting analysis, real-time PCR, and Sanger sequencing for the

examination of genetic stability of the entire construct of NK603 as well as in the regions flanking NK603. To perform such screening, it was necessary to develop specific PCR primers for the NK603 insert. Twenty-five specific primer pairs and PCR reactions were used to screen a total number of 340 samples. In addition to the screening, the NK603 zygosity was determined by a PCR-based testing method. Differences to the published patent sequence occurring in all samples were detected in two locations of the transgenic DNA sequence. These differences were also found in certified NK603 reference material.

DOI: [10.1007/s00217-016-2749-2](https://doi.org/10.1007/s00217-016-2749-2)

Publication Type: J

***Record 7 of 13.** Search terms matched: BT(9); CORN(1); CRY1AB(3); MAIZE(12); RESISTANT(1); ZEA MAYS(1)

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Accession Number: CABI:20173120676

Document Type: Journal article

Author(s): Zhang Bing; Yang Yan; Zhou Xiang; Shen Ping; Peng YuFa; Li YunHe

Title: A laboratory assessment of the potential effect of Cry1Ab/Cry2Aj-containing *Bt* maize pollen on *Folsomia candida* by toxicological and biochemical analyses.

Source: Environmental Pollution, 222 94-100; 2017

Language: English

Abstract: The common soil arthropod *Folsomia candida* can survive well when fed only maize pollen and thus may be exposed to insecticidal proteins by ingesting insect-resistant genetically engineered maize pollen containing *Bacillus thuringiensis* (Bt) proteins when being released into the soil. Laboratory experiments were conducted to assess the potential effects of Cry1Ab/Cry2Aj-producing transgenic Bt maize (Shuangkang 12-5) pollen on *F. candida* fitness. Survival, development, and the reproduction were not significantly reduced when *F. candida* fed on Bt maize pollen rather than on non-Bt maize pollen, but these parameters were significantly reduced when *F. candida* fed on non-Bt maize pollen containing the protease inhibitor E-64 at 75 g/g pollen. The intrinsic rate of increase (rm) was not significantly reduced when *F. candida* fed on Bt maize pollen but was significantly reduced when *F. candida* fed on non-Bt maize pollen containing E-64. The activities of antioxidant-related enzymes in *F. candida* were not significantly affected when *F. candida* fed on Bt maize pollen but were significantly increased when *F. candida* fed on non-Bt pollen containing E-64. The results demonstrate that consumption of Bt maize pollen containing Cry1Ab/Cry2Aj has no lethal or sublethal effects on *F. candida*.

DOI: [10.1016/j.envpol.2016.12.079](https://doi.org/10.1016/j.envpol.2016.12.079)

Publication Type: J

***Record 8 of 13.** Search terms matched: CRY1AB(1); LEPIDOPTERA(1)

*[Click Here to View Full Record](#)

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Accession Number: CABI:20173099873

Document Type: Journal article

Author(s): Liu LaiPan; Gao MeiJing; Yang Song; Liu ShaoYan; Wu YiDong; Carriere, Y.; Yang YiHua

Title: Resistance to *Bacillus thuringiensis* toxin Cry2Ab and survival on single-toxin and pyramided cotton in cotton bollworm from China.

Source: Evolutionary Applications, 10 (2):170-179; 2017

Language: English

Abstract: Evolution of *Helicoverpa armigera* resistance to *Bacillus thuringiensis* (Bt) cotton producing Cry1Ac is progressing in northern China, and replacement of Cry1Ac cotton by pyramided Bt cotton has been considered to counter such resistance. Here, we investigated four of the eight conditions underlying success of the refuge strategy for delaying resistance to Cry1Ac+Cry2Ab cotton, a pyramid that has been used extensively against *H. armigera* outside China. Laboratory bioassays of a Cry2Ab-selected strain (An2Ab) and a related unselected strain (An) reveal that resistance to Cry2Ab (130-fold) was nearly dominant, autosomally inherited, and controlled by more than one locus. Strong cross-resistance occurred between Cry2Ab and Cry2Aa (81-fold). Weaker cross-resistance (18- to 22-fold) between Cry2Ab and Cry1A toxins was also present and significantly increased survival of An2Ab relative to An on cotton cultivars producing the fusion protein Cry1Ac/Cry1Ab or Cry1Ac. Survival on Cry1Ac+Cry2Ab cotton was also significantly higher in An2Ab than in An, showing that redundant killing on this pyramid was incomplete. Survival on non-Bt cotton did not differ significantly between An2Ab and An, indicating an absence of fitness costs affecting this trait. These results indicate that a switch to three-toxin pyramided cotton could be valuable for increasing durability of Bt cotton in China.

Publication Type: J

***Record 9 of 13.** Search terms matched: BT(9); CORN(1); CRY1AB(4); MAIZE(11); MON810(1); ZEA MAYS(1)

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*Order Full Text []

Accession Number: CABI:20173121162

Document Type: Journal article

Author(s): Shu YingHua; Zhang YanYan; Zeng HuiLan; Zhang YaHui; Wang JianWu

Title: Effects of Cry1Ab Bt maize straw return on bacterial community of earthworm *Eisenia fetida*.

Source: Chemosphere, 173 1-13; 2017

Language: English

Abstract: The eco-toxicological effects of *Bacillus thuringiensis* (Bt) maize on earthworm life-history traits were widely studied and the results were controversial, while their effects on earthworm bacterial community have been rarely studied. Here, effects of two hybrids of Bt maize [5422Bt1 (event Bt11) and 5422CBCL (MON810)] straw return on *Eisenia fetida* bacterial community were investigated by the terminal restriction fragment length polymorphism (T-RFLP) and polymerase chain reaction-denaturing gradient gel electrophoresis (PCR-DGGE) combining with DNA sequencing, compared to near-isogenic non-Bt maize (5422).

Bt maize straw return had significant effects on soil nutrients, especially for available nitrogen (N). The significant differences were shown in soil bacterial community between Bt and non-Bt maize treatments on the 75th and 90th d, which was closely correlated with soil available N, P and K rather than Cry1Ab protein. There was no statistically significant difference in the bacterial community of earthworm gut contents between Bt and non-Bt maize treatments. The significant differences in the bacterial community of earthworm casts were found among three maize varieties treatments, which were closely correlated with Cry1Ab protein and N levels. The differentiated bacterial species in earthworm casts mainly belonged to Proteobacteria, including Brevundimonas, Caulobacter, Pseudomonas, Stenotrophomonas, Methylobacterium, Asticcacaulis and Achromobacter etc., which were associated with the mineralization, metabolic process and degradation of plants residues. Therefore, Bt maize straw return caused changes in the bacterial community of E. fetida casts, which was possibly caused by the direct (Cry1Ab protein) and non-expected effects (N levels) of Bt maize straw.

Publication Type: J

***Record 10 of 13.** Search terms matched: BT(5); CORN(9); CRY1AB(4); MAIZE(1); RESISTANT(1); ZEA MAYS(1)

*[Click Here to View Full Record](#)

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Accession Number: CABI:20173123885

Document Type: Journal article

Author(s): Liu YanMin; Liu QingSong; Wang YaNan; Chen XiuPing; Song XinYuan; Romeis, J.; Li YunHe; Peng YuFa

Title: Ingestion of *Bt* corn pollen containing Cry1Ab/2Aj or Cry1Ac does not harm *Propylea japonica* larvae.

Source: Scientific Reports, 6 (23507):srep23507; 2016

Language: English

Abstract: *Propylea japonica* (Thunberg) (Coleoptera: Coccinellidae) is a prevalent pollen consumer in corn fields and is therefore exposed to insecticidal proteins contained in the pollen of insect-resistant transgenic corn cultivars expressing Cry proteins derived from *Bacillus thuringiensis* (Bt). In the present study, the potential effect of Cry1Ab/2Aj- or Cry1Ac-containing transgenic Bt corn pollen on the fitness of *P. japonica* larvae was evaluated. The results show that the larval developmental time was significantly shorter when *P. japonica* larvae were fed pollen from Bt corn cultivars rather than control pollen but that pupation rate, eclosion rate, and adult fresh weight were not significantly affected. In the feeding experiments, the stability of the Cry proteins in the food sources was confirmed. When Bt corn pollen passed through the gut of *P. japonica*, 23% of Cry1Ab/2Aj was digested. The results demonstrate that consumption of Bt corn pollen containing Cry1Ab/2Aj or Cry1Ac has no detrimental effect on *P. japonica* larvae; the shortened developmental time of larvae that consumed these proteins was likely attributable to unknown differences in the nutritional composition between the Bt-transgenic and control corn pollen.

Publication Type: J

*Record 11 of 13. Search terms matched: CRY1AB(1); LEPIDOPTERA(1); YIELD(1)

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Accession Number: CABI:20173124338

Document Type: Journal article

Author(s): Li ChuanMing; Han GuangJie; Liu Qin; Qi JianHang; Xu Jian

Title: Cultural characteristics and insecticidal activity of *Bacillus thuringiensis* strain Bt-8.

Source: Journal of Southern Agriculture, 47 (12):2072-2077; 2016

Language: Chinese

Language of Summary: English

Abstract: Objective: The present study was conducted to investigate biological characteristics and insecticidal activity of *Bacillus thuringiensis* (Bt) strain Bt-8, in order to provide a reference for industrial production. Method: The cultural characteristics, endogenous plasmids and insecticidal crystallin proteins (ICPs) varieties of *B. thuringiensis* strains Bt-8, Bt2671 and Bt7-9 were observed and analyzed after cultured with LB medium. Bt-8, Bt2671 and Bt7-9 were cultured in fermentative medium, then ICPs were isolated, and its insecticidal spectrum and relation between concentration and bio-potency were analyzed by biological activity assay and national standard detection method of toxin proteins. Result: Results showed that, Bt-8 had typical cultural characteristics of *B. thuringiensis*, ICPs were diamond or oval-shaped in the late stage of vegetative growth. However, Bt-8 was easy to regermination because of shorter stability time of spore. Bt-8 had four types of endogenous plasmids with the length of 24, 16, 8 and 7 kb, and the main genes of ICPs included cry1Ac and cry1Ab. Insecticidal activity analysis showed that, survival number of Bt-8 was significantly lower than that of Bt2671, whereas metabolism yield of ICPs was significantly increased. The bio-potency of Bt-8 was increased by 30.4% compared with that of Bt2671. Bt-8 had a widespread insecticidal spectrum against lepidopterous pest, such as *Plutella xylostella*, *Ectropis obliqua* Prout, *Cnaphalocrocis medinalis* and so on. Conclusion: The bio-potency, insecticidal spectrum and toxin proteins-producing ability of Bt-8 are significantly higher than those of Bt2671, therefore, it has potential for development of new Bt preparations with high content.

Publication Type: J

*Record 12 of 13. Search terms matched: BT(5); CORN(11); LEPIDOPTERA(1); MAIZE(1); ZEA MAYS(1)

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Accession Number: CABI:20173110412

Document Type: Journal article

Author(s): Silva, G. V.; Bueno, A. de F.; Bortolotto, O. C.; Santos, A. C. dos; Pomari-Fernandes, A.

Title: Biological characteristics of black armyworm *Spodoptera cosmioides* on genetically modified soybean and corn crops that express insecticide *Cry* proteins.

Source: Revista Brasileira de Entomologia, 60 (3):255-259; 2016

Language: English

Abstract: This study aimed to evaluate the development and reproduction of the black armyworm, *Spodoptera cosmioides* when larvae fed on leaves of Bt-corn hybrids, expressing a single Cry1F and also Cry1F, Cry1A.105 and Cry2Ab2 in pyramided corn and their non-Bt-isoline (hybrid 2B688), as well as on leaves of two soybean isolines expressing the Cry1Ac protein and its non-Bt isolate (A5547-227). We also assessed the effect of these Bt and non-Bt plants on the leaf consumption rate of *S. cosmioides* larvae. This pest was unable to develop when fed on any of the corn isolines (Bt and non-Bt). When both 1st and 3rd instar larvae were fed on corn leaf, mortality was 100% in both Bt and non-Bt corn. In contrast, when corn leaves were offered to 5th instar larvae, there were survivors. Defoliation and leaf consumption was higher with non-Bt corn than with both of the Bt corn isolines. There was no negative effect of Bt soybean leaves on the development and reproduction of *S. cosmioides* with respect to all evaluated parameters. Our study indicates that both Bt and non-Bt corn adversely affect the development of *S. cosmioides* while Bt soybean did not affect its biology, suggesting that this lepidopteran has major potential to become an important pest in Bt soybean crops.

DOI: [10.1016/j.rbe.2016.04.005](https://doi.org/10.1016/j.rbe.2016.04.005)

Publication Type: J

***Record 13 of 13.** Search terms matched: BT(1); CORN(2); MAIZE(3); ZEA MAYS(1)

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Accession Number: CABI:20173110430

Document Type: Journal article

Author(s): Resende, D. C.; Mendes, S. M.; Marucci, R. C.; Silva, A. de C.; Campanha, M. M.; Waquil, J. M.

Title: Does *Bt* maize cultivation affect the non-target insect community in the agro ecosystem?

Source: Revista Brasileira de Entomologia, 60 (1):82-93; 2016

Language: English

Abstract: The cultivation of genetically modified crops in Brazil has led to the need to assess the impacts of this technology on non-target species. Under field conditions, the potential effect on insect biodiversity was evaluated by comparing a homogeneous corn field with conventional and transgenic maize, expressing different Bt proteins in seven counties of Minas Gerais, Brazil. The richness pattern of non-target insect species, secondary pests and natural enemies were observed. The results do not support the hypothesis that Bt protein affects insect biodiversity. The richness and diversity data of insects studied were dependent on the location and other factors, such as the use of insecticides, which may be a major factor where they are used.

DOI: [10.1016/j.rbe.2015.12.001](https://doi.org/10.1016/j.rbe.2015.12.001)

Publication Type: J

***Record 1 of 11.** Search terms matched: BORER(4); BORERS(4); BT(5); CORN(1); LEPIDOPTERA(2); MAIZE(7); RESISTANT(1); ZEA MAYS(1)

*[Click Here to View Full Record](#)

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Accession Number: CABI:20173144977

Document Type: Journal article

Author(s): Berg, J. van den

Title: Insect resistance management in Bt maize: wild host plants of stem borers do not serve as refuges in Africa.

Source: Journal of Economic Entomology, 110 (1):221-229; 2017

Language: English

Abstract: Resistance evolution by target pests threatens the sustainability of Bt maize in Africa where insect resistance management (IRM) strategies are faced by unique challenges. The assumptions, on which current IRM strategies for stem borers are based, are not all valid for African maize stem borer species. The high dose-refuge strategy which is used to delay resistance evolution relies heavily on the presence of appropriate refuges (non-Bt plants) where pests are not under selection pressure and where sufficient numbers of Bt-susceptible individuals are produced to mate with possible survivors on the Bt maize crop. Misidentification of stem borer species and inaccurate reporting on wild host plant diversity over the past six decades created the perception that grasses will contribute to IRM strategies for these pests in Africa. Desired characteristics of refuge plants are that they should be good pest hosts, implying that larval survival is high and that it produces sufficient numbers of high-quality moths. Refuge plants should also have large cover abundance in areas where Bt maize is planted. While wild host plants may suffice in IRM strategies for polyphagous pests, this is not the case with stenophagous pests. This review discusses data of ecological studies and stem borer surveys conducted over the past decade and shows that wild host plants are unsuitable for development and survival of sufficient numbers of stem borer individuals. These grasses rather act as dead-end-trap plants and do not comply with refuge requirements of producing 500 susceptible individuals for every one resistant individual that survives on Bt maize.

Publication Type: J

*Record 2 of 11. Search terms matched: CRY1AB(2); YIELD(2)

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Accession Number: CABI:20173152771

Document Type: Journal article

Author(s): Jiang Yang; Ling Lin; Zhang LingLi; Domingo, A.; Cai MingLi; Li ChengFang; Zhan Ming; Wang JinPing; Cao CouGui

Title: Different response of an elite *Bt* restorer line of hybrid rice (*Oryza sativa* L.) in adaptation to nitrogen deficiency.

Source: Acta Physiologiae Plantarum, 39 (3):89; 2017

Language: English

Abstract: Transgenic *Bacillus thuringiensis* (Bt) rice have been reported to acquire effective resistance against the target pests; however, the insertion and expression of alien Bt genes may have some unintended effects on the growth characteristics of rice. A screen-house experiment was conducted and repeated twice to investigate the growth characteristics and Bt protein expressions in two Bt rice lines [MH63 (Cry2A*) and MH63 (Cry1Ab/Ac)], which had

different Bt protein expression levels in leaves, under zero nitrogen (N0) and recommended nitrogen (NR) fertilizer applications. Compared to the counterpart MH63, MH63 (Cry2A*) under N0 experienced accelerated leaf senescence and a lower internal N use efficiency (IEN), resulting in a 23.2% decrease in grain yield and a lower accumulated biomass. These variations were revealed to be correlated to the higher ratio of the Bt protein content to the soluble protein content (BTC/SPC) with a maximum value of 4.3 per mil in MH63 (Cry2A*) leaves in the late growth stage. Under NR, no differences in growth characteristics between MH63 (Cry2A*) and MH63 were found. The growth characteristics of MH63 (Cry1Ab/Ac), with a lower BTC/SPC in the late growth stage compared to MH63 (Cry2A*), were identical to those of MH63 under the two N applications. Results show that the transgenic Bt rice MH63 (Cry2A*), with a relatively higher Bt protein expression in the late growth stage, had an inferior adaptation to nitrogen deficiency compared to its non-Bt counterpart. And this inferior adaptation was found to be correlated with the higher BTC/SPC in MH63 (Cry2A*) leaves in the late growth stage.

Publication Type: J

***Record 3 of 11.** Search terms matched: BORER(6); CORN(15); LEPIDOPTERA(4); MAIZE(1); OSTRINIA(5); PROTECT(1); ZEA MAYS(1)

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Accession Number: CABI:20173144957

Document Type: Journal article

Author(s): Gagnon, A. E.; Audette, C.; Duval, B.; Boisclair, J.

Title: Can the use of *Trichogramma ostriniae* (Hymenoptera: Trichogrammatidae) to control *Ostrinia nubilalis* (Lepidoptera: Crambidae) be economically sustainable for processing sweet corn?

Source: Journal of Economic Entomology, 110 (1):59-66; 2017

Language: English

Abstract: European corn borer, *Ostrinia nubilalis* (Hubner) (Lepidoptera: Crambidae), is the main pest causing damage to sweet corn in North America. Conventional management with multiple use of insecticides is a common practice for processing sweet corn. In Canada, the use of *Trichogramma* spp. began in the 1990s, but the adoption of this approach for European corn borer management is still limited to the fresh market of sweet corn. *Trichogramma ostriniae* (Peng & Chen) has great potential as a biological control agent for large areas such as in processing sweet corn. The objective of this study was to evaluate an economically and environmentally sustainable alternative to insecticides for controlling European corn borer populations in processing sweet corn. During the growing season, the mean number of larvae decreased after insecticide (0.070.04) and *Trichogramma* (1.320.59) treatments compared with the control (2.420.72). At harvest, damages associated with European corn borer were similar after *Trichogramma* (1.00.7%) and insecticide (1.00.6%) treatments, but significantly lower than the control (8.73.3%). This study showed that the use of *T. ostriniae* can significantly decrease the pressure exerted by European corn borer and its damage on corn ears. This outcome is particularly interesting considering that it was achieved with lower doses of *Trichogramma*, a lower number of releases, and on large crop areas, compared with what is actually done to protect fresh market corn from European corn borer. Under these conditions,

the use of Trichogramma is an economically and competitive alternative to insecticide applications.

Publication Type: J

***Record 4 of 11.** Search terms matched: BORER(1); CORN(6); CRY1AB(7); LEPIDOPTERA(1); MAIZE(1); MON810(1); OSTRINIA(5); RESISTANT(4); ZEA MAYS(1)

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Accession Number: CABI:20173147939

Document Type: Journal article

Author(s): Yao JianXiu; Zhu YuCheng; Lu NanYan; Buschman, L. L.; Zhu KunYan

Title: Comparisons of transcriptional profiles of gut genes between Cry1Ab-resistant and susceptible strains of *Ostrinia nubilalis* revealed genes possibly related to the adaptation of resistant larvae to transgenic Cry1Ab corn.

Source: International Journal of Molecular Sciences, 18 (2):301; 2017

Language: English

Abstract: A microarray developed on the basis of 2895 unique transcripts from larval gut was used to compare gut gene expression profiles between a laboratory-selected Cry1Ab-resistant (R) strain and its isoline susceptible (S) strain of the European corn borer (*Ostrinia nubilalis*) after the larvae were fed the leaves of transgenic corn (MON810) expressing Cry1Ab or its non-transgenic isoline for 6 h. We revealed 398 gut genes differentially expressed (i.e., either up- or down-regulated genes with expression ratio ≥ 2.0) in S-strain, but only 264 gut genes differentially expressed in R-strain after being fed transgenic corn leaves. Although the percentages of down-regulated genes among the total number of differentially expressed genes (50% in S-strain and 45% in R-strain) were similar between the R- and S-strains, the expression ratios of down-regulated genes were much higher in S-strain than in R-strain. We revealed that 17 and 9 significantly up- or down-regulated gut genes from S and R-strain, respectively, including serine proteases and aminopeptidases. These genes may be associated with Cry1Ab toxicity by degradation, binding, and cellular defense. Overall, our study suggests enhanced adaptation of Cry1Ab-resistant larvae on transgenic Cry1Ab corn as revealed by lower number and lower ratios of differentially expressed genes in R-strain than in S-strain of *O. nubilalis*.

Publication Type: J

***Record 5 of 11.** Search terms matched: BT(4); CORN(1); MAIZE(10); MON810(1); ZEA MAYS(1)

*[Click Here to View Full Record](#)

*Order Full Text []

Accession Number: CABI:20173142431

Document Type: Journal article

Author(s): Mashiane, R. A.; Ezeokoli, O. T.; Adeleke, R. A.; Bezuidenhout, C. C.

Title: Metagenomic analyses of bacterial endophytes associated with the phyllosphere of a Bt maize cultivar and its isogenic parental line from South Africa.

Source: World Journal of Microbiology & Biotechnology, 33 (4):80; 2017

Language: English

Abstract: Genetic modification of maize with *Bacillus thuringiensis* (Bt) cry proteins may predispose shifts in the bacterial endophytes' community associated with maize shoots. In this study, the diversity of bacterial endophytes associated with a Bt maize genotype (Mon810) and its isogenic non-transgenic parental line were investigated at pre-flowering (50 days) and post-flowering (90 days) developmental stages. PCR-DGGE and high throughput sequencing on the Illumina MiSeq sequencer were used to characterize bacterial 16S rRNA gene diversity in leaves, stems, seeds and tassels. PCR-DGGE profile revealed similarity as well as differences between bacterial communities of shoots in both cultivars and at both developmental stages. A total of 1771 operational taxonomic units (OTUs) were obtained from the MiSeq and assigned into 14 phyla, 27 classes, 58 orders, 116 families and 247 genera. Differences in alpha and beta diversity measures of OTUs between the phyllospheres of both genotypes were not significant ($P > .05$) at all developmental stages. In all cultivars, OTU diversity reduced with plant development. OTUs belonging to the phyla Proteobacteria were dominant in all maize phyllospheres. The class Gammaproteobacteria was dominant in Bt maize while, Alphaproteobacteria and Actinobacteria were dominant in non-Bt maize phyllospheres. Differences in the abundance of some genera, including *Acidovorax*, *Burkerholderia*, *Brachy bacterium*, *Enterobacter* and *Rhodococcus*, whose species are known beneficial endophytes were observed between cultivars. Hierarchical cluster analysis further suggests that the bacterial endophyte communities of both maize genotypes associate differently (are dissimilar). Overall, the results suggest that bacterial endophytes community differed more across developmental stages than between maize genotypes.

Publication Type: J

***Record 6 of 11.** Search terms matched: BORER(2); BORERS(2); BT(2); CORN(1); CRY1AB(3); LEPIDOPTERA(3); MAIZE(6); MON 810(2); RESISTANT(3); ZEA MAYS(1)
*[Click Here to View Full Record](#)
*Order Full Text []

Accession Number: CABI:20173153418

Document Type: Journal article

Author(s): Yang GuoQing; Niu Ying; Head, G. P.; Price, P. A.; Huang FangNeng

Title: Performance of Cry1Ab-susceptible and -heterozygous resistant populations of sugarcane borer in sequential feedings on non-Bt and Bt maize plant tissue.

Source: *Entomologia Experimentalis et Applicata*, 162 (1):51-59; 2017

Language: English

Abstract: A seed mix strategy has been used to provide refuge to susceptible insects for resistance management in planting transgenic maize expressing *Bacillus thuringiensis* Berliner (Bt) proteins. To determine whether larval movement in a seed mix planting creates favorable conditions for resistant heterozygotes of a target pest, performance of Cry1Ab-susceptible (SS) and -heterozygous resistant (RS) populations of the sugarcane borer, *Diatraea saccharalis* (Fabricius) (Lepidoptera: Crambidae), was evaluated in sequential feeding on non-Bt and Cry1Ab (event MON 810) maize plant tissue. For each insect population, nine feeding sequences were employed. SS and RS feeding on non-Bt plants for their entire larval stages survived well and >60% of the adult pairs produced viable eggs, with an average of 269

progeny per female, whereas none of the two populations on Bt maize plants survived to the pupal stage. SS larvae could not develop to adults if the larvae fed on non-Bt plants for ≤ 15 days and then moved to Bt plants. In contrast, 4.2-29.2% of RS larvae that fed on non-Bt plants for ≥ 9 days and then moved to Bt plants developed to adults, and 63.6% of pairs of these adults produced viable eggs, with an average of 185 progeny per female. For SS larvae that fed on Bt plants for 1 or 2 days and then moved to non-Bt plants, few larvae developed to adults with varied emergence times, whereas 28.1 and 13.5% RS larvae feeding on Bt plants for 1 and 2 days, respectively, successfully developed to adults; 43.8% of pairs of these adults produced viable eggs, with an average of 220 progeny per female. For the case of the single Bt gene maize plants (event MON 810), the results suggest that RS insects may have advantages in survival and reproduction over SS if RS larvae hatch and feed on Bt plants during the first 1 or 2 days and then move to non-Bt plants. This advantage is less for RS larvae that hatch and feed on non-Bt plants first and then move to Bt plants, unless the larval movement occurs in the later stages (e.g., fourth or fifth instars).

DOI: [10.1111/eea.12502](https://doi.org/10.1111/eea.12502)

Publication Type: J

***Record 7 of 11.** Search terms matched: CRY1AB(10)

*[Click Here to View Full Record](#)

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Accession Number: CABI:20173147494

Document Type: Journal article

Author(s): Dong Sa; Zhang Xiao; Liu Yuan; Zhang CunZheng; Xie YaJing; Zhong JianFeng; Xu ChongXin; Liu XianJin

Title: Establishment of a sandwich enzyme-linked immunosorbent assay for specific detection of *Bacillus thuringiensis* (Bt) Cry1Ab toxin utilizing a monoclonal antibody produced with a novel hapten designed with molecular model.

Source: Analytical and Bioanalytical Chemistry, 409 (8):1985-1994; 2017

Language: English

Abstract: Cry1Ab toxin is commonly expressed in genetically modified crops in order to control chewing pests. At present, the detection method with enzyme-linked immunosorbent assay (ELISA) based on monoclonal antibody cannot specifically detect Cry1Ab toxin for Cry1Ab's amino acid sequence and spatial structure are highly similar to Cry1Ac toxin. In this study, based on molecular design, a novel hapten polypeptide was synthesized and conjugated to keyhole limpet hemocyanin (KLH). Then, through animal immunization with this antigen, a monoclonal antibody named 2C12, showing high affinity to Cry1Ab and having no cross reaction with Cry1Ac, was produced. The equilibrium dissociation constant (KD) value of Cry1Ab toxin with MAb 2C12 was 1.947×10^{-8} M. Based on this specific monoclonal antibody, a sandwich enzyme-linked immunosorbent assay (DAS-ELISA) was developed for the specific determination of Cry1Ab toxin and the LOD and LOQ values were determined as 0.470.11 and 2.430.19 ng mL⁻¹, respectively. The average recoveries of Cry1Ab from spiked rice leaf and rice flour samples ranged from 75 to 115%, with coefficient of variation (CV) less than 8.6% within the quantitation range (2.5-100 ng mL⁻¹), showing good accuracy for the quantitative detection of Cry1Ab toxin in agricultural samples. In conclusion, this study provides a new

approach for the production of high specific antibody and the newly developed DAS-ELISA is a useful method for Cry1Ab monitoring in agriculture products.

DOI: [10.1007/s00216-016-0146-0](https://doi.org/10.1007/s00216-016-0146-0)

Publication Type: J

*Record 8 of 11. Search terms matched: BORER(2); CRY1AB(7); LEPIDOPTERA(1)

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Accession Number: CABI:20173144140

Document Type: Journal article

Author(s): Wang, X. Y.; Du, L. X.; Liu, C. X.; Gong, L.; Han, L. Z.; Peng, Y. F.

Title: RNAi in the striped stem borer, *Chilo suppressalis*, establishes a functional role for aminopeptidase N in Cry1Ab intoxication.

Source: Journal of Invertebrate Pathology, 143 1-10; 2017

Language: English

Abstract: The striped stem borer, *Chilo suppressalis*, is a major target pest of transgenic rice expressing the Cry1Ab protein from the bacterium *Bacillus thuringiensis* (Bt) in China. Evolution of resistance in this pest is a major threat to the durability of Bt rice. Since Bt exerts its activity through binding to specific receptors in the midgut of target insects, identification of functional Cry1Ab receptors in the midgut of *C. suppressalis* larvae is crucial to evaluate potential resistance mechanisms and develop effective strategies for delaying insect resistance. In this work, we identified the putative Cry1Ab toxin-binding protein, aminopeptidase-N (APN), in the midgut of *C. suppressalis* by ligand blot and mass spectrometry. After cloning the full-length cDNAs encoding APN isoforms from the *C. suppressalis* larval midgut, we studied their spatiotemporal expression in different gut tissues and developmental stages. Furthermore, RNA interference (RNAi) against *C. suppressalis* aminopeptidases (CsAPNs) was employed to illustrate a functional role for CsAPNs in Cry1Ab toxicity to *C. suppressalis* larvae using injection and oral delivery of Stealth™ siRNA. Down-regulating the expression of CsAPNs by RNAi was closely associated with reduced susceptibility of *C. suppressalis* to Cry1Ab. These data provide the first direct evidence that CsAPNs participate in the mode of Cry1Ab action and may act as the functional receptor of Cry1A in *C. suppressalis* larvae.

DOI: [10.1016/j.jip.2016.11.004](https://doi.org/10.1016/j.jip.2016.11.004)

Publication Type: J

*Record 9 of 11. Search terms matched: BT(1); CORN(1); MAIZE(4); PROTECTIONISM(1); ZEA MAYS(1)

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Accession Number: CABI:20173147254

Document Type: Journal article, Conference paper

Author(s): Tagliabue, G.

Title: "GMO" maize and public health - a case of Schumpeterian policy vs. free market in the EU.

Source: Bio-based and Applied Economics, 5 (3):325-332; 2016

Conference: Fifth AIEEA Conference, Bologna, Italy, 16-17 June 2016.

Language: English

Abstract: EU lawmakers have long refused the cultivation of "Genetically Modified Organisms". An example of this struggle is the revision of the accepted level of contaminants in maize: rather than admitting that Bt maize is safer than "non-GMO" varieties, and therefore European farmers should be allowed not only to import it, but also to produce it, politicians have raised the threshold of the poisonous fumonisins that may be legally present in food and feed. This decision is an example of a "Schumpeterian" approach to policy, where public choices are not inspired by a science-based mindset, but are substantially dictated by a calculus of consent; economic/commercial protectionism has also been considered as a motivation. While scholars must continue to explain that every policy decision should have a basis in sound science, no way out of the "GMO" imbroglio seems to be foreseeable, as long as politicians stick to the Schumpeterian iron law.

Publication Type: J

***Record 10 of 11.** Search terms matched: BT(8); CORN(1); MAIZE(14); ZEA MAYS(1)

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Accession Number: CABI:20173146371

Document Type: Journal article

Author(s): Guo JingFei; He KangLai; Hellmich, R. L.; Bai ShuXiong; Zhang TianTao; Liu YunJun; Ahmed, T.; Wang ZhenYing

Title: Field trials to evaluate the effects of transgenic *cryIIe* maize on the community characteristics of arthropod natural enemies.

Source: Scientific Reports, 6 (22102):srep22102; 2016

Language: English

Abstract: Possible non-target effect of transgenic *cryIIe* maize exerts on natural enemy community biodiversity in the field is unresolved. In the present study, a 2-yr comparison of transgenic *cryIIe* maize (Event IE09S034, Bt maize) and its near isoline (Zong 31, non-Bt maize) on natural enemy community biodiversity were compared with whole plant inspections, pitfall traps and suction sampler. Natural enemy diversity indices (Shannon-Wiener', Simpson's and Pielou's index) and abundance suggested there were no significant differences between the two types of maize. The only exceptions were the Pielou's index for whole plant inspections in 2013 and abundance for pitfall traps in 2012, which were significantly higher in Bt maize than those of non-Bt maize. The main species of natural enemies were identical in Bt and non-Bt maize plots for each method and the three methods combined. For whole plant inspections, Bt maize had no time-dependent effect on the entire arthropod natural enemy community, and also no effect on community dissimilarities between Bt and non-Bt maize plots. These results suggested that despite the presence of a relatively minor difference in natural enemy communities between Bt and non-Bt maize, transgenic *cryIIe* maize had little, if any, effect on natural enemy community biodiversity.

Publication Type: B

***Record 11 of 11.** Search terms matched: BORER(1); BT(2); CORN(2); CRY1AB(2); LEPIDOPTERA(1); MAIZE(10); MON 810(2); OSTRINIA(2); ZEA MAYS(1)

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Accession Number: CABI:20173097149

Document Type: Conference paper

Author(s): Chrenkova, M.; Pomikalova, S.; Chrastinova, L.; Polacikova, M.; Formelova, Z.; Rajskey, M.; Mlynekova, Z.

Edited by: Rajcakova L.

Title: Effect of crimped maize grain ensiled with high moisture grains of transgenic Bt maize in fattening bulls [Conference poster].

Source: 17th International Conference, Forage Conservation, 27 - 29 September, 2016, Horny Smokovec, Slovak Republic, 159-162; 2016

Conference: 17th International Conference, Forage Conservation, 27 - 29 September, 2016, Horny Smokovec, Slovak Republic.

Language: English

Abstract: The maize event MON 810 carries the novel gene cry1Ab from a naturally soil bacterium, *Bacillus thuringiensis* (Bt). Thus the transgenic Bt-maize produces the insecticidal Cry1Ab protein which provides resistance against the European corn borer. However, the increasing use of genetically modified plants in the production of animal feed has raised concerns about their safety. A feeding trial was carried out with 40 Holstein breed bulls with an initial live weight 298 kg which were randomly distributed into 4 groups with 10 bulls in each, housed in boxes. The feed consisted of maize silage, lucerne silage, meadow hay, wheat, rape extr. meal, minerals and crimped maize grain in two feeding TMR with content of isogenic maize and transgenic maize (event MON 810) intended for bulls. Bulls were fed TMR diet for ad libitum intake. Water was provided ad libitum. The TMR contained 139.84 g.kg⁻¹ crude protein, 6.45 MJ.kg⁻¹ NEV, 155.3 g.kg⁻¹ crude fibre, 264.47 g.kg⁻¹ starch, fat 28.8 g.kg⁻¹, Ca 9.21 g.kg⁻¹, P 3.67 g.kg⁻¹, Na 2.06 g.kg⁻¹, Mg 2.18 g.kg⁻¹ and K 10.735 g.kg⁻¹ in dry matter. The feeding trial was conducted with 2*20 bulls from average live weight 298 kg to the average slaughtering weight 620 kg in control and 622 kg in experimental group. The live weight gain was 1.248 kg.d⁻¹ and 1.255 kg.d⁻¹. The experiment lasted for 258 days. Data were processed by analysis of variance. The significance of differences was evaluated by the t-test. In fattening experiments there were studied live weight growth of bulls and consumption of feed mixtures per unit of live weight growth. Obtained results demonstrate minimal, statistically non-significant differences of individual parameters in tested groups. Bulls were slaughtered at the age of 586 days after achieving the live weight 620.5 kg. Feeding of TMR with proportion Bt transgenic and isogenic control maize to Holstein breed bulls did not influence zootechnical parameters, as well as it has no negative effect on feed conversion, growth performance, meat quality and health status.

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