

Appendix 5.3 MON 810 Literature Review – List of all hits (June 2015 – May 2016) – Web of Science™ Core Collection database

***Record 1 of 9.**

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

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Title: Bacillus thuringiensis Cry1 AbMod toxin counters tolerance associated with low cadherin expression but not that associated with low alkaline phosphatase expression in Manduca sexta

Authors: Gomez, I; Flores, B; Bravo, A; Soberon, M

Author Full Names: Gomez, Isabel; Flores, Biviana; Bravo, Alejandra; Soberon, Mario

Source: PEPTIDES, 68 130-133; [10.1016/j.peptides.2014.08.012](https://doi.org/10.1016/j.peptides.2014.08.012) JUN 2015

Language: English

Abstract: To exert their toxic effect, Bacillus thuringiensis Cry1Ab toxin undergoes a sequential binding mechanism with different larval gut proteins including glycosyl-phosphatidyl-inositol anchored proteins like aminopeptidase-N (APN) or alkaline-phosphatase (ALP) and a transmembrane cadherin to form pre-pore structures that insert into the membrane. Cadherin binding induces oligomerization of the toxin by facilitating removal of the N-terminal region, while APN/ALP binding helps in oligomer membrane insertion. Cry1AbMod toxin was engineered to lack N-terminal region of the toxin and shown to counter resistance linked to cadherin mutations. In this manuscript we determined the toxicity of Cry1AbMod to Manduca sexta larvae silenced in the expression of cadherin, ALP or APN receptors. As previously reported Cry1Ab toxicity relied principally in ALP and cadherin in comparison to APN. Our data shows that Cry1AbMod counters resistance associated with low cadherin expression but was not effective against ALP silenced larvae. These results show that Cry1AbMod could be effective against resistance insects linked to mutations on binding molecules involved in toxin oligomerization but not against resistant insects linked to mutations on binding molecules involved in oligomer membrane insertion. (C) 2014 Elsevier Inc. All rights reserved.

ISSN: 0196-9781

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IDS Number: CI2JF

Unique ID: WOS:000354572200018

PubMed ID: 25239508

***Record 2 of 9.**

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

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

Title: Nitric oxide participates in the toxicity of Bacillus thuringiensis Cry1Ab toxin to kill Manduca sexta larvae

Authors: Chavez, C; Recio-Totoro, B; Flores-Escobar, B; Lanz-Mendoza, H; Sanchez, J; Soberon, M; Bravo, A

Author Full Names: Chavez, Carolina; Recio-Totoro, Benito; Flores-Escobar, Biviana; Lanz-Mendoza, Humberto; Sanchez, Jorge; Soberon, Mario; Bravo, Alejandra

Source: PEPTIDES, 68 134-139; [10.1016/j.peptides.2014.07.012](https://doi.org/10.1016/j.peptides.2014.07.012) JUN 2015

Language: English

Abstract: Nitric oxide (NO) produced by the nitric oxide synthase (NOS) enzyme is a reactive

oxygen molecule widely considered as important participant in the immune system of different organisms to confront microbial infections. In insects the NO molecule has also been implicated in immune response against microbial pathogens. *Bacillus thuringiensis* (Bt) is an insect-pathogenic bacterium that produces insecticidal proteins such as Cry toxins. These proteins kill insects because they form pores in the larval-midgut cells. Here we show that intoxication of *Manduca sexta* larvae with Cry1Ab activates expression of NOS with a corresponding increase in NO. This effect is not observed with a non-toxic mutant toxin Cry1Ab-E129K that is affected in pore formation. The increased production of NO triggered by intoxication with LC50 dose of Cry1Ab toxin is not associated with higher expression of antimicrobial peptides. NO participates in Cry1Ab toxicity since inhibition of NOS by selective L-NAME inhibitor prevented NO production and resulted in reduced mortality of the larvae. The fact that mortality was not completely abolished by L-NAME indicates that other processes participate in toxin action and induction of NO production upon Cry1Ab toxin administration accounts only for a part of the toxicity of this protein to *M. sexta* larvae. (C) 2014 Elsevier Inc. All rights reserved.

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IDS Number: CI2JF

Unique ID: WOS:000354572200019

PubMed ID: 25063056

***Record 3 of 9.**

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

***Order Full Text []**

Title: Aedes cadherin mediates the in vivo toxicity of the Cry11Aa toxin to *Aedes aegypti*

Authors: Lee, SB; Chen, JW; Aimanova, KG; Gill, SS

Author Full Names: Lee, Su-Bum; Chen, Jianwu; Aimanova, Karlygash G.; Gill, Sarjeet S.

Source: PEPTIDES, 68 140-147; [10.1016/j.peptides.2014.07.015](https://doi.org/10.1016/j.peptides.2014.07.015) JUN 2015

Language: English

Abstract: Cadherin plays an important role in the toxicity of *Bacillus thuringiensis* Cry proteins. We previously cloned a full-length cadherin from *Aedes aegypti* larvae and reported this protein binds Cry11Aa toxin from *B. thuringiensis* subsp. *israelensis* with high affinity, approximate to 16.7 nM. Based on these results, we investigated if *Aedes* cadherin is involved in the in vivo toxicity of Cry11Aa toxin to *Ae. aegypti*. We established a mosquito cell line stably expressing the full-length *Aedes* cadherin and transgenic mosquitoes with silenced *Aedes* cadherin expression. Cells expressing the *Aedes* cadherin showed increased sensitivity to Cry11Aa toxin. Cry11Aa toxin at 400 nM killed approximately 37% of the cells in 3h. Otherwise, transgenic mosquitoes with silenced *Aedes* cadherin expression showed increased tolerance to Cry11Aa toxin. Furthermore, cells expressing *Aedes* cadherin triggered Cry11Aa oligomerization. These results show the *Aedes* cadherin plays a pivotal role in Cry11Aa toxicity to *Ae. aegypti* larvae by mediating Cry11Aa oligomerization. However, since high toxicity was not obtained in cadherin-expressing cells, an additional receptor may be needed for manifestation of full toxicity. Moreover, cells expressing *Aedes* cadherin were sensitive to Cry4Aa and Cry11Ba, but not Cry4Ba. However transgenic mosquitoes with silenced *Aedes* cadherin expression showed no tolerance to Cry4Aa, Cry4Ba, and Cry11Ba toxins. These results suggest that while *Aedes*

cadherin may mediate Cry4Aa and Cry11Ba toxicity, this cadherin but is not the main receptor of Cry4Aa, Cry4Ba and Cry11Ba toxin in *Ae. aegypti*. (C) 2014 Elsevier Inc. All rights reserved.

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IDS Number: CI2JF

Unique ID: WOS:000354572200020

PubMed ID: 25064814

***Record 4 of 9.**

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

***Order Full Text []**

Title: Enhanced Indirect Photochemical Transformation of Histidine and Histamine through Association with Chromophoric Dissolved Organic Matter

Authors: Chu, CH; Lundeen, RA; Remucal, CK; Sander, M; McNeill, K

Author Full Names: Chu, Chiheng; Lundeen, Rachel A.; Remucal, Christina K.; Sander, Michael; McNeill, Kristopher

Source: ENVIRONMENTAL SCIENCE & TECHNOLOGY, 49 (9):5511-5519;
[10.1021/acs.est.5b00466](https://doi.org/10.1021/acs.est.5b00466) MAY 5 2015

Language: English

Abstract: Photochemical transformations greatly affect the stability and fate of amino acids (AAs) in sunlit aquatic ecosystems. Whereas the direct phototransformation of dissolved AAs is well investigated, their indirect photolysis in the presence of chromophoric dissolved organic matter (CDOM) is poorly understood. In aquatic systems, CDOM may act both as sorbent for AAs and as photosensitizer, creating microenvironments with high concentrations of photochemically produced reactive intermediates, such as singlet oxygen ($O_1(2)$). This study provides a systematic investigation of the indirect photochemical transformation of histidine (His) and histamine by $O_1(2)$ in solutions containing CDOM as a function of solution pH. Both His and histamine showed pH-dependent enhanced phototransformation in the CDOM systems as compared to systems in which model, low-molecular-weight $O_1(2)$ sensitizers were used. Enhanced reactivity resulted from sorption of His and histamine to CDOM and thus exposure to elevated $O_1(2)$ concentrations in the CDOM microenvironment. The extent of reactivity enhancement depended on solution pH via its effects on the protonation state of His, histamine, and CDOM. Sorption-enhanced reactivity was independently supported by depressed rate enhancements in the presence of a cosorbate that competitively displaced His and histamine from CDOM. Incorporating sorption and photochemical transformation processes into a reaction rate prediction model improved the description of the abiotic photochemical transformation rates of His in the presence of CDOM.

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eISSN: 1520-5851

IDS Number: CH6OL

Unique ID: WOS:000354155800032

PubMed ID: 25827214

***Record 5 of 9.**

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

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

Title: Fitness costs of Cry1F resistance in two populations of fall armyworm, *Spodoptera frugiperda* (JE Smith), collected from Puerto Rico and Florida

Authors: Dangal, V; Huang, FN

Author Full Names: Dangal, Vikash; Huang, Fangneng

Source: JOURNAL OF INVERTEBRATE PATHOLOGY, 127 81-86;
[10.1016/j.jip.2015.03.004](https://doi.org/10.1016/j.jip.2015.03.004) MAY 2015

Language: English

Abstract: The development of resistance in target pest populations is a threat to the sustainability of transgenic crops expressing *Bacillus thuringiensis* (Bt) proteins. Fall armyworm, *Spodoptera frugiperda* J.E. Smith), is a major target pest of Bt maize in North and South America. This insect is the first target pest that has developed field resistance to Bt maize at multiple locations in these regions. The objective of this study was to assess the fitness costs associated with the Cry1F resistance in two populations of *S. frugiperda* collected from Puerto Rico (RR-PR) and Florida (RR-FL). In the study, fitness costs were evaluated by comparing survival, growth, and developmental time of seven populations of *S. frugiperda* on (1) non-Bt meridic diet and (2) non-Bt maize leaf tissue and non-Bt diet. The seven populations were RR-PR, RR-FL, a Bt-susceptible strain (Bt-SS), and four F-1 populations developed from reciprocal crosses between Bt-SS and the two resistant populations. Biological parameters measured were neonate-to-adult survivorship, neonate-to-adult developmental time, 10 day larval weight on non-Bt maize leaf tissue, pupal weight, and sex ratios. Results of the study show that the Cry1F resistance in both RR-PR and RR-FL was associated with considerable fitness costs, especially for the Florida population. Compared to the Bt-susceptible population, RR-PR showed an average of 61.1% reduction in larval weight, 20.4% less in neonate-to-adult survivorship, and 3.7 days delay in neonate-to-adult developmental time. These fitness costs for RR-FL were 66.9%, 31.7% and 4.4 days, respectively. The fitness costs of RR-PR and RR-FL appeared to be non-recessive. The results indicate that a diversified genetic basis may exist for the Cry1F resistance in *S. frugiperda*. (C) 2015 Elsevier Inc. All rights reserved.

ISSN: 0022-2011

eISSN: 1096-0805

IDS Number: C11KQ

Unique ID: WOS:000354503500013

PubMed ID: 25791021

***Record 6 of 9.**

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

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

Title: Binding analysis of *Bacillus thuringiensis* Cry1 proteins in the sugarcane borer, *Diatraea saccharalis* (Lepidoptera: Crambidae)

Authors: Davolos, CC; Hernandez-Martinez, P; Crialesi-Legori, PCB; Desiderio, JA; Ferre, J; Escriche, B; Lemos, MVF

Author Full Names: Davolos, Camila C.; Hernandez-Martinez, Patricia; Crialesi-Legori, Paula C. B.; Desiderio, Janete A.; Ferre, Juan; Escriche, Baltasar; Lemos, Manoel Victor F.

Source: JOURNAL OF INVERTEBRATE PATHOLOGY, 127 32-34;
[10.1016/j.jip.2015.01.013](https://doi.org/10.1016/j.jip.2015.01.013) MAY 2015

Language: English

Abstract: Sugarcane borer (*Diatraea saccharalis*, F.) is an important corn pest in South America and United States. The aim of the present study was to analyze the susceptibility and binding interactions of three Cry1A proteins and Cry1Fa in a Brazilian *D. saccharalis* population. The results showed that Cry1Ab was the most active, followed by Cry1Ac, Cry1Fa and Cry1Aa. All Cry1-biotinylated proteins tested bound specifically to the *D. saccharalis* brush border membrane vesicles (BBMV). Heterologous competition assays showed shared binding sites for all Cry1A proteins and another one shared by Cry1Fa and Cry1Ab. Thus, pyramiding Cry1Aa/Cry1Ac and Cry1F proteins would be a recommended strategy for managing this pest. (C) 2015 Elsevier Inc. All rights reserved.

ISSN: 0022-2011

eISSN: 1096-0805

IDS Number: CIIKQ

Unique ID: WOS:000354503500005

PubMed ID: 25736726

***Record 7 of 9.**

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

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

Title: Occurrence of molecularly diverse Bt Cry toxin-resistant mutations in insect pests of Bt(+) corn and cotton crops and remedial approaches

Authors: Kumar, S; Kumari, R

Author Full Names: Kumar, Sushil; Kumari, Renu

Source: CURRENT SCIENCE, 108 (8):1483-1490; APR 25 2015

Language: English

Abstract: Cultivation of Bt(+) genotypes has dispensed with insecticidal sprays and thereby corn and cotton farmers have hugely benefited worldwide. Recent recordings of genetically diverse Cry-resistance in insect pests of Bt(+) corn and cotton fields have raised grave concern. Curiously, bulk of Cry-resistant pink bollworms found in certain Bt(+) cotton fields in India proved homozygous for multiple linked mutations. Besides, dominantly inheritable Cry-resistance and cross resistance between different Cry-proteins have also been noted. To stem evolution of resistance against anti-insect protein-toxins, new nematology research on IPM procedures, complementary to refuge and Cry stacking technologies is imminently needed.

ISSN: 0011-3891

IDS Number: CIIKI

Unique ID: WOS:000354502700019

***Record 8 of 9.**

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

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

Title: Effects of Pyramided Bt Corn and Blended Refuges on Western Corn Rootworm and Northern Corn Rootworm (Coleoptera: Chrysomelidae)

Authors: Keweshan, RS; Head, GP; Gassmann, AJ

Author Full Names: Keweshan, Ryan S.; Head, Graham P.; Gassmann, Aaron J.

Source: JOURNAL OF ECONOMIC ENTOMOLOGY, 108 (2):720-729; [10.1093/jee/tov005](#)
APR 2015

Language: English

Abstract: The western corn rootworm, *Diabrotica virgifera virgifera* LeConte, and the northern corn rootworm, *Diabrotica barberi* Smith & Lawrence (Coleoptera: Chrysomelidae), are major pests of corn (*Zea mays* L). Several transgenic corn events producing insecticidal toxins derived from the bacterium *Bacillus thuringiensis* (Bt) kill corn rootworm larvae and reduce injury to corn roots. However, planting of Bt corn imposes selection on rootworm populations to evolve Bt resistance. The refuge strategy and pyramiding of multiple Bt toxins can delay resistance to Bt crops. In this study, we assessed the impact of four treatments-1) non-Bt corn, 2) Cry3Bb1 corn, 3) corn pyramided with Cry3Bb1 and Cry34/35Ab1, and 4) pyramided corn with a blended refuge-on survival, time of adult emergence, and size of western and northern corn rootworm. All treatments with Bt corn led to significant reductions in the number of adults that emerged per plot. However, at one location, we identified Cry3Bb1-resistant western corn rootworm. In some cases Bt treatments reduced size of adults and delayed time of adult emergence, with effects most pronounced for pyramided corn. For both species, the number of adults that emerged from pyramided corn with a blended refuge was significantly lower than expected, based solely on emergence from pure stands of pyramided corn and non-Bt corn. The results of this study indicate that pyramided corn with a blended refuge substantially reduces survival of both western and northern corn rootworm, and as such, should be a useful tool within the context of a broader integrated pest management strategy.

ISSN: 0022-0493

eISSN: 1938-291X

IDS Number: CJ1ZL

Unique ID: WOS:000355283600037

***Record 9 of 9.**

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

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

Title: Susceptibility of Nebraska Western Corn Rootworm (Coleoptera: Chrysomelidae) Populations to Bt Corn Events

Authors: Wangila, DS; Gassmann, AJ; Petzold-Maxwell, JL; French, BW; Meinke, LJ

Author Full Names: Wangila, David S.; Gassmann, Aaron J.; Petzold-Maxwell, Jennifer L.; French, B. Wade; Meinke, Lance J.

Source: JOURNAL OF ECONOMIC ENTOMOLOGY, 108 (2):742-751; [10.1093/jee/tou063](#)
APR 2015

Language: English

Abstract: Transgenic plants have been widely adopted by growers to manage the western corn rootworm, *Diabrotica virgifera virgifera* LeConte, in field corn. Because of reduced efficacy in some Nebraska fields after repeated use of Cry3Bb1-expressing hybrids, single plant bioassays were conducted in 2012 and 2013 to characterize the susceptibility of western corn rootworm populations to the rootworm-active proteins Cry3Bb1, mCry3A, and Cry34/35Ab1. Results demonstrate that there are heritable differences in susceptibility of Nebraska western corn rootworm populations to rootworm-active Bt traits. Proportional survival and corrected survival data coupled with field histories collectively support the conclusion that a level of field resistance to Cry3Bb1 has evolved in some Nebraska populations in response to selection pressure and that cross-resistance exists between Cry3Bb1 and mCry3A. There was no apparent cross-resistance between Cry34/35Ab1 and either Cry3Bb1 or mCry3A. The potential implications of these results on current and future corn rootworm management strategies are discussed.

ISSN: 0022-0493

eISSN: 1938-291X

IDS Number: CJ1ZL

Unique ID: WOS:000355283600040

*Record 1 of 12. Search terms matched: BT MAIZE(1); BT-MAIZE(1); CRY1AB(10); MAIZE(2)

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

*Order Full Text []

Title: The fate and transport of the **Cry1Ab** protein in an agricultural field and laboratory aquatic microcosms

Authors: Strain, KE; Lydy, MJ

Author Full Names: Strain, Katherine E.; Lydy, Michael J.

Source: CHEMOSPHERE, 132 94-100; [10.1016/j.chemosphere.2015.03.005](https://doi.org/10.1016/j.chemosphere.2015.03.005) AUG 2015

Language: English

Abstract: Genetically engineered crops expressing insecticidal crystalline proteins derived from *Bacillus thuringiensis* (Bt), were commercialized almost two decades ago as a means to manage agricultural pests. The Bt proteins are highly specific and only lethal upon ingestion, limiting the scope of toxicity to target insects. However, concern of exposure to non-target organisms and negative public perceptions regarding Bt crops has caused controversy surrounding their use. The objective of this research was to monitor the fate and transport of a Bt protein, Cry1Ab, in a large-scale agricultural field containing maize expressing the Cry1Ab protein and a non-Bt near isoline, and in aquatic microcosms. The highest environmental concentrations of the Cry1Ab protein were found in runoff water and sediment, up to 130 ng L⁻¹ and 143 ng g⁻¹ dry weight, respectively, with the Cry1Ab protein detected in both Bt and non-Bt maize fields. As surface runoff and residual crop debris can transport Bt proteins to waterways adjacent to agricultural fields, a series of laboratory experiments were conducted to determine the potential fate of the Cry1Ab protein under different conditions. The results showed that sediment type and temperature can influence the degradation of the Cry1Ab protein in an aquatic system and that the Cry1Ab protein can persist for up to two months. Although Cry1Ab protein concentrations measured in the field soil indicate little exposure to terrestrial organisms, the consistent input of Bt-contaminated runoff and crop debris into agricultural waterways is relevant to understanding potential consequences to aquatic species. (C) 2015 Elsevier Ltd. All rights reserved.

ISSN: 0045-6535

eISSN: 1879-1298

IDS Number: CK0GE

Unique ID: WOS:000355882900013

PubMed ID: 25828252

*Record 2 of 12. Search terms matched: CRY1AB(4); MAIZE(1)

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

*Order Full Text []

Title: Discrimination of Transgenic Rice containing the **Cry1Ab** Protein using Terahertz Spectroscopy and Chemometrics

Authors: Xu, WD; Xie, LJ; Ye, ZZ; Gao, WL; Yao, Y; Chen, M; Qin, JY; Ying, YB

Author Full Names: Xu, Wendao; Xie, Lijuan; Ye, Zunzhong; Gao, Weilu; Yao, Yang; Chen, Min; Qin, Jianyuan; Ying, Yibin

Source: SCIENTIFIC REPORTS, 5 [10.1038/srep11115](https://doi.org/10.1038/srep11115) JUL 8 2015

Language: English

Abstract: Spectroscopic techniques combined with chemometrics methods have proven to be effective tools for the discrimination of objects with similar properties. In this work, terahertz time-domain spectroscopy (THz-TDS) combined with discriminate analysis (DA) and principal component analysis (PCA) with derivative pretreatments was performed to differentiate transgenic rice (Hua Hui 1, containing the Cry1Ab protein) from its parent (Ming Hui 63). Both rice samples and the Cry1Ab protein were ground and pressed into pellets for terahertz (THz) measurements. The resulting time-domain spectra were transformed into frequency-domain spectra, and then, the transmittances of the rice and Cry1Ab protein were calculated. By applying the first derivative of the THz spectra in conjunction with the DA model, the discrimination of transgenic from non-transgenic rice was possible with accuracies up to 89.4% and 85.0% for the calibration set and validation set, respectively. The results indicated that THz spectroscopic techniques and chemometrics methods could be new feasible ways to differentiate transgenic rice.

ISSN: 2045-2322

Article Number: 11115

IDS Number: CM3GY

Unique ID: WOS:000357571300001

PubMed ID: 26154950

***Record 3 of 12.** Search terms matched: CORN(1); CRY1AB(1)

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

*Order Full Text []

Title: Genetically Modified Crops: Towards Agricultural Growth, Agricultural Development, or Agricultural Sustainability?

Authors: Azadi, H; Ghanian, M; Ghuchani, OM; Rafiaani, P; Taning, CNT; Hajivand, RY; Dogot, T

Author Full Names: Azadi, Hossein; Ghanian, Mansour; Ghuchani, Omid M.; Rafiaani, Parisa; Taning, Clauvis N. T.; Hajivand, Roghaye Y.; Dogot, Thomas

Source: FOOD REVIEWS INTERNATIONAL, 31 (3):195-221;
[10.1080/87559129.2014.994816](https://doi.org/10.1080/87559129.2014.994816) JUL 3 2015

Language: English

Abstract: The present debate on how to increase global food production in a sustainable way has focused on arguments over the pros and cons of genetically modified (GM) crops. Scientists in both public and private sectors clearly regard GM technology as a major new set of tools, whereas industry sees it as an opportunity for increased profits. However, it remains questionable whether GM crops can contribute to agricultural growth, agricultural development, and agricultural sustainability. This review paper examines and discusses the role of GM crops in agricultural growth, agricultural development, and agricultural sustainability. Although the contribution of GM crops to agriculture productivity is obvious in certain regions, their contributions to agricultural development and sustainability remain uncertain.

ISSN: 8755-9129

eISSN: 1525-6103

IDS Number: CK4ZG

Unique ID: WOS:000356231300001

***Record 4 of 12.** Search terms matched: BT CORN(1); CRY1AB(1); MAIZE(1); PROTECTION(2)

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

Title: Mercury and Other Trace Elements in Ohio River Fish Collected Near Coal-Fired Power Plants: Interspecific Patterns and Consideration of Consumption Risks

Authors: Reash, RJ; Brown, L; Merritt, K

Author Full Names: Reash, Robin J.; Brown, Lauren; Merritt, Karen

Source: INTEGRATED ENVIRONMENTAL ASSESSMENT AND MANAGEMENT, 11 (3):474-480; [10.1002/ieam.1618](https://doi.org/10.1002/ieam.1618) JUL 2015

Language: English

Abstract: Many coal-fired electric generating facilities in the United States are discharging higher loads of Hg, Se, and other chemicals to receiving streams due to the installation of flue gas desulfurization (FGD) air pollution control units. There are regulatory concerns about the potential increased uptake of these bioaccumulative trace elements into food webs. We evaluated the concentrations of As, total Hg (THg), methylmercury (MeHg), and Se in Ohio River fish collected proximal to coal-fired power plants, of which 75% operate FGD systems. Fillet samples (n = 50) from 6 fish species representing 3 trophic levels were analyzed. Geometric mean fillet concentrations of THg (wet wt), MeHg (wet wt), and Se (dry wt) in 3 species were 0.136, 0.1181, and 3.19 mg/kg (sauger); 0.123, 0.1013, and 1.56 mg/kg (channel catfish); and 0.127, 0.0914, and 3.30 mg/kg (hybrid striped bass). For all species analyzed, only 3 fillet samples (6% of total) had MeHg concentrations that exceeded the US Environmental Protection Agency (USEPA) human health criterion (0.3 mg/kg wet wt); all of these were freshwater drum aged ≥ 19 y. None of the samples analyzed exceeded the USEPA proposed muscle and whole body Se thresholds for protection against reproductive effects in freshwater fish. All but 8 fillet samples had a total As concentration less than 1.0 mg/kg dry wt. Mean Se health benefit values (HBVSe) for all species were ≥ 4 , indicating that potential Hg-related health risks associated with consumption of Ohio River fish are likely to be offset by adequate Se concentrations. Overall, we observed no measurable evidence of enhanced trace element bioaccumulation associated with proximity to power plant FGD facilities, however, some enhanced bioaccumulation could have occurred in the wastewater mixing zones. Furthermore, available evidence indicates that, due to hydraulic and physical factors, the main stem Ohio River appears to have low net Hg methylation potential. (C) 2015 SETAC

ISSN: 1551-3777

eISSN: 1551-3793

IDS Number: CL5RZ

Unique ID: WOS:000357019400016

PubMed ID: 25586716

***Record 5 of 12.** Search terms matched: BORER(2); BORERS(1); BT CORN(1); CORN(5);

LEPIDOPTERA(1); MAIZE(6); OSTRINIA(2); PROTECTED(1)

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

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

Title: Spatial and numerical relationships of arthropod communities associated with key pests of **maize**

Authors: Lundgren, JG; McDonald, T; Rand, TA; Fausti, SW

Author Full Names: Lundgren, J. G.; McDonald, T.; Rand, T. A.; Fausti, S. W.

Source: JOURNAL OF APPLIED ENTOMOLOGY, 139 (6):446-456; SI [10.1111/jen.12215](https://doi.org/10.1111/jen.12215)
JUL 2015

Language: English

Abstract: Pest management largely focuses on managing individual pest species with little concern for the diverse communities that co-occur with key pests and potentially shape their population dynamics. During anthesis, we described the foliar arthropod communities on 53 maize farms throughout the region of eastern South Dakota. The resulting communities were examined for trends in local associations in the abundances of taxa with key pests in the system (rootworms [*Diabrotica* spp.], European corn borers [*Ostrinia nubilalis*], aphids and Western bean cutworm [*Striacosta albicosta*]) using regression analyses. Regional spatial clustering in the abundances of key pests with members of the community was explored using Moran's I test statistic. The distributions of rootworms and European corn borer were mapped. A total of 37185 arthropods representing at least 91 taxa were collected in South Dakota maize; there was an average of 5.06 predators and 8.29 herbivores found per plant. Key pests were never found at economically threatening levels (with one exception for *Diabrotica*). Numerous species were consistently numerically associated with each of the key pests across the farms during anthesis. Occasionally, these pests shared species with which they were locally associated with; for example, coccinellid egg abundances were predictive of the abundances of all key pest species except rootworm adults. Spatial analysis across the region suggested that species co-occurred with key pests based on local characteristics surrounding the fields, rather than as a result of regional characteristics. Exceptions were documented; namely aphids and Western bean cutworms that spatially clustered with a handful of other members of the community. The results of the study point out that the abundances of key pests of maize were interconnected through indirect associations in the abundances of other members of the community. These associations may be useful for manipulating maize agroecosystems to minimize the effects of maize pests.

ISSN: 0931-2048

eISSN: 1439-0418

IDS Number: CLOEM

Unique ID: WOS:000356612400006

***Record 6 of 12.** Search terms matched: BT CORN(3); CORN(3); PROTECT(1)

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

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

Title: A Site-Specific Ecological Risk Assessment for **Corn**-Associated Insecticides

Authors: Whiting, SA; Lydy, MJ

Author Full Names: Whiting, Sara A.; Lydy, Michael J.

Source: INTEGRATED ENVIRONMENTAL ASSESSMENT AND MANAGEMENT, 11 (3):445-458; [10.1002/ieam.1613](https://doi.org/10.1002/ieam.1613) JUL 2015

Language: English

Abstract: A site-specific ecological risk assessment (ERA) was conducted to examine the simultaneous use of genetically modified corn (Bt corn) with a neonicotinoid seed coating, clothianidin, and use of a granular insecticide, tefluthrin, to protect crops from pest damage. A field study was conducted on site, and exposure data from the literature were summarized to determine the matrices and exposure concentrations that nontarget species could typically experience within an agricultural ecosystem. To determine ecological effects on nontarget species, acute toxicity bioassays were conducted on earthworms (*Eisenia fetida*), amphipods (*Hyalella azteca*), and Elmid riffle beetle larvae (*Ancyronyx* spp.) in which the test species were exposed to single insecticides as well as the mixture of the 3 insecticides. In the risk characterization section of the ERA, stressor-response profiles for each species tested were compared with field distributions of the insecticides, and a margin of safety at the 10th percentile (MOS10) was calculated to estimate risk. No acute toxicity was observed in any of the 3 nontarget species after exposure to senescent Bt corn leaf tissue. Large MOS10 values were calculated for clothianidin to the nontarget species. When bioassays were compared with tefluthrin field distributions, very low MOS10 values were calculated for earthworms (0.06) and *H. azteca* (0.08) because the environmental concentrations often exceeded the stressor-response profile. No increased toxicity was observed when nontarget species were exposed to a mixture of the 3 insecticides. In summary, the genetically modified corn insecticidal proteins and clothianidin were not found at environmental concentrations exceeding benchmark values for ecological effects, but tefluthrin was consistently detected in the environment at levels that could be causing toxicity to nontarget species, especially if this pyrethroid is able to travel off site. (C) 2015 SETAC

ISSN: 1551-3777

eISSN: 1551-3793

IDS Number: CL5RZ

Unique ID: WOS:000357019400014

PubMed ID: 25557061

***Record 7 of 12.** Search terms matched: CORN(1); CRY1AB(1); LEPIDOPTERA(4)

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

*Order Full Text []

Title: Effects of dietary protein to carbohydrate ratio on Bt toxicity and fitness costs of resistance in *Helicoverpa zea*

Authors: Orpet, RJ; Degain, BA; Unnithan, GC; Welch, KL; Tabashnik, BE; Carriere, Y

Author Full Names: Orpet, Robert J.; Degain, Ben A.; Unnithan, Gopalan C.; Welch, Kara L.; Tabashnik, Bruce E.; Carriere, Yves

Source: ENTOMOLOGIA EXPERIMENTALIS ET APPLICATA, 156 (1):28-36; [10.1111/eea.12308](https://doi.org/10.1111/eea.12308) JUL 2015

Language: English

Abstract: The ratio of dietary protein to carbohydrate (P:C) affects the feeding performance of

insect herbivores and was recently shown to affect susceptibility to Bt toxins and fitness costs of resistance in *Trichoplusia ni* Hubner. Here, we used laboratory experiments with larvae reared on artificial diet to determine whether dietary P:C ratio affects responses to Bt toxin Cry1Ac and fitness costs of resistance in *Helicoverpa zea* Boddie (Lepidoptera: Noctuidae). We tested a *H. zea* strain that was selected for resistance to Cry1Ac in the laboratory (GA-R) and its field-derived parent strain (GA), which was not selected in the laboratory. Relative to GA, GA-R had 14-fold resistance to Cry1Ac. The P:C ratio of diet did not affect susceptibility to Cry1Ac of GA-R. However, against GA, Cry1Ac was least toxic on the diet with the lowest P:C ratio (35:65) and most toxic on the diet with the highest P:C ratio (90:10). Diets of all P:C ratios except 80:20 induced a fitness cost of lower pupal weight in GA-R relative to GA for males, females, or both. Considered together with previous results, the new findings reported here indicate that the effects of P:C ratio on responses to Cry1Ac and fitness costs vary between species and between strains within species.

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eISSN: 1570-7458

IDS Number: CK1HS

Unique ID: WOS:000355958700003

***Record 8 of 12.** Search terms matched: BT MAIZE(5); CORN(5); MAIZE(8); RESISTANT(5); ZEA MAYS(1)

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

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

Title: Fitness costs of resistance to Cry3Bb1 **maize** by western **corn** rootworm

Authors: Hoffmann, AM; French, BW; Hellmich, RL; Lauter, N; Gassmann, AJ

Author Full Names: Hoffmann, A. M.; French, B. W.; Hellmich, R. L.; Lauter, N.; Gassmann, A. J.

Source: JOURNAL OF APPLIED ENTOMOLOGY, 139 (6):403-415; SI [10.1111/jen.12209](https://doi.org/10.1111/jen.12209)
JUL 2015

Language: English

Abstract: Crops producing toxins derived from the bacterium *Bacillus thuringiensis* (Bt) are widely planted to manage insect pests including western corn rootworm, *Diabrotica virgifera virgifera* LeConte (Coleoptera: Chrysomelidae), which is a significant pest of maize in the United States and Europe. However, the widespread use of Bt maize places intense selection pressure on pest populations to evolve resistance, and field-evolved resistance to Bt maize by western corn rootworm has been documented in the United States. In conjunction with non-Bt refuges, fitness costs of Bt resistance can delay resistance evolution. Fitness costs arise in the absence of Bt toxin when individuals with resistance alleles have lower fitness than Bt-susceptible genotypes. We quantified the level of resistance and fitness costs of resistance for a strain of western corn rootworm with laboratory-selected resistance to transgenic maize (*Zea mays* L.) producing Bt toxin Cry3Bb1. Survival to adulthood on Cry3Bb1 maize was more than twofold higher for resistant insects vs. susceptible insects, which is similar to the magnitude of resistance first observed in the field. Fitness costs were measured in two experiments; the first used maize hybrids and the second used inbred lines. The experiment with maize hybrids compared resistant and susceptible strains while the experiment with maize inbreds compared resistant, susceptible

and heterozygous genotypes. The only non-recessive fitness cost detected (i.e. cost affecting heterozygotes) was for adult size. Recessive fitness costs (i.e. costs affecting the resistant strain) were observed for developmental rate, female survival and egg viability. However, when reared on non-Bt maize, the resistant strain also displayed higher fecundity, higher survival for males and greater adult longevity compared to the susceptible strain. These results suggest that resistance to Bt maize by western corn rootworm may not impose substantial fitness costs, and consequently, may evolve quickly and persist once present.

ISSN: 0931-2048

eISSN: 1439-0418

IDS Number: CLOEM

Unique ID: WOS:000356612400002

***Record 9 of 12.** Search terms matched: BT CORN(1); BT MAIZE(3); CORN(1); MAIZE(3); PROTECTED(1); RESISTANT(1); TOLERANCE(1)

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

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

Title: Risk Assessment of Genetically Engineered **Maize Resistant** to *Diabrotica* spp.: Influence on Above-Ground Arthropods in the Czech Republic

Authors: Svobodova, Z; Habustova, OS; Hutchison, WD; Hussein, HM; Sehnal, F

Author Full Names: Svobodova, Zdenka; Habustova, Oxana Skokova; Hutchison, William D.; Hussein, Hany M.; Sehnal, Frantisek

Source: PLOS ONE, 10 (6):[10.1371/journal.pone.0130656](https://doi.org/10.1371/journal.pone.0130656) JUN 17 2015

Language: English

Abstract: Transgenic maize MON88017, expressing the Cry3Bb1 toxin from *Bacillus thuringiensis* (Bt maize), confers resistance to corn rootworms (*Diabrotica* spp.) and provides tolerance to the herbicide glyphosate. However, prior to commercialization, substantial assessment of potential effects on non-target organisms within agroecosystems is required. The MON88017 event was therefore evaluated under field conditions in Southern Bohemia in 2009-2011, to detect possible impacts on the above-ground arthropod species. The study compared MON88017, its near-isogenic non-Bt hybrid DK315 (treated or not treated with the soil insecticide Dursban 10G) and two non-Bt reference hybrids (KIPOUS and PR38N86). Each hybrid was grown on five 0.5 ha plots distributed in a 14-ha field with a Latin square design. Semiquantitative ELISA was used to verify Cry3Bb1 toxin levels in the Bt maize. The species spectrum of non-target invertebrates changed during seasons and was affected by weather conditions. The thrips *Frankliniella occidentalis* was the most abundant species in all three successive years. The next most common species were aphids *Rhopalosiphum padi* and *Metopolophium dirhodum*. Frequently observed predators included *Orius* spp. and several species within the Coccinellidae. Throughout the three-year study, analysis of variance indicated some significant differences ($P < 0.05$). Multivariate analysis showed that the abundance and diversity of plant dwelling insects was similar in maize with the same genetic background, for both Bt (MON88017) and non-Bt (DK315) untreated or insecticide treated. KIPOUS and PR38N86 showed some differences in species abundance relative to the Bt maize and its near-isogenic hybrid. However, the effect of management regime on arthropod community was insignificant and accounted only for a negligible portion of the variability.

ISSN: 1932-6203

Article Number: e0130656

IDS Number: CK9NS

Unique ID: WOS:000356567400152

PubMed ID: 26083254

***Record 10 of 12.** Search terms matched: BT MAIZE(3); CORN(10); MAIZE(2); ZEA MAYS(1)

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

Title: Effect of Seed Blends and Soil-Insecticide on Western and Northern **Corn** Rootworm Emergence from mCry3A+eCry3.1Ab **Bt Maize**

Authors: Frank, DL; Kurtz, R; Tinsley, NA; Gassmann, AJ; Meinke, LJ; Moellenbeck, D; Gray, ME; Bledsoe, LW; Krupke, CH; Estes, RE; Weber, P; Hibbard, BE

Author Full Names: Frank, Daniel L.; Kurtz, Ryan; Tinsley, Nicholas A.; Gassmann, Aaron J.; Meinke, Lance J.; Moellenbeck, Daniel; Gray, Michael E.; Bledsoe, Larry W.; Krupke, Christian H.; Estes, Ronald E.; Weber, Patrick; Hibbard, Bruce E.

Source: JOURNAL OF ECONOMIC ENTOMOLOGY, 108 (3):1260-1270; [10.1093/jee/tov081](https://doi.org/10.1093/jee/tov081)
JUN 2015

Language: English

Abstract: Seed blends containing various ratios of transgenic Bt maize (*Zea mays* L.) expressing the mCry3A + eCry3.1Ab proteins and non-Bt maize (near-isoline maize) were deployed alone and in combination with a soil applied pyrethroid insecticide (Force CS) to evaluate the emergence of the western corn rootworm, *Diabrotica virgifera virgifera* LeConte, in a total of nine field environments across the Midwestern United States in 2010 and 2011. Northern corn rootworm, *Diabrotica barberi* Smith & Lawrence emergence was also evaluated in four of these environments. Both western and northern corn rootworm beetle emergence from all Bt treatments was significantly reduced when compared with beetle emergence from near-isoline treatments. Averaged across all environments, western corn rootworm beetle emergence from 95:5, 90:10, and 80:20 seed blend ratios of mCry3A + eCry3.1Ab: near-isoline were 2.6-, 4.2-, and 6.7-fold greater than that from the 100:0 ratio treatment. Northern corn rootworm emergence from the same seed blend treatments resulted in 2.8-, 3.2-, and 4.2-fold more beetles than from the 100:0 treatment. The addition of Force CS (tefluthrin) significantly reduced western corn rootworm beetle emergence for each of the three treatments to which it was applied. Force CS also significantly delayed the number of days to 50% beetle emergence in western corn rootworms. Time to 50% beetle emergence in the 100% mCry3A + eCry3.1Ab treatment with Force CS was delayed 13.7 d when compared with western corn rootworm beetle emergence on near-isoline corn. These data are discussed in terms of rootworm resistance management.

ISSN: 0022-0493

eISSN: 1938-291X

IDS Number: CK5CF

Unique ID: WOS:000356239000053

***Record 11 of 12.** Search terms matched: MAIZE(5); ZEA MAYS(2)

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

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

Title: QUANTIFICATION OF GENETICALLY MODIFIED **MAIZE** WITH qPCR AND dPCR TECHNIQUES

Authors: Gutierrez-Angoa, LE; Castillo-Duran, LC; Gomez-Casielo, BE; Acatzi-Silva, AI

Author Full Names: Gutierrez-Angoa, Lizbeth E.; Castillo-Duran, Luis C.; Gomez-Casielo, Blanca E.; Acatzi-Silva, Abraham I.

Source: AGROCIENCIA, 49 (4):373-394; MAY-JUN 2015

Language: English

Abstract: In 2009 in Mexico, permission was given to release genetically modified maize (*Zea mays* L.) into the environment. This made it necessary to detect, identify and quantify genetically modified organisms (GMO) in the country's crops. The objective of this study was to validate the technique of absolute quantification of leaf mixtures in mass fraction of GM maize using real time (qPCR) and digital (dPCR) polymerase chain reaction (PCR) technique. Mixed leaves of maize modified with the MON810 event were prepared with conventional maize and analyzed with the qPCR technique. A certified reference plasmid and DNA obtained from a leaf with the MON810 modification were used as calibrants; besides, the dPCR technique was utilized since it allows a precise measurement of the number of DNA initial copies in the samples and does not require the utilization of calibrants. The test in qPCR complied with validation criteria, such as quantification limit, dynamic interval, amplification efficiency, correlation coefficient and estimation of uncertainty. Moreover, the dPCR technique was validated prior to quantification of the mixtures with the certified reference materials (CRM). Once the dPCR technique was validated, the GM material in the mixtures were quantified, and the results of the two techniques were comparable, indicating that they can be applied in quantifying genetic modification in crops and emit the results in mass fraction or copy number. The results show that quantification of genetically modified crop material in Mexico is possible with reliable results.

ISSN: 1405-3195

IDS Number: CL4FZ

Unique ID: WOS:000356909300003

***Record 12 of 12.** Search terms matched: MAIZE(6); YIELD(1); ZEA-MAYS(1)

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

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

Title: Influence of plant developmental stage on DNA **yield** and extractability in MON810 **maize**

Authors: Taverniers, I; De Meyer, L; Van Droogenbroeck, B; Messens, K; De Loose, M

Author Full Names: Taverniers, Isabel; De Meyer, Laurens; Van Droogenbroeck, Bart; Messens, Kathy; De Loose, Marc

Source: AGRICULTURAL AND FOOD SCIENCE, 24 (2):128-138; 2015

Language: English

Abstract: The amount and extractability of DNA in different parts of MON810 GM hybrid was studied during different developmental stages. To quantify GM contents, an evaluation was performed of the effect of plant development stage on DNA density. To this end, the evolution of

weights, absolute DNA yields, DNA densities and ratios of endosperm and embryo relative to total maize kernel were studied. Sampling at four stages during the growth shows an influence on relative GM quantification based on haploid genome equivalents, due to the specific maize seed composition and differences in DNA extractability from different seed tissues. During plant growth, plant parts with potential GM genes (embryo in kernel and cob on total plant) increase in importance on weight and DNA concentration level, while the endosperm drops in relative importance. Expected % GM maize values are calculated for a whole field harvest of grain maize.

ISSN: 1459-6067

eISSN: 1795-1895

IDS Number: CM0CC

Unique ID: WOS:000357344800006

***Record 1 of 9.** Search terms matched: BT(1); CORN(7)

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

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

Title: The causes and unintended consequences of a paradigm shift in corn production practices

Authors: Fausti, SW

Author Full Names: Fausti, Scott W.

Source: ENVIRONMENTAL SCIENCE & POLICY, 52 41-50; [10.1016/j.envsci.2015.04.017](https://doi.org/10.1016/j.envsci.2015.04.017)
OCT 2015

Language: English

Abstract: Independent but simultaneously occurring changes in U.S. agricultural and energy policies in conjunction with advances in biotechnology converged to create an economic and regulatory environment that incentivized corn acreage expansion. Advancements in Bt seed and ethanol production technologies contributed to scale efficiency gains in corn and biofuel production. These advancements were accompanied by changes in market forces that altered the balance between corn and other agricultural crop production. The causal linkages among Bt adoption, ethanol production, and corn production are explored along with a discussion of how this shift toward corn production generated unexpected economic and environmental consequences. Alternative policy solutions to mitigate the negative consequences and enhance the resiliency of U.S. agriculture are discussed. (C) 2015 The Author. Published by Elsevier Ltd.

ISSN: 1462-9011

eISSN: 1873-6416

IDS Number: CN8OD

Unique ID: WOS:000358699600005

***Record 2 of 9.** Search terms matched: BT(1); MAIZE(1)

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

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

Title: Evolution of BT maize and HT soybean production and cost of coexistence in Romania

Authors: Beciu, S; Dinu, T; Ghidurus, M; Ladaru, R; Calin, A

Author Full Names: Beciu, Silviu; Dinu, Toma; Ghidurus, Mihaela; Ladaru, Raluca; Calin, Alexandru

Source: JOURNAL OF BIOTECHNOLOGY, 208 S106-S106; S [10.1016/j.jbiotec.2015.06.333](https://doi.org/10.1016/j.jbiotec.2015.06.333)
AUG 20 2015

Language: English

ISSN: 0168-1656

eISSN: 1873-4863

IDS Number: CO3UW

Unique ID: WOS:000359087000333

***Record 3 of 9.** Search terms matched: BORER(1); BORERS(2); BT(2); CORN(1); LEPIDOPTERA(2); MAIZE(7); SESAMIA(1)

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

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

Title: Baseline sensitivity of maize borers in India to the *Bacillus thuringiensis* insecticidal proteins Cry1A.105 and Cry2Ab2

Authors: Jalali, SK; Yadavalli, L; Ojha, R; Kumar, P; Sulaikhabeevi, SB; Sharma, R; Nair, R; Kadanur, RC; Kamath, SP; Komarlingam, MS

Author Full Names: Jalali, Sushil K.; Yadavalli, Lalitha; Ojha, Rakshit; Kumar, Pradyumn; Sulaikhabeevi, Suby B.; Sharma, Reema; Nair, Rupa; Kadanur, Ravi C.; Kamath, Subray P.; Komarlingam, Mohan S.

Source: PEST MANAGEMENT SCIENCE, 71 (8):1082-1090; [10.1002/ps.3888](https://doi.org/10.1002/ps.3888) AUG 2015

Language: English

Abstract: BACKGROUND Among the major pests of maize in India are two stem borers, *Chilo partellus* (Swinhoe) and *Sesamia inferens* (Walker), and an earworm, *Helicoverpa armigera* (Hubner). As a pest control strategy, transgenic *Bacillus thuringiensis* (Bt) maize hybrids are undergoing regulatory trials in India. We have determined the sensitivity of the target lepidopterans to the insecticidal Bt proteins expressed in Bt maize, as this determines product efficacy and the resistance management strategy to be adopted. Maize hybrids with event MON89034 express two insecticidal Bt proteins, Cry1A.105 and Cry2Ab2. RESULTSSensitivity profiles of 53 populations of *C. partellus*, 21 populations of *S. inferens* and 21 populations of *H. armigera*, collected between 2008 and 2013 from maize-growing areas in India, to Cry1A.105 and Cry2Ab2 proteins were generated through dose-response assays. Cry1A.105 protein was the most effective to neonates of *C. partellus* (mean MIC90 range 0.30-1.0 $\mu\text{g mL}^{-1}$) and *H. armigera* (mean MIC90 range 0.71-8.22 $\mu\text{g mL}^{-1}$), whereas Cry2Ab2 (mean MIC90 range 0.65-1.70 $\mu\text{g mL}^{-1}$) was the most effective to *S. inferens*. CONCLUSION Populations of *C. partellus*, *S. inferens* and *H. armigera* were susceptible to the Bt proteins Cry1A.105 and Cry2Ab2. The Bt sensitivity data will serve as precommercialisation benchmarks for resistance monitoring purposes. (c) 2014 Society of Chemical Industry

ISSN: 1526-498X

eISSN: 1526-4998

IDS Number: CM3QG

Unique ID: WOS:000357597400006

PubMed ID: 25143318

***Record 4 of 9.** Search terms matched: BORER(3); CORN(3); LEPIDOPTERA(2); OSTRINIA(3); RESISTANT(6)

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

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

Title: Transcriptional analysis of susceptible and resistant European corn borer strains and their response to Cry1F protoxin

Authors: Vellichirammal, NN; Wang, HC; Eyun, SI; Moriyama, EN; Coates, BS; Miller, NJ; Siegfried, BD

Author Full Names: Vellichirammal, Neetha Nanoth; Wang, Haichuan; Eyun, Seong-il; Moriyama, Etsuko N.; Coates, Brad S.; Miller, Nicholas J.; Siegfried, Blair D.

Source: BMC GENOMICS, 16 [10.1186/s12864-015-1751-6](https://doi.org/10.1186/s12864-015-1751-6) JUL 29 2015

Language: English

Abstract: Background: Despite a number of recent reports of insect resistance to transgenic crops expressing insecticidal toxins from *Bacillus thuringiensis* (Bt), little is known about the mechanism of resistance to these toxins. The purpose of this study is to identify genes associated with the mechanism of Cry1F toxin resistance in European corn borer (*Ostrinia nubilalis* Hubner). For this, we compared the global transcriptomic response of laboratory selected resistant and susceptible *O. nubilalis* strain to Cry1F toxin. We further identified constitutive transcriptional differences between the two strains. Results: An *O. nubilalis* midgut transcriptome of 36,125 transcripts was assembled de novo from 106 million Illumina HiSeq and Roche 454 reads and used as a reference for estimation of differential gene expression analysis. Evaluation of gene expression profiles of midgut tissues from the Cry1F susceptible and resistant strains after toxin exposure identified a suite of genes that responded to the toxin in the susceptible strain ($n = 1,654$), but almost 20-fold fewer in the resistant strain ($n = 84$). A total of 5,455 midgut transcripts showed significant constitutive expression differences between Cry1F susceptible and resistant strains. Transcripts coding for previously identified Cry toxin receptors, cadherin and alkaline phosphatase and proteases were also differentially expressed in the midgut of the susceptible and resistant strains. Conclusions: Our current study provides a valuable resource for further molecular characterization of Bt resistance and insect response to Cry1F toxin in *O. nubilalis* and other pest species.

ISSN: 1471-2164

Article Number: 558

IDS Number: CN6SP

Unique ID: WOS:000358564800004

***Record 5 of 9.** Search terms matched: CRY1AB(1); MAIZE(3); MON 810(2)

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

*Order Full Text []

Title: New multiplex PCR methods for rapid screening of genetically modified organisms in foods

Authors: Datukishvili, N; Kutateladze, T; Gabriadze, I; Bitskinashvili, K; Vishnepolsky, B

Author Full Names: Datukishvili, Nelly; Kutateladze, Tamara; Gabriadze, Inga; Bitskinashvili, Kakha; Vishnepolsky, Boris

Source: FRONTIERS IN MICROBIOLOGY, 6 [10.3389/fmicb.2015.00757](https://doi.org/10.3389/fmicb.2015.00757) JUL 24 2015

Language: English

Abstract: We present novel multiplex PCR methods for rapid and reliable screening of genetically modified organisms (GMOs). New designed PCR primers targeting four frequently used GMO specific sequences permitted identification of new DNA markers, in particular 141 bp fragment of cauliflower mosaic virus (CaMV) 35S promoter, 224 bp fragment of *Agrobacterium tumefaciens* nopaline synthase (NOS) terminator, 256 bp fragment of 5-enolpyruvylshikimate-phosphate synthase (epsps) gene and 258 bp fragment of Cry1Ab delta-endotoxin (cry1 Ab) gene for GMO screening. The certified reference materials containing Roundup Ready soybean (RRS) and maize MON 810 were applied for the development and optimization of uniplex and multiplex PCR systems. Evaluation of amplification products by agarose gel electrophoresis using negative and positive controls confirmed high specificity and sensitivity at 0.1% GMO for

both RRS and MON 810. The fourplex PCR was developed and optimized that allows simultaneous detection of three common transgenic elements, such as: CaMV 35S promoter, NOS terminator, epsps gene together with soybean-specific lectin gene. The triplex PCR developed enables simultaneous identification of transgenic elements, such as: 35S promoter and cryl Ab gene together with maize zein gene. The analysis of different processed foods demonstrated that multiplex PCR methods developed in this study are useful for accurate and fast screening of GM food products.

ISSN: 1664-302X

Article Number: 757

IDS Number: CO0WT

Unique ID: WOS:000358875100001

PubMed ID: 26257724

***Record 6 of 9.** Search terms matched: BT(1); CORN(1); RESISTANT(1)

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

*Order Full Text []

Title: Toxicological, Biochemical, and Histopathological Analyses Demonstrating That Cry1C and Cry2A Are Not Toxic to Larvae of the Honeybee, *Apis mellifera*

Authors: Wang, YY; Li, YH; Huang, ZY; Chen, XP; Romeis, J; Dai, PL; Peng, YF

Author Full Names: Wang, Yuan-Yuan; Li, Yun-He; Huang, Zachary Y.; Chen, Xiu-Ping; Romeis, Joerg; Dai, Ping-Li; Peng, Yu-Fa

Source: JOURNAL OF AGRICULTURAL AND FOOD CHEMISTRY, 63 (27):6126-6132; [10.1021/acs.jafc.5b01662](https://doi.org/10.1021/acs.jafc.5b01662) JUL 15 2015

Language: English

Abstract: The honey bee, *Apis mellifera*, is commonly used as a test species for the regulatory risk assessment of insect-resistant genetically engineered (IRGE) plants. In the current study, a dietary exposure assay was developed, validated, and used to assess the potential toxicity of Cry1C and Cry2A proteins from *Bacillus thuringiensis* (Bt) to *A. mellifera* larvae; Cry1C and Cry2A are produced by different IRGE crops. The assay, which uses the soybean trypsin inhibitor (SBTI) as a positive control and bovine serum albumin (BSA) as a negative control, was used to measure the responses of *A. mellifera* larvae to high concentrations of Cry1C and Cry2A. Survival was reduced and development was delayed when larvae were fed SBTI (1 mg/g diet) but were unaffected when larvae were fed BSA (400 µg/g), Cry1C (50 µg/g), or Cry2A (400 µg/g). The enzymatic activities of *A. mellifera* larvae were not altered and their midgut brush border membranes (BBMs) were not damaged after being fed with diets containing BSA, Cry1C, or Cry2A; however, enzymatic activities were increased and BBMs were damaged when diets contained SBTI. The study confirms that Cry1C and Cry2A have no acute toxicity to *A. mellifera* larvae at concentrations >10 times higher than those detected in pollen from Bt plants.

ISSN: 0021-8561

eISSN: 1520-5118

IDS Number: CN1NI

Unique ID: WOS:000358186300004

PubMed ID: 26084400

***Record 7 of 9.** Search terms matched: BT(1); LEPIDOPTERA(1); MAIZE(1); RESISTANT(4)

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

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

Title: Homo logs to Cry toxin receptor genes in a de novo transcriptome and their altered expression in resistant *Spodoptera litura* larvae

Authors: Gong, L; Wang, HD; Qi, JW; Han, LZ; Hu, MY; Jurat-Fuentes, JL

Author Full Names: Gong, Liang; Wang, Huidong; Qi, Jiangwei; Han, Lanzhi; Hu, Meiyong; Jurat-Fuentes, Juan Luis

Source: JOURNAL OF INVERTEBRATE PATHOLOGY, 129 1-6; [10.1016/j.jip.2015.05.008](https://doi.org/10.1016/j.jip.2015.05.008)
JUL 2015

Language: English

Abstract: Insect resistance threatens sustainability of insecticides based on Cry proteins from the bacterium *Bacillus thuringiensis* (Bt). Since high levels of resistance to Cry proteins involve alterations in Cry-binding midgut receptors, their identification is needed to develop resistance management strategies. Through Illumina sequencing we generated a transcriptome containing 16,161 annotated unigenes for the Oriental leafworm (*Spodoptera litura*). Transcriptome mining identified 6 contigs with identity to reported lepidopteran Cry toxin receptors. Using PCR we confirmed their expression during the larval stage and compared their quantitative expression in larvae from susceptible and a field-derived Cry1 Ca resistant strain of *S. litura*. Among reduced transcript levels detected for most tested contigs in the Cry1 Ca-resistant *S. litura* larvae, the most dramatic reduction (up to 99%) was detected for alkaline phosphatase contigs. This study significantly expands *S. litura* transcriptomic resources and provides preliminary identification of putative receptor genes with altered expression in *S. litura* resistant to Cry1Ca toxin. (C) 2015 Elsevier Inc. All rights reserved,

ISSN: 0022-2011

eISSN: 1096-0805

IDS Number: CN0MV

Unique ID: WOS:000358108600001

PubMed ID: 25981133

***Record 8 of 9.** Search terms matched: CORN(1); MAIZE(8); MON 810(3)

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

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

Title: The use of genetically modified Roundup Ready soyabean meal and genetically modified MON 810 maize in broiler chicken diets. Part 1. Effects on performance and blood lymphocyte subpopulations

Authors: Czerwinski, J; Bogacki, M; Jalali, BM; Konieczka, P; Smulikowska, S

Author Full Names: Czerwinski, J.; Bogacki, M.; Jalali, B. M.; Konieczka, P.; Smulikowska, S.

Source: JOURNAL OF ANIMAL AND FEED SCIENCES, 24 (2):134-143; 2015

Language: English

Abstract: The effects of genetically modified (GM) soyabean meal (SBM) and GM maize (MON

810) on the performance and immunological response of broiler chickens were studied. Eight diets were prepared based on conventional or GM SBM (GTS 40-3-2) combined with non-modified maize cvs. Clarica or PR39 F58 or their isogenic GM counterparts, cvs. Bacilla or PR39 F56. Diets were fed in mash form from day one of age to 192 Ross 308 broiler females, allocated to 8 groups, 24 birds per group. From day 8 to 28 of age, 18 chickens per group were kept in individual cages and performance parameters were measured. After slaughter the shares of T helper and T cytotoxic cells in the blood were determined in 8 birds per group. The feed conversion ratio (FCR) of birds fed GM SBM was better by 3.2% than in birds fed conventional SBM ($P < 0.01$). The performance of birds fed GM maize did not differ from those fed conventional maize, but body weight gain was lower and FCR worse by 3.3% in birds fed diets with Clarica/Bacilla compared with the PR 39 cultivar. The shares of circulating lymphocytes in their entire population averaged 10% to 17% and 6.5 to 12.2% (T helper and T cytotoxic, respectively) for all groups except the group fed conventional cv. Clarica maize and non-modified SBM (31% and 20.6%, respectively). It may be concluded that the use of GM GTS 40-3-2 soyabean meal and GM MON 810 maize in broiler diets did not negatively affect the feed efficiency and blood lymphocyte subpopulations of broilers.

ISSN: 1230-1388

IDS Number: CM0IZ

Unique ID: WOS:000357362900007

***Record 9 of 9.** Search terms matched: BT(1); CORN(1); MAIZE(9); MON 810(2)

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

*Order Full Text []

Title: The use of genetically modified Roundup Ready soyabean meal and genetically modified MON 810 maize in broiler chicken diets. Part 2. Functional status of the small intestine

Authors: Czerwinski, J; Slupecka-Ziemilska, M; Wolinski, J; Barszcz, M; Konieczka, P; Smulikowska, S

Author Full Names: Czerwinski, J.; Slupecka-Ziemilska, M.; Wolinski, J.; Barszcz, M.; Konieczka, P.; Smulikowska, S.

Source: JOURNAL OF ANIMAL AND FEED SCIENCES, 24 (2):144-152; 2015

Language: English

Abstract: The effects of genetically modified (GM) soyabean meal (SBM) and GM maize on the functional status of the small intestine of broiler chickens was studied. Eight diets were prepared, based on conventional or GM SBM (GTS 40-3-2) combined with non-modified maize cvs. Clarica and PR39 F58 or their isogenic GM (MON 810) counterparts cvs. Bacilla or PR39 F56. Diets were fed in mash form from days 1 to 30 of age to 192 Ross 308 broiler females, assigned to 8 groups and kept in individual cages from day 8 of life. The functional status of the small intestine was studied in 8 birds per group after slaughter. The investigation included morphological evaluation of jejunum and ileum sections, calculation of apoptotic and mitotic indices, and measurement of DNA damage in jejuna] epithelial cells. There were no statistically significant differences in morphological parameters of the jejunum and ileum except the width of the tunica mucosa in the jejunum, which was greater in birds fed GM than in those given conventional maize. GM SBM had no effect on the apoptotic and mitotic indices in the crypt area or in villi tips, while GM maize did not affect these indices in the crypt area, but increased the

apoptotic index in the villi tips of the jejunum. Neither substituting conventional SBM by GM SBM, nor conventional maize by GM maize induced significant DNA damage in the epithelial cells of the jejunum. Our results indicate that the functional development and maturation of the small intestinal epithelium is not greatly modified by the use of GM SBM and GM maize in broiler diets.

ISSN: 1230-1388

IDS Number: CM0IZ

Unique ID: WOS:000357362900008

***Record 1 of 9.** Search terms matched: BT(2); CORN(1); CRY1AB(8); MAIZE(2); MON810(1)

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

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

Title: Fate of the insecticidal Cry1Ab protein of GM crops in two agricultural soils as revealed by C-14-tracer studies

Authors: Valldor, P; Miethling-Graff, R; Martens, R; Tebbe, CC

Author Full Names: Valldor, Petra; Miethling-Graff, Rona; Martens, Rainer; Tebbe, Christoph C.

Source: APPLIED MICROBIOLOGY AND BIOTECHNOLOGY, 99 (17):7333-7341;
[10.1007/s00253-015-6655-5](https://doi.org/10.1007/s00253-015-6655-5) SEP 2015

Language: English

Abstract: Insecticidal delta-endotoxins of *Bacillus thuringiensis* are among the most abundant recombinant proteins released by genetically modified (GM) crops into agricultural soils worldwide. However, there is still controversy about their degradation and accumulation in soils. In this study, C-14-labelled Cry1Ab protein was applied to soil microcosms at two concentrations (14 and 50 $\mu\text{g g}^{-1}$ soil) to quantify the mineralization of Cry1Ab, its incorporation into the soil microbial biomass, and its persistence in two soils which strongly differed in their texture but not in silt or pH. Furthermore, ELISA was used to quantify Cry1Ab and its potential immunoreactive breakdown products in aqueous soil extracts. In both soils, (CO₂)-C-14-production was initially very high and then declined during a total monitoring period of up to 135 days. A total of 16 to 23 % of the C-14 activity was incorporated after 29 to 37 days into the soil microbial biomass, indicating that Cry1Ab protein was utilized by microorganisms as a growth substrate. Adsorption in the clay-rich soil was the most important factor limiting microbial degradation; as indicated by higher degradation rates in the more sandy soil, extremely low concentrations of immunoreactive Cry1Ab molecules in the soils' aqueous extracts and a higher amount of C-14 activity bound to the soil with more clay. Ecological risk assessments of Bt-crops should therefore consider that the very low concentrations of extractable Cry1Ab do not reflect the actual elimination of the protein from soils but that, on the other hand, desorbed proteins mineralize quickly due to efficient microbial degradation.

ISSN: 0175-7598

eISSN: 1432-0614

IDS Number: CP2WY

Unique ID: WOS:000359739600031

PubMed ID: 25967657

***Record 2 of 9.** Search terms matched: BORER(1); BT(1); CORN(2); MAIZE(1); PROTECTION(1)

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

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

Title: Safe use of Cry genes in genetically modified crops

Authors: Rahman, M; Zaman, M; Shaheen, T; Irem, S; Zafar, Y

Author Full Names: Rahman, M.; Zaman, Muhammad; Shaheen, Tayyaba; Irem, Samra; Zafar, Yusuf

Source: ENVIRONMENTAL CHEMISTRY LETTERS, 13 (3):239-249; [10.1007/s10311-015-0508-4](https://doi.org/10.1007/s10311-015-0508-4) SEP 2015

Language: English

Abstract: Genomic technologies have been used to improve cultivated crop species. For example, Bt genes such as Cry1Ac, Cry2Ab, Cry1F and Cry3Bb1 are derived from *Bacillus thuringiensis*, a soil bacterium. Such genes provide protection against lepidopteran insect pests. Bt genes have been introduced in corn, cotton, soybean, rice, potato and canola. Genetically modified (GM)-cotton, containing the Cry1Ac gene, was released for cultivation in the mid-1990s in the USA and later in 28 countries including China and India. Potential harmful effects of the Bt-crops on non-targets were assessed before release into the environment. Most commonly, cultivation of the Bt-crops was found safe. Safety was tested using various experiments including: the insertional impact of transgene and its regulatory elements on plant phenotype and agronomic performance; effect on non-target organisms; and nutritional impacts on multiple experimental models, albeit the studies were conducted for limited durations. However, skeptics always claim for conducting extensive clinical as well as field trials and also cast doubt on methods and procedures of calculating the ecological risks. This debate got further momentum especially after the publication of reports on substantial reduction in monarch butterfly caterpillars when exposed to Bt-maize pollen-though later nullified-and detection of traces of transgene in various tissues of experimental animals. It is generally accepted that procedures, methods and protocols for evaluating the potential risks of GM-crops and foods should be standardized for building confidence of all stakeholders. Efforts should be exerted in deploying genes of interest, marker genes and regulatory sequences invoking no or little issues of potential risks to the ecosystem.

ISSN: 1610-3653

eISSN: 1610-3661

IDS Number: CO8UG

Unique ID: WOS:000359447000002

*Record 3 of 9. Search terms matched: CRY1AB(1)

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

*Order Full Text []

Title: A 90 Day Safety Assessment of Genetically Modified Rice Expressing Cry1Ab/1Ac Protein Using an Aquatic Animal Model (vol 63, pg 3627, 2015)

Authors: Zhu, HJ; Chen, Y; Li, YH; Wang, JM; Ding, JT; Chen, XP; Peng, YF

Author Full Names: Zhu, Hao-Jun; Chen, Yi; Li, Yun-He; Wang, Jia-Mei; Ding, Jia-Tong; Chen, Xiu-Ping; Peng, Yu-Fa

Source: JOURNAL OF AGRICULTURAL AND FOOD CHEMISTRY, 63 (33):7462-7462; [10.1021/acs.jafc.5b03809](https://doi.org/10.1021/acs.jafc.5b03809) AUG 26 2015

Language: English

ISSN: 0021-8561

eISSN: 1520-5118

IDS Number: CQ0XO

Unique ID: WOS:000360322100018

PubMed ID: 26264730

***Record 4 of 9.** Search terms matched: MAIZE(1); MON810(1)

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

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

Title: A highly sensitive and specific method for the screening detection of genetically modified organisms based on digital PCR without pretreatment

Authors: Fu, W; Zhu, PY; Wang, CG; Huang, KL; Du, ZX; Tian, WY; Wang, Q; Wang, HY; Xu, WT; Zhu, SF

Author Full Names: Fu, Wei; Zhu, Pengyu; Wang, Chenguang; Huang, Kunlun; Du, Zhixin; Tian, Wenyong; Wang, Qin; Wang, Huiyu; Xu, Wentao; Zhu, Shuifang

Source: SCIENTIFIC REPORTS, 5 [10.1038/srep12715](https://doi.org/10.1038/srep12715) AUG 4 2015

Language: English

Abstract: Digital PCR has developed rapidly since it was first reported in the 1990s. It was recently reported that an improved method facilitated the detection of genetically modified organisms (GMOs). However, to use this improved method, the samples must be pretreated, which could introduce inaccuracy into the results. In our study, we explored a pretreatment-free digital PCR detection method for the screening for GMOs. We chose the CaMV35s promoter and the NOS terminator as the templates in our assay. To determine the specificity of our method, 9 events of GMOs were collected, including MON810, MON863, TC1507, MIR604, MIR162, GA21, T25, NK603 and Bt176. Moreover, the sensitivity, intra-laboratory and inter-laboratory reproducibility of our detection method were assessed. The results showed that the limit of detection of our method was 0.1%, which was lower than the labeling threshold level of the EU. The specificity and stability among the 9 events were consistent, respectively. The intra-laboratory and inter-laboratory reproducibility were both good. Finally, the perfect fitness for the detection of eight double-blind samples indicated the good practicability of our method. In conclusion, the method in our study would allow more sensitive, specific and stable screening detection of the GMO content of international trading products.

ISSN: 2045-2322

Article Number: 12715

IDS Number: CO4AW

Unique ID: WOS:000359103400002

PubMed ID: 26239916

***Record 5 of 9.** Search terms matched: BT(2); CRY1AB(3); MAIZE(7); MON810(3)

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

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

Title: Chronic Responses of *Daphnia magna* Under Dietary Exposure to Leaves of a Transgenic (Event MON810) Bt-Maize Hybrid and its Conventional Near-Isoline

Authors: Holderbaum, DF; Cuhra, M; Wickson, F; Orth, AI; Nodari, RO; Bohn, T

Author Full Names: Holderbaum, Daniel Ferreira; Cuhra, Marek; Wickson, Fern; Orth, Afonso Inacio; Nodari, Rubens Onofre; Bohn, Thomas

Source: JOURNAL OF TOXICOLOGY AND ENVIRONMENTAL HEALTH-PART A-CURRENT ISSUES, 78 (15):993-1007; [10.1080/15287394.2015.1037877](https://doi.org/10.1080/15287394.2015.1037877) AUG 3 2015

Language: English

Abstract: Insect resistance is the second most common trait globally in cultivated genetically modified (GM) plants. Resistance is usually obtained by introducing into the plant's genome genes from the bacterium *Bacillus thuringiensis* (Bt) coding for insecticidal proteins (Cry proteins or toxins) that target insect pests. The aim of this study was to examine the hypothesis that a chronic, high-dose dietary exposure to leaves of a Bt-maize hybrid (GM event MON810, expressing a transgenic or recombinant Cry1Ab toxin), exerted no adverse effects on fitness parameters of the aquatic nontarget organism *Daphnia magna* (water flea) when compared to an identical control diet based on leaves of the non-GM near-isoline. Cry1Ab was immunologically detected and quantified in GM maize leaf material used for *Daphnia* feed. A 69-kD protein near Bt's active core-toxin size and a 34-kD protein were identified. The *D. magna* bioassay showed a resource allocation to production of resting eggs and early fecundity in *D. magna* fed GM maize, with adverse effects for body size and fecundity later in life. This is the first study to examine GM-plant leaf material in the *D. magna* model, and provides of negative fitness effects of a MON810 maize hybrid in a nontarget model organism under chronic, high dietary exposure. Based upon these results, it is postulated that the observed transgenic proteins exert a nontarget effect in *D. magna* and/or unintended changes were produced in the maize genome/metabolome by the transformation process, producing a nutritional difference between GM-maize and non-GM near-isoline.

ISSN: 1528-7394

eISSN: 1087-2620

IDS Number: CP0ZT

Unique ID: WOS:000359606300003

***Record 6 of 9.** Search terms matched: CORN(5); CRY1AB(8); LEPIDOPTERA(2); ZEA MAYS(1)

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

*Order Full Text []

Title: Inhibition of *Helicoverpa zea* (Lepidoptera: Noctuidae) Growth by Transgenic Corn Expressing Bt Toxins and Development of Resistance to Cry1Ab

Authors: Reisig, DD; Reay-Jones, FPF

Author Full Names: Reisig, Dominic D.; Reay-Jones, Francis P. F.

Source: ENVIRONMENTAL ENTOMOLOGY, 44 (4):1275-1285; [10.1093/ee/nvv076](https://doi.org/10.1093/ee/nvv076) AUG 2015

Language: English

Abstract: Transgenic corn, *Zea mays* L., that expresses the *Bacillus thuringiensis* (Bt) toxin Cry1Ab is only moderately toxic to *Helicoverpa zea* (Boddie) and has been planted commercially since 1996. Growth and development of *H. zea* was monitored to determine potential changes in susceptibility to this toxin over time. Small plots of corn hybrids expressing Cry1F, Cry1F x Cry1Ab, Cry1Ab x Cry3Bb1, Cry1A.105 x Cry2Ab2 x Cry3Bb1, Cry1A.105 x Cry2Ab2, and Vip3Aa20 x Cry1Ab x mCry3A were planted in both 2012 and 2013 in North and South Carolina

with paired non-Bt hybrids from the same genetic background. *H. zea* larvae were sampled on three time periods from ears and the following factors were measured: kernel area injured (cm²) by *H. zea* larvae, larval number per ear, larval weight, larval length, and larval head width. Pupae were sampled on a single time period and the following factors recorded: number per ear, weight, time to eclosion, and the number that eclosed. There was no reduction in larval weight, number of insect entering the pupal stadium, pupal weight, time to eclosion, and number of pupae able to successfully eclose to adulthood in the hybrid expressing Cry1Ab compared with a non-Bt paired hybrid. As Cry1Ab affected these in 1996, *H. zea* may be developing resistance to Cry1Ab in corn, although these results are not comprehensive, given the limited sampling period, size, and geography. We also found that the negative impacts on larval growth and development were greater in corn hybrids with pyramided traits compared with single traits.

ISSN: 0046-225X

eISSN: 1938-2936

IDS Number: CP1WN

Unique ID: WOS:000359668100038

PubMed ID: 26314074

***Record 7 of 9.** Search terms matched: CRY1AB(1); PROTECTION(2); RESISTANT(1)

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

***Order Full Text []**

Title: Comparative performance of modified full-length and truncated *Bacillus thuringiensis*-cry1Ac genes in transgenic tomato

Authors: Koul, B; Yadav, R; Sanyal, I; Amla, DV

Author Full Names: Koul, Bhupendra; Yadav, Reena; Sanyal, Indraneel; Amla, Devindra Vijay

Source: SPRINGERPLUS, 4 [10.1186/s40064-015-0991-x](https://doi.org/10.1186/s40064-015-0991-x) APR 30 2015

Language: English

Abstract: Background: Bt-cry1Ac gene has been reputedly effective against *Helicoverpa armigera* a notorious lepidopteran pest. Reports on the expression of full-length and truncated cry1Ac genes in plants for effective resistance against *Helicoverpa* sp. have been documented however, their performance is still ambiguous. Moreover, the question remains to be addressed that truncation of 3' end of the native gene was documented and suggested for active insecticidal toxin production while the most successful transgenic event(s) of commercialized-cotton are based on full-length of the cry gene. Therefore, we performed a comparative study on the efficacy of the two versions of cry1Ac genes (full-length: 3,510 bp and truncated: 1,845 bp) in T-0 and T-1 transgenic tomato plants and analyzed the extent of protection against *H. armigera* and also compared the results with our previous findings related to a successful transgenic tomato line Ab25E, expressing cry1Ab gene. The integration of cry1Ac gene(s) in T-0 transgenic plants and its inheritance in T-1 progeny was observed by PCR, RT-PCR and Southern blot hybridization analysis while, the toxin integrity, expression and toxicity was monitored by Western immunoassay, DAS-ELISA and insect bioassay respectively. Results: An average transformation frequency and Bt-Cry protein content of 16.93 +/- 2.10 and 0.0020-0.0128% of total soluble protein (TSP) was obtained with pRD400 vector (Trcry1Ac) while, a much lower value of 9.30 +/- 2.041 and 0.0001. 0.0026% of TSP was observed with pNBRI-1 vector (Flcry1Ac), respectively. The promising Trcry1Ac T-0 transgenic plants and their T-1 progeny gave full

protection from *H. armigera*. Although Flcry1Ac gene showed lower transformation frequency and lower expression, it showed higher toxicity to *H. armigera* when compared with truncated Trcry1Ac gene. Conclusions: The full-length cry1Ac gene can be redesigned for higher expression and performance in dicots or a hybrid gene could be designed having a blend of strong receptor binding and stable expression characteristics for enhanced efficacy and toxicity to the susceptible insects.

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Article Number: 203

IDS Number: CO5MB

Unique ID: WOS:000359202100004

PubMed ID: 25977893

***Record 8 of 9.** Search terms matched: BT(2); CORN(7)

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

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

Title: Effects of Bt cry1Ah corn pollen on immature worker survival and development of *Apis cerana cerana*

Authors: Dai, PL; Zhou, W; Zhang, J; Lang, ZH; Zhou, T; Wang, Q; Cui, HJ; Jiang, WY; Wu, YY

Author Full Names: Dai, Ping-Li; Zhou, Wei; Zhang, Jie; Lang, Zhi-Hong; Zhou, Ting; Wang, Qiang; Cui, Hong-Juan; Jiang, Wei-Yu; Wu, Yan-Yan

Source: JOURNAL OF APICULTURAL RESEARCH, 54 (1):72-76;

[10.1080/00218839.2015.1035075](https://doi.org/10.1080/00218839.2015.1035075) JAN 1 2015

Language: English

Abstract: The honey bee may be exposed to insecticidal proteins from transgenic plants via pollen. An assessment of the impact of such exposures on the honey bee is an essential part of the risk assessment process for transgenic *Bacillus thuringiensis* (Bt) corn. The effects of dietary transgenic Bt corn pollen on honey bee immature workers of *Apis cerana cerana* were examined by feeding trials in colonies. Four- to six-day-old honey bee worker larvae were fed various pollens (cry1Ah corn pollen, regular corn pollen, mixed bee pollen and control) and then sampled to record their survival and development. There were no significant differences in capping rate, emergence rate and immature stage among treatments. Our studies suggest that cry1Ah corn pollen carries no risk for the survival and development of *A. c. cerana* immature workers.

ISSN: 0021-8839

eISSN: 2078-6913

IDS Number: CP1PU

Unique ID: WOS:000359648500010

***Record 9 of 9.** Search terms matched: CRY1AB(1); MAIZE(1); TOLERANCE(3)

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

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

Title: GENETIC TRANSFORMATION AND EXPRESSION DETECTION OF TOBACCO BY

USING A MULTI-GENE PLANT TRANSFORMATION VECTOR

Authors: Ren, Y; Dong, Y; Zhang, J; Qiu, T; Yang, M

Author Full Names: Ren, Y.; Dong, Y.; Zhang, J.; Qiu, T.; Yang, M.

Source: JOURNAL OF ANIMAL AND PLANT SCIENCES, 25 (3):13-21; 1 SI 2015

Language: English

Abstract: Tobacco was transformed by employing the plant transformation vector p209-Cry1Ac-Cry3A-BADH by using Agrobacterium-mediated method to obtain completely regenerated plants screened by kanamycin sulfate. PCR detection indicated out of the nine lines in which NPT II gene was detected, Cry1Ac, Cry3A, and BADH were detected in seven lines; Cry1Ac and Cry3A were detected in one line; and Cry1Ac was detected in one line. Fluorescence quantitative PCR detection indicated in all target gene lines, three target genes were differentially expressed at the transcriptional level in four lines. BADH expression was absent in three lines. ELISA analysis revealed Cry1Ac and Cry3A toxin expression were detected in all target gene lines. The content of Cry3A toxin (up to 13,749.30 ng.g(-1)) was significantly higher than that of Cry1Ac toxin (up to 290.70 ng.g(-1)). The indoor insect-resistance test showed each transgenic line with insectresistant gene inhibited the survival, growth, and development of *Prodenia litura* (Fabricius) larvae to varying degrees. Average corrected mortality of five lines was significantly higher than that of control, reaching up to 70.6%. Two lines were selected for further salt-tolerance research, and results showed transgenic lines had an individual salt tolerance compared with control.

ISSN: 1018-7081

IDS Number: CO9EG

Unique ID: WOS:000359475000003

*Record 1 of 9. Search terms matched: BT(1); LEPIDOPTERA(2); MAIZE(1)

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

*Order Full Text []

Title: Secondary metabolites from Neotropical Annonaceae: Screening, bioguided fractionation, and toxicity to *Spodoptera frugiperda* (JE Smith) (Lepidoptera: Noctuidae)

Authors: Ansante, TF; Ribeiro, LD; Bicalho, KU; Fernandes, JB; da Silva, MFDF; Vieira, PC; Vendramim, JD

Author Full Names: Ansante, Thiago Felipe; Ribeiro, Leandro do Prado; Bicalho, Keylla Utherdyany; Fernandes, Joao Batista; das Gracas Fernandes da Silva, Maria Fatima; Vieira, Paulo Cezar; Vendramim, Jose Djair

Source: INDUSTRIAL CROPS AND PRODUCTS, 74 969-976; [10.1016/j.indcrop.2015.05.058](https://doi.org/10.1016/j.indcrop.2015.05.058)
NOV 15 2015

Language: English

Abstract: Annonaceae species are interesting sources of structurally diverse compounds with insecticidal properties. Therefore, a screening assay was conducted on ethanolic extracts prepared from the leaves, branches, and seeds of different Annonaceae species (*Annona cacans* Warming, *Annona montana* Macfadyen, *Annona mucosa* Jacquin, *Annona reticulata* Linnaeus, *Annona sylvatica* A. St.-Hil., and *Duguetia lanceolata* A. St.-Hil.) to detect promising sources of compounds with action against *Spodoptera frugiperda* (J.E. Smith) (Lepidoptera: Noctuidae). The ethanolic extract from *A. mucosa* seeds (ESAM) was the most active treatment, causing significant acute toxicity (LC50=842.9 mg kg(-1)) and pronounced larval growth inhibition (EC50 = 580.4 mg kg(-1)) after 7 days of exposure to an ESAM-treated diet. Furthermore, ethanolic extracts (at 1000 mg kg(-1)) from seeds of *A. cacans*, *A. montana*, *A. mucosa*, and *A. sylvatica*; leaves and branches of *A. reticulata*; and *D. lanceolata* leaves only caused sublethal effects, reducing the *S. frugiperda* larval weight. Nevertheless, ESAM (at LC90) showed an efficacy similar to that of two commercial insecticides of natural [azadirachtin +3-tigloylazadirachtol (Azamax (R) 1.2 EC)] and synthetic [chlorantraniliprole (Premio (R) 20 SC)] origins, which were tested at the registered concentration for *S. frugiperda* control. Thus, using different chromatographic techniques, bioguided fractionations were conducted and led to the isolation of acetogenin bis-tetrahydrofuran rolliniastatin-1, which was identified as the primary compound from the most active fractions of ESAM. This compound, which caused both strong mortality and pronounced growth inhibition to *S. frugiperda*, may be a useful component for the integrated management of this important pest species. (C) 2015 Elsevier B.V. All rights reserved.

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eISSN: 1872-633X

IDS Number: CQ9QD

Unique ID: WOS:000360948900121

*Record 2 of 9. Search terms matched: BT(2); CORN(2); CRY1AB(1); LEPIDOPTERA(1); MAIZE(7); MON810(3)

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

*Order Full Text []

Title: Flea beetles (Coleoptera: Chrysomelidae, Alticinae) in Bt- (MON810) and near isogenic maize stands: Species composition and activity densities in Hungarian fields

Authors: Szenasi, A; Marko, V

Author Full Names: Szenasi, Agnes; Marko, Viktor

Source: CROP PROTECTION, 77 38-44; [10.1016/j.cropro.2015.07.008](https://doi.org/10.1016/j.cropro.2015.07.008) NOV 2015

Language: English

Abstract: Flea beetles (Chrysomelidae, Alticinae) were collected with Pherocon AM yellow sticky traps in maize plots to compare the assemblages from transgenic Bt- (genetic event MON810, producing Cry1Ab protein effective against lepidopteran pests) and near isogenic maize in Hungary. Altogether, 51,348 flea beetle individuals from 26 species were collected. The dominant species were *Phyllotreta atra* (F.) and *Phyllotreta vittula* (Redtenbacher). Their abundances along with other (non-P. atra and non-P. vittula) flea beetle species showed no significant differences between Bt- and isogenic maize plots. Similarly, no difference was found between Bt maize and isogenic maize plots in the species richness of the flea beetle assemblages. (C) 2015 Elsevier Ltd. All rights reserved.

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eISSN: 1873-6904

IDS Number: CR8CY

Unique ID: WOS:000361579900006

*Record 3 of 9. Search terms matched: BT(7); CRY1AB(4); MAIZE(8); MON810(1)

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

*Order Full Text []

Title: Multilevel assessment of Cry1Ab Bt-maize straw return affecting the earthworm *Eisenia fetida*

Authors: Shu, YH; Zhang, YY; Cheng, MM; Zeng, HL; Wang, JW

Author Full Names: Shu, Yinghua; Zhang, Yanyan; Cheng, Miaomiao; Zeng, Huilan; Wang, Jianwu

Source: CHEMOSPHERE, 137 59-69; [10.1016/j.chemosphere.2015.05.038](https://doi.org/10.1016/j.chemosphere.2015.05.038) OCT 2015

Language: English

Abstract: Non-target effects of two varieties of *Bacillus thuringiensis* (Bt)-maize straw (5422Bt1 [event Bt11] and 5422CBCL [MON810]) return on the *Eisenia fetida* were investigated by using multilevel assessments, compared to near-isogenic non-Bt-maize (5422). 5422Bt1 straw return had no deleterious effects on adult earthworms and had significantly positive effects on juveniles over three generations. Negative, no, and positive effects on adults treated with 5422CBCL straw were observed in the 1st, 2nd and 3rd generation, respectively. Negative and positive effects were observed on juveniles produced from the 1st- and 2nd-generation adults treated with 5422CBCL straw, respectively. Glutathione peroxidase activity of earthworms from Bt-maize treatments was significantly higher than that of control on the 90th d. Translationally controlled tumour protein (TCTP) and superoxide dismutase (SOD) genes were down-regulated, while annetocin (ANN) expression was up-regulated in 5422Bt1 treatments. TCTP and SOD genes were up-regulated, while ANN and heat shock protein 70 were down-regulated in *E. fetida* from 5422CBCL treatments. Enzyme-linked immunosorbent assay revealed that Cry1Ab released from 5422Bt1 and 5422CBCL straw degraded rapidly on the 15th and 30th d and had a slow decline in the rest testing time. Cry1Ab concentrations in the soil, casts and guts of earthworm significantly

decreased over the course of the experiment. This study was the first to evaluate generational effects of Bt-maize straw return on earthworms under laboratory conditions. The responses of enzymes activity and genes expression may contribute to better understand above different effects of Bt-maize straw return on earthworms from the 1st generation. (C) 2015 Elsevier Ltd. All rights reserved.

ISSN: 0045-6535

eISSN: 1879-1298

IDS Number: CQ8OG

Unique ID: WOS:000360867100008

PubMed ID: 26011413

***Record 4 of 9.** Search terms matched: BORER(1); BORERS(1); CRY1AB(2); LEPIDOPTERA(1); SESAMIA(3); TOLERANCE(1)

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Title: Chilo suppressalis and Sesamia inferens display different susceptibility responses to Cry1A insecticidal proteins

Authors: Li, B; Xu, YY; Han, C; Han, LZ; Hou, ML; Peng, YF

Author Full Names: Li, Bo; Xu, Yangyang; Han, Cao; Han, Lanzhi; Hou, Maolin; Peng, Yufa

Source: PEST MANAGEMENT SCIENCE, 71 (10):1433-1440; [10.1002/ps.3948](https://doi.org/10.1002/ps.3948) OCT 2015

Language: English

Abstract: BACKGROUND Chilo suppressalis and Sesamia inferens are important lepidopteran rice pests that occur concurrently in rice-growing areas of China. The development of transgenic rice expressing Cry1A insecticidal proteins has provided a useful strategy for controlling these pests. RESULTSThis study evaluated the baseline susceptibilities of C. suppressalis and S. inferens to Cry1A, as well as their responses to selection with Cry1A. Wide geographic variation in susceptibility was observed across all field populations. Within a given population, the LC50 of both Cry1Ab and Cry1Ac against S. inferens was drastically higher than that of C. suppressalis. Large LC50 differences (74.6-fold) were detected between the two species for Cry1Ab in the Poyang population, while small differences (3.6-fold) were detected for Cry1Ac in the Changsha population. The Cry1Ac LC50 of C. suppressalis and S. inferens increased 8.4- and 4.4-fold after 21 and eight selection generations respectively. Additionally, the estimated realised heritabilities (h^2) of Cry1Ac tolerance were 0.11 in C. suppressalis and 0.292 in S. inferens. CONCLUSIONSS. inferens exhibited a significantly lower susceptibility and more rapidly evolved resistance to Cry1A compared with C. suppressalis. Therefore, S. inferens is more likely to evolve increased resistance, which threatens the sustainability of rice expressing Cry1A protein. (c) 2014 Society of Chemical Industry

ISSN: 1526-498X

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IDS Number: CQ5GY

Unique ID: WOS:000360632600011

PubMed ID: 25469810

*Record 5 of 9. Search terms matched: MAIZE(1); MON810(1); PROTECTIVE(3)

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

*Order Full Text []

Title: Sequence and Temperature Influence on Kinetics of DNA Strand Displacement at Gold Electrode Surfaces

Authors: Biala, K; Sedova, A; Flechsig, GU

Author Full Names: Biala, Katarzyna; Sedova, Ada; Flechsig, Gerd-Uwe

Source: ACS APPLIED MATERIALS & INTERFACES, 7 (36):19948-19959;
[10.1021/acsami.5b04435](https://doi.org/10.1021/acsami.5b04435) SEP 16 2015

Language: English

Abstract: Understanding complex contributions of surface environment to tethered nucleic acid sensing experiments has proven challenging, yet it is important because it is essential for interpretation and calibration of indispensable methods, such as microarrays. We investigate the effects of DNA sequence and solution temperature gradients on the kinetics of strand displacement at heated gold wire electrodes, and at gold disc electrodes in a heated solution. Addition of a terminal double mismatch (toehold) provides a reduction in strand displacement energy barriers sufficient to probe the secondary mechanisms involved in the hybridization process. In four different DNA capture probe sequences (relevant for the identification of genetically modified maize MON810), all but one revealed a high activation energy up to 200 kJ/mol during hybridization, that we attribute to displacement of protective strands by capture probes. Protective strands contain 4 to 5 mismatches to ease their displacement by the surface-confined probes at the gold electrodes. A low activation energy (30 kJ/mol) was observed for the sequence whose protective strand contained a toehold and one central mismatch, its kinetic curves displayed significantly different shapes, and we observed a reduced maximum signal intensity as compared to other sequences. These findings point to potential sequence-related contributions to oligonucleotide diffusion influencing kinetics. Additionally, for all sequences studied with heated wire electrodes, we observed a 23 K lower optimal hybridization temperature in comparison with disc electrodes in heated solution, and greatly reduced voltammetric signals after taking into account electrode surface area. We propose that thermodiffusion due to temperature gradients may influence both hybridization and strand displacement kinetics at heated microelectrodes, an explanation supported by computational fluid dynamics. DNA assays with surface-confined capture probes and temperature gradients should not neglect potential influences of thermodiffusion as well as sequence-related effects. Furthermore, studies attempting to characterize surface-tethered environments should consider thermodiffusion if temperature gradients are involved.

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Unique ID: WOS:000361501700012

PubMed ID: 26302819

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

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

*Order Full Text []

Title: Identification, inheritance, and fitness costs of Cry2Ab2 resistance in a field-derived population of sugarcane borer, *Diatraea saccharalis* (F.) (Lepidoptera: Crambidae)

Authors: Huang, FN; Chen, M; Gowda, A; Clark, TL; McNulty, BC; Yang, F; Niu, Y

Author Full Names: Huang, Fangneng; Chen, Mao; Gowda, Anilkumar; Clark, Thomas L.; McNulty, Brain C.; Yang, Fei; Niu, Ying

Source: JOURNAL OF INVERTEBRATE PATHOLOGY, 130 116-123;
[10.1016/j.jip.2015.07.007](https://doi.org/10.1016/j.jip.2015.07.007) SEP 2015

Language: English

Abstract: The sugarcane borer, *Diatraea saccharalis* (F.), is one of the major target pests of transgenic maize, *Zea mays*, expressing *Bacillus thuringiensis* (Bt) proteins in South America and mid-southern region of the U.S. The MON89034 maize expresses Cry2Ab2 and Cry1 A.105 Bt proteins and it was developed to provide better control of key lepidopteran pests of maize including *D. saccharalis*. The objectives of this study were to select and characterize the resistance of *D. saccharalis* to Cry2Ab2 using a non-commercial Cry2Ab2 single gene Bt maize line. A Cry2Ab2-resistant strain (Cry2Ab2-RR) of *D. saccharalis* was established from 28 two-parent families collected from fields in northeast Louisiana, U.S. The Cry2Ab2-RR showed a high level of resistance to Cry2Ab2 in both diet-incorporated and whole maize plant bioassays. The Cry2Ab2 resistance in *D. saccharalis* was likely inherited as a single or a few tightly linked autosomal genes. The resistance was non-recessive and not associated with fitness costs. The results should provide valuable information in resistance monitoring, assessing resistance risk, and developing effective management strategies for the sustainable use of Bt maize technology for managing maize stalk borers. (C) 2015 Elsevier Inc. All rights reserved.

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IDS Number: CR3UO

Unique ID: WOS:000361258800017

PubMed ID: 26205174

*Record 7 of 9. Search terms matched: CRY1AB(1); CRYIAB(1); LEPIDOPTERA(1)

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

*Order Full Text []

Title: Molecular Screening and Bioactivity of Native *Bacillus thuringiensis* Isolates

Authors: Unalmis, S; Ayvaz, A; Yilmaz, S; Azizoglu, U

Author Full Names: Unalmis, S.; Ayvaz, A.; Yilmaz, S.; Azizoglu, U.

Source: JOURNAL OF AGRICULTURAL SCIENCE AND TECHNOLOGY, 17 (5):1197-1207; SEP-OCT 2015

Language: English

Abstract: *Bacillus thuringiensis* strains were isolated from various soil samples collected from different regions of Kahramanmaraş in Turkey and were characterized by their colony morphology, PCR method with cryIAb/Ac, cryID, cry2 and cyt2 primers, and SDS-PAGE of crystal proteins with 130-140 and 60-70 kDa molecular weights. Plasmid profiles of selected isolates were also analyzed. Among the cry genes studied, cry1Ab/Ac was found to be the most common one (60%) in local isolates. Bioactivity tests were carried out under laboratory

conditions to assess the efficacy of isolates against the third instar larvae of the stored product insects; *Anagasta kuehniella* and *Plodia interpunctella*. Toxicity values of the isolates varied between 20.00-53.33% for *A. kuehniella* and 20.00-55.56% for *P. interpunctella* at 1,000 µg g⁻¹ concentration. Out of 55 isolates, ST13.1 was found to be the most effective against *A. kuehniella*. Also, ST7.2, ST7.3, and ST8.2 isolates yielded remarkable control against *P. interpunctella*. Further research is recommended to investigate the efficacy of these promising Bt isolates against other pest insect species.

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IDS Number: CQ4OR

Unique ID: WOS:000360584900011

***Record 8 of 9.** Search terms matched: BT(2); CORN(7); MAIZE(2); RESISTANT(1); ZEA MAYS(1)

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

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

Title: Impact of the Bt Corn Proteins Cry34/35Ab1 and Cry3Bb1, Alone or Pyramided, on Western Corn Rootworm (Coleoptera: Chrysomelidae) Beetle Emergence in the Field

Authors: Hitchon, AJ; Smith, JL; French, BW; Schaafsma, AW

Author Full Names: Hitchon, A. J.; Smith, J. L.; French, B. W.; Schaafsma, A. W.

Source: JOURNAL OF ECONOMIC ENTOMOLOGY, 108 (4):1986-1993; [10.1093/jee/tov125](#)
AUG 2015

Language: English

Abstract: Western corn rootworm, *Diabrotica virgifera virgifera* LeConte, is a major pest of corn, *Zea mays* L. The effect of the Bt proteins Cry34/35Ab1 and Cry3Bb1, alone or pyramided in corn hybrids on *D. v. virgifera* adult emergence was evaluated in field experiments for 3 yr. Experiments were infested artificially with 2,500 viable *D. v. virgifera* eggs per row meter of corn. The reduction in beetle emergence compared with non-Bt controls, from Cry34/35Ab1, Cry3Bb1, and the pyramided hybrids ranged from 64.3 to 97.4%, 91.1 to 95.2%, and 98.1 to 99.6%, respectively. The sex ratio of emerged beetles was usually female-biased from the Cry3Bb1 and pyramided treatments, but not from Cry34/35Ab1 treatment alone. Emergence from all Bt hybrids was delayed compared with the control, with the delay longest from the pyramided hybrid. In 2013, three egg infestation levels were tested, with density-dependent mortality observed at 1,250 viable eggs per row meter. The effect of Bt proteins on the emergence timing and sex ratio of *D. v. virgifera* may impact the suitability of resistance management plans, specifically the effectiveness of the refuge strategy. Susceptible males emerging from refuge might not be synchronized to mate with potentially resistant females emerging later from Bt corn hybrids.

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IDS Number: CQ5ER

Unique ID: WOS:000360626600061

***Record 9 of 9.** Search terms matched: CRY1AB(1); LEPIDOPTERA(1)

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

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

Title: Cry Proteins from *Bacillus thuringiensis* Active against Diamondback Moth and Fall Armyworm

Authors: Silva, MC; Siqueira, HAA; Silva, LM; Marques, EJ; Barros, R

Author Full Names: Silva, M. C.; Siqueira, H. A. A.; Silva, L. M.; Marques, E. J.; Barros, R.

Source: NEOTROPICAL ENTOMOLOGY, 44 (4):392-401; [10.1007/s13744-015-0302-9](https://doi.org/10.1007/s13744-015-0302-9) AUG 2015

Language: English

Abstract: Biopesticides based on *Bacillus thuringiensis* and genetically modified plants with genes from this bacterium have been used to control *Plutella xylostella* (L.) and *Spodoptera frugiperda* (J.E. Smith). However, the selection pressure imposed by these technologies may undermine the efficiency of this important alternative to synthetic insecticides. Toxins with different modes of action allow a satisfactory control of these insects. The purpose of this study was to characterize the protein and gene contents of 20 *B. thuringiensis* isolates from soil and insect samples collected in several areas of Northeast Brazil which are active against *P. xylostella* and *S. frugiperda*. Protein profiles were obtained by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE). Polymerase chain reaction assays were used to determine toxin genes present within bacterial isolates. The protein profile of the majority of the isolates produced bands of approximately 130 kDa, suggesting the presence of Cry1, Cry8 and Cry9 proteins. The gene content of the isolates of *B. thuringiensis* investigated showed different gene profiles. Isolates LIIT-4306 and LIIT-4311 were the most actives against both species, with LC50 of 0.03 and 0.02x 10⁸ spores mL⁽⁻¹⁾, respectively, for *P. xylostella*, and LC50 of 0.001x 10⁸ spores mL⁽⁻¹⁾ for *S. frugiperda*. These isolates carried the cry1, cry1Aa, cry1Ab, cry1Ac, cry1B, cry1C, cry1D, cry1F, cry2, cry2A, cry8, and cry9C genes. The obtained gene profiles showed great potential for the control of *P. xylostella* and *S. frugiperda*, primarily because of the presence of several cry1A genes, which are found in isolates of *B. thuringiensis* active against these insects.

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Unique ID: WOS:000360926100011

PubMed ID: 26070631

*Record 1 of 15. Search terms matched: BT(1); MAIZE(1); TOLERANCE(1); TOLERANT(1); YIELD(1)

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

*Order Full Text []

Title: Influence of genetically modified organisms on agro-ecosystem processes

Authors: Kolseth, AK; D'Hertefeldt, T; Emmerich, M; Forabosco, F; Marklund, S; Cheeke, TE; Hallin, S; Weih, M

Author Full Names: Kolseth, Anna-Karin; D'Hertefeldt, Tina; Emmerich, Maren; Forabosco, Flavio; Marklund, Stefan; Cheeke, Tanya E.; Hallin, Sara; Weih, Martin

Source: AGRICULTURE ECOSYSTEMS & ENVIRONMENT, 214 96-106;
[10.1016/j.agee.2015.08.021](https://doi.org/10.1016/j.agee.2015.08.021) DEC 27 2015

Language: English

Abstract: Biotechnology offers extensive possibilities to incorporate new traits into organisms. Genetically modified (GM) traits relevant for agro-ecosystems include traits such as pest resistance and herbicide tolerance in crop plants, increased growth rate in fish and livestock, and enhanced nitrogen-fixation capabilities of soil microbes. In this review, we evaluated the direct and indirect trait-specific effects of GM plants, microbes, and animals on ecosystem processes and found that most of the effects of genetically modified organisms (GMOs) on ecosystem processes are indirect and are the result of associated changes in management strategy rather than a direct effect of the GMOs. Conflicting results on the performance and effects of GMOs are frequently reported, especially regarding crop yield and impacts on soil organisms. This is partly because methods with different levels of resolution have been used in different ecological contexts. Overall, there is little evidence that the effects of GM traits on ecosystem processes act with different mechanisms from those of traits modified using conventional methods. However, little is known about trait-specific effects of GMOs on ecosystem processes even though GMOs have been used for more than three decades. In particular, studies linking genetically modified traits to ecosystem processes at longer time scales are rare, but needed for evaluating trait effects, especially in an evolutionary context. In addition, biotechnology may provide a unique tool for gaining insights into the links between traits and ecosystem processes when integrated into basic ecological research. (C) 2015 Elsevier B.V. All rights reserved.

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IDS Number: CT2CA

Unique ID: WOS:000362608400010

*Record 2 of 15. Search terms matched: CORN(2); CRY1AB(4); TOLERANT(1); ZEA-MAYS(1)

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

*Order Full Text []

Title: Effects of a diet containing genetically modified rice expressing the **Cry1Ab/1Ac** protein (*Bacillus thuringiensis* toxin) on broiler chickens

Authors: Li, ZY; Gao, Y; Zhang, MH; Feng, JH; Xiong, YD

Author Full Names: Li, Zeyang; Gao, Yang; Zhang, Minhong; Feng, Jinghai; Xiong, Yandan

Source: ARCHIVES OF ANIMAL NUTRITION, 69 (6):487-498;
[10.1080/1745039X.2015.1087749](https://doi.org/10.1080/1745039X.2015.1087749) NOV 2 2015

Language: English

Abstract: The aim of this study was to evaluate the effect of feeding *Bacillus thuringiensis* (Bt) rice expressing the Cry1Ab/1Ac protein on broiler chicken. The genetically modified (GM) Bt rice was compared with the corresponding non-GM rice regarding performance of feeding groups, their health status, relative organ weights, biochemical serum parameters and occurrence of Cry1Ab/1Ac gene fragments. One hundred and eighty day-old Arbor Acres female broilers with the same health condition were randomly allocated to the two treatments (6 replicate cages with 15 broilers in each cage per treatment). They received diets containing GM rice (GM group) or its parental non-GM rice (non-GM group) at 52-57% of the air-dried diet for 42 days. The results show that the transgenic rice had a similar nutrient composition as the non-GM rice and had no adverse effects on chicken growth, biochemical serum parameters and necropsy during the 42-day feeding period. In birds fed the GM rice, no transgenic gene fragments were detected in the samples of blood, liver, kidneys, spleen, jejunum, ileum, duodenum and muscle tissue. In conclusion, the results suggest that Bt rice expressing Cry1Ab/1Ac protein has no adverse effects on broiler chicken. Therefore, it can be considered as safe and used as feed source for broiler chicken.

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IDS Number: CU1WW

Unique ID: WOS:000363314000005

PubMed ID: 26414482

***Record 3 of 15.** Search terms matched: CRY1AB(4)

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

*Order Full Text []

Title: Nanobody-based electrochemical immunoassay for *Bacillus thuringiensis* **Cry1Ab** toxin by detecting the enzymatic formation of polyaniline

Authors: Zhu, M; Li, M; Li, GH; Zhou, ZK; Liu, H; Lei, HT; Shen, YF; Wan, YK

Author Full Names: Zhu, Min; Li, Min; Li, Guanghui; Zhou, Zikai; Liu, Hong; Lei, Hongtao; Shen, Yanfei; Wan, Yakun

Source: MICROCHIMICA ACTA, 182 (15-16):2451-2459; [10.1007/s00604-015-1602-9](https://doi.org/10.1007/s00604-015-1602-9) NOV 2015

Language: English

Abstract: We describe an electrochemical immunoassay for the Cry1Ab toxin that is produced by *Bacillus thuringiensis*. It is making use of a nanobody (a heavy-chain only antibody) that was selected from an immune phage displayed library. A biotinylated primary nanobody and a HRP-conjugated secondary nanobody were applied in a sandwich immunoassay where horseradish peroxidase (HRP) is used to produce polyaniline (PANI) from aniline. PANI can be easily detected by differential pulse voltammetry at a working voltage as low as 40 mV (vs. Ag/AgCl) which makes the assay fairly selective. This immunoassay for Cry1Ab has an analytical range from 0.1 to 1000 ng (TM) mL⁻¹ and a 0.07 ng (TM) mL⁻¹ lower limit of detection. The

average recoveries of the toxin from spiked samples are in the range from 102 to 114 %, with a relative standard deviation of < 7.5 %. The results demonstrated that the assay represented an attractive alternative to existing immunoassays in enabling affordable, sensitive, robust and specific determination of this toxin.

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IDS Number: CT8BB

Unique ID: WOS:000363038800011

***Record 4 of 15.** Search terms matched: BT(2); CORN(2); CRY1AB(1); LEPIDOPTERA(1); MAIZE(7); MON810(3)

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

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

Title: Flea beetles (Coleoptera: Chrysomelidae, Alticinae) in Bt- (**MON810**) and near isogenic maize stands: Species composition and activity densities in Hungarian fields

Authors: Szenasi, A; Marko, V

Author Full Names: Szenasi, Agnes; Marko, Viktor

Source: CROP PROTECTION, 77 38-44; [10.1016/j.cropro.2015.07.008](https://doi.org/10.1016/j.cropro.2015.07.008) NOV 2015

Language: English

Abstract: Flea beetles (Chrysomelidae, Alticinae) were collected with Pherocon AM yellow sticky traps in maize plots to compare the assemblages from transgenic Bt- (genetic event MON810, producing Cry1Ab protein effective against lepidopteran pests) and near isogenic maize in Hungary. Altogether, 51,348 flea beetle individuals from 26 species were collected. The dominant species were *Phyllotreta atra* (F.) and *Phyllotreta vittula* (Redtenbacher). Their abundances along with other (non-*P. atra* and non-*P. vittula*) flea beetle species showed no significant differences between Bt- and isogenic maize plots. Similarly, no difference was found between Bt maize and isogenic maize plots in the species richness of the flea beetle assemblages. (C) 2015 Elsevier Ltd. All rights reserved.

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IDS Number: CR8CY

Unique ID: WOS:000361579900006

***Record 5 of 15.** Search terms matched: BORER(2); BT(1); CORN(2); CRY1AB(3); LEPIDOPTERA(1); MAIZE(1); OSTRINIA(2); RESISTANT(2)

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

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

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

Authors: Xu, LN; Ling, YH; Wang, YQ; Wang, ZY; Hu, BJ; Zhou, ZY; Hu, F; He, KL

Author Full Names: Xu, Li-Na; Ling, Ying-Hui; Wang, Yue-Qin; Wang, Zhen-Ying; Hu, Ben-Jin; Zhou, Zi-Yan; Hu, Fei; He, Kang-Lai

Source: SCIENTIFIC REPORTS, 5 [10.1038/srep15461](https://doi.org/10.1038/srep15461) OCT 21 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.

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Article Number: 15461

IDS Number: CT9FO

Unique ID: WOS:000363122400002

PubMed ID: 26486179

*Record 6 of 15. Search terms matched: BT(4); CORN(1); CRY1AB(2); LEPIDOPTERA(1); MAIZE(8)

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

*Order Full Text []

Title: Cross-Resistance between Cry1 Proteins in Fall Armyworm (*Spodoptera frugiperda*) May Affect the Durability of Current Pyramided **Bt Maize** Hybrids in Brazil

Authors: Bernardi, D; Salmeron, E; Horikoshi, RJ; Bernardi, O; Dourado, PM; Carvalho, RA; Martinelli, S; Head, GP; Omoto, C

Author Full Names: Bernardi, Daniel; Salmeron, Eloisa; Horikoshi, Renato Jun; Bernardi, Oderlei; Dourado, Patrick Marques; Carvalho, Renato Assis; Martinelli, Samuel; Head, Graham P.; Omoto, Celso

Source: PLOS ONE, 10 (10):[10.1371/journal.pone.0140130](https://doi.org/10.1371/journal.pone.0140130) OCT 16 2015

Language: English

Abstract: Genetically modified plants expressing insecticidal proteins from *Bacillus thuringiensis* (Bt) offer valuable options for managing insect pests with considerable environmental and economic benefits. Despite the benefits provided by Bt crops, the continuous expression of these insecticidal proteins imposes strong selection for resistance in target pest populations. Bt maize (*Zeamays*) hybrids have been successful in controlling fall armyworm (*Spodoptera frugiperda*), the main maize pest in Brazil since 2008; however, field-evolved resistance to the protein Cry1F has recently been reported. Therefore it is important to

assess the possibility of cross-resistance between Cry1F and other Cry proteins expressed in Bt maize hybrids. In this study, an F-2 screen followed by subsequent selection on MON 89034 maize was used to select an *S. frugiperda* strain (RR) able to survive on the Bt maize event MON 89034, which expresses the Cry1A.105 and Cry2Ab2 proteins. Field-collected insects from maize expressing the Cry1F protein (event TC1507) represented most of the positive (resistance allele-containing) (iso)families found. The RR strain showed high levels of resistance to Cry1F, which apparently also conferred high levels of cross resistance to Cry1A.105 and Cry1Ab, but had only low-level (10-fold) resistance to Cry2Ab2. Life history studies to investigate fitness costs associated with the resistance in RR strain revealed only small reductions in reproductive rate when compared to susceptible and heterozygous strains, but the RR strain produced 32.2% and 28.4% fewer females from each female relative to the SS and RS (pooled) strains, respectively. Consistent with the lack of significant resistance to Cry2Ab2, MON 89034 maize in combination with appropriate management practices continues to provide effective control of *S. frugiperda* in Brazil. Nevertheless, the occurrence of Cry1F resistance in *S. frugiperda* across Brazil, and the cross-resistance to Cry1Ab and Cry1A.105, indicates that current Cry1-based maize hybrids face a challenge in managing *S. frugiperda* in Brazil and highlights the importance of effective insect resistance management for these technologies.

ISSN: 1932-6203

Article Number: e0140130

IDS Number: CU0DF

Unique ID: WOS:000363185500028

PubMed ID: 26473961

*Record 7 of 15. Search terms matched: BORER(1); CORN(1); CRY1AB(1); LEPIDOPTERA(2)

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

*Order Full Text []

Title: Bt rice does not disrupt the host-searching behavior of the parasitoid *Cotesia chilonis*

Authors: Liu, QS; Romeis, J; Yu, HL; Zhang, YJ; Li, YH; Peng, YF

Author Full Names: Liu, Qingsong; Romeis, Joerg; Yu, Huilin; Zhang, Yongjun; Li, Yunhe; Peng, Yufa

Source: SCIENTIFIC REPORTS, 5 [10.1038/srep15295](https://doi.org/10.1038/srep15295) OCT 15 2015

Language: English

Abstract: We determined whether plant volatiles help explain why *Cotesia chilonis* (a parasitoid of the target pest *Chilo suppressalis*) is less abundant in Bt than in non-Bt rice fields. Olfactometer studies revealed that *C. chilonis* females responded similarly to undamaged Bt and non-Bt rice plants. Parasitoids preferred rice plants damaged by 3rd-instar larvae of *C. suppressalis*, but did not differentiate between caterpillar-infested Bt and non-Bt plants. According to GC-MS analyses of rice plant volatiles, undamaged Bt and non-Bt rice plants emitted the same number of volatile compounds and there were no significant differences in the quantity of each volatile compound between the treatments. When plants were infested with and damaged by *C. suppressalis* larvae, both Bt and non-Bt rice plants emitted higher numbers and larger amounts of volatile compounds than undamaged plants, but there were no significant differences between Bt and non-Bt plants. These results demonstrate that the volatile-mediated

interactions of rice plants with the parasitoid *C. chilonis* were not disrupted by the genetic engineering of the plants. We infer that parasitoid numbers are lower in Bt than in non-Bt fields because damage and volatile induction by *C. suppressalis* larvae are greatly reduced in Bt fields.

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Article Number: 15295

IDS Number: CT4UX

Unique ID: WOS:000362803900002

PubMed ID: 26470012

***Record 8 of 15.** Search terms matched: BORER(2); CORN(1); CRY1AB(2); OSTRINIA(1); RESISTANT(3)

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

*Order Full Text []

Title: Dual mode of action of Bt proteins: protoxin efficacy against **resistant** insects

Authors: Tabashnik, BE; Zhang, M; Fabrick, JA; Wu, YD; Gao, MJ; Huang, FN; Wei, JZ; Zhang, J; Yelich, A; Unnithan, GC; Bravo, A; Soberon, M; Carriere, Y; Li, XC

Author Full Names: Tabashnik, Bruce E.; Zhang, Min; Fabrick, Jeffrey A.; Wu, Yidong; Gao, Meijing; Huang, Fangneng; Wei, Jizhen; Zhang, Jie; Yelich, Alexander; Unnithan, Gopalan C.; Bravo, Alejandra; Soberon, Mario; Carriere, Yves; Li, Xianchun

Source: SCIENTIFIC REPORTS, 5 [10.1038/srep15107](https://doi.org/10.1038/srep15107) OCT 12 2015

Language: English

Abstract: Transgenic crops that produce *Bacillus thuringiensis* (Bt) proteins for pest control are grown extensively, but insect adaptation can reduce their effectiveness. Established mode of action models assert that Bt proteins Cry1Ab and Cry1Ac are produced as inactive protoxins that require conversion to a smaller activated form to exert toxicity. However, contrary to this widely accepted paradigm, we report evidence from seven resistant strains of three major crop pests showing that Cry1Ab and Cry1Ac protoxins were generally more potent than the corresponding activated toxins. Moreover, resistance was higher to activated toxins than protoxins in eight of nine cases evaluated in this study. These data and previously reported results support a new model in which protoxins and activated toxins kill insects via different pathways. Recognizing that protoxins can be more potent than activated toxins against resistant insects may help to enhance and sustain the efficacy of transgenic Bt crops.

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Article Number: 15107

IDS Number: CT1MC

Unique ID: WOS:000362561500001

PubMed ID: 26455902

***Record 9 of 15.** Search terms matched: BT(3); CORN(12); MAIZE(2)

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

*Order Full Text []

Title: Inheritance and Fitness Costs of Resistance to Cry3Bb1 **Corn** by Western **Corn** Rootworm

(Coleoptera: Chrysomelidae)

Authors: Ingber, DA; Gassmann, AJ

Author Full Names: Ingber, David A.; Gassmann, Aaron J.

Source: JOURNAL OF ECONOMIC ENTOMOLOGY, 108 (5):2421-2432; [10.1093/jee/tov199](https://doi.org/10.1093/jee/tov199) OCT 2015

Language: English

Abstract: Transgenic crops that produce insecticidal toxins derived from the bacterium *Bacillus thuringiensis* (Bt) are widely planted to manage pest insects. One of the primary pests targeted by Bt corn in the United States is western corn rootworm, *Diabrotica virgifera virgifera* LeConte (Coleoptera: Chrysomelidae). Cry3Bb1 corn for management of western corn rootworm was commercialized in 2003, and beginning in 2009, populations of western corn rootworm with field-evolved resistance to Cry3Bb1 corn were found in Iowa. Here we quantify the magnitude, inheritance, and fitness costs of resistance to Cry3Bb1 corn in two strains (Hopkinton and Cresco) derived from field populations that evolved resistance to Cry3Bb1 corn. For Hopkinton, we found evidence for complete resistance to Cry3Bb1 corn and nonrecessive inheritance. Additionally, no fitness costs of Cry3Bb1 resistance were detected for Hopkinton. For Cresco, resistance was incomplete and recessive, and we detected fitness costs affecting developmental rate, survival to adulthood, and fecundity. These results suggest that variation may exist among field populations in both the inheritance and accompanying fitness costs of resistance. To the extent that field populations exhibit nonrecessive inheritance and a lack of fitness cost, this will favor more rapid evolution of resistance than would be expected when resistance is functionally recessive and is accompanied by fitness costs.

ISSN: 0022-0493

eISSN: 1938-291X

IDS Number: CT5DQ

Unique ID: WOS:000362828300030

PubMed ID: 26453731

*Record 10 of 15. Search terms matched: CRY1AB(4); MAIZE(1); RESISTANT(1)

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

*Order Full Text []

Title: Degradation and detection of transgenic *Bacillus thuringiensis* DNA and proteins in flour of three genetically modified rice events submitted to a set of thermal processes

Authors: Wang, XF; Chen, XY; Xu, JF; Dai, C; Shen, WB

Author Full Names: Wang, Xiaofu; Chen, Xiaoyun; Xu, Junfeng; Dai, Chen; Shen, Wenbiao

Source: FOOD AND CHEMICAL TOXICOLOGY, 84 89-98; [10.1016/j.fct.2015.08.010](https://doi.org/10.1016/j.fct.2015.08.010) OCT 2015

Language: English

Abstract: This study aimed to investigate the degradation of three transgenic *Bacillus thuringiensis* (Bt) genes (Cry1Ab, Cry1Ac, and Cry1Ab/Ac) and the corresponding encoded Bt proteins in KMD1, KF6, and TT51-1 rice powder, respectively, following autoclaving, cooking, baking, or microwaving. Exogenous Bt genes were more stable than the endogenous sucrose phosphate synthase (SPS) gene, and short DNA fragments were detected more frequently than

long DNA fragments in both the Bt and SPS genes. Autoclaving, cooking (boiling in water, 30 min), and baking (200 degrees C, 30 min) induced the most severe Bt protein degradation effects, and Cry1Ab protein was more stable than Cry1Ac and Cry1Ab/Ac protein, which was further confirmed by baking samples at 180 degrees C for different periods of time. Microwaving induced mild degradation of the Bt and SPS genes, and Bt proteins, whereas baking (180 degrees C, 15 min), cooking and autoclaving led to further degradation, and baking (200 degrees C, 30 min) induced the most severe degradation. The findings of the study indicated that degradation of the Bt genes and proteins somewhat correlated with the treatment intensity. Polymerase chain reaction, enzyme-linked immunosorbent assay, and lateral flow tests were used to detect the corresponding transgenic components. Strategies for detecting transgenic ingredients in highly processed foods are discussed. (C) 2015 Elsevier Ltd. All rights reserved.

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IDS Number: CT5OR

Unique ID: WOS:000362860200011

PubMed ID: 26277627

***Record 11 of 15.** Search terms matched: BORER(1); BORERS(2); CRY1AB(5); LEPIDOPTERA(1)

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

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

Title: Development of photoperiod- and thermo-sensitive male sterility rice expressing transgene *Bacillus thuringiensis*

Authors: Liu, X; Zhang, JW; Zhang, CC; Wang, LC; Chen, H; Zhu, ZR; Tu, JM

Author Full Names: Liu, Xin; Zhang, Jiwen; Zhang, Cuicui; Wang, Liangchao; Chen, Hao; Zhu, Zengrong; Tu, Jumin

Source: BREEDING SCIENCE, 65 (4):333-339; [10.1270/jsbbs.65.333](https://doi.org/10.1270/jsbbs.65.333) SEP 2015

Language: English

Abstract: Stem borers and leaffolders are the main pests that cause severe damage in rice (*Oryza saliva* L.) production worldwide. We developed the first photoperiod- and thermo-sensitive male sterility (PTSMS) rice 208S with the cry1Ab/1Ac *Bacillus thuringiensis* (Bt) gene, through sexual crossing with Huahui 1 (elite line with the cry1Ab/1Ac gene). The novel 208S and its hybrids presented high and stable resistance to stem borers and leaffolders, and the content of Cry1Ab/1Ac protein in chlorophyllous tissues achieved the identical level as donor and showed little accumulation in non-chlorophyllous tissue. No dominant dosage effect in the Bt gene was observed in 208S and its derived hybrids. An analysis of fertility transition traits indicated that 208S was completely sterile under long day length/high temperature, but partially fertile under short day length/low temperature. With fine grain quality and favorable combining ability, 208S had no observed negative effects on fertility and agronomic traits from Bt (cry1Ab/1Ac). Additionally, 208S as a male sterile line showed no fertility decrease caused by Bt transgenic process, as it is the case in Huahui 1. Thus, 208S has great application value in two-line hybrid production for insect resistance, and can also be used as a bridge material in rice Bt transgenic breeding.

ISSN: 1344-7610

eISSN: 1347-3735

IDS Number: CU3PP

Unique ID: WOS:000363437600006

PubMed ID: 26366116

***Record 12 of 15.** Search terms matched: CORN(8); CRY1AB(1); LEPIDOPTERA(2); MAIZE(1); RESISTANT(1); ZEA MAYS(1)

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

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

Title: Genetically modified **maize resistant to corn** earworm (**Lepidoptera: Noctuidae**) in Sinaloa, Mexico

Authors: Aguirre, LA; Hernandez, A; Flores, M; Frias, GA; Cerna, E; Landeros, J; Harris, MK

Author Full Names: Aguirre, Luis A.; Hernandez, Agustin; Flores, Mariano; Frias, Gustavo A.; Cerna, Ernesto; Landeros, Jeronimo; Harris, Marvin K.

Source: FLORIDA ENTOMOLOGIST, 98 (3):SEP 2015

Language: English

Abstract: *Helicoverpa zea* (Boddie) (Lepidoptera: Noctuidae), the corn earworm, is a key pest causing damage to corn *Zea mays* L. (Poales: Poaceae). The development of hybrids expressing Cry1Ab, Vip3Aa20, and mCry3A protein of *Bacillus thuringiensis* Berliner (Bt) (Bacillales: Bacillaceae) is an option to control this insect. Corn hybrids Agrisure (TM) 3000 GT, Agrisure (R) Viptera (TM) 3110, and Agrisure (R) Viptera (TM) 3111 were tested for corn earworm suppression in the agricultural region of Sinaloa during the 2011, 2012, and 2013 autumn-winter growing seasons, and compared with their respective isolines. Gallery length on the ear and the number of damaged ears were evaluated. The genetically modified hybrids demonstrated the effectiveness of inserted proteins to confer resistance to the corn earworm by killing the pest or reducing its growth and damage to the ear. Based on the results, Agrisure (TM) 3000 GT, Agrisure (R) Viptera (TM) 3110, and Agrisure (R) Viptera (TM) 3111 are useful elements for an integrated pest management program on corn in Sinaloa, Mexico.

ISSN: 0015-4040

eISSN: 1938-5102

IDS Number: CS2QC

Unique ID: WOS:000361915000001

***Record 13 of 15.** Search terms matched: BORER(1); CRY1AB(3)

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

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

Title: **Cry1Ab** rice does not impact biological characters and functional response of *Cyrtorhinus lividipennis* preying on *Nilaparvata lugens* eggs

Authors: Chen, Y; Lai, FX; Sun, YQ; Hong, LY; Tian, JC; Zhang, ZT; Fu, Q

Author Full Names: Chen Yang; Lai Feng-xiang; Sun Yan-qun; Hong Li-ying; Tian Jun-ce; Zhang Zhi-tao; Fu Qiang

Source: JOURNAL OF INTEGRATIVE AGRICULTURE, 14 (10):2011-2018; [10.1016/S2095-3119\(14\)60978-3](https://doi.org/10.1016/S2095-3119(14)60978-3) 2015

Language: English

Abstract: One concern about the use of transgenic plants is their potential risk to natural enemies. In this study, using the eggs of the rice brown planthopper, *Nilaparvata lugens*, as a food source, we investigated the effects of Cry1Ab rice on the biological characteristics and functional response of an important predator *Cyrtorhinus lividipennis*. The results showed that the survival ability (adult emergence rate and egg hatching rate), development (egg duration, nymphal developmental duration), adult fresh weight, adult longevity and fecundity of *C. lividipennis* on Bt rice plants were not significantly different compared to those on non-Bt rice plants. Furthermore, two important parameters of functional response (instantaneous search rate and handling time) were not significantly affected by Bt rice. In conclusion, the tested Cry1Ab rice does not adversely impact the biological character and functional response of *C. lividipennis*.

ISSN: 2095-3119

IDS Number: CT70P

Unique ID: WOS:000363004700010

***Record 14 of 15.** Search terms matched: CRY1AB(1); RESISTANT(4)

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

*Order Full Text []

Title: Impacts of transgenic poplar-cotton agro-ecosystems upon target pests and non-target insects under field conditions

Authors: Zhang, DJ; Liu, JX; Lu, ZY; Li, CL; Comada, E; Yang, MS

Author Full Names: Zhang, D. J.; Liu, J. X.; Lu, Z. Y.; Li, C. L.; Comada, E.; Yang, M. S.

Source: GENETICS AND MOLECULAR RESEARCH, 14 (3):8125-8136;
[10.4238/2015.July.27.1](https://doi.org/10.4238/2015.July.27.1) 2015

Language: English

Abstract: Poplar-cotton agro-ecosystems are the main agricultural planting modes of cotton fields in China. With increasing acres devoted to transgenic insect-resistant poplar and transgenic insect-resistant cotton, studies examining the effects of transgenic plants on target and non-target insects become increasingly important. We systematically surveyed populations of both target pests and non-target insects for 4 different combinations of poplar-cotton eco-systems over 3 years. Transgenic Bt cotton strongly resisted the target insects Fall webworm moth [*Hyphantria cunea* (Drury)], *Sylepta derogata* Fabricius, and American bollworm (*Heliothis armigera*), but no clear impact on nontarget insect cotton aphids (*Aphis gossypii*). Importantly, intercrops containing transgenic Pb29 poplar significantly increased the inhibitory effects of Bt cotton on Fall webworm moth in ecosystem IV. Highly resistant Pb29 poplar reduced populations of the target pests *Grnsonoma minutara* Hubner and non-target insect poplar leaf aphid (*Chaitophorus po-pulialbae*), while Fall webworm moth populations were unaffected. We determined the effects of Bt toxin from transgenic poplar and cotton on target and non-target pests in different ecosystems of cotton-poplar intercrops and identified the synergistic effects of such combinations toward both target and non-target insects.

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IDS Number: CS9OR

Unique ID: WOS:000362421100092

PubMed ID: 26345739

***Record 15 of 15.** Search terms matched: MAIZE(1); MON810(1); PROTECTION(1)

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

*Order Full Text []

Title: Highly specific detection of genetic modification events using an enzyme-linked probe hybridization chip

Authors: Zhang, MZ; Zhang, XF; Chen, XM; Chen, X; Wu, S; Xu, LL

Author Full Names: Zhang, M. Z.; Zhang, X. F.; Chen, X. M.; Chen, X.; Wu, S.; Xu, L. L.

Source: GENETICS AND MOLECULAR RESEARCH, 14 (3):9298-9305;
[10.4238/2015.August.10.10](#) 2015

Language: English

Abstract: The enzyme-linked probe hybridization chip utilizes a method based on ligase-hybridizing probe chip technology, with the principle of using thio-primers for protection against enzyme digestion, and using lambda DNA exonuclease to cut multiple PCR products obtained from the sample being tested into single-strand chains for hybridization. The 5'-end amino-labeled probe was fixed onto the aldehyde chip, and hybridized with the single-stranded PCR product, followed by addition of a fluorescent-modified probe that was then enzymatically linked with the adjacent, substrate-bound probe in order to achieve highly specific, parallel, and high-throughput detection. Specificity and sensitivity testing demonstrated that enzyme-linked probe hybridization technology could be applied to the specific detection of eight genetic modification events at the same time, with a sensitivity reaching 0.1% and the achievement of accurate, efficient, and stable results.

ISSN: 1676-5680

IDS Number: CS9OV

Unique ID: WOS:000362421500074

PubMed ID: 26345863

***Record 1 of 5.** Search terms matched: BORER(1); BT(7); CORN(3); LEPIDOPTERA(1); MAIZE(9); PROTECTION(1)

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

*Order Full Text []

Title: Risk assessment of the cultivation of a stacked **Bt-maize** variety (MON89034 x MON88017) for nematode communities

Authors: Hoss, S; Reiff, N; Ottermanns, R; Pagel-Wieder, S; Dohrmann, AB; Tebbe, CC; Traunspurger, W

Author Full Names: Hoess, Sebastian; Reiff, Nicola; Ottermanns, Richard; Pagel-Wieder, Sibylle; Dohrmann, Anja B.; Tebbe, Christoph C.; Traunspurger, Walter

Source: SOIL BIOLOGY & BIOCHEMISTRY, 91 109-118; [10.1016/j.soilbio.2015.08.022](https://doi.org/10.1016/j.soilbio.2015.08.022) DEC 2015

Language: English

Abstract: Genetically modified Bt-maize MON89034 x MON88017 contains three different genes derived from *Bacillus thuringiensis* (Bt) which enable protection against insect pests, due to expression of three different insecticidal crystal proteins (Cry proteins), i.e., Cry1A.105 and Cry2Ab2 against the European corn borer and Cry3Bb1 against the Western corn root worm. Nematodes are important organisms in agricultural soil ecosystems, and on fields with Bt-maize cultivation they will be exposed to Cry proteins released into the soil from roots or plant residues. The objective of this study was to analyze in a field experiment the effect of Bt-maize MON89034 x MON88017 on nematodes as non-target organisms. Nematode communities from soil planted with the Bt-maize were compared to those from soil planted with the near-isogenic cultivar (with and without chemical insecticide treatment) and two conventional maize cultivars. The experimental field consisted of 40 plots in a completely randomized block design (eight plots for each treatment), which were monitored over two growing seasons (2008 and 2009) at six sampling dates for nematode diversity at the genus level in the rhizosphere soil. Physicochemical soil properties and Cry protein concentrations were also analyzed. Nematodes showed very high abundances, as well as a high diversity of taxa and functional guilds, indicating the relevance of maize fields as their habitat. Neither Bt-maize cultivation, nor insecticide treatment adversely affected abundance or, community structure of nematode assemblages in field plots compared to several non-Bt cultivars including a near-isogenic cultivar. This confirmed the risk estimations based on the analyzed soil concentrations of extractable Cry protein, not exceeding 4.8 ng g(-1) soil dry weight and thus revealing a safe toxicity-exposure ratio of >20. (C) 2015 Elsevier Ltd. All rights reserved.

ISSN: 0038-0717

IDS Number: CV8CA

Unique ID: WOS:000364502900013

***Record 2 of 5.** Search terms matched: BORER(1); BT(5); CORN(3); CRY1AB(3); LEPIDOPTERA(1); MAIZE(6); MON810(3); RESISTANT(3)

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

*Order Full Text []

Title: Inheritance, fitness costs, incomplete resistance and feeding preferences in a laboratory-selected **MON810-resistant** strain of the true armyworm *Mythimna unipuncta*

Authors: Garcia, M; Ortego, F; Hernandez-Crespo, P; Farinos, GP; Castanera, P

Author Full Names: Garcia, Matias; Ortego, Felix; Hernandez-Crespo, Pedro; Farinos, Gema P.; Castanera, Pedro

Source: PEST MANAGEMENT SCIENCE, 71 (12):1631-1639; [10.1002/ps.3971](https://doi.org/10.1002/ps.3971) DEC 2015

Language: English

Abstract: BACKGROUNDThe low efficacy of MON810 maize against *Mythimna unipuncta* represents a scenario of non-compliance with the high-dose' strategy, raising concerns about potential resistance development and outbreaks of this secondary pest. The present study offers insight into the different components related to resistance in a laboratory-selected MON810-resistant (MR) strain of *M. unipuncta*. RESULTSThe resistance in the MR strain is autosomal and inherited as a partially dominant trait. We have found a lack of fitness costs in this strain for essential life history traits, reproductive potential and most of the population growth parameters analysed, the only exception being an increment in the mean generation time. Larvae of the MR strain reared on *Bacillus thuringiensis* (Bt) maize took longer to develop, presented a high adult cumulative emergence time and had lower growth rate than those reared on non-Bt maize, suggesting the existence of incomplete resistance. Feeding preference assays reveal a low discrimination between Bt and conventional maize. CONCLUSIONBoth resistant and heterozygous larvae of *M. unipuncta* survive the Cry1Ab toxin expressed on Bt maize, with a weak fitness cost for the homozygous larvae, indicating the potential risk of field-evolved resistance and its relevance to resistance monitoring. (c) 2015 Society of Chemical Industry

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IDS Number: CU7BH

Unique ID: WOS:000363689400008

PubMed ID: 25565147

*Record 3 of 5. Search terms matched: CRY1AB(1); RESISTANT(1)

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

*Order Full Text []

Title: Bt crops benefit natural enemies to control non-target pests

Authors: Tian, JC; Yao, J; Long, LP; Romeis, J; Shelton, AM

Author Full Names: Tian, Jun-Ce; Yao, Ju; Long, Li-Ping; Romeis, Joerg; Shelton, Anthony M.

Source: Scientific Reports, 5 [10.1038/srep16636](https://doi.org/10.1038/srep16636) NOV 12 2015

Language: English

Abstract: Crops producing insecticidal crystal (Cry) proteins from *Bacillus thuringiensis* (Bt) control important lepidopteran pests. However, pests such as aphids not susceptible to Cry proteins may require other integrated pest management (IPM) tactics, including biological control. We fed aphids on Bt and non-Bt plants and analyzed the Bt protein residue in aphids and compared the effects of Bt plants and a pyrethroid, lambda-cyhalothrin, on the performance of three natural enemies (predators: *Coleomegilla maculata* and *Eupeodes americanus*; parasitoid *Aphidius colemani*) of the green peach aphid, *Myzus persicae*. No Bt protein residues in aphids were detected and no significant differences were recorded in the performance of pyrethroid-resistant aphids that fed on Bt broccoli expressing Cry1Ab or Cry1C, or on non-Bt broccoli

plants treated or not treated with the pyrethroid. This indicated the aphids were not affected by the Cry proteins or the pyrethroid, thus removing any effect of prey quality. Tri-trophic experiments demonstrated that no *C. maculata* and *E. americanus* survived consumption of pyrethroid-treated aphids and that ovipositional behavior of *A. colemani* was impaired when provided with pyrethroid-treated aphids. In contrast, natural enemies were not affected when fed aphids reared on Bt broccoli, thus demonstrating the safety of these Bt plants for IPM.

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Article Number: 16636

IDS Number: CV7PW

Unique ID: WOS:000364467500001

PubMed ID: 26559133

***Record 4 of 5.** Search terms matched: CRY1AB(1)

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

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

Title: Assessing the Indirect Photochemical Transformation of Dissolved Combined Amino Acids through the Use of Systematically Designed Histidine-Containing Oligopeptides

Authors: Chu, CH; Lundeen, RA; Sander, M; McNeill, K

Author Full Names: Chu, Chiheng; Lundeen, Rachel A.; Sander, Michael; McNeill, Kristopher

Source: ENVIRONMENTAL SCIENCE & TECHNOLOGY, 49 (21):12798-12807;
[10.1021/acs.est.5b03498](https://doi.org/10.1021/acs.est.5b03498) NOV 3 2015

Language: English

Abstract: Photooxidation is an important abiotic transformation pathway for amino acids (AAs) in sunlit waters. Although dissolved free AAs are well studied, the photooxidation of dissolved combined AAs (DCAAs) remains poorly investigated. This study is a systematic investigation of the effect of neighboring photostable AA residues (i.e., aliphatic, cationic, anionic, or aromatic residues) on the environmental indirect photochemical transformation of histidine (His) in His-containing oligopeptides. The pK(a) values of His residues in the studied oligopeptides were found to be between 4.3 and 8.1. Accordingly, the phototransformation rate constants of the His-containing oligopeptides were highly pH-dependent in an environmentally relevant pH range with higher reactivity for neutral His than for the protonated species. The photostable AA residues significantly modulated the photoreactivity of oligopeptides either through altering the accessibility of His to photochemically produced oxidants or through shifting the pK(a) values of His residues. In addition, the influence of neighboring photostable AA residues on the sorption-enhanced phototransformation of oligopeptides in solutions containing chromophoric dissolved organic matter (CDOM) was assessed. The constituent photostable AA residues promoted sorption of His-containing oligopeptides to CDOM macromolecules through electrostatic attraction, hydrophobic effects, and/or low-barrier hydrogen bonds, and subsequently increased the apparent phototransformation rate constants by up to 2 orders of magnitude.

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IDS Number: CV6BI

Unique ID: WOS:000364355300023

PubMed ID: 26425803

***Record 5 of 5.** Search terms matched: CRY1AB(1)

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

***Order Full Text []**

Title: "Study of Bacillus thuringiensis **Cry1Ab** and Cry1Ac protoxins interaction with cadherin-like receptor from Manduca sexta"

Authors: Pena-Cardena, A; Bravo, A; Soberon, M; Gomez, I

Author Full Names: Pena-Cardena, Arlen; Bravo, Alejandra; Soberon, Mario; Gomez, Isabel

Source: PROTEIN SCIENCE, 24 14-15; 1 SI OCT 2015

Language: English

ISSN: 0961-8368

eISSN: 1469-896X

IDS Number: CU6QS

Unique ID: WOS:000363658100026

*Record 1 of 9. Search terms matched: BORER(2); CORN(2); CRY1AB(2); LEPIDOPTERA(1); OSTRINIA(1)

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

*Order Full Text []

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

Authors: Willcoxon, MI; Dennis, JR; Lau, SI; Xie, WP; You, Y; Leng, S; Fong, RC; Yamamoto, T

Author Full Names: Willcoxon, Michi Izumi; Dennis, Jaclyn R.; Lau, Sabina I.; Xie, Weiping; You, You; Leng, Song; Fong, Ryan C.; Yamamoto, Takashi

Source: JOURNAL OF BIOTECHNOLOGY, 217 72-81; [10.1016/j.jbiotec.2015.10.021](https://doi.org/10.1016/j.jbiotec.2015.10.021) JAN 10 2016

Language: English

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 (R) 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. (C) 2015 Elsevier B.V. All rights reserved.

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IDS Number: CY9WU

Unique ID: WOS:000366757900010

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

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

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

Title: Resistance to dual-gene **Bt maize** in *Spodoptera frugiperda*: selection, inheritance, and cross-resistance to other transgenic events

Authors: Santos-Amaya, OF; Rodrigues, JVC; Souza, TC; Tavares, CS; Campos, SO; Guedes, RNC; Pereira, EJG

Author Full Names: Santos-Amaya, Oscar F.; Rodrigues, Joao V. C.; Souza, Thadeu C.; Tavares, Clebson S.; Campos, Silverio O.; Guedes, Raul N. C.; Pereira, Eliseu J. G.

Source: SCIENTIFIC REPORTS, 5 [10.1038/srep18243](https://doi.org/10.1038/srep18243) DEC 17 2015

Language: English

Abstract: Transgenic crop "pyramids" producing two or more *Bacillus thuringiensis* (Bt) toxins active against the same pest are used to delay evolution of resistance in insect pest populations. Laboratory and greenhouse experiments were performed with fall armyworm, *Spodoptera frugiperda*, to characterize resistance to Bt maize producing Cry1A.105 and Cry2Ab and test some assumptions of the "pyramid" resistance management strategy. Selection of a field-derived strain of *S. frugiperda* already resistant to Cry1F maize with Cry1A.105 + Cry2Ab maize for ten generations produced resistance that allowed the larvae to colonize and complete the life cycle on these Bt maize plants. Greenhouse experiments revealed that the resistance was completely recessive ($D_x = 0$), incomplete, autosomal, and without maternal effects or cross-resistance to the Vip3Aa20 toxin produced in other Bt maize events. This profile of resistance supports some of the assumptions of the pyramid strategy for resistance management. However, laboratory experiments with purified Bt toxin and plant leaf tissue showed that resistance to Cry1A.105 + Cry2Ab2 maize further increased resistance to Cry1Fa, which indicates that populations of fall armyworm have high potential for developing resistance to some currently available pyramided maize used against this pest, especially where resistance to Cry1Fa was reported in the field.

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Article Number: 18243

IDS Number: CY7GC

Unique ID: WOS:000366575600001

PubMed ID: 26675246

***Record 3 of 9.** Search terms matched: CRY1AB(1); MAIZE(1); RESISTANT(4)

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Title: Binding and Oligomerization of Modified and Native Bt Toxins in **Resistant** and Susceptible Pink Bollworm

Authors: Ocelotl, J; Sanchez, J; Arroyo, R; Garcia-Gomez, BI; Gomez, I; Unnithan, GC; Tabashnik, BE; Bravo, A; Soberon, M

Author Full Names: Ocelotl, Josue; Sanchez, Jorge; Arroyo, Raquel; Garcia-Gomez, Blanca I.; Gomez, Isabel; Unnithan, Gopalan C.; Tabashnik, Bruce E.; Bravo, Alejandra; Soberon, Mario

Source: PLOS ONE, 10 (12):[10.1371/journal.pone.0144086](https://doi.org/10.1371/journal.pone.0144086) DEC 3 2015

Language: English

Abstract: Insecticidal proteins from *Bacillus thuringiensis* (Bt) are used extensively in sprays and transgenic crops for pest control, but their efficacy is reduced when pests evolve resistance. Better understanding of the mode of action of Bt toxins and the mechanisms of insect resistance is needed to enhance the durability of these important alternatives to conventional insecticides. Mode of action models agree that binding of Bt toxins to midgut proteins such as cadherin is essential for toxicity, but some details remain unresolved, such as the role of toxin oligomers. In this study, we evaluated how Bt toxin Cry1Ac and its genetically engineered counterpart Cry1AcMod interact with brush border membrane vesicles (BBMV) from resistant and susceptible larvae of *Pectinophora gossypiella* (pink bollworm), a global pest of cotton. Compared with Cry1Ac, Cry1AcMod lacks 56 amino acids at the amino-terminus including helix alpha-1; previous work showed that Cry1AcMod formed oligomers in vitro without cadherin and killed *P. gossypiella* larvae harboring cadherin mutations linked with > 1000-fold resistance to Cry1Ac. Here we found that resistance to Cry1Ac was associated with reduced oligomer formation and insertion. In contrast, Cry1AcMod formed oligomers in BBMV from resistant larvae. These results confirm the role of cadherin in oligomerization of Cry1Ac in susceptible larvae and imply that forming oligomers without cadherin promotes toxicity of Cry1AcMod against resistant *P. gossypiella* larvae that have cadherin mutations.

ISSN: 1932-6203

Article Number: e0144086

IDS Number: CX9QI

Unique ID: WOS:000366040000053

***Record 4 of 9.** Search terms matched: BT(9); CORN(2); CRY1AB(1); LEPIDOPTERA(4); MAIZE(16); PROTECTED(7)

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

*Order Full Text []

Title: Potential exposure of butterflies in **protected** habitats by **Bt maize** cultivation: A case study in Switzerland

Authors: Lang, A; Oehen, B; Ross, JH; Bieri, K; Steinbrich, A

Author Full Names: Lang, Andreas; Oehen, Bernadette; Ross, Jan-Henning; Bieri, Katharina; Steinbrich, Andreas

Source: BIOLOGICAL CONSERVATION, 192 369-377; [10.1016/j.biocon.2015.10.006](https://doi.org/10.1016/j.biocon.2015.10.006) DEC 2015

Language: English

Abstract: Transgenic Bt maize can produce insecticidal Cry proteins toxic to butterflies and moths (Lepidoptera). In protected habitats near maize fields, Bt maize pollen containing the toxin can be drifted by wind onto host plants of Lepidoptera, and inadvertently harm lepidopteran larvae feeding on these host plants. For a heterogeneous, agricultural landscape in Switzerland, we investigated the butterfly community of protected habitats and their potential exposure to possible cultivation of Bt maize, recorded the densities of maize pollen deposited on a butterfly host plant, simulated the effect of different pollen dispersal ranges and Bt maize adoption rates on the exposure of protected habitats, and explored the consequences of different buffer zones around protected habitats. On average, the 49 recorded butterfly species showed a temporal overlap of larvae of 50.10% +/- 30.09% with the maize pollen shedding period. Mean maize

pollen density on nettles (*Urtica dioica*) was 6.49 +/- 13.58 pollen/cm(2) (range: 0-100). Most of the pollen was deposited close to maize fields less than 30 m distance, but pollen also drifted onto host plants as far as 500 m away. In simulations, protected habitats were highly exposed to Bt maize pollen deposition even at low adoption rates of Bt maize, given that maize pollen is distributed to larger distances, The conflict between species conservation and Bt maize cultivation could be minimised by establishing buffer zones around protected habitats, where non-Bt maize is grown. The results and the known sensitivities of lepidopteran larvae to Bt suggest at least 50 m-100 m broad buffer zones, and case-specific risk assessments for distances above 100 m. (C) 2015 Elsevier B.V. All rights reserved.

ISSN: 0006-3207

eISSN: 1873-2917

IDS Number: CY6TB

Unique ID: WOS:000366540600041

***Record 5 of 9.** Search terms matched: CRY1AB(5); MAIZE(1)

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

*Order Full Text []

Title: INTERNAL QUALITY CONTROL OF AN ENZYME-LINKED IMMUNOASSAY FOR CRY1AB TOXIN DETECTION APPLIED IN ANIMAL TISSUES

Authors: Takacs, E; Nagy, A; Gelencser, E; Szekacs, A

Author Full Names: Takacs, E.; Nagy, A.; Gelencser, E.; Szekacs, A.

Source: ACTA ALIMENTARIA, 44 (4):593-600; [10.1556/066.2015.44.0032](https://doi.org/10.1556/066.2015.44.0032) DEC 2015

Language: English

Abstract: Reliable determination of microbial or transgenic Cry toxins is an essential issue in food and feed analyses, and enzyme-linked immunosorbent assays (ELISAs) are the method of choice for quantifying these toxins currently in food and environmental analysis. Internal Quality Control (IQC) is an indispensable method to assess accuracy, precision, and reproducibility of analytical measurements. To assess the utility of the ELISA method, IQC was performed on EnviroLogix Cry1Ab/Cry1Ac QualiPlate ELISA with manufacturer supplied analytical standards. Applicability of negative and positive controls (C- and C+) was examined by Shewhart Control Charts for bias and Control Chart of the Range of Duplicates for precision. Linear regression (up to 5 ng ml(-1) Cry1Ab concentration) of the commercial ELISA kit was compared to sigmoid calibration (up to 60 ng ml(-1) Cry1Ab concentration). For immunoassay optimization process, possible matrix effects in different liquid and solid vertebrate tissues were examined by determination of the limit of detection values in these matrices.

ISSN: 0139-3006

eISSN: 1588-2535

IDS Number: CW8XM

Unique ID: WOS:000365282700015

***Record 6 of 9.** Search terms matched: MAIZE(8); MON810(1)

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

*Order Full Text []

Title: Genetically modified crops in a 10-generation feeding trial on Japanese quails - Evaluation of its influence on birds' performance and body composition

Authors: Sartowska, KE; Korwin-Kossakowska, A; Sender, G

Author Full Names: Sartowska, K. E.; Korwin-Kossakowska, A.; Sender, G.

Source: POULTRY SCIENCE, 94 (12):2909-2916; [10.3382/ps/pev271](https://doi.org/10.3382/ps/pev271) DEC 2015

Language: English

Abstract: The effect of genetically modified (GM) feed components comprising soya bean meal and maize on the performance indices (reproduction, survival rate, growth, egg production, relative weight of chosen internal organs, and basic chemical composition of breast muscle and egg yolk) of Japanese quails was investigated during a 10-generation trial. A total number of 8,438 healthy quail chicks were used in the course of the trial. In each generation, birds were maintained in 3 experimental groups differing in the main feed components, i.e. 1) GM soya (Roundup Ready) and non-GM maize, 2) GM maize (MON810) and non-GM soya, and 3) non-GM soya and maize. The different feeds used did not influence any of the biological hatch indices, survival rate, or BW of young or adult quails. With regard to egg-laying performance, the GM maize group showed a better laying percentage and a higher egg mass production compared to the other groups; the GM soya group showed reduced average egg mass compared to the other groups, whereas the overall egg production level was the same as in the control group. Results showed a higher relative weight of breast muscle and gizzard in birds fed GM maize compared to the control group, whereas live BW and the relative weights of liver and heart were not different among groups. Meat from the GM soya group showed higher protein and lower fat levels compared to the control group. In the case of egg yolk, its chemical composition in the experimental groups did not differ from the control group. Even though some differences were found among the feeding groups, none could be judged as a negative influence of GM maize or GM soya in feed on the birds or final consumer products over 10 generations of Japanese quails.

ISSN: 0032-5791

eISSN: 1525-3171

IDS Number: CY9VJ

Unique ID: WOS:000366754100008

***Record 7 of 9.** Search terms matched: CRY1AB(1); TOLERANCE(1)

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

*Order Full Text []

Title: Excavating abiotic stress-related gene resources of terrestrial macroscopic cyanobacteria for crop genetic engineering: dawn and challenge

Authors: Ye, SF; Gao, X

Author Full Names: Ye, Shuifeng; Gao, Xiang

Source: BIOENGINEERED, 6 (6):313-315; [10.1080/21655979.2015.1091907](https://doi.org/10.1080/21655979.2015.1091907) NOV-DEC 2015

Language: English

Abstract: Genetically engineered (GE) crops with resistance to environmental stresses are one of the most important solutions for future food security. Numerous genes associated to plant stress resistance have been identified and characterized. However, the current reality is that only a few transgenic crops expressing prokaryotic genes are successfully applied in field conditions. These

few prokaryotic genes include *Agrobacterium* strain CP4 EPSPS gene, *Bacillus thuringiensis* Cry1Ab gene and a bacterial chaperonin gene. Thus, the excavation of potentially critical genes still remains an arduous task for crop engineering. Terrestrial macroscopic cyanobacteria, *Nostoc commune* and *Nostoc flagelliforme*, which exhibit extreme resistance to desiccation stress, may serve as new prokaryotic bioresources for excavating critical genes. Recently, their marker gene *wspA* was heterologously expressed in *Arabidopsis* plant and the transgenics exhibited more flourishing root systems than wild-type plants under osmotic stress condition. In addition, some new genes associated with drought response and adaptation in *N. flagelliforme* are being uncovered by our ongoing RNA-seq analysis. Although the relevant work about the terrestrial macroscopic cyanobacteria is still underway, we believe that the prospect of excavating their critical genes for application in GE crops is quite optimistic.

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eISSN: 2165-5987

IDS Number: CY4ZR

Unique ID: WOS:000366418000001

***Record 8 of 9.** Search terms matched: BORER(1); CORN(1); CRY1AB(1); CRY1 AB(1); LEPIDOPTERA(1)

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

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

Title: Cross-resistance to toxins used in pyramided Bt crops and resistance to Bt sprays in *Helicoverpa zea*

Authors: Welch, KL; Unnithan, GC; Degain, BA; Wei, JZ; Zhang, J; Li, XC; Tabashnik, BE; Carriere, Y

Author Full Names: Welch, Kara L.; Unnithan, Gopalan C.; Degain, Ben A.; Wei, Jizhen; Zhang, Jie; Li, Xianchun; Tabashnik, Bruce E.; Carriere, Yves

Source: JOURNAL OF INVERTEBRATE PATHOLOGY, 132 149-156;
[10.1016/j.jip.2015.10.003](https://doi.org/10.1016/j.jip.2015.10.003) NOV 2015

Language: English

Abstract: To delay evolution of resistance by insect pests, farmers are rapidly increasing their use of transgenic crops producing two or more *Bacillus thuringiensis* (Bt) toxins that kill the same pest. A key condition favoring durability of these "pyramided" crops is the absence of cross-resistance between toxins. Here we evaluated cross-resistance in the major lepidopteran pest *Helicoverpa zea* (Boddie) to Bt toxins used in pyramids. In the laboratory, we selected a strain of this pest with Bt toxin cry1Ac followed by selection with MVP II, a formulation containing a hybrid protoxin that is identical to cry1Ac in the active portion of the toxin and 98.5% identical overall. We calculated the resistance ratio as the EC50 (concentration causing mortality or failure to develop beyond the first instar of 50% of larvae) for the laboratory-selected strain divided by the EC50 for its field-derived parent strain that was not selected in the laboratory. The resistance ratio was 20.0-33.9 (mean = 27.0) for MVP II, 57.0 for cry1Ac, 51.3 for Cry1A.105, 22.4 for cry1Ab, 3.3 for Cry2Ab, 1.8 for cry1Fa, and 1.6 for Vip3Aa. Resistance ratios were 2.9 for DiPel ES and 2.0 for Agree VG, which are commercial Bt spray formulations containing cry1Ac, other Bt toxins, and Bt spores. By the conservative criterion of non-overlap of 95% fiducial limits, the EC50 was significantly higher for the selected strain than its parent strain

for MVP II, cry1Ac, Cry1A.105, cry1 Ab, Cry2Ab and DiPel ES. For cry1 Fa, Vip3Aa, and Agree VG, significantly lower susceptibility to a high concentration indicated low cross-resistance. The resistance ratio for toxins other than cry1Ac was associated with their amino acid sequence similarity to cry1Ac in domain II. Resistance to cry1 Ac and the observed cross-resistance to other Bt toxins could accelerate evolution of *H. zea* resistance to currently registered Bt sprays and pyramided Bt crops. (C) 2015 Elsevier Inc. All rights reserved.

ISSN: 0022-2011

eISSN: 1096-0805

IDS Number: CX3WM

Unique ID: WOS:000365630200016

PubMed ID: 26458274

***Record 9 of 9.** Search terms matched: CRY1AB(1); YIELD(1)

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

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

Title: Foreign Protein Detection in Transgenic Rice Revealed by Comparative Proteomic Analysis

Authors: Yang, YH; Dai, L; Zhu, KM; Xia, HC; Chen, L; Liu, HL; Chen, KP

Author Full Names: Yang, Yanhua; Dai, Li; Zhu, Keming; Xia, Hengchuan; Chen, Liang; Liu, Hailong; Chen, Keping

Source: CROP SCIENCE, 55 (5):2225-2233; [10.2135/cropsci2014.11.0799](https://doi.org/10.2135/cropsci2014.11.0799) SEP-OCT 2015

Language: English

Abstract: To investigate whether the foreign protein in transgenic rice (*Oryza sativa* L.) can be detected and then characterize the different proteins between transgenic rice and nontransgenic rice, we employed proteomic tools including two-dimensional electrophoresis (2-DE) and mass spectrometry (MS) to globally identify different proteins between Bt-'Minghui 63' (MH63) (with the fused Cry1Ab-Cry1Ac gene) and its non-transgenic control MH63. In all, 37 statistically different proteins between Bt-MH63 and MH63 were successfully identified, including six unique proteins in Bt-MH63. Gene ontology analysis showed that these six unique proteins were mainly involved in metabolic, catalytic, binding, and antioxidant process. Among these six unique proteins, two non-rice source proteins, phosphinothricin-N-acetyltransferase, were only expressed in germinating seed and seedling of Bt-MH63, but not in MH63, which were further confirmed by matrix-assisted laser desorption-ionization time of flight (MALDI-TOF) MS-MS analysis. Our work suggests that a comparative proteomic approach may be feasible for identifying foreign proteins and genes in rice.

ISSN: 0011-183X

eISSN: 1435-0653

IDS Number: CW5GT

Unique ID: WOS:000365024400033

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

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

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

Title: A rapid loop-mediated isothermal amplification method for detection of the modified GM cry1A gene in transgenic insect-resistant cotton and rice

Authors: Shen, PL; Geng, FZ; Yu, Y; Zhang, YZ; Wang, ZX; Li, ZH; Zhang, W; Shu, CL; Zhang, YJ; Tan, JX

Author Full Names: Shen, Peili; Geng, Fengzhen; Yu, Yan; Zhang, Yunzhe; Wang, Zhixin; Li, Zhihui; Zhang, Wei; Shu, Changlong; Zhang, Yongjun; Tan, Jianxin

Source: FOOD CONTROL, 62 357-364; [10.1016/j.foodcont.2015.10.035](https://doi.org/10.1016/j.foodcont.2015.10.035) APR 2016

Language: English

Abstract: Among the commercial genetically modified (GM) crops, the insect-resistant GM crops are the major cultivars that cry gene is introduced into. A cry1Ab/1Ac GM fusion gene (GFM cry1A) and a GM truncated cry1Ac gene (cry1Ac-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 cry1A" gene and a rapid visual loop-mediated isothermal amplification (LAMP) assay method for detection of GM cry1A in transgenic insect-resistant crops was established. The LAMP assay was performed at an optimal temperature of 65 degrees C for 60 min in the presence of a set of four specific primers recognized six distinct sequences of the GM cry1A gene. The rough detection limit to the GM cry1A 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 cry1A 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 cry1A gene comparing with PCR analysis. Therefore, this LAMP method will be a potential effective tool for screening the GM cry1A gene in GM crops which are widely plant in China and other developing countries. (C) 2015 Elsevier Ltd. All rights reserved.

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IDS Number: DB0TI

Unique ID: WOS:000368220000050

***Record 2 of 19.** Search terms matched: CRY1AB(1); CRY1 AB(1); MAIZE(1)

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

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

Title: A high-throughput liquid bead array-based screening technology for Bt presence in GMO manipulation

Authors: Fu, W; Wang, HY; Wang, CG; Mei, L; Lin, XM; Han, XQ; Zhu, SF

Author Full Names: Fu, Wei; Wang, Huiyu; Wang, Chenguang; Mei, Lin; Lin, Xiangmei; Han, Xueqing; Zhu, Shuifang

Source: BIOSENSORS & BIOELECTRONICS, 77 702-708; [10.1016/j.bios.2015.10.043](https://doi.org/10.1016/j.bios.2015.10.043) MAR 15 2016

Language: English

Abstract: The number of species and planting areas of genetically modified organisms (GMOs) has been rapidly developed during the past ten years. For the purpose of GMO inspection, quarantine and manipulation, we have now devised a high-throughput Bt-based GMOs screening method based on the liquid bead array. This novel method is based on the direct competitive recognition between biotinylated antibodies and beads-coupled antigens, searching for Bt presence in samples if it contains Bt Cry1 Aa, Bt Cry1 Ab, Bt Cry1 Ac, Bt Cry1 Ah, Bt Cry1 B, Bt Cry1 C, Bt Cry1 F, Bt Cry2 A, Bt Cry3 or Bt Cry9 C. Our method has a wide GMO species coverage so that more than 90% of the whole commercialized GMO species can be identified throughout the world. Under our optimization, specificity, sensitivity, repeatability and availability validation, the method shows a high specificity and 10-50 ng/mL sensitivity of quantification. We then assessed more than 1800 samples in the field and food market to prove capacity of our method in performing a high throughput screening work for GMO manipulation. Our method offers an applicant platform for further inspection and research on GMO plants. (C) 2015 Elsevier B.V. All rights reserved.

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eISSN: 1873-4235

IDS Number: CZ0AG

Unique ID: WOS:000366766900101

***Record 3 of 19.** Search terms matched: BT(1); CORN(1); LEPIDOPTERA(1); MAIZE(5); RESISTANT(2); TOLERANT(1)

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

*Order Full Text []

Title: Rove beetles (Coleoptera Staphylinidae)-Their abundance and competition with other predatory groups in **Bt maize** expressing Cry34Ab1, Cry35Ab1, Cry1F and CP4 EPSPS proteins

Authors: Palinkas, Z; Zalai, M; Szenasi, A; Kadar, F; Dorner, Z; Balog, A

Author Full Names: Palinkas, Zoltan; Zalai, Mihaly; Szenasi, Agnes; Kadar, Ferenc; Dorner, Zita; Balog, Adalbert

Source: CROP PROTECTION, 80 87-93; [10.1016/j.cropro.2015.11.001](https://doi.org/10.1016/j.cropro.2015.11.001) FEB 2016

Language: English

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. (C) 2015 Elsevier Ltd. All rights reserved.

ISSN: 0261-2194

eISSN: 1873-6904

IDS Number: CZ9IE

Unique ID: WOS:000367410500010

*Record 4 of 19. Search terms matched: BT(1); MAIZE(2)

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

*Order Full Text []

Title: Assessment of unanticipated unintended effects of genetically modified plants on non-target organisms: a controversy worthy of pursuit?

Authors: Devos, Y; Alvarez-Alfageme, F; Gennaro, A; Mestdagh, S

Author Full Names: Devos, Y.; Alvarez-Alfageme, F.; Gennaro, A.; Mestdagh, S.

Source: JOURNAL OF APPLIED ENTOMOLOGY, 140 (1-2):1-10; [10.1111/jen.12248](https://doi.org/10.1111/jen.12248) FEB 2016

Language: English

Abstract: A typical risk hypothesis addressed during the environmental risk assessment (ERA) of genetically modified (GM) plants for cultivation is that the novel traits intentionally introduced into GM plants do not adversely affect non-target organisms (NTOs). However, genetic modification may potentially also lead to unintended changes in the GM plant which could raise safety concerns. Therefore, the European Food Safety Authority (EFSA) advocates the characterization of ecological interactions between the GM plant and representative NTOs as part of the ERA of GM plants for cultivation in the European Union. Yet, this requirement is not unanimously accepted by stakeholders. Here, we present EFSA's approach to assess potential adverse effects on NTOs and summarize some of the stake-holders' views, mostly opposing EFSA's position on scientific grounds.

ISSN: 0931-2048

eISSN: 1439-0418

IDS Number: DA9QP

Unique ID: WOS:000368144900001

*Record 5 of 19. Search terms matched: BT(2); CORN(4); MAIZE(7); YIELD(6); ZEA MAYS(1)

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

*Order Full Text []

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

Authors: Estes, RE; Tinsley, NA; Gray, ME

Author Full Names: Estes, R. E.; Tinsley, N. A.; Gray, M. E.

Source: JOURNAL OF APPLIED ENTOMOLOGY, 140 (1-2):19-27; [10.1111/jen.12233](https://doi.org/10.1111/jen.12233) FEB 2016

Language: English

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 neoni-cotinoid 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.

ISSN: 0931-2048

eISSN: 1439-0418

IDS Number: DA9QP

Unique ID: WOS:000368144900003

***Record 6 of 19.** Search terms matched: BT(1); CORN(5); MAIZE(1)

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

*Order Full Text []

Title: Biological aspects of *Dichelops melacanthus* at three temperature, reared on immature 2B688Hx and 2B688 corn grains

Authors: Bortolotto, OC; Mikami, AY; Bueno, AD; Silva, GV; de Queiroz, AP

Author Full Names: Bortolotto, Orcial Ceolin; Mikami, Adriana Yatie; Bueno, Adeney de Freitas; Silva, Gabriela Vieira; de Queiroz, Ana Paula

Source: CIENCIA RURAL, 46 (2):254-259; [10.1590/0103-8478cr20150542](https://doi.org/10.1590/0103-8478cr20150542) FEB 2016

Language: Portuguese

Abstract: This study investigated the development of *Dichelops melacanthus* (Hemiptera: Pentatomidae) at different temperatures (19 +/- 1 degrees C, 25 +/- 1 degrees C and 31 +/- 1 degrees C) reared on 2B688Hx (expressing Cry1F insecticide protein to control lepidopterans target) immature corn grains. The temperature of 19 +/- 1 degrees C impaired the development of *D. melacanthus* and recorded the highest mortality of nymphs, lower weight and adult females laid no eggs. Moreover, the length of the nymphal biology, adult weight, fecundity and viability of eggs did not differ between temperatures 25 +/- 1 degrees C and 31 +/- 1 degrees C. It was also shown that the biological aspects of green belly stink bugs fed with 2B688Hx immature grains of corn do not differ from that develop with 2B688 isoline. This study showed that the biological cycle of *D. melacanthus* is favored at warmer temperature (until 31 +/- 1 degrees C),

and the consume of immature corn grain 2B688Hx does not affect its development.

ISSN: 0103-8478

eISSN: 1678-4596

IDS Number: CZ5HV

Unique ID: WOS:000367134300010

***Record 7 of 19.** Search terms matched: CRY1AB(1)

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

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

Title: Structure of bovine serum albumin adsorbed on silica investigated by quartz crystal microbalance

Authors: Jachimska, B; Tokarczyk, K; Lapeczynska, M; Puciul-Malinowska, A; Zapotoczny, S

Author Full Names: Jachimska, Barbara; Tokarczyk, Karolina; Lapeczynska, Marta; Puciul-Malinowska, Agnieszka; Zapotoczny, Szczepan

Source: COLLOIDS AND SURFACES A-PHYSCOCHEMICAL AND ENGINEERING ASPECTS, 489 163-172; [10.1016/j.colsurfa.2015.10.033](https://doi.org/10.1016/j.colsurfa.2015.10.033) JAN 20 2016

Language: English

Abstract: Adsorption of bovine serum albumin (BSA) on the surface of SiO₂ was investigated mainly using quartz crystal microbalance (QCM) with energy dissipation mode. BSA adsorption kinetics and coverage were determined as a function of pH of the solution with the ionic strength of 1×10^{-2} M. The maximum coverage was obtained in the pH range 4.5-5.4, near the protein isoelectric point. For pH larger than 5.4 and smaller than 4.5 a monotonic decrease of the adsorbed mass was observed. The images obtained using atomic force microscopy (AFM) method revealed various BSA structures depending on the pH at which they were adsorbed. The identified conformations were assigned to the compact triangular form with an effective length $L_{ef} = 8.3$ nm and the elongated one with length $L_{ef} = 26.7$ nm. The dependence between the structure of the protein layers formed on the surface and BSA conformations in solution was additionally followed by contact angle (CA) measurements. It turned out that CA values are very sensitive to the structure of BSA monolayers formed on the silica surface. Comparison of QCM and AFM data with those obtained by other indirect methods (CA) additionally enabled interpretation of the dependence of BSA adsorption on the pH of the solution. The obtained results confirmed the significant role of the highly anisotropic surface charge distribution of BSA molecules on the process of their adsorption. (C) 2015 Elsevier B.V. All rights reserved.

ISSN: 0927-7757

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IDS Number: CZ2NZ

Unique ID: WOS:000366943200019

***Record 8 of 19.** Search terms matched: BORER(1); BT(2); CORN(2); MAIZE(3)

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

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

Title: FUM Gene Expression Profile and Fumonisin Production by *Fusarium verticillioides*

Inoculated in Bt and Non-Bt Maize

Authors: Rocha, LO; Barroso, VM; Andrade, LJ; Pereira, GHA; Ferreira-Castro, FL; Duarte, AP; Michelotto, MD; Correa, B

Author Full Names: Rocha, Liliana O.; Barroso, Vinicius M.; Andrade, Ludmila J.; Pereira, Gustavo H. A.; Ferreira-Castro, Fabiane L.; Duarte, Aildson P.; Michelotto, Marcos D.; Correa, Benedito

Source: FRONTIERS IN MICROBIOLOGY, 6 [10.3389/fmicb.2015.01503](https://doi.org/10.3389/fmicb.2015.01503) JAN 6 2016

Language: English

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 B-1 and B-2 (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-BE 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 BE 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.

ISSN: 1664-302X

Article Number: 1503

IDS Number: DA4QV

Unique ID: WOS:000367786300003

*Record 9 of 19. Search terms matched: CRY1AB(1)

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

*Order Full Text []

Title: Enzymatic Hydrolysis of Polyester Thin Films: Real-Time Analysis of Film Mass Changes and Dissipation Dynamics

Authors: Zumstein, MT; Kohler, HPE; McNeill, K; Sander, M

Author Full Names: Zumstein, Michael Thomas; Kohler, Hans-Peter E.; McNeill, Kristopher; Sander, Michael

Source: ENVIRONMENTAL SCIENCE & TECHNOLOGY, 50 (1):197-206;
[10.1021/acs.est.5b04103](https://doi.org/10.1021/acs.est.5b04103) JAN 5 2016

Language: English

Abstract: Cleavage of ester bonds by extracellular microbial hydrolases is considered a key step during the breakdown of biodegradable polyester materials in natural and engineered systems.

Here we present a novel analytical approach for simultaneous detection of changes in the masses and rigidities of polyester thin films during enzymatic hydrolysis using a Quartz Crystal Microbalance with Dissipation monitoring (QCM-D). In experiments with poly(butylene succinate) (PBS) and the lipase of *Rhizopus oryzae* (RoL), we detected complete hydrolysis of PBS thin films at pH 5 and 40 degrees C that proceeded through soft and water-rich film intermediates. Increasing the temperature from 20 to 40 degrees C resulted in a larger increase of the enzymatic hydrolysis rate of PBS than of nonpolymeric dibutyl adipate. This finding was ascribed to elevated accessibility of ester bonds to the catalytic site of RoL due to increasing polyester chain mobility. When the pH of the solution was changed from 5 to 7, initial hydrolysis rates were little affected, while a softer film intermediate that lead to incomplete film hydrolysis was formed. Hydrolysis dynamics of PBS, poly(butylene adipate), poly(lactic acid), and poly(ethylene terephthalate) in assays with RoL showed distinct differences that we attribute to differences in the polyester structure.

ISSN: 0013-936X

eISSN: 1520-5851

IDS Number: DA5TU

Unique ID: WOS:000367866300023

PubMed ID: 26599203

***Record 10 of 19.** Search terms matched: CRY1AB(1); RESISTANT(3); TOLERANT(2)

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

*Order Full Text []

Title: New Technologies for Insect-**Resistant** and Herbicide-**Tolerant** Plants

Authors: Lombardo, L; Coppola, G; Zelasco, S

Author Full Names: Lombardo, Luca; Coppola, Gerardo; Zelasco, Samanta

Source: TRENDS IN BIOTECHNOLOGY, 34 (1):49-57; [10.1016/j.tibtech.2015.10.006](https://doi.org/10.1016/j.tibtech.2015.10.006) JAN 2016

Language: English

Abstract: The advent of modern molecular biology and recombinant DNA technology has resulted in a dramatic increase in the number of insect-resistant (IR) and herbicide-tolerant (HT) plant varieties, with great economic benefits for farmers. Nevertheless, the high selection pressure generated by control strategies for weed and insect populations has led to the evolution of herbicide and pesticide resistance. In the short term, the development of new techniques or the improvement of existing ones will provide further instruments to counter the appearance of resistant weeds and insects and to reduce the use of agro-chemicals. In this review, we examine some of the most promising new technologies for developing IR and HT plants, such as genome editing and antisense technologies.

ISSN: 0167-7799

IDS Number: DB0NX

Unique ID: WOS:000368205900006

PubMed ID: 26620971

*Record 11 of 19. Search terms matched: CRY 1AB(2)

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

*Order Full Text []

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

Authors: Li, JW; Li, HH; Wang, RR; Gao, XX; Wang, QC

Author Full Names: Li, Jing-Wei; Li, Hou-Hua; Wang, Ren-Rui; Gao, Xiao-Xia; Wang, Qiao-Chun

Source: ACTA PHYSIOLOGIAE PLANTARUM, 38 (1):[10.1007/s11738-015-2028-z](https://doi.org/10.1007/s11738-015-2028-z) JAN 2016

Language: English

Abstract: *Torenia fournieri*, 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. fournieri* 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 1Ab 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.

ISSN: 0137-5881

eISSN: 1861-1664

Article Number: UNSP 8

IDS Number: DA7WF

Unique ID: WOS:000368015100008

*Record 12 of 19. Search terms matched: BT(4); CORN(1); CRY1AB(3); MAIZE(7); MON810(1)

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

*Order Full Text []

Title: The **Cry1Ab** Protein Has Minor Effects on the Arbuscular Mycorrhizal Fungal Communities after Five Seasons of Continuous **Bt Maize** Cultivation

Authors: Zeng, HL; Tan, FX; Shu, YH; Zhang, YY; Feng, YJ; Wang, JW

Author Full Names: Zeng, Huilan; Tan, Fengxiao; Shu, Yinghua; Zhang, Yanyan; Feng, Yuanjiao; Wang, Jianwu

Source: PLOS ONE, 10 (12):[10.1371/journal.pone.0146041](https://doi.org/10.1371/journal.pone.0146041) DEC 30 2015

Language: English

Abstract: The cultivation of genetically modified plants (GMP) has raised concerns regarding the plants' ecological safety. A greenhouse experiment was conducted to assess the impact of five

seasons of continuous Bt (*Bacillus thuringiensis*) maize cultivation on the colonisation and community structure of the non-target organisms arbuscular mycorrhizal fungi (AMF) in the maize roots, bulk soils and rhizospheric soils using the terminal restriction fragment length polymorphism (T-RFLP) analysis of the 28S ribosomal DNA and sequencing methods. AMF colonisation was significantly higher in the two Bt maize lines that express Cry1Ab, 5422Bt1 (event Bt11) and 5422CBCL (MON810) than in the non-Bt isolate 5422. No significant differences were observed in the diversity of the AMF community between the roots, bulk soils and rhizospheric soils of the Bt and non-Bt maize cultivars. The AMF genus *Glomus* was dominant in most of the samples, as detected by DNA sequencing. A clustering analysis based on the DNA sequence data suggested that the sample types (i. e., the samples from the roots, bulk soils or rhizospheric soils) might have greater influence on the AMF community phylotypes than the maize cultivars. This study indicated that the Cry1Ab protein has minor effects on the AMF communities after five seasons of continuous Bt maize cultivation.

ISSN: 1932-6203

Article Number: e0146041

IDS Number: DA0TN

Unique ID: WOS:000367510500124

PubMed ID: 26717324

***Record 13 of 19.** Search terms matched: CRY1AB(1)

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

*Order Full Text []

Title: Comparing Gene Expression Profiles Between Bt and non-Bt Rice in Response to Brown Planthopper Infestation

Authors: Wang, F; Ning, D; Chen, Y; Dang, C; Han, NS; Liu, YE; Ye, GY

Author Full Names: Wang, Fang; Ning, Duo; Chen, Yang; Dang, Cong; Han, Nai-Shun; Liu, Yu'e; Ye, Gong-Yin

Source: FRONTIERS IN PLANT SCIENCE, 6 [10.3389/fpls.2015.01181](https://doi.org/10.3389/fpls.2015.01181) DEC 24 2015

Language: English

Abstract: Bt proteins are the most widely used insecticidal proteins in transgenic crops for improving insect resistance. We previously observed longer nymphal developmental duration and lower fecundity in brown planthopper (BPH) fed on Bt rice line KMD2, although Bt insecticidal protein Cry1Ab could rarely concentrate in this non-target rice pest. In the present study, we performed microarray analysis in an effort to detect Bt-independent variation, which might render Bt rice more defensive and/or less nutritious to BPH. We detected 3834 and 3273 differentially expressed probe sets in response to BPH infestation in non-Bt parent Xiushui 11 and Bt rice KMD2, respectively, only 439 of which showed significant differences in expression between rice lines. Our analysis revealed a shift from growth to defense responses in response to BPH infestation, which was also detected in many other studies of plants suffering biotic and abiotic stresses. Chlorophyll biosynthesis and basic metabolism pathways were inhibited in response to infestation. IAA and GA levels decreased as a result of the repression of biosynthesis related genes or the induction of inactivation related genes. In accordance with these observations, a number of IAA-, GA-, BR-signaling genes were downregulated in response to BPH. Thus, the growth of rice plants under BPH attack was reduced and defense related hormone signaling like

JA, SA and ET were activated. In addition, growth related hormone signaling pathways, such as GA, BR, and auxin signaling pathways, as well as ABA, were also found to be involved in BPH-induced defense. On the other side, 51 probe-sets (represented 50 genes) that most likely contribute to the impact of Bt rice on BPH were identified, including three early nodulin genes, four lipid metabolic genes, 14 stress response genes, three IF genes and genes with other functions. Two transcription factor genes, bHLH and MYB, together with lipid transfer protein genes LTPL65 and early nodulin gene ENOD93, are the most likely candidates for improving herbivore resistance in plants.

ISSN: 1664-462X

Article Number: 1181

IDS Number: CZ5JX

Unique ID: WOS:000367139800001

PubMed ID: 26734057

***Record 14 of 19.** Search terms matched: BT(1); MAIZE(2); ZEA-MAYS(1)

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

***Order Full Text []**

Title: Community Structure of Arbuscular Mycorrhizal Fungi in Rhizospheric Soil of a Transgenic High-Methionine Soybean and a Near Isogenic Variety

Authors: Liang, J; Meng, F; Sun, S; Wu, CX; Wu, HY; Zhang, MR; Zhang, HF; Zheng, XB; Song, XY; Zhang, ZG

Author Full Names: Liang, Jingang; Meng, Fang; Sun, Shi; Wu, Cunxiang; Wu, Haiying; Zhang, Mingrong; Zhang, Haifeng; Zheng, Xiaobo; Song, Xinyuan; Zhang, Zhengguang

Source: PLOS ONE, 10 (12):[10.1371/journal.pone.0145001](https://doi.org/10.1371/journal.pone.0145001) DEC 14 2015

Language: English

Abstract: The use of transgenic plants in agriculture provides many economic benefits, but it also raises concerns over the potential impact of transgenic plants on the environment. We here examined the impact of transgenic high-methionine soybean ZD91 on the arbuscular mycorrhizal (AM) fungal community structure in rhizosphere soil. Our investigations based on clone libraries were conducted in field trials at four growth stages of the crops each year from 2012 to 2013. A total of 155 operational taxonomic units (OTUs) of AM fungi were identified based on the sequences of small subunit ribosomal RNA (SSU rRNA) genes. There were no significant differences found in AM fungal diversity in rhizosphere soil during the same growth stage between transgenic soybean ZD91 and its non-transgenic parental soybean ZD. In addition, plant growth stage and year had the strongest effect on the AM fungal community structure while the genetically modified (GM) trait studied was the least explanatory factor. In conclusion, we found no indication that transgenic soybean ZD91 cultivation poses a risk for AM fungal communities in agricultural soils.

ISSN: 1932-6203

Article Number: e0145001

IDS Number: CY9GR

Unique ID: WOS:000366715900164

PubMed ID: 26658560

***Record 15 of 19.** Search terms matched: BORER(1); BT(3); CORN(5); CRY1AB(1); LEPIDOPTERA(1); MAIZE(2)

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

*Order Full Text []

Title: Bt Maize Seed Mixtures for *Helicoverpa zea* (**Lepidoptera**: Noctuidae): Larval Movement, Development, and Survival on Non-transgenic Maize

Authors: Burkness, EC; Cira, TM; Moser, SE; Hutchison, WD

Author Full Names: Burkness, Eric C.; Cira, T. M.; Moser, S. E.; Hutchison, W. D.

Source: JOURNAL OF ECONOMIC ENTOMOLOGY, 108 (6):2761-2769; [10.1093/jee/tov253](https://doi.org/10.1093/jee/tov253)
DEC 2015

Language: English

Abstract: In 2012 and 2013, field trials were conducted near Rosemount, MN, to assess the movement and development of *Helicoverpa zea* (Boddie) larvae on non-Bt refuge corn plants within a seed mixture of non-Bt and Bt corn. The Bt corn hybrid expressed three Bt toxins-Cry1Ab, Cry1F, and Vip3A. As the use of seed mixtures for insect resistance management (IRM) continues to be implemented, it is necessary to further characterize how this IRM approach impacts resistance development in ear-feeding Lepidopteran pests. The potential for Bt pollen movement and cross pollination of the non-Bt ears in a seed mixture may lead to Bt toxin exposure to larvae developing on those refuge ears. Larval movement and development by *H. zea*, feeding on non-Bt refuge plants adjacent to either transgenic Bt or non-Bt plants, were measured to investigate the potential for unintended Bt exposure. Non-Bt plants were infested with *H. zea* eggs and subplots were destructively sampled twice per week within each treatment to assess larval development, location, and kernel injury. Results indicate that *H. zea* larval movement between plants is relatively low, ranging from 2-16% of larvae, and occurs mainly after reaching the second instar. Refuge plants in seed mixtures did not produce equivalent numbers of *H. zea* larvae, kernel injury, and larval development differed as compared with a pure stand of non-Bt plants. This suggests that there may be costs to larvae developing on refuge plants within seed mixtures and additional studies are warranted to define potential impacts.

ISSN: 0022-0493

eISSN: 1938-291X

IDS Number: CZ6AD

Unique ID: WOS:000367182600031

***Record 16 of 19.** Search terms matched: BORER(2); BT(1); CORN(6); CRY1AB(2); LEPIDOPTERA(2)

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

*Order Full Text []

Title: Resistance Risk Assessment of *Spodoptera frugiperda* (**Lepidoptera**: Noctuidae) and *Diatraea saccharalis* (**Lepidoptera**: Crambidae) to Vip3Aa20 Insecticidal Protein Expressed in Corn

Authors: Bernardi, O; Bernardi, D; Amado, D; Sousa, RS; Fatochetto, J; Medeiros, FCL; Conville, J; Burd, T; Omoto, C

Author Full Names: Bernardi, Oderlei; Bernardi, Daniel; Amado, Douglas; Sousa, Renan S.; Fatochetto, Julio; Medeiros, Fernanda C. L.; Conville, Jared; Burd, Tony; Omoto, Celso

Source: JOURNAL OF ECONOMIC ENTOMOLOGY, 108 (6):2711-2719; [10.1093/jee/tov219](https://doi.org/10.1093/jee/tov219)
DEC 2015

Language: English

Abstract: Transgenic Agrisure Viptera 3 corn that expresses Cry1Ab, Vip3Aa20, and EPSPS proteins and Agrisure Viptera expressing Vip3Aa20 are used for control of Spodoptera frugiperda (J.E. Smith) and Diatraea saccharalis (F.) in Brazil. To support a resistance management program, resistance risk assessment studies were conducted to characterize the dose expression of Vip3Aa20 protein and level of control against these species. The Vip3Aa20 expression in Agrisure Viptera 3 and Agrisure Viptera decreased from V6 to V10 stage of growth. However, Vip3Aa20 expression in Agrisure Viptera 3 at V6 and V10 stages was 13- and 16-fold greater than Cry1Ab, respectively. The Vip3Aa20 expression in lyophilized tissue of Agrisure Viptera 3 and Agrisure Viptera diluted 25-fold in an artificial diet caused complete larval mortality of *S. frugiperda* and *D. saccharalis*. In contrast, lyophilized tissue of Bt11 at the same dilution does not provide complete mortality of these species. Agrisure Viptera 3 and Agrisure Viptera also caused a high level of mortality against *S. frugiperda* and *D. saccharalis*. Moreover, 100% mortality was observed for *S. frugiperda* larvae (neonates through fifth-instar larvae) when fed in corn with the Vip trait technology. Viptera corn achieves a high level of control against *S. frugiperda* and *D. saccharalis* providing a high dose, which is an important determination to support the refuge strategy for an effective resistance management program.

ISSN: 0022-0493

eISSN: 1938-291X

IDS Number: CZ6AD

Unique ID: WOS:000367182600025

*Record 17 of 19. Search terms matched: CRY1AB(11); LEPIDOPTERA(1)

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

*Order Full Text []

Title: Different Effects of *Bacillus thuringiensis* Toxin **Cry1Ab** on Midgut Cell Transmembrane Potential of *Mythimna separata* and *Agrotis ipsilon* Larvae

Authors: Wang, YY; Hu, ZN; Wu, WJ

Author Full Names: Wang, Yingying; Hu, Zhaonong; Wu, Wenjun

Source: TOXINS, 7 (12):5448-5458; [10.3390/toxins7124894](https://doi.org/10.3390/toxins7124894) DEC 2015

Language: English

Abstract: *Bacillus thuringiensis* (Bt) Cry toxins from the Cry1A family demonstrate significantly different toxicities against members of the family Noctuidae for unknown reasons. In this study, membrane potential was measured and analyzed in freshly isolated midgut samples from *Mythimna separata* and *Agrotis ipsilon* larvae under oral administration and in vitro incubation with Bt toxin Cry1Ab to elucidate the mechanism of action for further control of these pests. Bioassay results showed that the larvae of *M. separata* achieved a LD₅₀ of 258.84 ng/larva at 24 h after ingestion; *M. separata* larvae were at least eightfold more sensitive than *A. ipsilon* larvae to Cry1Ab. Force-feeding showed that the observed midgut apical-membrane potential (V-am) of

M. separata larvae was significantly depolarized from -82.9 ± 6.6 mV to -19.9 ± 7.2 mV at 8 h after ingestion of 1 g activated Cry1Ab, whereas no obvious changes were detected in *A. ipsilon* larvae with dosage of 5 g Cry1Ab. The activated Cry1Ab caused a distinct concentration-dependent depolarization of the apical membrane; V-am was reduced by 50% after 14.7 \pm 0.2, 9.8 \pm 0.4, and 7.6 \pm 0.6 min of treatment with 1, 5, and 10 g/mL Cry1Ab, respectively. Cry1Ab showed a minimal effect on *A. ipsilon* larvae even at 20 g/mL, and V-am decreased by 26.3% \pm 2.3% after 15 min. The concentrations of Cry1Ab displayed no significant effect on the basolateral side of the epithelium. The V-am of *A. ipsilon* (-33.19 ± 6.29 mV, n = 51) was only half that of *M. separata* (-80.94 ± 6.95 mV, n = 75). The different degrees of sensitivity to Cry1Ab were speculatively associated with various habits, as well as the diverse physiological or biochemical characteristics of the midgut cell membranes.

ISSN: 2072-6651

IDS Number: CZ3OI

Unique ID: WOS:000367013500042

PubMed ID: 26694463

***Record 18 of 19.** Search terms matched: CRY1AB(3); LEPIDOPTERA(1)

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

***Order Full Text []**

Title: Toxicity and binding capacity of Cry1 proteins to *Helicoverpa armigera* (**Lepidoptera: Noctuidae**) intestine receptors

Authors: Sebastiao, I; Lemes, ARN; Figueiredo, CS; Polanczyk, RA; Desiderio, JA; Lemos, MVF

Author Full Names: Sebastiao, Isis; Nunes Lemes, Ana Rita; Figueiredo, Camila Soares; Polanczyk, Ricardo Antonio; Desiderio, Janete Aparecida; Franco Lemos, Manoel Victor

Source: PESQUISA AGROPECUARIA BRASILEIRA, 50 (11):999-1005; [10.1590/S0100-204X2015001100002](https://doi.org/10.1590/S0100-204X2015001100002) NOV 2015

Language: Portuguese

Abstract: The objective of this work was to evaluate the toxicity and the binding capacity of the Cry1Aa, Cry1Ab, Cry1Ac, and Cry1Ca proteins, from *Bacillus thuringiensis*, to *Helicoverpa armigera* intestine receptors. Binding analysis of the activated proteins to the brush-border membrane vesicles (BBMV) in the midgut of *H. armigera*, besides heterologous competition assays to evaluate their binding capacity, was performed. Cry1Ac stood out as the most toxic protein, followed by Cry1Ab and Cry1Aa. The Cry1Ca protein had no toxicity to the caterpillars and, therefore, it was not possible to evaluate its LC50 and LC90 toxicity parameters. The Cry1Aa, Cry1Ab, and Cry1Ac proteins are able to bind themselves to the same receptor in the midgut membrane, which increases the risk of developing cross-resistance. Therefore, the use of these proteins together should be avoided.

ISSN: 0100-204X

eISSN: 1678-3921

IDS Number: CZ5ON

Unique ID: WOS:000367152000002

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

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

*Order Full Text []

Title: Loading and Light Degradation Characteristics of Bt Toxin on Nanogoethite: A Potential Material for Controlling the Environmental Risk of Bt Toxin

Authors: Zhou, XY; She, CM; Liu, HF

Author Full Names: Zhou, Xueyong; She, Chongmei; Liu, Huifen

Source: JOURNAL OF NANOMATERIALS, [10.1155/2015/849693](#) 2015

Language: English

Abstract: Transgenic Bt-modified crops release toxins into soil through root exudates and upon decomposition of residues. The fate of these toxins in soil has not been yet clearly elucidated. Nanogoethite was found to have a different influence on the lifetime and insecticidal activity of Bt toxin. The aim of this study was to elucidate the adsorption characteristics of Bt toxin on nanogoethite and its activity changes before and after adsorption. The adsorption of toxin on nanogoethite reached equilibrium within 5 h, and the adsorption isotherm of Bt toxin on nanogoethite conformed to the Langmuir equation ($R^2 > 0.9690$). In the range of pH from 6.0 to 8.0, larger adsorption occurred at lower pH value. The toxin adsorption decreased with the temperature between 10 and 50 degrees C. The results of FTIR, XRD, and SEM indicated that toxin did not influence the structure of nanogoethite and the adsorption of toxin only on the surface of nanogoethite. The LC50 value for bound toxin was higher than that of free toxin, and the nanogoethite greatly accelerated the degradation of toxin by ultraviolet irradiation. The above results suggested that nanogoethite is a potential material for controlling the environmental risk of toxin released by Bt transgenic plants.

ISSN: 1687-4110

eISSN: 1687-4129

Article Number: 849693

IDS Number: DA6SV

Unique ID: WOS:000367936500001

*Record 1 of 13. Search terms matched: CRY1AB(3); RESISTANT(1)

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

*Order Full Text []

Title: Loop replacements with gut-binding peptides in **Cry1Ab** domain II enhanced toxicity against the brown planthopper, *Nilaparvata lugens* (Stal)

Authors: Shao, ES; Lin, L; Chen, C; Chen, HZ; Zhuang, HH; Wu, SQ; Sha, L; Guan, X; Huang, ZP

Author Full Names: Shao, Ensi; Lin, Li; Chen, Chen; Chen, Hanze; Zhuang, Haohan; Wu, Songqing; Sha, Li; Guan, Xiong; Huang, Zhipeng

Source: SCIENTIFIC REPORTS, 6 [10.1038/srep20106](https://doi.org/10.1038/srep20106) FEB 1 2016

Language: English

Abstract: *Bacillus thuringiensis* (Bt) Cry toxins have been used widely in pest managements. However, Cry toxins are not effective against sap-sucking insects (Hemiptera), which limits the application of Bt for pest management. In order to extend the insecticidal spectrum of Bt toxins to the rice brown planthopper (BPH), *Nilaparvata lugens*, we modified Cry1Ab putative receptor binding domains with selected BPH gut-binding peptides (GBPs). Three surface exposed loops in the domain II of Cry1Ab were replaced with two GBPs (P2S and P1Z) respectively. Bioassay results showed that toxicity of modified toxin L2-P2S increased significantly (similar to 9 folds) against BPH nymphs. In addition, damage of midgut cells was observed from the nymphs fed with L2-P2S. Our results indicate that modifying Cry toxins based on the toxin-gut interactions can broaden the insecticidal spectrum of Bt toxin. This method provides another approach for the development of transgenic crops with novel insecticidal activity against hemipteran insects and insect populations resistant to current Bt transgenic crops.

ISSN: 2045-2322

Article Number: 20106

IDS Number: DC1SI

Unique ID: WOS:000368996700003

PubMed ID: 26830331

*Record 2 of 13. Search terms matched: CRY1AB(7); MAIZE(1)

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

*Order Full Text []

Title: The fate of fusion **Cry1Ab/1Ac** proteins from Bt-transgenic rice in soil and water

Authors: Liu, YB; Li, JS; Luo, ZL; Wang, HR; Liu, F

Author Full Names: Liu, Yongbo; Li, Junsheng; Luo, Zunlan; Wang, Huaru; Liu, Fang

Source: ECOTOXICOLOGY AND ENVIRONMENTAL SAFETY, 124 455-459;
[10.1016/j.ecoenv.2015.11.025](https://doi.org/10.1016/j.ecoenv.2015.11.025) FEB 2016

Language: English

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. (C) 2015 Elsevier Inc. All rights reserved.

ISSN: 0147-6513

eISSN: 1090-2414

IDS Number: DD4GR

Unique ID: WOS:000369881000053

***Record 3 of 13.** Search terms matched: BT(2); CORN(4); CRY1AB(1); LEPIDOPTERA(1); MAIZE(1); RESISTANT(1)

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

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

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

Authors: Jakka, SRK; Gong, L; Hasler, J; Banerjee, R; Sheets, JJ; Narva, K; Blanco, CA; Jurat-Fuentes, JL

Author Full Names: Jakka, Siva R. K.; Gong, Liang; Hasler, James; Banerjee, Rahul; Sheets, Joel J.; Narva, Kenneth; Blanco, Carlos A.; Jurat-Fuentes, Juan L.

Source: APPLIED AND ENVIRONMENTAL MICROBIOLOGY, 82 (4):1023-1034; [10.1128/AEM.02871-15](https://doi.org/10.1128/AEM.02871-15) FEB 2016

Language: English

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.

ISSN: 0099-2240

eISSN: 1098-5336

IDS Number: DC7CJ

Unique ID: WOS:000369375900005

***Record 4 of 13.** Search terms matched: BORERS(1); CRY1AB(2); LEPIDOPTERA(2); SESAMIA(1)

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

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

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

Authors: Wang, YN; Ke, KQ; Li, YH; Han, LZ; Liu, YM; Hua, HX; Peng, YF

Author Full Names: Wang, Ya-Nan; Ke, Kai-Qie; Li, Yun-He; Han, Lan-Zhi; Liu, Yan-Min; Hua, Hong-Xia; Peng, Yu-Fa

Source: INSECT SCIENCE, 23 (1):78-87; [10.1111/1744-7917.12178](https://doi.org/10.1111/1744-7917.12178) FEB 2016

Language: English

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.

ISSN: 1672-9609

eISSN: 1744-7917

IDS Number: DB9IG

Unique ID: WOS:000368829000008

PubMed ID: 25284137

***Record 5 of 13.** Search terms matched: BT(1); CORN(11); MAIZE(1); YIELD(8)

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

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

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

Authors: Tumbalam, P; Thelen, KD; Adkins, A; Dale, B; Balan, V; Gunawan, C; Gao, J

Author Full Names: Tumbalam, Pavani; Thelen, Kurt D.; Adkins, Andrew; Dale, Bruce; Balan, Venkatesh; Gunawan, Christa; Gao, Juan

Source: BIOMASS & BIOENERGY, 85 119-125; [10.1016/j.biombioe.2015.12.004](https://doi.org/10.1016/j.biombioe.2015.12.004) FEB 2016

Language: English

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 glucan and xylan levels. Analysis showed that there were no significant differences in total glucose or xylose levels nor in enzymatically hydrolyzable glucan 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. (C) 2015 Elsevier Ltd. All rights reserved.

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eISSN: 1873-2909

IDS Number: DB3TW

Unique ID: WOS:000368435800015

***Record 6 of 13.** Search terms matched: CRY1AB(1)

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

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

Title: Viruses at Solid Water Interfaces: A Systematic Assessment of Interactions Driving Adsorption

Authors: Armanious, A; Aeppli, M; Jacak, R; Refardt, D; Sigstam, T; Kohn, T; Sander, M

Author Full Names: Armanious, Antonius; Aeppli, Meret; Jacak, Ronald; Refardt, Dominik; Sigstam, Therese; Kohn, Tamar; Sander, Michael

Source: ENVIRONMENTAL SCIENCE & TECHNOLOGY, 50 (2):732-743;
[10.1021/acs.est5b04644](https://doi.org/10.1021/acs.est5b04644) JAN 19 2016

Language: English

Abstract: Adsorption to solid-water interfaces is a major process governing the fate of waterborne viruses in natural and engineered systems. The relative contributions of different interaction forces to adsorption and their dependence on the physicochemical properties of the

viruses remain, however, only poorly understood. Herein, we systematically studied the adsorption of four bacteriophages (MS2, φr, φGA, and φQ beta) to five model surfaces with varying surface chemistries and to three dissolved organic matter adlayers, as a function of solution pH and ionic strength, using quartz crystal microbalance with dissipation monitoring. The viruses were selected to have similar sizes and shapes but different surface charges, polarities, and topographies, as identified by modeling the distributions of amino acids in the virus capsids. Virus-sorbent interactions were governed by long-ranged electrostatics and favorable contributions from the hydrophobic effect, and shorter-ranged van der Waals interactions were of secondary importance. Steric effects depended on the topographic irregularities on both the virus and sorbent surfaces. Differences in the adsorption characteristics of the tested viruses were successfully linked to differences in their capsid surface properties. Besides identifying the major interaction forces, this work highlights the potential of computable virus surface charge and polarity descriptors to predict virus adsorption to solid-water interfaces.

ISSN: 0013-936X

eISSN: 1520-5851

IDS Number: DB5OL

Unique ID: WOS:000368563400024

PubMed ID: 26636722

***Record 7 of 13.** Search terms matched: BT(5); CORN(9); MAIZE(1); YIELD(1)

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

*Order Full Text []

Title: Effects of refuges on the evolution of resistance to transgenic **corn** by the western **corn** rootworm, *Diabrotica virgifera virgifera* LeConte

Authors: Deitloff, J; Dunbar, MW; Ingber, DA; Hibbard, BE; Gassmann, AJ

Author Full Names: Deitloff, Jennifer; Dunbar, Mike W.; Ingber, David A.; Hibbard, Bruce E.; Gassmann, Aaron J.

Source: PEST MANAGEMENT SCIENCE, 72 (1):190-198; [10.1002/ps.3988](https://doi.org/10.1002/ps.3988) JAN 2016

Language: English

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. (c) 2015 Society of Chemical Industry

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IDS Number: DC0XN

Unique ID: WOS:000368941400021

PubMed ID: 25652190

***Record 8 of 13.** Search terms matched: CRY1AB(1); PROTECTS(1); TOLERANCE(2)

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

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

Title: Bacillus thuringiensis Crystal Protein Cry6Aa Triggers Caenorhabditis elegans Necrosis Pathway Mediated by Aspartic Protease (ASP-1)

Authors: Zhang, FJ; Peng, DH; Cheng, CS; Zhou, W; Ju, SY; Wan, DF; Yu, ZQ; Shi, JW; Deng, YY; Wang, FS; Ye, XB; Hu, ZF; Lin, J; Ruan, LF; Sun, M

Author Full Names: Zhang, Fengjuan; Peng, Donghai; Cheng, Chunsheng; Zhou, Wei; Ju, Shouyong; Wan, Danfeng; Yu, Ziquan; Shi, Jianwei; Deng, Yaoyao; Wang, Fenshan; Ye, Xiaobo; Hu, Zhenfei; Lin, Jian; Ruan, Lifang; Sun, Ming

Source: PLOS PATHOGENS, 12 (1):[10.1371/journal.ppat.1005389](https://doi.org/10.1371/journal.ppat.1005389) JAN 2016

Language: English

Abstract: Cell death plays an important role in host-pathogen interactions. Crystal proteins (toxins) are essential components of Bacillus thuringiensis (Bt) biological pesticides because of their specific toxicity against insects and nematodes. However, the mode of action by which crystal toxins to induce cell death is not completely understood. Here we show that crystal toxin triggers cell death by necrosis signaling pathway using crystal toxin Cry6Aa-Caenorhabditis elegans toxin-host interaction system, which involves an increase in concentrations of cytoplasmic calcium, lysosomal lyses, uptake of propidium iodide, and burst of death fluorescence. We find that a deficiency in the necrosis pathway confers tolerance to Cry6Aa toxin. Intriguingly, the necrosis pathway is specifically triggered by Cry6Aa, not by Cry5Ba, whose amino acid sequence is different from that of Cry6Aa. Furthermore, Cry6Aa-induced necrosis pathway requires aspartic protease (ASP-1). In addition, ASP-1 protects Cry6Aa from over-degradation in C. elegans. This is the first demonstration that deficiency in necrosis pathway confers tolerance to Bt crystal protein, and that Cry6A triggers necrosis represents a newly added necrosis paradigm in the C. elegans. Understanding this model could lead to new strategies for nematode control.

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eISSN: 1553-7374

Article Number: e1005389

IDS Number: DC7BX

Unique ID: WOS:000369374500041

PubMed ID: 26795495

***Record 9 of 13.** Search terms matched: CRY1AB(1); LEPIDOPTERA(1); OSTRINIA(1); RESISTANT(1)

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

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

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

Authors: Shera, PS; Arora, R

Author Full Names: Shera, P. S.; Arora, Ramesh

Source: JOURNAL OF ENVIRONMENTAL BIOLOGY, 27 (1):121-127; JAN 2016

Language: English

Abstract: Oviposition and larval preference of spotted bollworm, *Earias vittella* (Fabricius) was assessed on four transgenic Bt cotton hybrids, viz. MRC 6304 Bt (*cry1Ac* gene), JKCH 1947 Bt (modified *cry1Ac* gene), NCEH 6R Bt (*cry1Ab/cry1Ac* fused gene) and MRC 7017 BG II (*cry1Ac* 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.

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IDS Number: DD8WX

Unique ID: WOS:000370208700018

***Record 10 of 13.** Search terms matched: BT(2); CORN(1); MAIZE(11); RESISTANT(1); YIELD(3)

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

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

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

Authors: Ma, BL; Zheng, ZM; Morrison, MJ; Gregorich, EG

Author Full Names: Ma, B. L.; Zheng, Z. M.; Morrison, M. J.; Gregorich, E. G.

Source: NUTRIENT CYCLING IN AGROECOSYSTEMS, 104 (1):93-105; [10.1007/s10705-016-9761-6](https://doi.org/10.1007/s10705-016-9761-6) JAN 2016

Language: English

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.

ISSN: 1385-1314

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IDS Number: DC1UX

Unique ID: WOS:000369003700008

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

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

***Order Full Text []**

Title: Cry1Ab/c in different stages of growth in transgenic rice Bt-shanyou63

Authors: Zhang, L; Shen, WJ; Fang, ZX; Liu, B

Author Full Names: Zhang, Li; Shen, Wenjing; Fang, Zhixiang; Liu, Biao

Source: FRONTIERS IN BIOSCIENCE-LANDMARK, 21 447-454; [10.2741/4400](#) JAN 1 2016

Language: English

Abstract: The relationship between the mRNA level and the corresponding protein level of the cry1Ab/c gene is not well characterized in transgenic rice (Bt-ShanYou63). In this study, we compared cry1Ab/c mRNA and its protein expression in leaves at different growth stages in Bt-ShanYou63 rice. The results demonstrated that both cry1Ab/c mRNA and its protein levels changed at all of the growth stages. The cry1Ab/c transcript levels in the leaves were highest during the grain filling stage (3.29, cry/actin) and lowest during the seeding stage (1.06, cry/actin), and the protein levels of Cry1Ab/c was also highest at the grain filling stage (5.71 $\mu\text{g} \times \text{g}^{-1}$ fresh weight, fw) and lowest during the seeding stage (2.08 $\mu\text{g} \times \text{g}^{-1}$ fw). There was a significant correlation between cry1Ab/c mRNA levels and the protein concentrations ($r = 0.742$, $p < 0.01$). However, a linear relationship was not observed between cry1Ab/c mRNA levels and the protein levels, and the trend for mRNA expression levels was not consistent with the Cry1Ab/c protein levels in the same growth period in Bt-ShanYou63 rice.

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IDS Number: DC2WD

Unique ID: WOS:000369078400015

PubMed ID: 26709785

***Record 12 of 13.** Search terms matched: BORER(4); BT(3); CORN(4); LEPIDOPTERA(1); MAIZE(8); OSTRINIA(1)

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

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

Title: The Effect of Farmers' Decisions on Pest Control with Bt Crops: A Billion Dollar Game of Strategy

Authors: Milne, AE; Bell, JR; Hutchison, WD; van den Bosch, F; Mitchell, PD; Crowder, D; Parnell, S; Whitmore, AP

Author Full Names: Milne, Alice E.; Bell, James R.; Hutchison, William D.; van den Bosch, Frank; Mitchell, Paul D.; Crowder, David; Parnell, Stephen; Whitmore, Andrew P.

Source: PLOS COMPUTATIONAL BIOLOGY, 11 (12):[10.1371/journal.pcbi.1004483](https://doi.org/10.1371/journal.pcbi.1004483) DEC 2015

Language: English

Abstract: A farmer's decision on whether to control a pest is usually based on the perceived threat of the pest locally and the guidance of commercial advisors. Therefore, farmers in a region are often influenced by similar circumstances, and this can create a coordinated response for pest control that is effective at a landscape scale. This coordinated response is not intentional, but is an emergent property of the system. We propose a framework for understanding the intrinsic feedback mechanisms between the actions of humans and the dynamics of pest populations and demonstrate this framework using the European corn borer, a serious pest in maize crops. We link a model of the European corn borer and a parasite in a landscape with a model that simulates the decisions of individual farmers on what type of maize to grow. Farmers chose whether to grow Bt-maize, which is toxic to the corn borer, or conventional maize for which the seed is cheaper. The problem is akin to the snow-drift problem in game theory; that is to say, if enough farmers choose to grow Bt maize then because the pest is suppressed an individual may benefit from growing conventional maize. We show that the communication network between farmers' and their perceptions of profit and loss affects landscape scale patterns in pest dynamics. We found that although adoption of Bt maize often brings increased financial returns, these rewards oscillate in response to the prevalence of pests.

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Article Number: e1004483

IDS Number: DB4ZJ

Unique ID: WOS:000368521900004

PubMed ID: 26720851

***Record 13 of 13.** Search terms matched: BT(1); LEPIDOPTERA(2); MAIZE(1); PROTECTION(1); RESISTANT(1)

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

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

Title: Effects of transgenic cabbage expressing Cry1Ac1 protein on target pests and the non-target arthropod community under field conditions

Authors: Kim, YJ; Moon, DB; Nam, KJ; Lee, JH; Harn, CH; Kim, CG

Author Full Names: Kim, Young-Joong; Moon, Doo-Bum; Nam, Ki Jung; Lee, Joon-Ho; Harn, Chee Hark; Kim, Chang-Gi

Source: JOURNAL OF ASIA-PACIFIC ENTOMOLOGY, 18 (4):657-668;
[10.1016/j.aspen.2015.07.015](https://doi.org/10.1016/j.aspen.2015.07.015) DEC 2015

Language: English

Abstract: Under field conditions, we investigated how transgenic Bt cabbage expressing the insecticidal Cry1Ac1 protein affects two target Lepidoptera species-*Plutella xylostella* (Plutellidae) and *Pieris rapae* (Pieridae)-as well as the structure of the local non-target arthropod community. When exposed to Bt cabbage Line 00, both species were significantly less abundant than when in the presence of the non-transgenic control. Transgenic line C24 had no apparent influence on those target populations. Multivariate analyses (PerMANOVA and NMDS) showed that composition of the non-target community was affected by sampling date but not by cabbage genotype. These results suggest that transgenic cabbage expressing Cry1Ac1 protein can be effective in controlling *P. xylostella* and *P. rapae* in the field and that its cultivation does not adversely affect non-target arthropods. (C) 2015 Korean Society of Applied Entomology, Taiwan Entomological Society and Malaysian Plant Protection Society. Published by Elsevier B.V. All rights reserved.

ISSN: 1226-8615

eISSN: 1876-7990

IDS Number: DC6SJ

Unique ID: WOS:000369349600004

***Record 1 of 19.** Search terms matched: BT(1); CORN(1); MAIZE(6)

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

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

Title: Selection of focal earthworm species as non-target soil organisms for environmental risk assessment of genetically modified plants

Authors: van Capelle, C; Schrader, S; Arpaia, S

Author Full Names: van Capelle, Christine; Schrader, Stefan; Arpaia, Salvatore

Source: SCIENCE OF THE TOTAL ENVIRONMENT, 548 360-369;
[10.1016/j.scitotenv.2015.12.165](https://doi.org/10.1016/j.scitotenv.2015.12.165) APR 1 2016

Language: English

Abstract: By means of a literature survey, earthworm species of significant relevance for soil functions in different biogeographical regions of Europe (Atlantic, Boreal, Mediterranean) were identified. These focal earthworm species, defined here according to the EFSA Guidance Document on the environmental risk assessment (ERA) of genetically modified plants, are typical for arable soils under crop rotations with maize and/or potatoes within the three regions represented by Ireland, Sweden and Spain, respectively. Focal earthworm species were selected following a matrix of four steps: Identification of functional groups, categorization of non-target species, ranking species on ecological criteria, and final selection of focal species. They are recommended as appropriate nontarget organisms to assess environmental risks of genetically modified (GM) crops; in this case maize and potatoes. In total, 44 literature sources on earthworms in arable cropping systems including maize or potato from Ireland, Sweden and Spain were collected, which present information on species diversity, individual density and specific relevance for soil functions. By means of condensed literature data, those species were identified which (i) play an important functional role in respective soil systems, (ii) are well adapted to the biogeographical regions, (iii) are expected to occur in high abundances under cultivation of maize or potato and (iv) fulfill the requirements for an ERA test system based on life-history traits. First, primary and secondary endogeic species were categorized as potential species. In step three, eight anecic and endogeic earthworm species belonging to the family Lumbricidae were ranked as relevant species: *Aporrectodea caliginosa*, *Aporrectodea rosea*, *Aporrectodea longa*, *Allolobophora chlorotica*, *Lumbricus terrestris*, *Lumbricus friendi*, *Octodrilus complanatus* and *Octolasion cyaneum*. Five out of these eight species are relevant for each biogeographical region with an overlap in the species. Finally, the earthworm species *Ap. caliginosa* (endogeic, secondary decomposer) and *L. terrestris* (anecic, primary decomposer) were selected as focal species. In the Mediterranean region *L. terrestris* may be substituted by the more relevant anecic species *L. friendi*. The selected focal species are recommended to be included in a standardized laboratory ERA test system based on life-history traits. (C) 2016 Elsevier B.V. All rights reserved.

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eISSN: 1879-1026

IDS Number: DD9LC

Unique ID: WOS:000370246000037

PubMed ID: 26803734

***Record 2 of 19.** Search terms matched: BT(10); CORN(2); CRY1AB(5); MAIZE(11);

MON810(1)

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

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

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

Authors: Arias-Martin, M; Garcia, M; Lucianez, MJ; Ortego, F; Castanera, P; Farinos, GP

Author Full Names: Arias-Martin, Maria; Garcia, Matias; Jose Lucianez, Ma; Ortego, Felix; Castanera, Pedro; Farinos, Gema P.

Source: AGRICULTURE ECOSYSTEMS & ENVIRONMENT, 220 125-134;
[10.1016/j.agee.2015.09.007](https://doi.org/10.1016/j.agee.2015.09.007) MAR 15 2016

Language: English

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. (C) 2015 Elsevier B.V. All rights reserved.

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IDS Number: DF2QW

Unique ID: WOS:000371189900014

***Record 3 of 19.** Search terms matched: BORER(1); BT(1); MAIZE(1)

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

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

Title: Cry1Ac Transgenic Sugarcane Does Not Affect the Diversity of Microbial Communities and Has No Significant Effect on Enzyme Activities in Rhizosphere Soil within One Crop Season

Authors: Zhou, DG; Xu, LP; Gao, SW; Guo, JL; Luo, J; You, Q; Que, YX

Author Full Names: Zhou, Dinggang; Xu, Liping; Gao, Shiwu; Guo, Jinlong; Luo, Jun; You, Qian; Que, Youxiong

Source: FRONTIERS IN PLANT SCIENCE, 7 [10.3389/fpls.2016.00265](https://doi.org/10.3389/fpls.2016.00265) MAR 8 2016

Language: English

Abstract: Cry1Ac transgenic sugarcane provides a promising way to control stem-borer pests. Biosafety assessment of soil ecosystem for cry1Ac transgenic sugarcane is urgently needed because of the important role of soil microorganisms in nutrient transformations and element cycling, however little is known. This study aimed to explore the potential impact of cry1Ac transgenic sugarcane on rhizosphere soil enzyme activities and microbial community diversity, and also to investigate whether the gene flow occurs through horizontal gene transfer. We found no horizontal gene flow from cry1Ac sugarcane to soil. No significant difference in the population of culturable microorganisms between the non-GM and cry1Ac transgenic sugarcane was observed, and there were no significant interactions between the sugarcane lines and the growth stages. A relatively consistent trend at community-level, represented by the functional diversity index, was found between the cry1Ac sugarcane and the non-transgenic lines. Most soil samples showed no significant difference in the activities of four soil enzymes: urease, protease, sucrose, and acid phosphate monoester between the non-transgenic and cry1Ac sugarcane lines. We conclude, based on one crop season, that the cry1Ac sugarcane lines may not affect the microbial community structure and functional diversity of the rhizosphere soil and have few negative effects on soil enzymes.

ISSN: 1664-462X

Article Number: 265

IDS Number: DF5NX

Unique ID: WOS:000371399900001

***Record 4 of 19.** Search terms matched: BORER(1); BT(3); CORN(1); LEPIDOPTERA(2); MAIZE(7); RESISTANT(2); ZEA MAYS(1)

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

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

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

Authors: Santos-Amaya, OF; Tavares, CS; Monteiro, HM; Teixeira, TPM; Guedes, RNC; Alves, AP; Pereira, EJG

Author Full Names: Santos-Amaya, Oscar F.; Tavares, Clebson S.; Monteiro, Hugo M.; Teixeira, Thais P. M.; Guedes, Raul N. C.; Alves, Analiza P.; Pereira, Eliseu J. G.

Source: CROP PROTECTION, 81 154-162; [10.1016/j.cropro.2015.12.014](https://doi.org/10.1016/j.cropro.2015.12.014) MAR 2016

Language: English

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 F-1 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. (C) 2015 Elsevier Ltd. All rights reserved.

ISSN: 0261-2194

eISSN: 1873-6904

IDS Number: DF9AS

Unique ID: WOS:000371653200021

***Record 5 of 19.** Search terms matched: BORER(1); BT(3); CORN(1); LEPIDOPTERA(4); MAIZE(9); RESISTANT(3); ZEA MAYS(2)

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

*Order Full Text []

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

Authors: Leite, NA; Mendes, SM; Santos-Amaya, OF; Santos, CA; Teixeira, TPM; Guedes, RNC; Pereira, EJG

Author Full Names: Leite, Natalia A.; Mendes, Simone M.; Santos-Amaya, Oscar F.; Santos, Chritiane A.; Teixeira, Thais P. M.; Guedes, Raul N. C.; Pereira, Eliseu J. G.

Source: ENTOMOLOGIA EXPERIMENTALIS ET APPLICATA, 158 (3):236-247;
[10.1111/eea.12399](https://doi.org/10.1111/eea.12399) MAR 2016

Language: English

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 F-1 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.

ISSN: 0013-8703

eISSN: 1570-7458

IDS Number: DE9JG

Unique ID: WOS:000370952200002

***Record 6 of 19.** Search terms matched: BORER(1); CRY1AB(1); RESISTANT(2)

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

*Order Full Text []

Title: Development of leaffolder **resistant** transgenic rice expressing cry2AX1 gene driven by green tissue-specific rbcS promoter

Authors: Manikandan, R; Balakrishnan, N; Sudhakar, D; Udayasuriyan, V

Author Full Names: Manikandan, R.; Balakrishnan, N.; Sudhakar, D.; Udayasuriyan, V.

Source: WORLD JOURNAL OF MICROBIOLOGY & BIOTECHNOLOGY, 32
(3):[10.1007/s11274-015-2006-z](https://doi.org/10.1007/s11274-015-2006-z) MAR 2016

Language: English

Abstract: The insecticidal cry genes of *Bacillus thuringiensis* (Bt) have been successfully used for development of insect resistant transgenic rice plants. In this study, a novel cry2AX1 gene consisting a sequence of cry2Aa and cry2Ac gene driven by rice rbcS promoter was introduced into a rice cultivar, ASD16. Among 27 putative rice transformants, 20 plants were found to be positive for cry2AX1 gene. The expression of Cry2AX1 protein in transgenic rice plants ranged from 5.95 to 122.40 ng/g of fresh leaf tissue. Stable integration of the transgene was confirmed in putative transformants of rice by Southern blot hybridization analysis. Insect bioassay on T-0 transgenic rice plants against rice leaffolder (*Cnaphalocrosis medinalis*) recorded larval mortality up to 83.33 %. Stable inheritance and expression of cry2AX1 gene in T-1 progenies was demonstrated using Southern and ELISA. The detached leaf bit bioassay with selected T-1 plants showed 83.33-90.00 % mortality against *C. medinalis*. The whole plant bioassay for T-1 plants with rice leaffolder showed significant level of resistance even at a lower level of Cry2AX1 expression varying from 131 to 158 ng/g fresh leaf tissue during tillering stage.

ISSN: 0959-3993

eISSN: 1573-0972

Article Number: UNSP 37

IDS Number: DF5YP

Unique ID: WOS:000371429200003

PubMed ID: 26867598

***Record 7 of 19.** Search terms matched: BORER(2); BORERS(1); BT(4); CORN(9); CRY1AB(2); LEPIDOPTERA(1); OSTRINIA(2)

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

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

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

Authors: Oyediran, I; Dively, G; Huang, FN; Burd, T

Author Full Names: Oyediran, Isaac; Dively, Galen; Huang, Fangneng; Burd, Tony

Source: CROP PROTECTION, 81 145-153; [10.1016/j.cropro.2015.12.008](https://doi.org/10.1016/j.cropro.2015.12.008) MAR 2016

Language: English

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 isolate 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. (C) 2015 Elsevier Ltd. All rights reserved.

ISSN: 0261-2194

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IDS Number: DF9AS

Unique ID: WOS:000371653200020

***Record 8 of 19.** Search terms matched: BT(3); MAIZE(4)

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

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

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

Authors: Steijven, K; Steffan-Dewenter, I; Hartel, S

Author Full Names: Steijven, Karin; Steffan-Dewenter, Ingolf; Haertel, Stephan

Source: APIDOLOGIE, 47 (2):216-226; [10.1007/s13592-015-0392-8](https://doi.org/10.1007/s13592-015-0392-8) MAR 2016

Language: English

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-dependence effects of GM plant material in an environmental risk assessment (ERA).

ISSN: 0044-8435

eISSN: 1297-9678

IDS Number: DF2GV

Unique ID: WOS:000371161500007

***Record 9 of 19.** Search terms matched: BORER(1); BT(8); CORN(1); MAIZE(13)

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

*Order Full Text []

Title: Field trials to evaluate the effects of transgenic cry1Ie **maize** on the community characteristics of arthropod natural enemies

Authors: Guo, JF; He, KL; Hellmich, RL; Bai, SX; Zhang, TT; Liu, YJ; Ahmed, T; Wang, ZY

Author Full Names: Guo, Jingfei; He, Kanglai; Hellmich, Richard L.; Bai, Shuxiong; Zhang, Tiantao; Liu, Yunjun; Ahmed, Tofael; Wang, Zhenying

Source: SCIENTIFIC REPORTS, 6 [10.1038/srep22102](https://doi.org/10.1038/srep22102) FEB 26 2016

Language: English

Abstract: Possible non-target effect of transgenic cry1Ie maize exerts on natural enemy community biodiversity in the field is unresolved. In the present study, a 2-yr comparison of transgenic cry1Ie 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 cry1Ie maize had little, if any, effect on natural enemy community biodiversity.

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Article Number: 22102

IDS Number: DE9AL

Unique ID: WOS:000370927700002

PubMed ID: 26915985

***Record 10 of 19.** Search terms matched: CRY1AB(7)

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

*Order Full Text []

Title: A Comprehensive Assessment of the Effects of Transgenic Cry1Ac/Cry1Ab Rice Huahui 1 on Adult *Micraspis discolor* (Fabricius) (Coleoptera: Coccinellidae)

Authors: Zhou, X; Guo, YL; Kong, H; Zuo, J; Huang, QX; Jia, RZ; Guo, AP; Xu, L

Author Full Names: Zhou, Xia; Guo, Yunling; Kong, Hua; Zuo, Jiao; Huang, Qixing; Jia, Ruizong; Guo, Anping; Xu, Lin

Source: PLOS ONE, 11 (2):[10.1371/journal.pone.0142714](https://doi.org/10.1371/journal.pone.0142714) FEB 25 2016

Language: English

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 lifetable parameters tested between Cry protein-containing and pure diet. Artificial diet containing E-64 (N-(trans-Epoxy succinyl)-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.

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Article Number: e0142714

IDS Number: DF2LW

Unique ID: WOS:000371175700002

PubMed ID: 26914608

*Record 11 of 19. Search terms matched: CRY1AB(2); RESISTANT(2)

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

*Order Full Text []

Title: Development of an Amino Acid-Functionalized Fluorescent Nanocarrier to Deliver a Toxin to Kill Insect Pests

Authors: Zheng, Y; You, SS; Ji, CD; Yin, MZ; Yang, WT; Shen, J

Author Full Names: Zheng, Yang; You, Shusen; Ji, Chendong; Yin, Meizhen; Yang, Wantai; Shen, Jie

Source: ADVANCED MATERIALS, 28 (7):1375-1380; [10.1002/adma.201504993](https://doi.org/10.1002/adma.201504993) FEB 17 2016

Language: English

Abstract: Large-scale cultivation of *Bacillus thuringiensis* Berliner (Bt) crops has led to the rapid development of drug resistance. Herein, a fluorescent star poly(amino acid) is synthesized with L-isoleucine functionalization for the efficient delivery of either positively or negatively charged exogenous proteins into live cells. Poly(amino acid)s (P1)/Cry1Ab complexes greatly increase the cytotoxicity of the Bt toxin, Cry1Ab, and efficiently kill Bt-resistant pests.

ISSN: 0935-9648

eISSN: 1521-4095

IDS Number: DD8QP

Unique ID: WOS:000370192200003

PubMed ID: 26640174

*Record 12 of 19. Search terms matched: BORER(1); BT(1); CORN(10); LEPIDOPTERA(4); MAIZE(1)

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

*Order Full Text []

Title: On-Plant Larval Movement and Feeding Behavior of Fall Armyworm (**Lepidoptera**: Noctuidae) on Reproductive **Corn** Stages

Authors: Pannuti, LER; Baldin, ELL; Hunt, TE; Paula-Moraes, SV

Author Full Names: Pannuti, L. E. R.; Baldin, E. L. L.; Hunt, T. E.; Paula-Moraes, S. V.

Source: ENVIRONMENTAL ENTOMOLOGY, 45 (1):192-200; [10.1093/ee/nvv159](https://doi.org/10.1093/ee/nvv159) FEB 2016

Language: English

Abstract: *Spodoptera frugiperda* J.E. Smith (fall armyworm) is considered one of the most destructive pests of corn throughout the Americas. Although this pest has been extensively studied, little is known about its larval movement and feeding behavior on reproductive compared to vegetative corn stages. Thus, we conducted studies with two corn stages (R1 and R3) and four corn plant zones (tassel, above ear, ear zone, and below ear) in the field at Concord, NE (USA), and in the field and greenhouse at Botucatu, SP (Brazil), to investigate on-plant larval movement. The effects of different corn tissues (opened tassel, closed tassel, silk, kernel, and leaf), two feeding sequence scenarios (closed tassel-leaf-silk-kernel and leaf-silk-kernel), and artificial diet (positive control) on larval survival and development were also evaluated in the laboratory. Ear zone has a strong effect on feeding choice and survival of fall armyworm larvae

regardless of reproductive corn stage. Feeding site choice is made by first-instar. Corn leaves of reproductive plants were not suitable for early instar development, but silk and kernel tissues had a positive effect on survival and development of fall armyworm larvae on reproductive stage corn.

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eISSN: 1938-2936

IDS Number: DD9UT

Unique ID: WOS:000370271900024

PubMed ID: 26476276

***Record 13 of 19.** Search terms matched: BT(6); CORN(6); LEPIDOPTERA(1); MAIZE(8)

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

*Order Full Text []

Title: Early Detection and Mitigation of Resistance to **Bt Maize** by Western **Corn** Rootworm (Coleoptera: Chrysomelidae)

Authors: Andow, DA; Pueppke, SG; Schaafsma, AW; Gassmann, AJ; Sappington, TW; Meinke, LJ; Mitche, PD; Hurley, TM; Hellmich, RL; Porterl, RP

Author Full Names: Andow, David A.; Pueppke, Steven G.; Schaafsma, Arthur W.; Gassmann, Aaron J.; Sappington, Thomas W.; Meinke, Lance J.; Mitche, Paul D.; Hurley, Terrance M.; Hellmich, Richard L.; Porterl, R. Pat

Source: JOURNAL OF ECONOMIC ENTOMOLOGY, 109 (1):1-12; [10.1093/jee/tov238](https://doi.org/10.1093/jee/tov238) FEB 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 proactive, 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.

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eISSN: 1938-291X

IDS Number: DD9VM

Unique ID: WOS:000370273800001

PubMed ID: 26362989

***Record 14 of 19.** Search terms matched: BT(1); CORN(3); LEPIDOPTERA(2); MAIZE(1)

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

Title: The Impact of Inter-Kernel Movement in the Evolution of Resistance to Dual-Toxin **Bt-Corn** Varieties in *Helicoverpa zea* (**Lepidoptera**: Noctuidae)

Authors: Caprio, MA; Martinez, JC; Porter, PA; Bynum, E

Author Full Names: Caprio, Michael A.; Martinez, Jeannette C.; Porter, Patrick A.; Bynum, Ed

Source: JOURNAL OF ECONOMIC ENTOMOLOGY, 109 (1):307-319; [10.1093/jee/tov295](https://doi.org/10.1093/jee/tov295)
FEB 2016

Language: English

Abstract: Seeds or kernels on hybrid plants are primarily F-2 tissue and will segregate for heterozygous alleles present in the parental F-1 hybrids. In the case of plants expressing Bt-toxins, the F-2 tissue in the kernels will express toxins as they would segregate in any F-2 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.

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eISSN: 1938-291X

IDS Number: DD9VM

Unique ID: WOS:000370273800041

PubMed ID: 26527792

***Record 15 of 19.** Search terms matched: BT(2); CORN(1); LEPIDOPTERA(3); MAIZE(4); MON810(1); RESISTANT(1); ZEA MAYS(1)

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

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

Title: Survival of **Corn** Earworm (**Lepidoptera**: Noctuidae) on **Bt Maize** and Cross-Pollinated Refuge Ears From Seed Blends

Authors: Crespo, ALB; Alves, AP; Wang, YW; Hong, BN; Flexner, JL; Catchot, A; Buntin, D;

Cook, D

Author Full Names: Crespo, Andre Luiz Barreto; Alves, Analiza Piovesan; Wang, Yiwei; Hong, Bonnie; Flexner, John Lindsey; Catchot, Angus; Buntin, David; Cook, Donald

Source: JOURNAL OF ECONOMIC ENTOMOLOGY, 109 (1):288-298; [10.1093/jee/tov272](https://doi.org/10.1093/jee/tov272)
FEB 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.

ISSN: 0022-0493

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IDS Number: DD9VM

Unique ID: WOS:000370273800039

PubMed ID: 26357846

***Record 16 of 19.** Search terms matched: BT(1); CORN(2); MAIZE(7); PROTECTED(1); RESISTANT(1); TOLERANCE(1)

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

*Order Full Text []

Title: Transportable data from non-target arthropod field studies for the environmental risk assessment of genetically modified **maize** expressing an insecticidal double-stranded RNA

Authors: Ahmad, A; Negri, I; Oliveira, W; Brown, C; Asiimwe, P; Sammons, B; Horak, M; Jiang, CJ; Carson, D

Author Full Names: Ahmad, Aqeel; Negri, Ignacio; Oliveira, Wladercir; Brown, Christopher; Asiimwe, Peter; Sammons, Bernard; Horak, Michael; Jiang, Changjian; Carson, David

Source: TRANSGENIC RESEARCH, 25 (1):1-17; [10.1007/s11248-015-9907-3](https://doi.org/10.1007/s11248-015-9907-3) FEB 2016

Language: English

Abstract: As part of an environmental risk assessment, the potential impact of genetically

modified (GM) maize MON 87411 on non-target arthropods (NTAs) was evaluated in the field. MON 87411 confers resistance to corn rootworm (CRW; *Diabrotica* spp.) by expressing an insecticidal double-stranded RNA (dsRNA) transcript and the Cry3Bb1 protein and tolerance to the herbicide glyphosate by producing the CP4 EPSPS protein. Field trials were conducted at 14 sites providing high geographic and environmental diversity within maize production areas from three geographic regions including the U.S., Argentina, and Brazil. MON 87411, the conventional control, and four commercial conventional reference hybrids were evaluated for NTA abundance and damage. Twenty arthropod taxa met minimum abundance criteria for valid statistical analysis. Nine of these taxa occurred in at least two of the three regions and in at least four sites across regions. These nine taxa included: aphid, predatory earwig, lacewing, ladybird beetle, leaf-hopper, minute pirate bug, parasitic wasp, sap beetle, and spider. In addition to wide regional distribution, these taxa encompass the ecological functions of herbivores, predators and parasitoids in maize agro-ecosystems. Thus, the nine arthropods may serve as representative taxa of maize agro-ecosystems, and thereby support that analysis of relevant data generated in one region can be transportable for the risk assessment of the same or similar GM crop products in another region. Across the 20 taxa analyzed, no statistically significant differences in abundance were detected between MON 87411 and the conventional control for 123 of the 128 individual-site comparisons (96.1 %). For the nine widely distributed taxa, no statistically significant differences in abundance were detected between MON 87411 and the conventional control. Furthermore, no statistically significant differences were detected between MON 87411 and the conventional control for 53 out of 56 individual-site comparisons (94.6 %) of NTA pest damage to the crop. In each case where a significant difference was observed in arthropod abundance or damage, the mean value for MON 87411 was within the reference range and/or the difference was not consistently observed across collection methods and/or sites. Thus, the differences were not representative of an adverse effect unfamiliar to maize and/or were not indicative of a consistent plant response associated with the GM traits. Results from this study support a conclusion of no adverse environmental impact of MON 87411 on NTAs compared to conventional maize and demonstrate the utility of relevant transportable data across regions for the ERA of GM crops.

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IDS Number: DF2FA

Unique ID: WOS:000371155500001

PubMed ID: 26433587

***Record 17 of 19.** Search terms matched: BT(2); LEPIDOPTERA(1); MAIZE(8)

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

***Order Full Text []**

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

Authors: Guo, YY; Tian, JC; Shi, WP; Dong, XH; Romeis, J; Naranjo, SE; Hellmich, RL; Shelton, AM

Author Full Names: Guo, Yan-Yan; Tian, Jun-Ce; Shi, Wang-Peng; Dong, Xue-Hui; Romeis,

Joerg; Naranjo, Steven E.; Hellmich, Richard L.; Shelton, Anthony M.

Source: TRANSGENIC RESEARCH, 25 (1):33-44; [10.1007/s11248-015-9917-1](https://doi.org/10.1007/s11248-015-9917-1) FEB 2016

Language: English

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 proteins 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.

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IDS Number: DF2FA

Unique ID: WOS:000371155500003

PubMed ID: 26545599

***Record 18 of 19.** Search terms matched: CORN(1); CRY1AB(1); MAIZE(1); RESISTANT(1)

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

*Order Full Text []

Title: Current trends in the global market of transgenic plants and environmental safety issues

Authors: Viktorov, AG

Author Full Names: Viktorov, A. G.

Source: RUSSIAN JOURNAL OF PLANT PHYSIOLOGY, 63 (1):38-45;

[10.1134/S1021443716010179](https://doi.org/10.1134/S1021443716010179) JAN 2016

Language: English

Abstract: The world market for the first generation of transgenic crops (insecticidal and herbicide-resistant plants) has been expanding since 2012, mostly owing to developing countries. The cautious attitude in the majority of economically developed countries to the first-generation transgenic agricultural crops is due to several objective circumstances: the negative impact of insecticidal Bt-crops on useful and endangered invertebrate species, the allergenic properties of Bt-toxin for humans, toxicity of glyphosate to humans and animals, the widely spreading resistance of weeds to glyphosate, the increasing resistance of harmful-insects to insecticidal Bt-

plants, the danger of-genetic pollution-of aboriginal plant varieties, and the flow of herbicide resistance traits to weed plants.

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IDS Number: DE1EU

Unique ID: WOS:000370370300004

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

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

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

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

Authors: Shera, PS; Arora, R

Author Full Names: Shera, P. S.; Arora, Ramesh

Source: JOURNAL OF ENVIRONMENTAL BIOLOGY, 37 (1):121-127; JAN 2016

Language: English

Abstract: Oviposition and larval preference of spotted bollworm, *Earias vittella* (Fabricius) was assessed on four transgenic Bt cotton hybrids, viz. MRC 6304 Bt (*cry1Ac* gene), JKCH 1947 Bt (modified *cry1Ac* gene), NCEH 6R Bt (*cry1Ab/cry1Ac* fused gene) and MRC 7017 BG II (*cry1Ac* 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.

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IDS Number: DD8WX

Unique ID: WOS:000370208700018

PubMed ID: 26930869

***Record 1 of 16.** Search terms matched: BORER(1); BT(11); CORN(11); LEPIDOPTERA(1); MAIZE(1)

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

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

Title: Pure Bt-crop and mixed seed sowing strategies for optimal economic profit in the face of pest resistance to pesticides and **Bt-corn**

Authors: Liang, JH; Tang, SY; Cheke, RA

Author Full Names: Liang, Juhua; Tang, Sanyi; Cheke, Robert A.

Source: APPLIED MATHEMATICS AND COMPUTATION, 283 6-21;
[10.1016/j.amc.2016.02.023](https://doi.org/10.1016/j.amc.2016.02.023) JUN 20 2016

Language: English

Abstract: With the evolution of pest resistance to Bt-corn, farmers' economic losses are increasing. However, a planting strategy with Bt-corn mixed with non-Bt-corn to fight the development of pest resistance can be efficient. Nevertheless, this mixed strategy poses questions such as (1) what is the optimal ratio of Bt-corn to non-Bt-corn that should be planted in a field? And (2) what is the main factor affecting the farmers' net present value? To address these questions, we propose and investigate a discrete pest growth model with pest resistance to Bt-corn. According to the model's economic functions, the main factors affecting the farmers' net present value are presented and discussed. By comparing the net present values of a pure Bt-corn planting strategy with the mixed planting strategy, an optimal planting strategy was devised. Moreover, the optimal ratio of Bt-corn to non-Bt-corn to be planted when the mixed planting strategy is implemented in the field was also investigated. (c) 2016 Elsevier Inc. All rights reserved.

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Unique ID: WOS:000373187400002

***Record 2 of 16.** Search terms matched: BORER(2); BT(1); CORN(2); CRY1AB(1); LEPIDOPTERA(1); MAIZE(7); OSTRINIA(1); RESISTANT(1)

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

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

Title: Frequency of *Bacillus thuringiensis* Cry1A.105 resistance alleles in field populations of the fall armyworm, *Spodoptera frugiperda*, in Louisiana and Florida

Authors: Huang, FN; Qureshi, JA; Head, GP; Price, PA; Levy, R; Yang, F; Niu, Y

Author Full Names: Huang, Fangneng; Qureshi, Jawwad A.; Head, Graham P.; Price, Paula A.; Levy, Ronnie; Yang, Fei; Niu, Ying

Source: CROP PROTECTION, 83 83-89; [10.1016/j.cropro.2016.01.019](https://doi.org/10.1016/j.cropro.2016.01.019) MAY 2016

Language: English

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 F-2 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. F-2 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. (C) 2016 Elsevier Ltd. All rights reserved.

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IDS Number: DH1PL

Unique ID: WOS:000372557300011

***Record 3 of 16.** Search terms matched: CRY1AB(1); MAIZE(1); RESISTANT(2); ZEA-MAYS(1)

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

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

Title: Current trends in Bt crops and their fate on associated microbial community dynamics: a review

Authors: Singh, AK; Dubey, SK

Author Full Names: Singh, Amit Kishore; Dubey, Suresh Kumar

Source: PROTOPLASMA, 253 (3):663-681; SI [10.1007/s00709-015-0903-5](https://doi.org/10.1007/s00709-015-0903-5) MAY 2016

Language: English

Abstract: Cry protein expressing insect-resistant trait is mostly deployed to control major devastating pests and minimize reliance on the conventional pesticides. However, the ethical and environmental issues are the major constraints in their acceptance, and consequently, the cultivation of genetically modified (GM) crops has invited intense debate. Since root exudates of *Bacillus thuringiensis* (Bt) crops harbor the insecticidal protein, there is a growing concern about the release and accumulation of soil-adsorbed Cry proteins and their impact on non-target microorganisms and soil microbial processes. This review pertains to reports from the laboratory studies and field trials to assess the Bt toxin proteins in soil microbes and the processes determining the soil quality in conjunction with the existing hypothesis and molecular approaches to elucidate the risk posed by the GM crops. Ecological perturbations hinder the risk aspect of soil microbiota in response to GM crops. Therefore, extensive research based on in vivo and interpretation of results using high-throughput techniques such as NGS on risk assessment are imperative to evaluate the impact of Bt crops to resolve the controversy related to their commercialization. But more studies are needed on the risk associated with stacked traits. Such

studies would strengthen our knowledge about the plant-microbe interactions.

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Unique ID: WOS:000373578500005

PubMed ID: 26560114

***Record 4 of 16.** Search terms matched: CRY1AB(1)

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

***Order Full Text []**

Title: Biomolecule-nanoparticle interactions: Elucidation of the thermodynamics by isothermal titration calorimetry

Authors: Huang, RX; Lau, BLT

Author Full Names: Huang, Rixiang; Lau, Boris L. T.

Source: BIOCHIMICA ET BIOPHYSICA ACTA-GENERAL SUBJECTS, 1860 (5):945-956; SI [10.1016/j.bbagen.2016.01.027](#) MAY 2016

Language: English

Abstract: Background: Nanomaterials (NMs) are often exposed to a broad range of biomolecules of different abundances. Biomolecule sorption driven by various interfacial forces determines the surface structure and composition of NMs, subsequently governs their functionality and the reactivity of the adsorbed biomolecules. Isothermal titration calorimetry (ITC) is a nondestructive technique that quantifies thermodynamic parameters through in-situ measurement of the heat absorption or release associated with an interaction. Scope of review: This review highlights the recent applications of ITC in understanding the thermodynamics of interactions between various nanoparticles (NPs) and biomolecules. Different aspects of a typical ITC experiment that are crucial for obtaining accurate and meaningful data, as well as the strengths, weaknesses, and challenges of ITC applications to NP research were discussed. Major conclusions: ITC reveals the driving forces behind biomolecule-NP interactions and the effects of the physicochemical properties of both NPs and biomolecules by quantifying the crucial thermodynamics parameters (e.g., binding stoichiometry, ΔH , ΔS , and ΔG). Complimentary techniques would strengthen the interpretation of ITC results for a more holistic understanding of biomolecule-NP interactions. General significance: The thermodynamic information revealed by ITC and its complimentary characterizations is important for understanding biomolecule-NP interactions that are fundamental to the biomedical and environmental applications of NMs and their toxicological effects. This article is part of a Special Issue entitled Microcalorimetry in the BioSciences - Principles and Applications, edited by Fadi Bou-Abdallah. (C) 2016 Elsevier B.V. All rights reserved.

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IDS Number: DI5LI

Unique ID: WOS:000373540200010

PubMed ID: 26851677

*Record 5 of 16. Search terms matched: BT(3); LEPIDOPTERA(1); MAIZE(6)

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

*Order Full Text []

Title: Dominance of Cry1F resistance in *Spodoptera frugiperda* (**Lepidoptera**: Noctuidae) on TC1507 **Bt maize** in Brazil

Authors: Farias, JR; Andow, DA; Horikoshi, RJ; Sorgatto, RJ; dos Santos, AC; Omoto, C

Author Full Names: Farias, Juliano R.; Andow, David A.; Horikoshi, Renato J.; Sorgatto, Rodrigo J.; dos Santos, Antonio C.; Omoto, Celso

Source: PEST MANAGEMENT SCIENCE, 72 (5):974-979; [10.1002/ps.4077](https://doi.org/10.1002/ps.4077) MAY 2016

Language: English

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. (c) 2015 Society of Chemical Industry

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IDS Number: DI6JM

Unique ID: WOS:000373605000015

PubMed ID: 26172071

*Record 6 of 16. Search terms matched: BT(1); MAIZE(1); RESISTANT(1)

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

*Order Full Text []

Title: Transgenic Cabbage Expressing Cry1Ac1 Does Not Affect the Survival and Growth of the Wolf Spider, *Pardosa astrigera* L. Koch (Araneae: Lycosidae)

Authors: Kim, YJ; Lee, JH; Harn, CH; Kim, CG

Author Full Names: Kim, Young-Joong; Lee, Joon-Ho; Harn, Chee Hark; Kim, Chang-Gi

Source: PLOS ONE, 11 (4):[10.1371/journal.pone.0153395](https://doi.org/10.1371/journal.pone.0153395) APR 7 2016

Language: English

Abstract: Both herbivores that consume transgenic crops and their predators can be exposed to

insecticidal proteins expressed in those crops. We conducted a tritrophic bioassay to evaluate the ecotoxicological impacts that Bt cabbage (*Brassica oleracea* var. *capitata*) expressing Cry1Ac1 protein might have on the wolf spider (*Pardosa astrigera*), a non-target generalist predator. Enzyme-Linked Immunosorbent Assays indicated that protein levels were 4.61 ng g(-1) dry weight in fruit flies (*Drosophila melanogaster*) fed with the transgenic cabbage and 1.86 ng g(-1) dry weight in the wolf spiders that preyed upon them. We also compared the life history traits of spiders collected from Bt versus non-Bt cabbage and found no significant differences in their growth, survival, and developmental rates. Because Bt cabbage did not affect the growth of fruit flies, we conclude that any indirect effects that this crop had on the wolf spider were probably not mediated by prey quality. Therefore, exposure to Cry1Ac1 protein when feeding upon prey containing that substance from transgenic cabbage has only a negligible influence on those non-target predatory spiders.

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Article Number: e0153395

IDS Number: DI6KO

Unique ID: WOS:000373608000128

PubMed ID: 27055120

***Record 7 of 16.** Search terms matched: CRY1AB(4)

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

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

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

Authors: Azizoglu, U; Ayvaz, A; Yilmaz, S; Temizgul, R

Author Full Names: Azizoglu, U.; Ayvaz, A.; Yilmaz, S.; Temizgul, R.

Source: JOURNAL OF APPLIED ENTOMOLOGY, 140 (3):223-227; [10.1111/jen.12241](https://doi.org/10.1111/jen.12241) APR 2016

Language: English

Abstract: Cry1Ab and Cry2Aa were overexpressed in *Escherichia coli* BL21(DE3), and their proportions were determined for evaluating their synergic and antagonistic interactions on *Ephestia 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.

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IDS Number: DG7QH

Unique ID: WOS:000372278300007

***Record 8 of 16.** Search terms matched: BT(1); CORN(2); LEPIDOPTERA(1)

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

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

Title: Can Pyramids and Seed Mixtures Delay Resistance to Bt Crops?

Authors: Carriere, Y; Fabrick, JA; Tabashnik, BE

Author Full Names: Carriere, Yves; Fabrick, Jeffrey A.; Tabashnik, Bruce E.

Source: TRENDS IN BIOTECHNOLOGY, 34 (4):291-302; [10.1016/j.tibtech.2015.12.011](https://doi.org/10.1016/j.tibtech.2015.12.011) APR 2016

Language: English

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.

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IDS Number: DI7BZ

Unique ID: WOS:000373655400005

PubMed ID: 26774592

***Record 9 of 16.** Search terms matched: BORER(2); BT(1); CORN(3); LEPIDOPTERA(6); MAIZE(5); OSTRINIA(3); RESISTANT(3); ZEA MAYS(1)

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

*Order Full Text []

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

Authors: Velez, AM; Alves, AP; Blankenship, EE; Siegfried, BD

Author Full Names: Velez, Ana Maria; Alves, Analiza P.; Blankenship, Erin E.; Siegfried, Blair D.

Source: ENTOMOLOGIA EXPERIMENTALIS ET APPLICATA, 159 (1):37-45; [10.1111/eea.12409](https://doi.org/10.1111/eea.12409) APR 2016

Language: English

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 isoline 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 30min 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.

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eISSN: 1570-7458

IDS Number: DI4QB

Unique ID: WOS:000373483300004

***Record 10 of 16.** Search terms matched: CRY1AB(8); RESISTANT(2)

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

*Order Full Text []

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

Authors: Tanaka, S; Miyamoto, K; Noda, H; Endo, H; Kikuta, S; Sato, R

Author Full Names: Tanaka, Shiho; Miyamoto, Kazuhisa; Noda, Hiroaki; Endo, Haruka; Kikuta, Shingo; Sato, Ryoichi

Source: PEPTIDES, 78 99-108; [10.1016/j.peptides.2016.01.006](https://doi.org/10.1016/j.peptides.2016.01.006) APR 2016

Language: English

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(+Y-234)] 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 BmABCC21R(+Y-234), 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. (C) 2016

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PubMed ID: 26928903

***Record 11 of 16.** Search terms matched: BT(5); CORN(2); MAIZE(7); ZEA MAYS(1)

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

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

Title: Sequential sampling plan for assessing **corn** rootworm (Coleoptera: Chrysomelidae) larval injury to **Bt maize**

Authors: Hong, BN; Nowatzki, TM; Sult, TS; Owens, ED; Pilcher, CD

Author Full Names: Hong, Bonnie; Nowatzki, Timothy M.; Sult, Theresa S.; Owens, Elizabeth D.; Pilcher, Clinton D.

Source: CROP PROTECTION, 82 36-44; [10.1016/j.cropro.2016.01.001](https://doi.org/10.1016/j.cropro.2016.01.001) APR 2016

Language: English

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. (C) 2016 Pioneer Hi-Bred International, Inc. Published by Elsevier Ltd.

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IDS Number: DH3LR

Unique ID: WOS:000372689000006

***Record 12 of 16.** Search terms matched: BT(1); CORN(1); MAIZE(1)

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

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

Title: A Review of Cry Protein Detection with Enzyme-Linked Immunosorbent Assays

Authors: Albright, VC; Hellmich, RL; Coats, JR

Author Full Names: Albright, Vurtice C., III; Hellmich, Richard L.; Coats, Joel R.

Source: JOURNAL OF AGRICULTURAL AND FOOD CHEMISTRY, 64 (11):2175-2189;
[10.1021/acs.jafc.5b03766](https://doi.org/10.1021/acs.jafc.5b03766) MAR 23 2016

Language: English

Abstract: The widespread use of Cry proteins in insecticide formulations and transgenic crops for insect control has led to an increased interest in the environmental fate of these proteins. Although several detection methods are available to monitor the fate of Cry proteins in the environment, enzyme-linked immunosorbent assays (ELISAs) have emerged as the preferred detection method, due to their cost-effectiveness, ease of use, and rapid results. Validation of ELISAs is necessary to ensure accurate measurements of Cry protein concentrations in the environment. Validation methodology has been extensively researched and published for the areas of sensitivity, specificity, accuracy, and precision; however, cross validation of ELISA results has been studied to a lesser extent. This review discusses the use of ELISAs for detection of Cry proteins in environmental samples and validation of ELISAs and introduces cross validation. The state of Cry protein environmental fate research is considered through a critical review of published literature to identify areas where the use of validation protocols can be improved.

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IDS Number: DH5TH

Unique ID: WOS:000372854300001

PubMed ID: 26949828

***Record 13 of 16.** Search terms matched: BT(5); CORN(8); CRY1AB(4); LEPIDOPTERA(1); MAIZE(1); RESISTANT(1)

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

*Order Full Text []

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

Authors: Liu, YM; Liu, QS; Wang, YA; Chen, XP; Song, XY; Romeis, J; Li, YH; Peng, YF

Author Full Names: Liu, Yanmin; Liu, Qingsong; Wang, Yanan; Chen, Xiuping; Song, Xinyuan; Romeis, Joerg; Li, Yunhe; Peng, Yufa

Source: SCIENTIFIC REPORTS, 6 [10.1038/srep23507](https://doi.org/10.1038/srep23507) MAR 23 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.

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Article Number: 23507

IDS Number: DH2IE

Unique ID: WOS:000372607500001

PubMed ID: 27005950

***Record 14 of 16.** Search terms matched: MAIZE(3); MON810(2)

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

*Order Full Text []

Title: Visual DNA Microarray Coupled with Multiplex-PCR for the Rapid Detection of Twelve Genetically Modified **Maize**

Authors: Li, YJ; Xiong, T; Wu, HW; Yang, YZ

Author Full Names: Li, Yongjin; Xiong, Tao; Wu, Huawei; Yang, Yazhen

Source: BIOCHIP JOURNAL, 10 (1):42-47; [10.1007/s13206-016-0106-y](https://doi.org/10.1007/s13206-016-0106-y) MAR 20 2016

Language: English

Abstract: We herein developed a visual DNA microarray system coupled with multiplex PCR (m-PCR) to rapidly detect twelve genetically modified maize (GMM). The microarray comprised short oligonucleotide probes complementary to the specific gene region for twelve different GMM. The m-PCR products annealed to the microarray probe were reacted with streptavidin-alkaline phosphatase conjugate and nitro blue tetrazolium/5-bromo-4-chloro-3'-indolylphosphate, p-toluidine salt (NBT/BCIP), resulting in blue spots that are easily visualized by unaided eyes for qualitative analysis. To ensure the reliability of this method, positive and negative hybridization controls were used in DNA microarray. Commercial GM materials (GMM: Bt176, Bt11, MON810, GA21, T25, MON88017, NK603, MON863, MON89034, DAS-59122-7, TC1507, MIR604; GM cotton: (MON1445, MON15985); GM soybean (Monsanto Roundup Ready soybean 40-3-2)) and non-GM materials were identified by this method and further confirmed by PCR and sequencing. The results showed that each probe consistently identified its corresponding GMM target very quickly and in a cost-effective and more time efficient way. The limit of detection is 0.5% for Bt176, Bt11, T25, MON88017, DAS59122-7, MON89034 and 1% for MON810, MIR604, GA21, MON863, NK603, TC1507. This method is advantageous because of rapid detection, cost-effectiveness and ease of use. These high specificity and sensitivity results demonstrate the feasibility of using this method in routine analysis GMOs.

ISSN: 1976-0280

eISSN: 2092-7843

IDS Number: DG9BT

Unique ID: WOS:000372378500006

***Record 15 of 16.** Search terms matched: BT(1); CORN(1); CRY1AB(4); MAIZE(1)

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

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

Title: Field studies show no significant effect of a **Cry1Ab/Ac** producing transgenic cotton on the fungal community structure in rhizosphere soil

Authors: Xie, M; Zhang, YJ; Peng, DL; Wu, G; Xu, P; Zhao, JJ; Zhang, ZR

Author Full Names: Xie, Ming; Zhang, Yan-Jun; Peng, De-Liang; Wu, Gang; Xu, Peng; Zhao, Jin-Jin; Zhang, Zhao-Rong

Source: EUROPEAN JOURNAL OF SOIL BIOLOGY, 73 69-76; [10.1016/j.ejsobi.2016.01.006](https://doi.org/10.1016/j.ejsobi.2016.01.006)
MAR-APR 2016

Language: English

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. (C) 2016 Elsevier Masson SAS. All rights reserved.

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eISSN: 1778-3615

IDS Number: DI5OZ

Unique ID: WOS:000373549800008

***Record 16 of 16.** Search terms matched: BT(1); CORN(2); LEPIDOPTERA(1); MAIZE(3); RESISTANT(1)

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

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

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

Authors: Resende, DC; Mendes, SM; Marucci, RC; Silva, AD; Campanha, MM; Waquil, JM

Author Full Names: Resende, Daniela Chaves; Mendes, Simone Martins; Marucci, Rosangela C.; Silva, Alessandra de Carvalho; Campanha, Monica Matoso; Waquil, Jose Magid

Source: REVISTA BRASILEIRA DE ENTOMOLOGIA, 60 (1):82-93;
[10.1016/j.rbe.2015.12.001](https://doi.org/10.1016/j.rbe.2015.12.001) JAN-MAR 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. (C) 2015 Sociedade Brasileira de Entomologia. Published by Elsevier Editora Ltda.

ISSN: 0085-5626

eISSN: 1806-9665

IDS Number: DG3WB

Unique ID: WOS:000372000100012

***Record 1 of 5.** Search terms matched: BT(1); CORN(1); MAIZE(2); TOLERANCE(1)

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

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

Title: Genetically modified crops in Switzerland: implications for agrosystem sustainability evidenced by multi-criteria model

Authors: Wohlfender-Buhler, D; Feusthuber, E; Wager, R; Mann, S; Aubry, SJ

Author Full Names: Wohlfender-Buhler, Doris; Feusthuber, Elisabeth; Wager, Robert; Mann, Stefan; Aubry, Sylvain J.

Source: AGRONOMY FOR SUSTAINABLE DEVELOPMENT, 36 (2):[10.1007/s13593-016-0367-9](https://doi.org/10.1007/s13593-016-0367-9) JUN 2016

Language: English

Abstract: In Switzerland, genetically modified (GM) crops have been banned in 2005 and have never been used in agriculture. The relevance and sustainability of genetically modified crops for agrosystems have been assessed following a mandate from the Swiss Parliament defined by the Federal Act on Agriculture (187d al. 1). For that, an ex ante study based on a multi-criteria decision analysis model that summarises literature and the opinion of experts has been done. The impacts of genetically modified crops on both environmental and socio-economical sustainability in Switzerland have been assessed. Here, we review four model crops for Swiss agriculture: maize, sugar beet, potato and apple. Each crop was compared for both conventional and genetically modified farming systems that contain a specific trait, namely insecticide production (*Bacillus thuringiensis* (Bt)), herbicide tolerance (HT), fungal resistance (FR), or bacterial resistance (BR). Results show that six out of seven scenarios showed a lower socio-economical sustainability for genetically modified compared to the conventional systems, whereas a slight improvement in the environmental component, mostly resources use, was observed in all scenarios. In conclusion, our work indicates that only carefully tailored and designed genetically modified crops would meet the high standard of requirements of Swiss agrosystems. Our model has thus allowed a quick diagnostic on the impact of genetically modified cultivation on sustainability.

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Article Number: 33

IDS Number: DL2EV

Unique ID: WOS:000375447100010

***Record 2 of 5.** Search terms matched: BT(1); LEPIDOPTERA(3); MAIZE(1)

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

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

Title: Bacterial Vegetative Insecticidal Proteins (Vip) from Entomopathogenic Bacteria

Authors: Chakroun, M; Banyuls, N; Bel, Y; Escriche, B; Ferre, J

Author Full Names: Chakroun, Maissa; Banyuls, Nuria; Bel, Yolanda; Escriche, Baltasar; Ferre, Juan

Source: MICROBIOLOGY AND MOLECULAR BIOLOGY REVIEWS, 80 (2):329-350;
[10.1128/MMBR.00060-15](https://doi.org/10.1128/MMBR.00060-15) JUN 2016

Language: English

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.

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IDS Number: DK6UZ

Unique ID: WOS:000375062300001

PubMed ID: 26935135

***Record 3 of 5.** Search terms matched: BT(4); CORN(7); LEPIDOPTERA(1); MAIZE(1); YIELDGARD(3)

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

*Order Full Text []

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

Authors: Bernardi, D; Bernardi, O; Horikoshi, RJ; Salmeron, E; Okuma, DM; Omoto, C

Author Full Names: Bernardi, Daniel; Bernardi, Oderlei; Horikoshi, Renato Jun; Salmeron, Eloisa; Okuma, Daniela Miyuki; Omoto, Celso

Source: CIENCIA RURAL, 46 (6):1019-1024; [10.1590/0103-8478cr20150047](https://doi.org/10.1590/0103-8478cr20150047) JUN 2016

Language: English

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.

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IDS Number: DK7BF

Unique ID: WOS:000375079100013

***Record 4 of 5.** Search terms matched: BORER(1); BT(1); CORN(5); CRY1AB(1); LEPIDOPTERA(4); OSTRINIA(1); RESISTANT(4); ZEA MAYS(1)

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

Title: Frequency of Cry1F Non-Recessive Resistance Alleles in North Carolina Field Populations of *Spodoptera frugiperda* (**Lepidoptera:** Noctuidae)

Authors: Li, GP; Reisig, D; Miao, J; Gould, F; Huang, FN; Feng, HQ

Author Full Names: Li, Guoping; Reisig, Dominic; Miao, Jin; Gould, Fred; Huang, Fangneng; Feng, Hongqiang

Source: PLOS ONE, 11 (4):[10.1371/journal.pone.0154492](https://doi.org/10.1371/journal.pone.0154492) APR 27 2016

Language: English

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 F-1/F-2 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.

ISSN: 1932-6203

Article Number: e0154492

IDS Number: DK5QZ

Unique ID: WOS:000374976200084

***Record 5 of 5.** Search terms matched: BT(1); CORN(2); MAIZE(5); YIELD(1); ZEA MAYS(2); ZEA-MAYS(1)

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

Title: Using Ancient Traits to Convert Soil Health into Crop **Yield:** Impact of Selection on

Maize Root and Rhizosphere Function

Authors: Schmidt, JE; Bowles, TM; Gaudin, ACM

Author Full Names: Schmidt, Jennifer E.; Bowles, Timothy M.; Gaudin, Amelie C. M.

Source: FRONTIERS IN PLANT SCIENCE, 7 [10.3389/fpls.2016.00373](https://doi.org/10.3389/fpls.2016.00373) MAR 30 2016

Language: English

Abstract: The effect of domestication and modern breeding on aboveground traits in maize (*Zea mays*) has been well-characterized, but the impact on root systems and the rhizosphere remain unclear. The transition from wild ecosystems to modern agriculture has focused on selecting traits that yielded the largest aboveground production with increasing levels of crop management and nutrient inputs. Root morphology, anatomy, and ecophysiological processes may have been affected by the substantial environmental and genetic shifts associated with this transition. As a result, root and rhizosphere traits that allow more efficient foraging and uptake in lower synthetic input environments might have been lost. The development of modern maize has led to a shift in microbiome community composition, but questions remain as to the dynamics and drivers of this change during maize evolution and its implications for resource acquisition and agroecosystem functioning under different management practices. Better understanding of how domestication and breeding affected root and rhizosphere microbial traits could inform breeding strategies, facilitate the sourcing of favorable alleles, and open new frontiers to improve resource use efficiency through greater integration of root development and ecophysiology with agroecosystem functioning.

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Article Number: 373

IDS Number: DH6AI

Unique ID: WOS:000372873000002

PubMed ID: 27066028