

Appendix 5.3 MON 810 literature review – List of all hits (June 2016-May 2017) -Web of Science™ Core Collection database

Record 1 of 50**Title:** Ground beetle acquisition of Cry1Ab from plant- and residue-based food webs**Author(s):** Andow, DA (Andow, D. A.); Zwahlen, C (Zwahlen, C.)**Source:** BIOLOGICAL CONTROL **Volume:** 103 **Pages:** 204-209 **DOI:** 10.1016/j.biocontrol.2016.09.009 **Published:** DEC 2016

Abstract: Ground beetles are significant predators in agricultural habitats. While many studies have characterized effects of Bt maize on various carabid species, few have examined the potential acquisition of Cry toxins from live plants versus plant residue. In this study, we examined how live Bt maize and Bt maize residue affect acquisition of Cry1Ab in six species. Adult beetles were collected live from fields with either current-year Bt maize, one-year-old Bt maize residue, two-year-old Bt maize residue, or fields without any Bt crops or residue for the past two years, and specimens were analyzed using ELISA. Observed Cry1Ab concentrations in the beetles were similar to that reported in previously published studies. Only one specimen of *Cyclotrachelus iowensis* acquired Cry1Ab from two-year-old maize residue. Three species acquired Cry1Ab from fields with either live plants or plant residue (*Cyclotrachelus iowensis*, *Poecilus lucublandus*, *Poecilus chalcites*), implying participation in both live-plant and residue-based food webs. Two species acquired toxin from fields with live plants, but not from fields with residue (*Bembidion quadrimaculatum*, *Elaphropus incurvus*), suggesting participation only in live plant-based food webs. One species did not acquire Cry1Ab from either live-plant or residue (*Scarites quadriceps*), suggesting that its food sources might not contain significant amounts of Cry1Ab. These results revealed significant differentiation among carabid species in their associations with live-plant and residue-based food webs in agricultural fields. (C) 2016 Elsevier Inc. All rights reserved.

Accession Number: WOS:000386468300024**ISSN:** 1049-9644**eISSN:** 1090-2112**Record 2 of 50****Title:** Movement and survival of *Busseola fusca* (Lepidoptera: Noctuidae) larvae within maize plantings with different ratios of non-Bt and Bt seed**Author(s):** Erasmus, A (Erasmus, Annemie); Marais, J (Marais, Jaco); Van den Berg, J (Van den Berg, Johnnie)**Source:** PEST MANAGEMENT SCIENCE **Volume:** 72 **Issue:** 12 **Pages:** 2287-2294 **DOI:** 10.1002/ps.4273 **Published:** DEC 2016

Abstract: BACKGROUNDProducts of plant biotechnology, for example genetically modified Bt maize, provide useful tools for pest management. The benefits provided by insect-resistant plants are, however, threatened by the evolution of resistance by target pest species. The high-dose/refuge insect resistance management strategy (IRM) as well as seed mixtures are globally used as IRM strategies. *Busseola fusca* (Lepidoptera: Noctuidae), the target stem borer of Bt maize in Africa, evolved resistance to Bt maize expressing Cry1Ab protein in South Africa. Owing to high larval mobility and subsequent sublethal exposure of larvae moving between non-Bt and Bt plants, more rapid resistance evolution has been proposed as a possibility with deployment of seed mixture strategies.

RESULTSLaboratory and field studies were conducted to study *B. fusca* larval mobility. In the laboratory, different scenarios of *B. fusca* larval movement between single-gene (Cry1Ab) and stacked-trait (Cry1A.105 and Cry2Ab2) Bt maize were studied. Data on larval survival and mass over time indicated that Cry proteins do not kill larvae above certain developmental stages. A 2 year field study with the single gene and the stacked event was conducted using seed mixtures containing 5, 10, 15 and 20% non-Bt seed as well as a control treatment (non-Bt seed only).

CONCLUSIONLarval movement continued for 5 weeks and resulted in a significant incidence of Bt and non-Bt damaged plants, indicating that the movement behaviour of *B. fusca* is of such a nature that seed mixtures as an IRM strategy may not be effective to delay resistance evolution. (c) 2016 Society of Chemical Industry

Accession Number: WOS:000386927800011**PubMed ID:** 26990107**ISSN:** 1526-498X**eISSN:** 1526-4998**Record 3 of 50****Title:** Frequency of Cry1F resistance alleles in *Spodoptera frugiperda* (Lepidoptera: Noctuidae) in Brazil**Author(s):** Farias, JR (Farias, Juliano R.); Andow, DA (Andow, David A.); Horikoshi, RJ (Horikoshi, Renato J.); Bernardi, D (Bernardi, Daniel); Ribeiro, RD (Ribeiro, Rebeca da S.); do Nascimento, ARB (do Nascimento, Antonio R. B.); dos Santos, AC (dos Santos, Antonio C.); Omoto, C (Omoto, Celso)**Source:** PEST MANAGEMENT SCIENCE **Volume:** 72 **Issue:** 12 **Pages:** 2295-2302 **DOI:** 10.1002/ps.4274 **Published:** DEC 2016

Abstract: BACKGROUNDThe frequency of resistance alleles is a major factor influencing the rate of resistance evolution. Here, we adapted the F-2 screen procedure for *Spodoptera frugiperda* (J. E. Smith) with a discriminating concentration assay, and extended associated statistical methods to estimate the frequency of resistance to Cry1F protein in *S. frugiperda* in Brazil when resistance was not rare.

RESULTSWe show that F-2 screen is efficient even when the resistance frequency is 0.250. It was possible to screen 517 isoparental lines from 12 populations sampled in five states of Brazil during the first half of 2012. Western Bahia had the highest allele frequency of Cry1F resistance, 0.192, with a 95% confidence interval (CI) between 0.163 and 0.220. All other states had a similar and lower frequency varying from 0.042 in Parana to 0.080 in Mato Grosso do Sul.

CONCLUSIONThe high frequency in western Bahia may be related to year-round availability of maize, the high population density of *S. frugiperda*, the lack of refuges and the high adoption rate of Cry1F maize. Cry1F resistance alleles were not rare and occurred at frequencies that have already compromised the useful life of TC1507 maize in western Bahia. (c) 2016 Society of Chemical Industry

Accession Number: WOS:000386927800012**PubMed ID:** 26990201**ISSN:** 1526-498X**eISSN:** 1526-4998**Record 4 of 50****Title:** Impedimetric immunosensors for the detection of Cry1Ab protein from genetically modified maize seeds**Author(s):** Freitas, M (Freitas, Maria); Correr, W (Correr, Wagner); Cancino-Bernardi, J (Cancino-Bernardi, Juliana); Barroso, MF (Fatima Barroso, M.); Delerue-Matos, C (Delerue-Matos, Cristina); Zucolotto, V (Zucolotto, Valtencir)**Source:** SENSORS AND ACTUATORS B-CHEMICAL **Volume:** 237 **Pages:** 702-709 **DOI:** 10.1016/j.snb.2016.06.149 **Published:** DEC 2016

Abstract: Regardless the controversies surrounding genetically modified organisms (GMO), their cultivation is constantly increasing and in according to the EU legislation, labeling is mandatory for products containing EU-authorized-GMO higher than 0.9%. Thereby, new analytical strategies for rapid and effective detection of GMO on foodstuffs are required. In this work, an electrochemical immunosensor for effective determination of Cry1Ab protein from MON810 transgenic maize (EU-authorized-GMO) is described. The immunosensor was developed onto indium tin oxide (ITO) electrodes modified by 3-aminopropyltrimethoxysilane (APTES) monolayer to covalently immobilize Anti-Cry1Ab polyclonal antibodies. The protein interaction with the polyclonal antibody (PAb) recognition platform was directly monitored and measured by cyclic voltammetry and electrochemical impedance spectroscopy using commercially Cry1Ab protein. After the analytical features optimization a linear response from 1 to 10 ng mL(-1), a limit of detection (LOD) of 0.37 ng mL(-1) and a limit of quantification (LOQ) of 1.23 ng mL(-1) - which provided accurate results (RSD <7.5%) - were achieved. The immunosensor allowed a simple and fast detection of Cry1Ab protein extracted from maize seeds with different GM maize mass percentages (0%, 0.5%, 1%, 2.5% and 5%). To crosscheck the detection of Cry1Ab protein, an enzyme-linked immunosorbent assay (ELISA) was used. The results indicate that the immunosensor is suitable for the transgenic protein Cry1Ab detection in GM maize representing a successfully tool to verify the compliance of the EU regulations. (C) 2016 Elsevier B.V. All rights reserved.

Accession Number: WOS:000384010500085**Author Identifiers:**

Author	ResearcherID Number	ORCID Number
Sao Carlos Institute of Physics, IFSC/USP	M-2664-2016	
ISSN: 0925-4005		

Record 5 of 50**Title:** People's reliance on the affect heuristic may result in a biased perception of gene technology**Author(s):** Siegrist, M (Siegrist, Michael); Sutterlin, B (Sutterlin, Bernadette)

Source: FOOD QUALITY AND PREFERENCE **Volume:** 54 **Pages:** 137-140 **DOI:** 10.1016/j.foodqual.2016.07.012 **Published:** DEC 2016

Abstract: In an experiment, we demonstrated that the same outcome of a new corn variety was evaluated less positively if it was from gene technology (GT) compared with conventional breeding technology (CT). The participants (N = 205) were randomly assigned to one of two experimental conditions-GT or CT. In the first step, the participants' affect associated with GT or CT plants was measured. Then, the participants read a hypothetical scenario about a new genetically modified (GT condition) or conventionally produced (CT condition) corn variety that was more resistant to the corn borer. They were presented with a matrix in which 1976 black (50%) and white (50%) cells were randomly scattered. The participants were informed that each cell represented a test plot and that the corn plants in the white test plots were not damaged by the corn borer. The participants were then asked to estimate the percentage of the plots infested by the corn borer and how effective they perceived the new corn variety was in resisting the pest. The results indicated that the participants assigned to the GT condition perceived the new corn variety as significantly less effective compared with the participants assigned to the CT condition. No significant difference was observed for estimated percentages. The results suggest that the difference in perceived effectiveness between genetically modified and conventionally bred corn can be explained by people's reliance on the affect heuristic. (C) 2016 Elsevier Ltd. All rights reserved.

Accession Number: WOS:000382592300015

Author Identifiers:

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

ISSN: 0950-3293

eISSN: 1873-6343

Record 6 of 50

Title: Yield trends under varying environmental conditions for sorghum and wheat across Australia

Author(s): Potgieter, AB (Potgieter, Andries B.); Lobell, DB (Lobell, David B.); Hammer, GL (Hammer, Graeme L.); Jordan, DR (Jordan, David R.); Davis, P (Davis, Peter); Brider, J (Brider, Jason)

Source: AGRICULTURAL AND FOREST METEOROLOGY **Volume:** 228 **Pages:** 276-285 **DOI:** 10.1016/j.agrformet.2016.07.004 **Published:** NOV 15 2016

Abstract: Globally as well as nationally, food production is being exposed to increased climatic and market volatility. The trend in sorghum yield in Australia has been consistent and positive over the last 30 years, while yield trends globally for other cereals like wheat, maize and rice have slowed. Australia is of interest not only as a major exporter in world markets, but also because considerable research effort has been focused on developing crops and practices that help to reduce the risks of yield losses under drought conditions. This study examines sorghum and wheat yield trends over the previous three to four decades in Australia after realistically accounting for the effects of year-to-year climate variability. We quantified the yield trends within three distinct types of crop stress environments (i.e. DRY: ENVT1, MODERATE: ENV2&WET: ENVT3). Overall trends in sorghum yields were 2.1% per year (44 kg/ha/year), which was nearly double that found for wheat (1.2% per year; 21 kg/ha/year). However, in dry environments, relative yield trends for sorghum were 3.6 times those for wheat, whereas in wet environments trends were similar. Likely technology and environmental factors underpinning these trends are discussed. (C) 2016 Elsevier B.V. All rights reserved.

Accession Number: WOS:000383295200023

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eISSN: 1873-2240

Record 7 of 50

Title: Effects of Periplocoside P from *Periploca sepium* on the Midgut Transmembrane Potential of *Mythimna separata* Larvae

Author(s): Wang, YY (Wang, YingYing); Qi, ZJ (Qi, Zhijun); Qi, M (Qi, Meng); Hu, ZN (Hu, Zhaonong); Wu, WJ (Wu, Wenjun)

Source: SCIENTIFIC REPORTS **Volume:** 6 **Article Number:** 36982 **DOI:** 10.1038/srep36982 **Published:** NOV 11 2016

Abstract: Periplocoside P (PSP) isolated from the root bark of *Periploca sepium* contains a pregnane glycoside skeleton and possesses high insecticidal properties. Preliminary studies indicated that PSP disrupts epithelial functions in the midgut of lepidopteran larvae. In the present study, we examined the effects of PSP on the apical and basolateral membrane voltages, V-a and V-bl, respectively, of cells from (1) midguts isolated from the larvae of the oriental armyworm *Mythimna separata* that were in vitro incubated with toxins and (2) midguts isolated from *M. separata* larvae force-fed with PSP. We compared the effects of PSP with the effects of the *Bacillus thuringiensis* toxin Cry1Ab and inactive periplocoside E (PSE) on the midgut epithelial cells. The results showed that V-a rapidly decreased in the presence of PSP in a time- and dose-dependent manner, similar to the effects of Cry1Ab. By contrast, PSE did not affect the V-a and V-bl. Additionally, PSP did not influence the V-bl. Given these results, we speculate that PSP may modulate transport mechanisms at the apical membrane of the midgut epithelial cells by inhibiting the V-type H⁺ ATPase.

Accession Number: WOS:000387475300001

PubMed ID: 27833169

ISSN: 2045-2322

Record 8 of 50

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

Author(s): Chen, HX (Chen, Hong-Xing); Yang, R (Yang, Rui); Yang, W (Yang, Wang); Zhang, L (Zhang, Liu); Camara, I (Camara, Ibrahimia); Dong, XH (Dong, Xue-Hui); Liu, YQ (Liu, Yi-Qing); Shi, WP (Shi, Wang-Peng)

Source: ENVIRONMENTAL SCIENCE AND POLLUTION RESEARCH **Volume:** 23 **Issue:** 21 **Pages:** 21511-21516 **DOI:** 10.1007/s11356-016-7340-7 **Published:** NOV 2016

Abstract: *Ostrinia furnacalis* (Guen,e) and *Helicoverpa armigera* (Hubner) are the most important pests of maize in China. A laboratory study and a 2-year field study on the efficacy of transgenic maize expressing the Cry1Ac protein BT38 against *O. furnacalis* and *H. armigera* were performed. We found that the husks, kernels, and silks of BT38 showed significant efficacy against larvae of *O. furnacalis* and *H. armigera*. In the field, when neonate larvae of *O. furnacalis* and *H. armigera* were on plants at different growth stages and when levels of leaf-damage or number of damaged silks were used to score efficacy, we found that BT38 showed significant insecticidal efficacy against *O. furnacalis* and *H. armigera*, but the non-Bt maize did not show significant efficacy against either pest. These results suggest that the insecticidal efficacy of Bt maize expressing the Cry1Ac protein could be useful in the integrated pest management of these key maize pests.

Accession Number: WOS:000387599600036

PubMed ID: 27510165

ISSN: 0944-1344

eISSN: 1614-7499

Record 9 of 50

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

Author(s): Zhang, YW (Zhang, Yuwen); Zhang, W (Zhang, Wei); Liu, Y (Liu, Yan); Wang, JH (Wang, Jianhua); Wang, GY (Wang, Guoying); Liu, YJ (Liu, Yunjun)

Source: ANALYTICAL AND BIOANALYTICAL CHEMISTRY **Volume:** 408 **Issue:** 28 **Pages:** 8231-8239 **DOI:** 10.1007/s00216-016-9938-5 **Published:** NOV 2016

Abstract: CryIIe is a kind of *Bacillus thuringiensis* (Bt) toxin protein which has a different action model than the CryIAb and CryIAc protein. The transgenic maize expressing CryIIe might be commercially used in the near future and it is urgent to develop a method to detect CryIIe protein in transgenic plants and their products. To develop an ELISA method, CryIIe protein was expressed in *Escherichia coli* strain Transetta DE3, purified with the Ni-NTA spin columns, and then validated by sequencing. Bioassay results showed that the purified CryIIe protein was highly toxic to the Asian corn borer. The polyclonal antibody (pAb) and the specific monoclonal antibody (mAb) 1G(4)2D(6) were generated from rabbit and mice which were immunized with CryIIe protein, respectively. Western blotting of crude CryIIe protein extracts was established by employing mAb 1G(4)2D(6), whereas the mAb 1G(4)2D(6) negligibly recognized other Bt proteins. Sandwich ELISA against CryIIe protein was established by coating with pAb and detecting with mAb 1G(4)2D(6). The limit of detection (LOD), the limit of quantification (LOQ), and the quantification range of the assay in different matrices of maize plant were determined as 0.27-0.51, 0.29-0.78, and 0.45-15.71 ng/mL, respectively. Recoveries of CryIIe protein spiked in different maize tissues ranged from 75.1 to 99.5%. The established sandwich ELISA was verified using transgenic maize overexpressing CryIIe. The results in this study suggested that the established ELISA method is effective for detecting CryIIe protein in transgenic plants.

Accession Number: WOS:000386693000034

PubMed ID: 27659816

ISSN: 1618-2642

eISSN: 1618-2650

Record 10 of 50

Title: Larval development of *Spodoptera eridania* and *Spodoptera frugiperda* fed on fresh ear of field corn expressing the Bt proteins (Cry1F and Cry1F+Cry1A.105+Cry2Ab2)

Author(s): Bortolotto, OC (Bortolotto, Orcial Ceolin); Bueno, AD (Bueno, Adeney de Freitas); de Queiroz, AP (de Queiroz, Ana Paula); Silva, GV (Silva, Gabriela Vieira)

Source: CIENCIA RURAL **Volume:** 46 **Issue:** 11 **Pages:** 1898-1901 **DOI:** 10.1590/0103-8478cr20151461 **Published:** NOV 2016

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

Accession Number: WOS:000385847000003

ISSN: 0103-8478

eISSN: 1678-4596

Record 11 of 50

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

Author(s): da Silva, KJ (da Silva, Kelly Justin); de Armas, RD (de Armas, Rafael Dutra); Soares, CRFS (Soares, Claudio Roberto F. S.); Ogliari, JB (Ogliari, Juliana Bernardi)

Source: WORLD JOURNAL OF MICROBIOLOGY & BIOTECHNOLOGY **Volume:** 32 **Issue:** 11 **Article Number:** 189 **DOI:** 10.1007/s11274-016-2149-6 **Published:** NOV 2016

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

Accession Number: WOS:000385145400016

PubMed ID: 27696288

ISSN: 0959-3993

eISSN: 1573-0972

Record 12 of 50

Title: Selection and application of broad-specificity human domain antibody for simultaneous detection of Bt Cry toxins

Author(s): Xu, CX (Xu, Chongxin); Zhang, X (Zhang, Xiao); Liu, XQ (Liu, Xiaoqin); Liu, Y (Liu, Yuan); Hu, XD (Hu, Xiaodan); Zhong, JF (Zhong, Jianfeng); Zhang, CZ (Zhang, Cunzheng); Liu, XJ (Liu, Xianjin)

Source: ANALYTICAL BIOCHEMISTRY **Volume:** 512 **Pages:** 70-77 **DOI:** 10.1016/j.ab.2016.08.012 **Published:** NOV 1 2016

Abstract: Bt Cry toxin is a kind of bio-toxins that used for genetically modified crops (GMC) transformation widely. In this study, total 15 positive clones could bind the Bt Cry toxins which isolated from a human domain antibody library by 5 rounds affinity selection. According to analyzing of PCR amplification and enzyme linked immunosorbent assay (ELISA), the most positive phage domain antibody (named F5) gene was cloned into the pET26b vector and expressed in *E. coli* BL21. The purified antibody was used to develop an indirect competitive ELISA (IC-ELISA) for Cry1Ab, Cry1Ac, Cry1B, Cry1C and Cry1F toxins, respectively. The working range of detection for standard curves in IC-ELISA were 0.258-1.407 $\mu\text{g/mL}$, the medium inhibition concentration (IC50) were 0.727-0.892 $\mu\text{g/mL}$ and detection limit (IC10) were 0.029-0.07414 $\mu\text{g/mL}$ for those Bt Cry toxins. The affinity of F5 domain antibody with Cry1Ab, Cry1Ac, Cry1B, Cry1C and Cry1F toxins were 1.21-5.94 $\times 10^7$ M⁻¹. The average recoveries of the 5 kinds of Bt Cry toxins from spiked wheat samples were ranged from 81.2%-100.8% with a CV at 2.5%-9.4%. The results showed that we successfully obtained the broad-specificity human domain antibody for simultaneous detection of Bt Cry toxins in agricultural product samples. (C) 2016 Elsevier Inc. All rights reserved.

Accession Number: WOS:000383413300008

PubMed ID: 27544649

ISSN: 0003-2697

eISSN: 1096-0309

Record 13 of 50

Title: Resistance of Bt-maize (MON810) against the stem borers *Busseola fusca* (Fuller) and *Chilo partellus* (Swinhoe) and its yield performance in Kenya

Author(s): Tefera, T (Tefera, Tadele); Mugo, S (Mugo, Stephen); Mwimali, M (Mwimali, Murenga); Anani, B (Anani, Bruce); Tende, R (Tende, Regina); Beyene, Y (Beyene, Yoseph); Gichuki, S (Gichuki, Simon); Oikeh, SO (Oikeh, Sylvester O.); Nang'ayo, F (Nang'ayo, Francis); Okeno, J (Okeno, James); Njeru, E (Njeru, Evans); Pillay, K (Pillay, Kiru); Meisel, B (Meisel, Barbara); Prasanna, BM (Prasanna, B. M.)

Source: CROP PROTECTION **Volume:** 89 **Pages:** 202-208 **DOI:** 10.1016/j.cropro.2016.07.023 **Published:** NOV 2016

Abstract: A study was conducted to assess the performance of maize hybrids with Bt event MON810 (Bt-hybrids) against the maize stem borer *Busseola fusca* (Fuller) in a biosafety greenhouse (BGH) and against the spotted stem borer *Chilo partellus* (Swinhoe) under confined field trials (CFT) in Kenya for three seasons during 2013-2014. The study comprised 14 non-commercialized hybrids (seven pairs of near-isogenic Bt and non-Bt hybrids) and four non-Bt commercial hybrids. Each plant was artificially infested twice with 10 first instar larvae. In CFT, plants were infested with *C. partellus* 14 and 24 days after planting; in BGH, plants were infested with *B. fusca* 21 and 31 days after planting. In CFT, the seven Bt hybrids significantly differed from their non-Bt counterparts for leaf damage, number of exit holes, percent tunnel length, and grain yield. When averaged over three seasons, Bt-hybrids gave the highest grain yield (9.7 t ha⁻¹), followed by non-Bt hybrids (6.9 t ha⁻¹) and commercial checks (6 t ha⁻¹). Bt-hybrids had the least number of exit holes and percent tunnel length in all the seasons as compared to the non-Bt hybrids and commercial checks. In BGH trials, Bt-hybrids consistently suffered less leaf damage than their non-Bt near isolines. The study demonstrated that MON810 was effective in controlling *B. fusca* and *C. partellus*. Bt-maize, therefore, has great potential to reduce the risk of maize grain losses in Africa due to stem borers, and will enable the smallholder farmers to produce high-quality grain with increased yield, reduced insecticide inputs, and improved food security. (C) 2016 The Authors. Published by Elsevier Ltd.

Accession Number: WOS:000383826400027

PubMed ID: 27812235

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eISSN: 1873-6904

Record 14 of 50

Title: Cry1Ab-expressing rice did not influence expression of fecundity-related genes in the wolf spider *Pardosa pseudoannulata*

Author(s): Wang, J (Wang, Juan); Peng, YD (Peng, Yuan-De); He, C (He, Chao); Wei, BY (Wei, Bao-Yang); Liang, YS (Liang, Yun-Shan); Yang, HL (Yang, Hui-Lin); Wang, Z (Wang, Zhi); Stanley, D (Stanley, David); Song, QS (Song, Qi-Sheng)

Source: GENE **Volume:** 592 **Issue:** 1-7 **Pages:** 1-7 **DOI:** 10.1016/j.gene.2016.07.041 **Published:** OCT 30 2016

Abstract: The impact of *Bacillus thuringiensis* (Bt) toxin proteins on non-target predatory arthropods is not well understood at the cellular and molecular levels. Here, we investigated the potential effects of Cry1Ab expressing rice on fecundity of the wolf spider, *Pardosa pseudoannulata*, and some of the underlying molecular mechanisms. The results indicated that brown planthoppers (BPHs) reared on Cry1Ab-expressing rice accumulated the Cry toxin and that reproductive parameters (pre-oviposition period, post-oviposition stage, number of eggs, and egg hatching rate) of the spiders that consumed BPHs reared on Bt rice were not different from those that consumed

BPHs reared on the non-Bt control rice. The accumulated Cry1Ab did not influence several vitellin (Vt) parameters, including stored energy and amino acid composition, during one generation. We considered the possibility that the Cry toxins exert their influence on beneficial predators via more subtle effects detectable at the molecular level in terms of gene expression. This led us to transcriptome analysis to detect differentially expressed genes in the ovaries of spiders exposed to dietary Cry1Ab and their counterpart control spiders. Eight genes, associated with vitellogenesis, vitellogenin receptor activity, and vitellin membrane formation were not differentially expressed between ovaries from the treated and control spiders, confirmed by qPCR analysis. We infer that dietary Cry1Ab expressing rice does not influence fecundity, nor expression levels of Vt-associated genes in *P. pseudoannulata*. (C) 2016 Published by Elsevier B.V.

Accession Number: WOS:000383304600001

PubMed ID: 27452121

ISSN: 0378-1119

eISSN: 1879-0038

Record 15 of 50

Title: Effective dominance of resistance of *Spodoptera frugiperda* to Bt maize and cotton varieties: implications for resistance management

Author(s): Horikoshi, RJ (Horikoshi, Renato J.); Bernardi, D (Bernardi, Daniel); Bernardi, O (Bernardi, Oderlei); Malaquias, JB (Malaquias, Jose B.); Okuma, DM (Okuma, Daniela M.); Miraldo, LL (Miraldo, Leonardo L.); Amaral, FSDE (e Amaral, Fernando S. de A.); Omoto, C (Omoto, Celso)

Source: SCIENTIFIC REPORTS **Volume:** 6 **Article Number:** 34864 **DOI:** 10.1038/srep34864 **Published:** OCT 10 2016

Abstract: The resistance of fall armyworm (FAW), *Spodoptera frugiperda*, has been characterized to some Cry and Vip3A proteins of *Bacillus thuringiensis* (Bt) expressed in transgenic maize in Brazil. Here we evaluated the effective dominance of resistance based on the survival of neonates from selected Bt-resistant, heterozygous, and susceptible (Sus) strains of FAW on different Bt maize and cotton varieties. High survival of strains resistant to the Cry1F (HX-R), Cry1A. 105/Cry2Ab (VT-R) and Cry1A. 105/Cry2Ab/Cry1F (PW-R) proteins was detected on Herculex, YieldGard VT PRO and PowerCore maize. Our Vip3A-resistant strain (Vip-R) exhibited high survival on Herculex, Agrisure Viptera and Agrisure Viptera 3 maize. However, the heterozygous from HX-R x Sus, VT-R x Sus, PW-R x Sus and Vip-R x Sus had complete mortality on YieldGard VT PRO, PowerCore, Agrisure Viptera, and Agrisure Viptera 3, whereas the HX-R x Sus and Vip-R x Sus strains survived on Herculex maize. On Bt cotton, the HX-R, VT-R and PW-R strains exhibited high survival on Bollgard II. All resistant strains survived on WideStrike, but only PW-R and Vip-R x Sus survived on TwinLink. Our study provides useful data to aid in the understanding of the effectiveness of the refuge strategy for Insect Resistance Management of Bt plants.

Accession Number: WOS:000385144400001

PubMed ID: 27721425

Author Identifiers:

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

ISSN: 2045-2322

Record 16 of 50

Title: Effects of Field History on Corn Root Injury and Adult Abundance of Northern and Western Corn Rootworm (Coleoptera: Chrysomelidae)

Author(s): Dunbar, MW (Dunbar, Mike W.); O'Neal, ME (O'Neal, Matthew E.); Gassmann, AJ (Gassmann, Aaron J.)

Source: JOURNAL OF ECONOMIC ENTOMOLOGY **Volume:** 109 **Issue:** 5 **Pages:** 2096-2104 **DOI:** 10.1093/jee/tow163 **Published:** OCT 2016

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

Accession Number: WOS:000386136700018

PubMed ID: 27498115

ISSN: 0022-0493

eISSN: 1938-291X

Record 17 of 50

Title: Estimating E-Race European Corn Borer (Lepidoptera: Crambidae) Adult Activity in Snap Bean Fields Based on Corn Planting Intensity and Their Activity in Corn in New York Agroecosystems

Author(s): Schmidt-Jeffris, RA (Schmidt-Jeffris, Rebecca A.); Huseeth, AS (Huseeth, Anders S.); Nault, BA (Nault, Brian A.)

Source: JOURNAL OF ECONOMIC ENTOMOLOGY **Volume:** 109 **Issue:** 5 **Pages:** 2210-2214 **DOI:** 10.1093/jee/tow149 **Published:** OCT 2016

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

Accession Number: WOS:000386136700032

ISSN: 0022-0493

eISSN: 1938-291X

Record 18 of 50

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

Author(s): Zeljenkova, D (Zeljenkova, Dagmar); Alacova, R (Alacova, Radka); Ondrejko, J (Ondrejko, Julia); Ambrusova, K (Ambrusova, Katarina); Bartusova, M (Bartusova, Maria); Kebis, A (Kebis, Anton); Kovriznych, J (Kovriznych, Jevgenij); Rollerova, E (Rollerova, Eva); Szabova, E (Szabova, Elena); Wimmerova, S (Wimmerova, Sonja); Cernak, M (Cernak, Martin); Krivosikova, Z (Krivosikova, Zora); Kuricova, M (Kuricova, Miroslava); Liskova, A (Liskova, Aurelia); Spustova, V (Spustova, Viera); Tulinska, J (Tulinska, Jana); Levkut, M (Levkut, Mikulas); Revajova, V (Revajova, Viera); Sevcikova, Z (Sevcikova, Zuzana); Schmidt, K (Schmidt, Kerstin); Schmidtko, J (Schmidtko, Joerg); Schmidt, P (Schmidt, Paul); La Paz, JL (La Paz, Jose Luis); Corujo, M (Corujo, Maria); Pla, M (Pla, Maria); Kleter, GA (Kleter, Gijs A.); Kok, EJ (Kok, Esther J.); Sharbati, J (Sharbati, Jutta); Bohmer, M (Bohmer, Marc); Bohmer, N (Bohmer, Nils); Einspanier, R (Einspanier, Ralf); Adel-Patient, K (Adel-Patient, Karine); Spok, A (Spok, Armin); Poting, A (Poting, Annette); Kohl, C (Kohl, Christian); Wilhelm, R (Wilhelm, Ralf); Schiemann, J (Schiemann, Joachim); Steinberg, P (Steinberg, Pablo)

Source: ARCHIVES OF TOXICOLOGY **Volume:** 90 **Issue:** 10 **Pages:** 2531-2562 **DOI:** 10.1007/s00204-016-1798-4 **Published:** OCT 2016

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

Accession Number: WOS:000385654600014**PubMed ID:** 27439414**ISSN:** 0340-5761**eISSN:** 1432-0738**Record 19 of 50****Title:** Integrating Insect, Resistance, and Floral Resource Management in Weed Control Decision-Making**Author(s):** DiTommaso, A (DiTommaso, Antonio); Averill, KM (Averill, Kristine M.); Hoffmann, MP (Hoffmann, Michael P.); Fuchsberg, JR (Fuchsberg, Jeffrey R.); Losey, JE (Losey, John E.)**Source:** WEED SCIENCE **Volume:** 64 **Issue:** 4 **Pages:** 743-756 **DOI:** 10.1614/WS-D-16-00052.1 **Published:** OCT-DEC 2016

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

Accession Number: WOS:000386055100021**ISSN:** 0043-1745**eISSN:** 1550-2759**Record 20 of 50****Title:** Marker-free transgenic rice expressing the vegetative insecticidal protein (Vip) of *Bacillus thuringiensis* shows broad insecticidal properties**Author(s):** Pradhan, S (Pradhan, Subrata); Chakraborty, A (Chakraborty, Anirban); Sikdar, N (Sikdar, Narattam); Chakraborty, S (Chakraborty, Saikat); Bhattacharyya, J (Bhattacharyya, Jagannath); Mitra, J (Mitra, Joy); Manna, A (Manna, Anulina); Gupta, SD (Gupta, Snehasish Dutta); Sen, SK (Sen, Soumitra Kumar)**Source:** PLANTA **Volume:** 244 **Issue:** 4 **Pages:** 789-804 **DOI:** 10.1007/s00425-016-2535-1 **Published:** OCT 2016

Abstract: Genetically engineered rice lines with broad insecticidal properties against major lepidopteran pests were generated using a synthetic, truncated form of vegetative insecticidal protein (Syn vip3BR) from *Bacillus thuringiensis*. The selectable marker gene and the redundant transgene(s) were eliminated through Cre/lox mediated recombination and genetic segregation to make consumer friendly Bt -rice.

For sustainable resistance against lepidopteran insect pests, chloroplast targeted synthetic version of bioactive core component of a vegetative insecticidal protein (Syn vip3BR) of *Bacillus thuringiensis* was expressed in rice under the control of green-tissue specific ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit gene promoter. The transgenic plants (in *Oryza sativa indica Swarna cultivar*) showed high insect mortality rate in vitro against major rice pests, yellow stem borer (*Scirpophaga incertulas*), rice leaf folder (*Cnaphalocrocis medinalis*) and rice horn caterpillar (*Melanitis leda ismene*) in T-1 generation, indicating insecticidal potency of Syn vip3BR. Under field conditions, the T-1 plants showed considerable resistance against leaf folders and stem borers. The expression cassette (vip-lox-hpt-lox) as well as another vector with chimeric cre recombinase gene under constitutive rice ubiquitin1 gene promoter was designed for the elimination of selectable marker hygromycin phosphotransferase (hptII) gene. Crossing experiments were performed between T-1 plants with single insertion site of vip-lox-hpt-lox T-DNA and one T-1 plant with moderate expression of cre recombinase with linked bialaphos resistance (syn bar) gene. Marker gene excision was achieved in hybrids with up to 41.18 % recombination efficiency. Insect resistant transgenic lines, devoid of selectable marker and redundant transgene(s) (hptII + cre-syn bar), were established in subsequent generation through genetic segregation.

Accession Number: WOS:000382939900003**PubMed ID:** 27165311**ISSN:** 0032-0935**eISSN:** 1432-2048**Record 21 of 50****Title:** Functional dominance of different aged larvae of Bt-resistant *Spodoptera frugiperda* (Lepidoptera: Noctuidae) on transgenic maize expressing Vip3Aa20 protein**Author(s):** Miraldo, LL (Miraldo, Leonardo L.); Bernardi, O (Bernardi, Oederlei); Horikoshi, RJ (Horikoshi, Renato J.); Amaral, FSAE (Amaral, Fernando S. A. e); Bernardi, D (Bernardi, Daniel); Omoto, C (Omoto, Celso)**Source:** CROP PROTECTION **Volume:** 88 **Pages:** 65-71 **DOI:** 10.1016/j.cropro.2016.06.004 **Published:** OCT 2016

Abstract: Fall armyworm (FAW), *Spodoptera frugiperda* (J. E. Smith), is the main target pest of transgenic maize expressing insecticidal proteins from *Bacillus thuringiensis* Berliner (Bt) in Brazil. To optimize resistance management strategies, we evaluated the functional dominance of different aged larvae of Bt-resistant FAW on Vip3Aa20 maize. We measured the survival and development of Vip3Aa20-resistant, -heterozygote, and -susceptible strains on MIR162 (expressing Vip3Aa20) and Bt11 x MIR162 x GA21 (expressing Vip3Aa20 and Cry1Ab) maize. The resistant strain, from neonate to sixth instar, showed more than 72% survival on Vip3Aa20 maize. From surviving larvae, more than 64 and 54% developed to pupae and adults, respectively. In contrast, heterozygote and susceptible strains showed no larval survival up to fourth instar, and less than 25% larval survival in the fifth and sixth instar on Vip3Aa20 maize. These larvae produced less than 21% of pupae and adults. The development time of FAW strains from neonate to-adult exposed to Vip3Aa20 maize was similar; however, the resistant strain showed an increase of 2 d when compared to those fed only non-Bt maize. In summary, the resistance of *S. frugiperda* to Vip3Aa20 maize is functionally recessive from neonate up to fourth instar larvae. However, high larval survival of resistant strain and some survival of heterozygote larvae in advanced instars on Vip3Aa20 maize were observed. These results will be important for designing insect resistance management to Bt maize plants expressing Vip3Aa20 protein in Brazil. (C) 2016 Elsevier Ltd. All rights reserved.

Accession Number: WOS:000382350900009**Author Identifiers:**

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

ISSN: 0261-2194**eISSN:** 1873-6904**Record 22 of 50****Title:** Performance of Cry1A.105-selected fall armyworm (Lepidoptera: Noctuidae) on transgenic maize plants containing single or pyramided Bt genes**Author(s):** Niu, Y (Niu, Ying); Head, GP (Head, Graham P.); Price, PA (Price, Paula A.); Huang, FN (Huang, Fangneng)**Source:** CROP PROTECTION **Volume:** 88 **Pages:** 79-87 **DOI:** 10.1016/j.cropro.2016.06.005 **Published:** OCT 2016

Abstract: Cry1A.105 is a Cry protein expressed in some transgenic *Bacillus thuringiensis* (Bt) maize products. In this study, performance of five populations of fall armyworm, *Spodoptera frugiperda* (J.E. Smith), were evaluated on four non-Bt and eight commercial and experimental Bt maize hybrids/lines (hereafter referred as maize products). The five insect populations included one Cry1A.105-susceptible strain, two Cry1A.105-resistant strains, and two F-1 heterozygous genotypes. The eight Bt maize hybrids/lines consisted of five single-gene Bt maize products containing Cry1A.105, Cry2Ab2, Cry1F, or Cry1Ab protein, and three pyramided Bt maize products expressing Cry1A.105/Cry2Ab2, Cry1A.105/Cry2Ab2/Cry1F, or Cry1A13/Vip3A for targeting aboveground lepidopteran maize pests. In the study, neonates of each population were tested on leaf tissues in the laboratory and whole plants in the greenhouse. Cry1A.105 and Cry1F maize killed 92.2-100% susceptible larvae in both test methods, while resistant larvae survived well on these two maize products. Performance of the two F1 populations on Cry1A.105 and Cry1F maize varied between the two test methods. In leaf tissue bioassay, Cry1Ab maize was marginally effective against the susceptible population. In contrast, few live larvae and little leaf injury from any of the five populations were observed on Cry2Ab2 and the three pyramided Bt maize products. The results of this study showed evidence of cross resistance of the Cry1A.105-resistant *S. frugiperda* to Cry1F and Cry1Ab maize, but not to the Bt maize products containing Cry2Ab2 or Vip3A. Data generated from this study will be useful in developing resistance management strategies for the sustainable use of Bt maize technology. (C) 2016 Elsevier Ltd. All rights reserved.

Accession Number: WOS:000382350900011

ISSN: 0261-2194

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Record 23 of 50

Title: Genetically modified rice Bt-Shanyou63 expressing Cry1Ab/c protein does not harm *Daphnia magna*

Author(s): Zhang, L (Zhang, Li); Guo, RQ (Guo, Ruqing); Fang, ZX (Fang, Zhixiang); Liu, B (Liu, Biao)

Source: ECOTOXICOLOGY AND ENVIRONMENTAL SAFETY **Volume:** 132 **Pages:** 196-201 **DOI:** 10.1016/j.ecoenv.2016.06.011 **Published:** OCT 2016

Abstract: The genetically modified (GM) rice Bt-ShanYou63 (Bt-SY63) received an official biosafety certificate while its safety remained in dispute. In a lifelong study, *Daphnia magna* were experimentally fed a basal diet of rice flours from Bt-SY63 or its parental rice ShanYou63 (SY63) at concentrations of 0.2 mg, 0.3 mg, or 0.4 mg C (per individual per day). Overall the survival, body size, and reproduction of the animals were comparable between Bt-SY63 and ShanYou63. The results showed that no significant differences were observed in growth and reproduction parameters between *D. magna* fed GM and non-GM flour and no dose-related changes occurred in all the values. Based on the different parameters assessed, the GM rice Bt-SY63 is a safe food source for *D. magna* that does not differ in quality from non-GM rice. (C) 2016 Published by Elsevier Inc.

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PubMed ID: 27322607

ISSN: 0147-6513

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Record 24 of 50

Title: Immunotoxicological Evaluation of Genetically Modified Rice Expressing Cry1Ab/Ac Protein (TT51-1) by a 6-Month Feeding Study on Cynomolgus Monkeys

Author(s): Tan, XY (Tan, Xiaoyan); Zhou, XB (Zhou, Xiaobing); Tang, Y (Tang, Yao); Lv, JJ (Lv, Jianjun); Zhang, L (Zhang, Lin); Sun, L (Sun, Li); Yang, YW (Yang, Yanwei); Miao, YF (Miao, Yufa); Jiang, H (Jiang, Hua); Chen, GF (Chen, Gaofeng); Huang, ZY (Huang, Zhiying); Wang, X (Wang, Xue)

Source: PLOS ONE **Volume:** 11 **Issue:** 9 **Article Number:** e0163879 **DOI:** 10.1371/journal.pone.0163879 **Published:** SEP 29 2016

Abstract: The present study was performed to evaluate the food safety of TT51-1, a new type of genetically modified rice that expresses the Cry1Ab/Ac protein (Bt toxin) and is highly resistant to most lepidopteran pests. Sixteen male and 16 female cynomolgus monkeys were randomly divided into four groups: conventional rice (non-genetically modified rice, non-GM rice), positive control, 17.5% genetically modified rice (GM rice) and 70% GM rice. Monkeys in the non-GM rice, positive control, and GM rice groups were fed on diets containing 70% non-GM rice, 17.5% GM rice or 70% GM rice, respectively, for 182 days, whereas animals in the positive group were intravenously injected with cyclophosphamide every other day for a total of four injections before the last treatment. Six months of treatment did not yield abnormal observations. Specifically, the following parameters did not significantly differ between the non-GM rice group and GM rice groups: body weight, food consumption, electrocardiogram, hematology, immuno-phenotyping of lymphocytes in the peripheral blood, mitogen-induced peripheral blood lymphocyte proliferation, splenocyte proliferation, KLH-T cell-dependent antibody response, organ weights and ratios, and histological appearance ($p > 0.05$). Animals from the GM rice group differed from animals in the non-GM rice group ($p < 0.05$) in several parameters: specifically, their body temperatures and serum alanine aminotransferase (ALT) levels were higher, whereas their levels of serum K⁺, Cl⁻ and cytokines (IL-2, IL-4 and IL-5) were lower. Because dose- or time-dependent changes were not observed in this study and animals appeared histologically normal, the aforementioned differences were not considered to be adverse or related to the treatment with GM rice. In conclusion, a 6-month feeding study of TT51-1 did not show adverse immunotoxicological effects on cynomolgus monkeys.

Accession Number: WOS:000384328500133

PubMed ID: 27684490

ISSN: 1932-6203

Record 25 of 50

Title: Effects of Bt-transgenic rice cultivation on planktonic communities in paddy fields and adjacent ditches

Author(s): Liu, YB (Liu, Yongbo); Liu, F (Liu, Fang); Wang, C (Wang, Chao); Quan, ZJ (Quan, Zhanjun); Li, JS (Li, Junsheng)

Source: SCIENCE OF THE TOTAL ENVIRONMENT **Volume:** 565 **Pages:** 690-697 **DOI:** 10.1016/j.scitotenv.2016.05.103 **Published:** SEP 15 2016

Abstract: The non-target effects of transgenic plants are issues of concern; however, their impacts in cultivated agricultural fields and adjacent natural aquatic ecosystems are poorly understood. We conducted field experiments during two growing seasons to determine the effects of cultivating *Bacillus thuringiensis* (Bt)-transgenic rice on the phytoplankton and zooplankton communities in a paddy field and an adjacent ditch. Bt toxin was detected in soil but not in water. Water quality was not significantly different between non-Bt and Bt rice fields, but varied among up-, mid-and downstream locations in the ditch. Cultivation of Bt-transgenic rice had no effects on zooplankton communities. Phytoplankton abundance and biodiversity were not significantly different between transgenic and non-transgenic rice fields in 2013; however, phytoplankton were more abundant in the transgenic rice field than in the non-transgenic rice field in 2014. Water quality and rice type explained 65.9% and 12.8% of this difference in 2014, respectively. Phytoplankton and zooplankton were more abundant in mid-and downstream, than upstream, locations in the ditch, an effect that we attribute to water quality differences. Thus, the release of Bt toxins into field water during the cultivation of transgenic crops had no direct negative effects on plankton community composition, but indirect effects that alter environmental conditions should be taken into account during the processes of management planning and policymaking. (C) 2016 Elsevier B.V. All rights reserved.

Accession Number: WOS:000378206300070

PubMed ID: 27219503

Author Identifiers:

Author	ResearcherID Number	ORCID Number
Liu, Yongbo	H-3984-2015	0000-0003-1618-8813

ISSN: 0048-9697

eISSN: 1879-1026

Record 26 of 50

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

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

Source: BULLETIN OF ENTOMOLOGICAL RESEARCH **Volume:** 106 **Issue:** 5 **Pages:** 591-597 **DOI:** 10.1017/S0007485316000249 **Published:** SEP 2016

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

Accession Number: WOS:000384238800004

PubMed ID: 27112423

Author Identifiers:

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

ISSN: 0007-4853

eISSN: 1475-2670

Record 27 of 50

Title: Detection of DNA fragments from wheat in blood of animals

Author(s): Trojan, V (Trojan, Vaclav); Vyhnanek, T (Vyhnanek, Tomas); Stastnik, O (Stastnik, Ondrej); Mrkvicova, E (Mrkvicova, Eva); Mares, J (Mares, Jan); Havel, L (Havel, Ladislav)

Source: JOURNAL FUR VERBRAUCHERSCHUTZ UND LEBENSMITTELSICHERHEIT-JOURNAL OF CONSUMER PROTECTION AND FOOD SAFETY **Volume:** 11 **Issue:** 3 **Pages:** 259-264 **DOI:** 10.1007/s00003-016-1035-3 **Published:** SEP 2016

Abstract: Delivery of foreign DNA is still a very controversial issue, especially in relation to genetically modified organisms. It is not necessary to use genetically modified feed to verify the possible transfer of DNA from food into the body. In this study, we evaluated the possible transfer of DNA from wheat forage (of single component diet) into the blood of three different organisms. DNA isolation kits were used to isolate total DNA from blood and feed. Blood was taken for analysis from rats (after 23 days feeding wheat), broilers (15 days), and carp (34 days). Housekeeping genes were used to verify blood samples (rats: glyceraldehyde-3-phosphate dehydrogenase/GAPDH/, broilers: growth hormone gene/GCH/and carp: small ribosomal subunit/40S/). We used GAPDH and actin to determine whether DNA from wheat was transferred into animal blood. No purple and common wheat DNA fragments were detected in the blood of any animal tested, suggesting no transfer of the tested wheat DNA into the body. Various contents of anthocyanins in the feeding variants had no effect on the transfer of wheat DNA into the blood of animals. Our results correspond to some studies that have not proved transfer DNA from genetically modified feed into the target organism.

Accession Number: WOS:000382704600006

ISSN: 1661-5751

eISSN: 1661-5867

Record 28 of 50

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

Author(s): Morse, S (Morse, Stephen)

Source: OUTLOOK ON AGRICULTURE **Volume:** 45 **Issue:** 3 **Pages:** 206-214 **DOI:** 10.1177/0030727016666237 **Published:** SEP 2016

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

Accession Number: WOS:000382952900009

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Record 29 of 50

Title: A 52-week safety study in cynomolgus macaques for genetically modified rice expressing Cry1Ab/1Ac protein

Author(s): Mao, J (Mao, Jie); Sun, X (Sun, Xing); Cheng, JH (Cheng, Jian-Hua); Shi, YJ (Shi, Yong-Jie); Wang, XZ (Wang, Xin-Zheng); Qin, JJ (Qin, Jun-Jie); Sang, ZH (Sang, Zhi-Hong); He, K (He, Kun); Xia, Q (Xia, Qing)

Source: FOOD AND CHEMICAL TOXICOLOGY **Volume:** 95 **Pages:** 1-11 **DOI:** 10.1016/j.fct.2016.06.015 **Published:** SEP 2016

Abstract: A 52-week feeding study in cynomolgus macaques was carried out to evaluate the safety of Bt rice Huahui 1 (HH1), a transgenic rice line expressing Cry1Ab/1Ac protein. Monkeys were fed a diet with 20% or 60% HH1 rice, 20% or 60% parental rice (Minghui 63, MH63), normal diet, normal diet spiked with purified recombinant Cry1Ab/1Ac fusion protein or bovine serum albumin (BSA) respectively. During the feeding trial, clinical observations were conducted daily, and multiple parameters, including body weight, body temperature, electrocardiogram, hematology, blood biochemistry, serum metabolome and gut microbiome were examined at regular intervals. Upon sacrifice, the organs were weighed, and the macroscopic, microscopic and electron microscopic examinations were performed. The results show no adverse or toxic effects of Bt rice HUH or Cry1Ab/1Ac fusion protein on monkeys. Therefore, the present 52-week primate feeding study suggests that the transgenic rice containing Cry1Ab/1Ac is equivalent to its parental rice line MH63. (C) 2016 Elsevier Ltd. All rights reserved.

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Record 30 of 50

Title: Safety assessment of GM plants: An updated review of the scientific literature

Author(s): Domingo, JL (Domingo, Jose L.)

Source: FOOD AND CHEMICAL TOXICOLOGY **Volume:** 95 **Pages:** 12-18 **DOI:** 10.1016/j.fct.2016.06.013 **Published:** SEP 2016

Abstract: In a wide revision of the literature conducted in 2000, I noted that the information in scientific journals on the safety of genetically modified (GM) foods in general, and GM plants in particular, was scarce. Of "course, it was not sufficient to guarantee that the consumption of these products should not mean risks for the health of the consumers. Because of the scientific interest in GM organisms (GMOs), as well as the great concern that the consumption of GM foods/plants has raised in a number of countries, I conducted two subsequent revisions (2007 and 2011) on the adverse/toxic effects of GM plants. In the present review, I have updated the information on the potential adverse health effects of GM plants consumed as food and/or feed. With only a few exceptions, the reported studies in the last six years show rather similar conclusions; that is to say, the assessed GM soybeans, rice, corn/maize and wheat would be as safe as the parental species of these plants. However, in spite of the notable increase in the available information, studies on the long-term health effects of GM plants, including tests of mutagenicity, teratogenicity and carcinogenicity seem to be still clearly necessary. (C) 2016 Elsevier Ltd. All rights reserved.

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PubMed ID: 27317828

Author Identifiers:

Author	ResearcherID Number	ORCID Number
Domingo, Jose L		0000-0001-6647-9470

ISSN: 0278-6915

eISSN: 1873-6351

Record 31 of 50

Title: Long-term toxicity study on genetically modified corn with cry1Ac gene in a Wuzhishan miniature pig model

Author(s): Chen, L (Chen, Liang); Sun, Z (Sun, Zhe); Liu, QW (Liu, Quanwei); Zhong, RQ (Zhong, Ruqing); Tan, SY (Tan, Shuyi); Yang, XG (Yang, Xiaoguang); Zhang, HF (Zhang, Hongfu)

Source: JOURNAL OF THE SCIENCE OF FOOD AND AGRICULTURE **Volume:** 96 **Issue:** 12 **Pages:** 4207-4214 **DOI:** 10.1002/jsfa.7624 **Published:** SEP 2016

Abstract: BACKGROUNDThe objective of the present study was to investigate the chronic effect of transgenic maize lines by the insertion of the cry1Ac gene from Bacillus thuringiensis (Bt) on the growth performance, immune response and health using a Wuzhishan miniature pig model through a 196-day feeding study. RESULTSBased on the gender and weight, 72 Wuzhishan miniature pigs were randomly assigned one of the diets containing 65% non-transgenic isogenic corn or Bt corn at three stages of growth (day 0-69, 70-134 and 135-196). The potential toxicological effects of transgenic corn on pigs were explored. No difference between the diet treatments for growth performance and haematology parameters at any stages of growth. Although subtle differences in serum content of alanine aminotransferase, relative kidney weight and some immune response were observed between the Bt group and isogenic group, they were not considered as diet treatment-related.

CONCLUSIONLong-term feeding Bt corn carrying cry1Ac genes to Wuzhishan miniature pigs did not indicate adverse effects on the growth, immune response and health indicators at any stages of growth. (c) 2016 Society of Chemical Industry

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PubMed ID: 26777397

ISSN: 0022-5142

eISSN: 1097-0010

Record 32 of 50**Title:** Field-evolved resistance to Cry1Ab maize by Spodoptera frugiperda in Brazil**Author(s):** Omoto, C (Omoto, Celso); Bernardi, O (Bernardi, Oderlei); Salmeron, E (Salmeron, Eloisa); Sorgatto, RJ (Sorgatto, Rodrigo J.); Dourado, PM (Dourado, Patrick M.); Crivellari, A (Crivellari, Augusto); Carvalho, RA (Carvalho, Renato A.); Willse, A (Willse, Alan); Martinelli, S (Martinelli, Samuel); Head, GP (Head, Graham P.)**Source:** PEST MANAGEMENT SCIENCE **Volume:** 72 **Issue:** 9 **Pages:** 1727-1736 **DOI:** 10.1002/ps.4201 **Published:** SEP 2016**Abstract:** BACKGROUNDThe first Bt maize in Brazil was launched in 2008 and contained the MON 810 event, which expresses Cry1Ab protein. Although the Cry1Ab dose in MON 810 is not high against fall armyworm (FAW), Spodoptera frugiperda (J.E. Smith), MON 810 provided commercial levels of control. To support insect resistance management in Brazil, the baseline and ongoing susceptibility of FAW was examined using protein bioassays, and the level of control and life history parameters of FAW were evaluated on MON 810 maize.**RESULTS**Baseline diet overlay assays with Cry1Ab (16 µg cm⁻²) caused 76.3% mortality to field FAW populations sampled in 2009. Moderate mortality (48.8%) and significant growth inhibition (88.4%) were verified in leaf-disc bioassays. In greenhouse trials, MON 810 had significantly less damage than non-Bt maize. The surviving FAW larvae on MON 810 (22.4%) had a 5.5 day increase in life cycle time and a 24% reduction in population growth rate. Resistance monitoring (2010-2015) showed a significant reduction in Cry1Ab susceptibility of FAW over time. Additionally, a significant reduction in the field efficacy of MON 810 maize against FAW was observed in different regions from crop season 2009 to 2013.**CONCLUSION**The decrease in susceptibility to Cry1Ab was expected, but the specific contributions to this resistance by MON 810 maize cannot be distinguished from cross-resistance to Cry1Ab caused by exposure to Cry1F maize. Technologies combining multiple novel insecticidal traits with no cross-resistance to the current Cry1 proteins and high activity against the same target pests should be pursued in Brazil and similar environments. (c) 2015 Society of Chemical Industry**Accession Number:** WOS:000380729400011**PubMed ID:** 26617261**Author Identifiers:**

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

ISSN: 1526-498X

eISSN: 1526-4998

Record 33 of 50**Title:** Selection and characterization of resistance to the Vip3Aa20 protein from Bacillus thuringiensis in Spodoptera frugiperda**Author(s):** Bernardi, O (Bernardi, Oderlei); Bernardi, D (Bernardi, Daniel); Horikoshi, RJ (Horikoshi, Renato J.); Okuma, DM (Okuma, Daniela M.); Miraldo, LL (Miraldo, Leonardo L.); Fatoresso, J (Fatoresso, Julio); Medeiros, FCL (Medeiros, Fernanda C. L.); Burd, T (Burd, Tony); Omoto, C (Omoto, Celso)**Source:** PEST MANAGEMENT SCIENCE **Volume:** 72 **Issue:** 9 **Pages:** 1794-1802 **DOI:** 10.1002/ps.4223 **Published:** SEP 2016**Abstract:** BACKGROUNDSpodoptera frugiperda is one the main target pests of maize events expressing Vip3Aa20 protein from Bacillus thuringiensis (Bt) in Brazil. In this study, we selected a resistant strain of S. frugiperda on Bt maize expressing Vip3Aa20 protein and characterized the inheritance and fitness costs of the resistance.**RESULTS**The resistance ratio of the Vip3Aa20-resistant strain of S. frugiperda was >3200-fold. Neonates of the Vip3Aa20-resistant strain were able to survive and emerge as fertile adults on Vip3Aa20 maize, while larvae from susceptible and heterozygous strains did not survive. The inheritance of Vip3Aa20 resistance was autosomal recessive and monogenic. Life history studies to investigate fitness cost revealed an 11% reduction in the survival rate until adult stage and a approximate to 50% lower reproductive rate of the Vip3Aa20-resistant strain compared with susceptible and heterozygous strains.**CONCLUSION**This is the first characterization of S. frugiperda resistance to Vip3Aa protein. Our results provide useful information for resistance management programs designed to prevent or delay resistance evolution to Vip3Aa proteins in S. frugiperda. (c) 2016 Society of Chemical Industry**Accession Number:** WOS:000380729400020**PubMed ID:** 26733182**Author Identifiers:**

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

ISSN: 1526-498X

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Record 34 of 50**Title:** Genetic Basis of Cry1F-Resistance in a Laboratory Selected Asian Corn Borer Strain and Its Cross-Resistance to Other Bacillus thuringiensis Toxins**Author(s):** Wang, YQ (Wang, Yueqin); Wang, YD (Wang, Yidong); Wang, ZY (Wang, Zhenying); Bravo, A (Bravo, Alejandra); Soberon, M (Soberon, Mario); He, KL (He, Kanglai)**Source:** PLOS ONE **Volume:** 11 **Issue:** 8 **Article Number:** e0161189 **DOI:** 10.1371/journal.pone.0161189 **Published:** AUG 12 2016**Abstract:** The Asian corn borer (ACB), *Ostrinia furnacalis* (Guenee) (Lepidoptera: Crambidae), is the most destructive insect pest of corn in China. Susceptibility to the Cry1F toxin derived from *Bacillus thuringiensis* has been demonstrated for ACB, suggesting the potential for Cry1F inclusion as part of an insect pest management program. Insects can develop resistance to Cry toxins, which threatens the development and use of Bt formulations and Bt crops in the field. To determine possible resistance mechanisms to Cry1F, a Cry1F-resistant colony of ACB (ACB-FR) that exhibited more than 1700-fold resistance was established through selection experiments after 49 generations of selection under laboratory conditions. The ACB-FR strain showed moderate cross-resistance to Cry1Ab and Cry1Ac of 22.8- and 26.9-fold, respectively, marginally cross-resistance to Cry1Ah (3.7-fold), and no cross-resistance to Cry1Ie (0.6-fold). The bioassay responses of progeny from reciprocal F-1 crosses to different Cry1 toxin concentrations indicated that the resistance trait to Cry1Ab, Cry1Ac and Cry1F has autosomal inheritance with no maternal effect or sex linked. The effective dominance (h) of F-1 offspring was calculated at different concentrations of Cry1F, showing that h decreased as concentration of Cry1F increased. Finally, the analysis of actual and expected mortality of the progeny from a backcross (F-1 x resistant strain) indicated that the inheritance of the resistance to Cry1F in ACB-FR was due to more than one locus. The present study provides an understanding of the genetic basis of Cry1F resistance in ACB-FR and also shows that pyramiding Cry1F with Cry1Ah or Cry1Ie could be used as a strategy to delay the development of ACB resistance to Bt proteins.**Accession Number:** WOS:000381382100060

ISSN: 1932-6203

Record 35 of 50**Title:** Highly Monodisperse Fe₃O₄@Au Superparamagnetic Nanoparticles as Reproducible Platform for Genosensing Genetically Modified Organisms**Author(s):** Freitas, M (Freitas, Maria); Couto, MS (Couto, Maria Sa); Barroso, MF (Barroso, Maria Fatima); Pereira, C (Pereira, Clara); de-los-Santos-Alvarez, N (de-los-Santos-Alvarez, Noemi); Miranda-Ordieres, AJ (Miranda-Ordieres, Arturo J.); Lobo-Castanon, MJ (Jesus Lobo-Castanon, Maria); Delerue-Matos, C (Delerue-Matos, Cristina)**Source:** ACS SENSORS **Volume:** 1 **Issue:** 8 **Pages:** 1044-1053 **DOI:** 10.1021/acssensors.6b00182 **Published:** AUG 2016**Abstract:** Several routes have been developed to prepare magnetic core-shell Fe₃O₄@Au nanoparticles (MNPs). However, only highly monodisperse MNPs are suitable for analytical applications. Herein, we describe the detection of GMO through the use of gold-coated MNPs with fine-tuned properties as platforms. The MNPs were prepared through a procedure that involves the preparation of Fe₃O₄ cores by thermal decomposition and their coating through reduction of a gold precursor. Different Fe₃O₄:Au precursor molar ratios (1:1; 1:4; 1:7) were tested on the Fe₃O₄ encapsulation. Monodisperse quasi-spherical core shell Fe₃O₄@Au were obtained for the 1:4 and 1:7 ratios, in contrast, the 1:1 ratio did not lead to complete encapsulation of Fe₃O₄ cores. Therefore, the Fe₃O₄@Au obtained from higher Fe₃O₄:HAuCl₄ ratios were tested as platforms for an electrochemical genosensing to detect MON810. The best performance was achieved with the Fe₃O₄@Au prepared from 1:4 ratio (10.0 ± 1.7 nm). A DNA probe covalently linked to a carboxylated self-assembled monolayer and a fluorescein isothiocyanate (FITC) signaling probe were used in a sandwich assay format. Labeling with anti-FITC-peroxidase Fab fragment conjugate allowed chronoamperometric measurements of the enzyme activity captured on Fe₃O₄@Au placed on screen-printed electrodes upon the hybridization event. The genosensing provided a linear range from 0.25 to 2.5 nM, LOD of 0.15 nM, with a reproducibility <4%.

Certified samples containing the transgenic event were measured without further purification after PCR amplification. The results highlight the efficiency of the genosay for the MON810 detection, opening new horizons to achieve a low-cost analysis out of large laboratory facilities to verify the compliance of GMO regulations.

Accession Number: WOS:000385465200013

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Record 36 of 50

Title: Hematotoxicity and Genotoxicity Evaluations in Swiss Mice Intraperitoneally Exposed to *Bacillus thuringiensis* (var *kurstaki*) Spore Crystals Genetically Modified to Express Individually Cry1Aa, Cry1Ab, Cry1Ac, or Cry2Aa

Author(s): Mezzomo, BP (Mezzomo, Belin Poletto); Miranda-Vilela, AL (Miranda-Vilela, Ana Luisa); Barbosa, LCP (Pereira Barbosa, Lilian Carla); Albernaz, VL (Albernaz, Vanessa Lima); Grisolia, CK (Grisolia, Cesar Koppe)

Source: ENVIRONMENTAL TOXICOLOGY **Volume:** 31 **Issue:** 8 **Pages:** 970-978 **DOI:** 10.1002/tox.22106 **Published:** AUG 2016

Abstract: *Bacillus thuringiensis* (Bt) has been widely used in foliar sprays as part of integrated pest management strategies against insect pests of agricultural crops. Since the advent of genetically modified plants expressing Bt delta-endotoxins, the bioavailability of Cry proteins has increased, and therefore for biosafety reasons their adverse effects should be studied, mainly for nontarget organisms. We evaluated, in Swiss mice, the hematotoxicity and genotoxicity of the genetically modified strains of Bt spore crystals Cry1Aa, 1Ab, 1Ac, or 2Aa at 27 mg/kg, and Cry1Aa, 1Ab and 2Aa also at 136 and 270 mg/kg, administered with a single intraperitoneal injection 24 h before euthanasia. Controls received filtered water or cyclophosphamide. Blood samples collected by cardiac puncture were used to perform hemogram, and bone marrow was extracted for the micronucleus test. Bt spore crystals presented toxicity for lymphocytes when in higher doses, which varied according to the type of spore crystal studied, besides promoting cytotoxic and genotoxic effects for the erythroid lineage of bone marrow, mainly at highest doses. Although the profile of such adverse side effects can be related to their high level of exposure, which is not commonly found in the environment, results indicated that these Bt spore crystals were not harmless to mice. This suggests that a more specific approach should be taken to increase knowledge about their toxicological properties and to establish the toxicological risks to nontarget organisms. (C) 2015 Wiley Periodicals, Inc.

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Record 37 of 50

Title: Intraguild Competition of Three Noctuid Maize Pests

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

Source: ENVIRONMENTAL ENTOMOLOGY **Volume:** 45 **Issue:** 4 **Pages:** 999-1008 **DOI:** 10.1093/ee/nvw068 **Published:** AUG 2016

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

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PubMed ID: 27330146

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Record 38 of 50

Title: Effects of Transgenic Bt Rice on Nontarget *Rhopalosiphum maidis* (Homoptera: Aphididae)

Author(s): Ren, SP (Ren, Shao-peng); Yang, F (Yang, Fan); Gao, MQ (Gao, Ming-qing); Pu, DQ (Pu, De-qiang); Shi, M (Shi, Min); Ye, GY (Ye, Gong-yin); Shen, ZC (Shen, Zhi-cheng); Chen, XX (Chen, Xue-xin)

Source: ENVIRONMENTAL ENTOMOLOGY **Volume:** 45 **Issue:** 4 **Pages:** 1090-1096 **DOI:** 10.1093/ee/nvw064 **Published:** AUG 2016

Abstract: The effects of three transgenic *Bacillus thuringiensis* (Bt) rice lines, KMD1, KMD2, and G8-7, on biological parameters and population dynamics of nontarget insect, *Rhopalosiphum maidis* (Fitch) (Homoptera: Aphididae), were investigated in the laboratory and field. No significant differences were found between Bt and non-Bt rice lines for aphid survival. The developmental time of *R. maidis* that fed on KMD1 and KMD2 did not differ significantly from those of the individuals feeding on the parental variety Xiushui11, but significantly prolonged developmental time was observed on G8-7 as compared with its parental variety Xiushui110. Aphid fecundity was significantly higher on Bt than on parental rice. A 2-yr field survey indicated that Bt rice did not significantly affect the population dynamics of *R. maidis* in comparison with non-Bt rice. Additionally, guttation droplets of Bt rice and aphids feeding on Bt rice were analyzed for presence of Cry1Ab using ELISA. No Cry1Ab protein was found in aphid adults feeding on Bt rice lines both in the laboratory and field. By using the guttation droplets from the top of rice seedlings, we designed a novel method to collect phloem sap, and found that relatively low concentrations were detected in the guttation droplets from Bt rice lines. In conclusion, although the Bt rice lines tested in this study stimulate the fecundity of *R. maidis*, the aphid population density did not increase in Bt rice fields.

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Record 39 of 50

Title: Evaluation of Potential Fitness Costs Associated With eCry3.1Ab Resistance in *Diabrotica virgifera virgifera* (Coleoptera: Chrysomelidae)

Author(s): Geisert, RW (Geisert, Ryan W.); Hibbard, BE (Hibbard, Bruce E.)

Source: JOURNAL OF ECONOMIC ENTOMOLOGY **Volume:** 109 **Issue:** 4 **Pages:** 1853-1858 **DOI:** 10.1093/jee/tow095 **Published:** AUG 2016

Abstract: Both an eCry3.1Ab-selected and paired control western corn rootworm, *Diabrotica virgifera virgifera* LeConte, colony were tested for adult longevity, egg oviposition, egg viability, and larval development in order to evaluate the potential fitness costs associated with eCry3.1Ab resistance. Adult longevity experiments were conducted by pairing virgin males and females together in plastic boxes supplied with food, water, and ovipositional medium and observed for survival time. Eggs were also collected from the ovipositional medium once a week to determine average egg oviposition and egg viability. Larval development time experiments were conducted by infesting seedling assays with 25 neonate larvae and recording larval recovery after several days. Adult longevity, average egg oviposition, and larval development time results indicated a lack of fitness costs associated with eCry3.1Ab resistance in the western corn rootworm. Results of egg viability indicated a fitness advantage for the eCry3.1Ab-selected colony with a significantly higher egg hatch than the control.

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PubMed ID: 27151470

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Record 40 of 50

Title: Impact of Lepidoptera (Crambidae, Noctuidae, and Pyralidae) Pests on Corn Containing Pyramided Bt Traits and a Blended Refuge in the Southern United States

Author(s): Reay-Jones, FPF (Reay-Jones, F. P. F.); Bessin, RT (Bessin, R. T.); Brewer, MJ (Brewer, M. J.); Buntin, DG (Buntin, D. G.); Catchot, AL (Catchot, A. L.); Cook, DR (Cook, D. R.); Flanders, KL (Flanders, K. L.); Kerns, DL (Kerns, D. L.); Porter, RP (Porter, R. P.); Reising, DD (Reising, D. D.); Stewart, SD (Stewart, S. D.); Rice, ME (Rice, M. E.)

Source: JOURNAL OF ECONOMIC ENTOMOLOGY **Volume:** 109 **Issue:** 4 **Pages:** 1859-1871 **DOI:** 10.1093/jee/tow109 **Published:** AUG 2016

Abstract: Blended refuge for transgenic plants expressing *Bacillus thuringiensis* (Bt) toxins has been approved in the northern United States as a resistance management strategy alternative to a structured refuge. A three-year study (2012-2014) was conducted with 54 trials across nine states in the southern United States to evaluate plant injury from lepidopteran pests of corn and yield in a corn hybrid expressing Cry1F x Cry1Ab x Vip3Aa20 (Pioneer Brand Optimum Leptra) planted as a pure stand and in refuge blends of 5, 10, and 20% in both early and late plantings. Injury by corn earworm, *Helicoverpa zea* Boddie (Lepidoptera: Noctuidae), and fall armyworm, *Spodoptera frugiperda* (J. E. Smith) (Lepidoptera: Noctuidae), was generally proportional to the percentage of non-Bt corn within each refuge blend. Across locations, ear injury in plots with 100% Cry1F x Cry1Ab x Vip3Aa20 (Optimum Leptra) corn ranged from no injury to a maximum of 0.42 cm² per ear in Mississippi in 2013. Leaf injury ratings in 100% non-Bt plots in early and late planted trials in 2014 were 86- and 70-fold greater than in 100% Cry1F x Cry1Ab x Vip3Aa20 (Optimum Leptra) plots. Plants in plots with blended refuges had significantly greater leaf injury in 2012 (5, 10, and 20% refuge blends), in the early-planted corn in 2013 (10 and 20% only), and in both early- and late-planted corn in 2014 (20% only) as compared with leaf injury in a pure stand of Cry1F x Cry1Ab x Vip3Aa20 (Optimum Leptra) seen during these years. Corn ears in plots with blended refuges also had significantly greater area of kernels injured in 2012 (5, 10, and 20%), in early- and late-planted corn in 2013 (5, 10, and 20%), and in early (10 and 20% only) and late-planted corn (5, 10, and 20%) in 2014 as compared with ear injury in a pure stand of Cry1F x Cry1Ab x Vip3Aa20 (Optimum Leptra) seen during these years. Infestations of southwestern corn borer, *Diatraea grandiosella* Dyar (Lepidoptera: Crambidae), were also significantly reduced by Cry1F x Cry1Ab x Vip3Aa20 (Optimum Leptra). Despite these differences in injury, yield averaged across locations varied among refuge blends only in the late-planted trials in 2013, with greater yields in the 0% refuge blend than in the 20% blend; however, when examining yield separately by location, only two of nine locations had higher yields in the 100% Bt plots than in any of the blended refuge plots. As a complement to studying the contribution of blended refuge to delaying resistance, quantifying injury and yield in a range of refuge blends is a necessary step to provide management information on the range of lepidopteran pests that occur in the southern United States.

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Record 41 of 50

Title: Evidence of Resistance to Cry34/35Ab1 Corn by Western Corn Rootworm (Coleoptera: Chrysomelidae): Root Injury in the Field and Larval Survival in Plant-Based Bioassays

Author(s): Gassmann, AJ (Gassmann, Aaron J.); Shrestha, RB (Shrestha, Ram B.); Jakka, SRK (Jakka, Siva R. K.); Dunbar, MW (Dunbar, Mike W.); Clifton, EH (Clifton, Eric H.); Paolino, AR (Paolino, Aubrey R.); Ingber, DA (Ingber, David A.); French, BW (French, B. Wade); Masloski, KE (Masloski, Kenneth E.); Dounda, JW (Dounda, John W.); St Clair, CR (St Clair, Coy R.)

Source: JOURNAL OF ECONOMIC ENTOMOLOGY **Volume:** 109 **Issue:** 4 **Pages:** 1872-1880 **DOI:** 10.1093/jee/tow110 **Published:** AUG 2016

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

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PubMed ID: 27329619

ISSN: 0022-0493

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Record 42 of 50

Title: Effects of feeding transgenic corn with mCry1Ac or maroACC gene to laying hens for 12 weeks on growth, egg quality and organ health

Author(s): Zhong, RQ (Zhong, R. Q.); Chen, L (Chen, L.); Gao, LX (Gao, L. X.); Zhang, LL (Zhang, L. L.); Yao, B (Yao, B.); Yang, XG (Yang, X. G.); Zhang, HF (Zhang, H. F.)

Source: ANIMAL **Volume:** 10 **Issue:** 8 **Pages:** 1280-1287 **DOI:** 10.1017/S1751731116000203 **Published:** AUG 2016

Abstract: The objective of the present study was to investigate the effect of feeding two transgenic corn lines containing the mCry1Ac gene from *Bacillus thuringiensis* strain (BT-799) and the maroACC gene from *Agrobacterium tumefaciens* strain (CC-2), respectively, on growth, egg quality and organ health indicators. Expression of the mCry1Ac gene confers resistance to *Pyrausta nubilalis* and the maroACC gene confers tolerance to herbicides. Healthy hens (n=96 placed in cages; 3 hens/cage) were randomly assigned to one of four corn-soybean meal dietary treatments (8 cages/treatment) formulated with the following corn: non-transgenic near-isoline control corn (control), BT-799 corn, CC-2 corn and commercially available non-transgenic reference corn (reference). The experiment was divided into three 4-week phases (week 1 to 4, week 5 to 8 and week 9 to 12), during which hens were fed mash diets. Performance (BW, feed intake and egg production) and egg quality were determined. Following slaughter at the end of 12 weeks of feeding (n=8/treatment), carcass yield and organ weights (heart, liver, spleen, lung, kidneys, stomach and ovary) were recorded; organs and intestines were sampled for histological analysis. Analysis of serum biochemistry parameters to assess the liver and kidney function were performed. No differences in BW, egg production and production efficiency were observed between hens consuming the control diet and hens consuming the BT-799 or CC-2 diet. Haugh unit measures and egg component weights were similar between the control and test groups. Carcass yield was not affected by the diet treatment. Similar organosomatic indices and serum parameters did not indicate the characteristics of organ dysfunction. All observed values of the BT-799 and CC-2 groups were within the calculated tolerance intervals. This research indicates that the performance, egg quality, organ health and carcass yield of laying hens fed diets containing the BT-799 or CC-2 corn line were similar to that of laying hens fed diets formulated with the non-transgenic near-isoline corn with comparable genetic backgrounds.

Accession Number: WOS:000381285600005

PubMed ID: 26915544

ISSN: 1751-7311

eISSN: 1751-732X

Record 43 of 50

Title: Monitoring carabid indicators could reveal environmental impacts of genetically modified maize

Author(s): Lee, MS (Lee, Marina S.); Albajes, R (Albajes, Ramon)

Source: AGRICULTURAL AND FOREST ENTOMOLOGY **Volume:** 18 **Issue:** 3 **Pages:** 238-249 **DOI:** 10.1111/afe.12156 **Published:** AUG 2016

Abstract: 1 Post market monitoring of GM crops is mandatory in EU states where they are grown commercially. Carabid beetles are very sensitive to environmental changes and may be used as indicators to monitor impacts of transgenic crops. This study aimed to assess which, where and when carabids should be sampled for improved postmarket monitoring.

2 Carabids were pitfall-trapped in maize fields, field margins, alfalfa and semi-natural vegetation across three regions of NE Spain, during 2 years, and three sampling dates.

3 Overall, 9193 carabids of 42 species were identified, aggregated into trophic groups and used for calculating community measures. The best indicator was *Pseudoophonus rufipes* (De Geer), satisfying criteria of abundance, relevance, sensitivity, ease of sampling, and sufficient statistical power. The carnivore group should also be monitored as an indicator of biodiversity and invertebrate biological control.

4 The best sampling location was the field margin where carabids are exposed to GM maize and are abundant enough to require smaller sample sizes to detect population changes.

5 Finally, sampling should concentrate around maize pollen-shed when carabid abundance is highest.

6 This study provides baseline data and shows that carabids can cost effectively improve detection capacity of postmarket monitoring.

Accession Number: WOS:000379423700006

ISSN: 1461-9555

eISSN: 1461-9563

Record 44 of 50

Title: Functional diversity of staphylinid beetles (Coleoptera: Staphylinidae) in maize fields: testing the possible effect of genetically modified, insect resistant maize

Author(s): Svobodova, Z (Svobodova, Z.); Habustova, OS (Habustova, O. Skokova); Bohac, J (Bohac, J.); Sehnal, F (Sehnal, F.)

Source: BULLETIN OF ENTOMOLOGICAL RESEARCH **Volume:** 106 **Issue:** 4 **Pages:** 432-445 **DOI:** 10.1017/S000748531500111X **Published:** AUG 2016

Abstract: Staphylinid beetles are recommended bioindicators for the pre-market environmental risk assessment of genetically modified (GM) insect protected maize expressing the Cry3Bb1 toxin. Our multiannual study is a unique European analysis of a staphylinid community within a 14 ha maize field. GM maize, its near-isogenic hybrid (with or without insecticide treatment), and two other reference hybrids were each grown in five 0.5 ha plots. The opportunity for exposure to Cry toxin from plant residues ploughed into the soil was shown by the presence of saprophagous dipteran larvae that are common prey of predatory staphylinid species and hosts of the parasitoid species. 2587 individuals belonging to 77 staphylinid species were sampled using pitfall traps. *Lesteva longolytrata* (31%), *Oxyptoda acuminata* (12%), *Aloconota sulcifrons* (8%) and *Anotylus rugosus* (7%) were the most abundant beetles in the field. Bionomics, food specialization, temperature requirements and size group were assigned for 25 most common species. These traits determine the occurrence of staphylinid beetles in the field, the food sources they could utilize and thus also their likely contact with the Cry3Bb1 toxin. Statistical analysis of activity abundance, Rao indices and multivariate analysis of distribution of particular categories of functional traits in the field showed negligible effects of the experimental treatments, including the GM maize, upon the staphylinid community. Staphylinid beetles represent a considerably diverse part of epigeic field fauna with wide food specialization; these features render them suitable for the assessment of environmental safety of GM insect protected maize. However, the availability of prey and the presence of particular staphylinid species and their abundance are highly variable; this complicates the interpretation of the results.

Accession Number: WOS:000379418000002

PubMed ID: 26781035

Author Identifiers:

Author	ResearcherID Number	ORCID Number
Skokova Habustova, Oxana	H-1412-2014	
Svobodova, Zdenka	L-2361-2015	

ISSN: 0007-4853

eISSN: 1475-2670

Record 45 of 50

Title: Heritability of Wing Size and Shape of the Rice and Corn Strains of Spodoptera frugiperda (JE Smith) (Lepidoptera: Noctuidae)

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

Source: NEOTROPICAL ENTOMOLOGY **Volume:** 45 **Issue:** 4 **Pages:** 411-419 **DOI:** 10.1007/s13744-016-0393-y **Published:** AUG 2016

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

Accession Number: WOS:000379710000011

PubMed ID: 27044394

ISSN: 1519-566X

eISSN: 1678-8052

Record 46 of 50

Title: Quality of laboratory studies assessing effects of Bt-proteins on non-target organisms: minimal criteria for acceptability

Author(s): De Schrijver, A (De Schrijver, Adinda); Devos, Y (Devos, Yann); De Clercq, P (De Clercq, Patrick); Gathmann, A (Gathmann, Achim); Romeis, J (Romeis, Jorg)

Source: TRANSGENIC RESEARCH **Volume:** 25 **Issue:** 4 **Pages:** 395-411 **DOI:** 10.1007/s11248-016-9950-8 **Published:** AUG 2016

Abstract: The potential risks that genetically modified plants may pose to non-target organisms and the ecosystem services they contribute to are assessed as part of pre-market risk assessments. This paper reviews the early tier studies testing the hypothesis whether exposure to plant-produced Cry34/35Ab1 proteins as a result of cultivation of maize 59122 is harmful to valued non-target organisms, in particular Arthropoda and Annelida. The available studies were assessed for their scientific quality by considering a set of criteria determining their relevance and reliability. As a case-study, this exercise revealed that when not all quality criteria are met, weighing the robustness of the study and its relevance for risk assessment is not obvious. Applying a worst-case expected environmental concentration of bioactive toxins equivalent to that present in the transgenic crop, confirming exposure of the test species to the test substance, and the use of a negative control were identified as minimum criteria to be met to guarantee sufficiently reliable data. This exercise stresses the importance of conducting studies meeting certain quality standards as this minimises the probability of erroneous or inconclusive results and increases confidence in the results and adds certainty to the conclusions drawn.

Accession Number: WOS:000379028300001

PubMed ID: 26980555

Author Identifiers:

Author	ResearcherID Number	ORCID Number
De Clercq, Patrick	B-5721-2015	0000-0003-0664-1602

ISSN: 0962-8819

eISSN: 1573-9368

Record 47 of 50

Title: Discovery of midgut genes for the RNA interference control of corn rootworm

Author(s): Hu, X (Hu, Xu); Richtman, NM (Richtman, Nina M.); Zhao, JZ (Zhao, Jian-Zhou); Duncan, KE (Duncan, Keith E.); Niu, XP (Niu, Xiping); Procyk, LA (Procyk, Lisa A.); Oneal, MA (Oneal, Meghan A.); Kernodle, BM (Kernodle, Bliss M.); Steimel, JP (Steimel, Joseph P.); Crane, VC (Crane, Virginia C.); Sandahl, G (Sandahl, Gary); Ritland, JL (Ritland, Julie L.); Howard, RJ (Howard, Richard J.); Presnail, JK (Presnail, James K.); Lu, AL (Lu, Albert L.); Wu, GS (Wu, Gusui)

Source: SCIENTIFIC REPORTS **Volume:** 6 **Article Number:** 30542 **DOI:** 10.1038/srep30542 **Published:** JUL 28 2016

Abstract: RNA interference (RNAi) is a promising new technology for corn rootworm control. This paper presents the discovery of new gene targets - *dvssj1* and *dvssj2*, in western corn rootworm (WCR). *Dvssj1* and *dvssj2* are orthologs of the *Drosophila* genes *snakeskin* (*ssk*) and *mesh*, respectively. These genes encode membrane proteins associated with smooth septate junctions (SSJ) which are required for intestinal barrier function. Based on bioinformatics analysis, *dvssj1* appears to be an arthropod-specific gene. Diet based insect feeding assays using double-stranded RNA (dsRNA) targeting *dvssj1* and *dvssj2* demonstrate targeted mRNA suppression, larval growth inhibition, and mortality. In RNAi treated WCR, injury to the midgut was manifested by "blebbing" of the midgut epithelium into the gut lumen. Ultrastructural examination of midgut epithelial cells revealed apoptosis and regenerative activities. Transgenic plants expressing dsRNA targeting *dvssj1* show insecticidal activity and significant plant protection from WCR damage. The data indicate that *dvssj1* and *dvssj2* are effective gene targets for the control of WCR using RNAi technology, by apparent suppression of production of their respective smooth septate junction membrane proteins located within the intestinal lining, leading to growth inhibition and mortality.

Accession Number: WOS:000380975000001

PubMed ID: 27464714

ISSN: 2045-2322

Record 48 of 50

Title: Sixteen Years of Bt Maize in the EU Hotspot: Why Has Resistance Not Evolved? (vol 11, e0154200, 2016)

Author(s): Castanera, P (Castanera, Pedro); Farinos, GP (Farinos, Gema P.); Ortego, F (Ortego, Felix); Andow, DA (Andow, David A.)

Source: PLOS ONE **Volume:** 11 **Issue:** 7 **Article Number:** e0160294 **DOI:** 10.1371/journal.pone.0160294 **Published:** JUL 25 2016

Accession Number: WOS:000381515200074

Author Identifiers:

Author	ResearcherID Number	ORCID Number
FARINOS, GEMA	D-9849-2015	0000-0002-4952-5372

ISSN: 1932-6203

Record 49 of 50

Title: Production and Characterization of Monoclonal Antibody Broadly Recognizing Cry1 Toxins by Use of Designed Polypeptide as Hapten

Author(s): Dong, S (Dong, Sa); Zhang, CZ (Zhang, Cunzheng); Zhang, X (Zhang, Xiao); Liu, Y (Liu, Yuan); Zhong, JF (Zhong, Jianfeng); Xie, YJ (Xie, Yajing); Xu, CX (Xu, Chongxin); Ding, Y (Ding, Ying); Zhang, LQ (Zhang, Liuquan); Liu, XJ (Liu, Xianjin)

Source: ANALYTICAL CHEMISTRY **Volume:** 88 **Issue:** 14 **Pages:** 7023-7032 **DOI:** 10.1021/acs.analchem.6b00429 **Published:** JUL 19 2016

Abstract: In this study, by use of synthesized polypeptides as haptens, a monoclonal antibody with broad recognition against seven major Cry1 toxins (Cry1Aa, Cry1Ab, Cry1Ac, Cry1B, Cry1C, Cry1E, and Cry1F) has been produced and characterized. First, by comparing the three-dimensional structures of seven Cry1 toxins, analyzing the conserved sequences, and considering the antigenicity and hydrophilicity, three polypeptides (T1, T2, and T3) have been chosen and coupled to keyhole limpet hemocyanin as immunogens for the generic monoclonal antibody (Mab) generation. Thereafter, a double antibody sandwich enzyme-linked immunosorbent assay method (DAS-ELISA) was developed for simultaneous determination of seven Cry1 toxins. The results revealed that the haptens T1, T2, and T3 had different effects in the production of antibodies. Among them, the obtained Mab (strain 2D3) generated by T2 can recognize seven Cry1 toxins simultaneously. Equilibrium dissociation constant (K-D) values for seven Cry1 toxins with Mab 2D3 were 1.198 X 10(-8) M for Cry1Aa, 2.197 X 10(-8) M for Cry1Ab, 1.367 X 10(-8) M for Cry1Ac, 2.092 X 10(-8) M for Cry1B, 5.177 X 10(-8) M for Cry1C, 4.016 X 10(-8) M for Cry1E, and 3.497 X 10(-8) M for Cry1F. For 2D3-based DAS-ELISA, the limits of detection (LOD) and limits of quantification (LOQ) can reach IS and 30 ng.mL(-1) for each Cry1 toxin, respectively. Our study is the first report of a broadly specific immunoassay for multidetermination of seven major Cry1 toxins, and it will provide a new idea and technical routes for development of multidetermination immunoassays.

Accession Number: WOS:000380296800012

PubMed ID: 27341419

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eISSN: 1520-6882

Record 50 of 50

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

Author(s): Silva, GV (Silva, Gabriela Vieira); Bueno, AD (Bueno, Adeney de Freitas); Bortolotto, OC (Bortolotto, Orcial Ceolin); dos Santos, AC (dos Santos, Antonio Cesar); Pomari-Fernandes, A (Pomari-Fernandes, Aline)

Source: REVISTA BRASILEIRA DE ENTOMOLOGIA **Volume:** 60 **Issue:** 3 **Pages:** 255-259 **DOI:** 10.1016/j.rbe.2016.04.005 **Published:** JUL-SEP 2016

Abstract: This study aimed to evaluate the development and reproduction of the black armyworm, Spodoptera cosmioides when larvae fed on leaves of Bt-corn hybrids, expressing a single Cry1F and also Cry1F, Cry1A. 105 and Cry2Ab2 in pyramided corn and their non-Bt-isoline (hybrid 2B688), as well as on leaves of two soybean isolines expressing the Cry1Ac protein and its non-Bt isoline (A5547-227). We also assessed the effect of these Bt and non-Bt plants on the leaf consumption rate of S. cosmioides larvae. This pest was unable to develop when fed on any of the corn isolines (Bt and non-Bt). When both 1st and 3rd instar larvae were fed on corn leaf, mortality was 100% in both Bt and non-Bt corn. In contrast, when corn leaves were offered to 5th instar larvae, there were survivors. Defoliation and leaf consumption was higher with non-Bt corn than with both of the Bt corn isolines. There was no negative effect of Bt soybean leaves on the development and reproduction of S. cosmioides with respect to all evaluated parameters. Our study indicates that both Bt and non-Bt corn adversely affect the development of S. cosmioides while Bt soybean did not affect its biology, suggesting that this lepidopteran has major potential to become an important pest in Bt soybean crops. (C) 2016 Sociedade Brasileira de Entomologia. Published by Elsevier Editora Ltda.

Accession Number: WOS:000382153200011

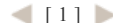
ISSN: 0085-5626

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Record 1 of 50**Title:** Expression of cry1Ab gene from a novel *Bacillus thuringiensis* strain SY49-1 active on pest insects**Author(s):** Azizoglu, U (Azizoglu, Ugur); Ayvaz, A (Ayvaz, Abdurrahman); Yilmaz, S (Yilmaz, Semih); Karaborklu, S (Karaborklu, Salih); Temizgul, R (Temizgul, Ridvan)**Source:** BRAZILIAN JOURNAL OF MICROBIOLOGY **Volume:** 47 **Issue:** 3 **Pages:** 597-602 **DOI:** 10.1016/j.bjm.2016.04.011 **Published:** JUL-SEP 2016**Abstract:** In this study, the cry1Ab gene of previously characterized and Lepidoptera-, Diptera-, and Coleoptera-active *Bacillus thuringiensis* SY49-1 strain was cloned, expressed and individually tested on *Ephesthia kuehniella* (Lepidoptera: Pyralidae) and *Plodia interpunctella* (Lepidoptera: Pyralidae) larvae. pET-cry1Ab plasmids were constructed by ligating the cry1Ab into pET28a (+) expression vector. Constructed plasmids were transferred to an *Escherichia coli* BL21 (DE3) strain rendered competent with CaCl₂. Isopropyl beta-D-1-thiogalactopyranoside was used to induce the expression of cry1Ab in *E. coli* BL21(DE3), and consequently, similar to 130 kDa of Cry1Ab was obtained. Bioassay results indicated that recombinant Cry1Ab at a dose of 1000 µg g⁻¹ caused 40% and 64% mortality on *P. interpunctella* and *E. kuehniella* larvae, respectively. However, the mortality rates of Bt SY49-1 strains' spore-crystal mixture at the same dose were observed to be 70% on *P. interpunctella* and 90% on *E. kuehniella* larvae. The results indicated that cry1Ab may be considered as a good candidate in transgenic crop production and as an alternative biocontrol agent in controlling stored product moths. (C) 2016 Sociedade Brasileira de Microbiologia. Published by Elsevier Editora Ltda. This is an open access article under the CC BY-NC-ND license**Accession Number:** WOS:000381101200010**PubMed ID:** 27143037**ISSN:** 1517-8382**eISSN:** 1678-4405**Record 2 of 50****Title:** Toxicity of *Bacillus thuringiensis* crystal proteins against eri silkworm, *Samia cynthia ricini* (Lepidoptera: Saturniidae)**Author(s):** Kumar, DS (Kumar, Donthula Sandeep); Tarakeswari, M (Tarakeswari, Muddanuru); Lakshminarayana, M (Lakshminarayana, Maddukuri); Sujatha, M (Sujatha, Mulpuri)**Source:** JOURNAL OF INVERTEBRATE PATHOLOGY **Volume:** 138 **Pages:** 116-119 **DOI:** 10.1016/j.jip.2016.06.012 **Published:** JUL 2016**Abstract:** Ten purified crystal proteins of *Bacillus thuringiensis* (Bt) were tested at concentrations ranging from 2.93 to 3000 ng/cm² for their toxicity to eri silkworm through protein paint bioassays using castor leaves. Based on LC50 values, Cry1Aa (2.6 ng/cm²) was highly toxic followed by Cry1Ac (29.3 ng/cm²) and Cry1Ab (68.7 ng/cm²). The Cry1Ca and Cry1Ea proteins were moderately toxic to eri silkworm larvae and resulted in 23% and 28% mortality, respectively at the highest concentration tested (3000 ng/cm²). Only reduction in larval weight was observed with Cry2Aa, Cry1Da and Cry9Aa proteins while Cry3Aa and Cry1Ba proteins were found to be nontoxic. (C) 2016 Elsevier Inc. All rights reserved.**Accession Number:** WOS:000380385000017**ISSN:** 0022-2011**eISSN:** 1096-0805**Record 3 of 50****Title:** Arthropod Diversity and Abundance in Wild Rice, *Oryza rufipogon*, in the Mekong Delta, Vietnam**Author(s):** Cuong, NL (Ngo Luc Cuong); Langellotto, GA (Langellotto, Gail A.); Thuy, TL (Tran Loc Thuy); Quynh, V (Vu Quynh); Thuy, NTT (Nguyen Thi Thanh Thuy); Barrion, AT (Barrion, Alberto T.); Chen, YH (Chen, Yolanda H.)**Source:** ANNALS OF THE ENTOMOLOGICAL SOCIETY OF AMERICA **Volume:** 109 **Issue:** 4 **Pages:** 542-554 **DOI:** 10.1093/aea/saw017 **Published:** JUL 2016**Abstract:** Very little is known about the arthropods associated with the wild ancestors of agricultural crops. Given that wild relatives of crop plants are subjected to human pressures of habitat loss and transgene flow, baseline levels of arthropod biodiversity and community composition are urgently needed to detect declines associated with anthropogenic disturbance. Here, we sampled arthropod abundance and community composition on the wild ancestor of cultivated rice, *Oryza rufipogon* Griffiths, in the Mekong Delta of Vietnam to ask: 1) Do arthropods associated with *O. rufipogon* fluctuate temporally and spatially in terms of community composition, diversity, and abundance? 2) What is the abundance and diversity of lepidopteran and hemipteran species associated with *O. rufipogon* across sites and seasons? We found a total of 578 arthropod taxa, distributed across 178 families in 17 orders. Rarefied species richness and arthropod abundance did not vary across the sampled stands of *O. rufipogon*, but did vary across the years. Arthropod abundance and metrics dependent upon abundance generally declined over the observation period, suggesting that the sampling effects or other unobservable factors may have contributed to the decline in the arthropod community. Overall, predators dominated the community composition, followed by detritivores and herbivores. Predatory and herbivorous taxa were the most speciose guilds. We found 45 unique taxa of Lepidoptera, many of which were previously undescribed on rice. Given that wild relatives such as *Oryza rufipogon* support a diverse arthropod community, this study provides a baseline evaluation of the arthropod community in this important native habitat.**Accession Number:** WOS:000380220600006**ISSN:** 0013-8746**eISSN:** 1938-2901**Record 4 of 50****Title:** Gut microbiota of *Busseola fusca* (Lepidoptera: Noctuidae)**Author(s):** Snyman, M (Snyman, Maxi); Gupta, AK (Gupta, Arvind Kumar); Bezuidenhout, CC (Bezuidenhout, Cornelius Carlos); Claassens, S (Claassens, Sarina); van den Berg, J (van den Berg, Johnnie)**Source:** WORLD JOURNAL OF MICROBIOLOGY & BIOTECHNOLOGY **Volume:** 32 **Issue:** 7 **Article Number:** 115 **DOI:** 10.1007/s11274-016-2066-8 **Published:** JUL 2016**Abstract:** *Busseola fusca* (Fuller) (Lepidoptera: Noctuidae) is a stemborer pest that attacks maize (*Zea mays*) throughout sub-Saharan Africa. Genetically modified maize has been shown to be effective against *B. fusca*. However, resistance of *B. fusca* against Bt-maize has developed and spread throughout South Africa. Previous studies suggested that gut microbiota contribute to mortality across a range of Lepidoptera. To fully assess the role of microbiota within the gut, it is essential to understand the microbiota harboured by natural *B. fusca* populations. This study aimed to identify the gut-associated bacteria by 16S rRNA gene sequencing. A total of 78 bacterial strains were characterised from the midgut of *B. fusca* larvae that were collected from 30 sites across the maize producing region of South Africa. Molecular phylogenetic analyses revealed bacteria affiliated to Proteobacteria, Actinobacteria, and Firmicutes. Taxonomic distribution placed these isolates into 15 different genera representing 20 species. The majority of bacteria identified belong to the genera *Bacillus*, *Enterococcus*, and *Klebsiella*. The *B. fusca* gut represents an intriguing and unexplored niche for analysing microbial ecology. The study could provide opportunities for developing new targets for pest management and contribute to understanding the phenomenon of resistance evolution of this species.**Accession Number:** WOS:000379023800010**PubMed ID:** 27263010**Author Identifiers:**

Author	ResearcherID Number	ORCID Number
Claassens, Sarina	F-8944-2010	0000-0003-3955-4361

ISSN: 0959-3993**eISSN:** 1573-0972**Record 5 of 50****Title:** Transgenic Bt (Cry1Ab/Ac) rice lines with different genetic backgrounds exhibit superior field performance under pesticide-free environment**Author(s):** Jiang, Y (Jiang, Yang); Ling, L (Ling, Lin); Zhang, LL (Zhang, Lingli); Wang, KX (Wang, Kangxu); Cai, ML (Cai, Mingli); Zhan, M (Zhan, Ming); Li, CF (Li, Chengfang); Wang, JP (Wang, Jinping); Chen, X (Chen, Xuan); Lin, YJ (Lin, Yongjun); Cao, CG (Cao, Cougui)**Source:** FIELD CROPS RESEARCH **Volume:** 193 **Pages:** 117-122 **DOI:** 10.1016/j.fcr.2016.03.014 **Published:** JUL 2016

Abstract: Transgenic rice with Cry Bacillus thuringiensis (Bt) genes have been developed in the last few decades. The performance of transgenic rice, especially the yield and resistance, must be meticulously evaluated prior to commercial production. In this study, yield and resistance performance of newly bred transgenic Bt (Cry1Ab/Ac) rice lines with different genetic backgrounds were first investigated under pesticide-free field environment. Transgenic Bt (Cry1Ab/Ac) rice lines showed high insect resistances and superior agronomic traits, resulting in obvious yield advantages ranging from 9.1% to 38.0% over their respective non-Bt control lines. Bt protein content (BTC) was similar among the Bt (Cry1Ab/Ac) rice lines in different years, while it was much higher in leaves than in stems of the Bt (Cry1Ab/Ac) rice lines. Different genetic backgrounds of Bt (Cry1Ab/Ac) rice lines affected the yield advantage but had no influence on the resistance and BTC. The results suggested that Bt (Cry1Ab/Ac) rice lines have gained obvious yield advantages and high resistances regardless of genetic background under pesticide-free environment. (C) 2016 Published by Elsevier B.V.

Accession Number: WOS:000377739200011

ISSN: 0378-4290

eISSN: 1872-6852

Record 6 of 50

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

Author(s): Turkec, A (Turkec, Aydin); Lucas, SJ (Lucas, Stuart J.); Karlik, E (Karlik, Elif)

Source: JOURNAL OF THE SCIENCE OF FOOD AND AGRICULTURE **Volume:** 96 **Issue:** 9 **Pages:** 3173-3179 **DOI:** 10.1002/jfsa.7496 **Published:** JUL 2016

Abstract: BACKGROUND: EU legislation strictly controls use of genetically modified (GM) crops in food and feed products, and requires them to be labelled if the totalGMcontent is greater than 9 g kg(-1) (for approvedGMcrops). We screened maize-containing food and feed products from Turkey to assess the prevalence of GM material.

RESULTS: With this aim, 83 food and feed products - none labelled as containing GMmaterial -were screened using multiplex real-time polymerase chain reaction (PCR) for four common GMelements (35S/NOS/bar/FMV). Of these, 18.2% of feeds and 6% of food samples tested positive for one or more of these elements, andwere subjected to event-specific PCR to identify whichGM organisms they contained. Most samples were negative for the approved GM events tested, suggesting that they may contain adventitious GM contaminants. One sample was shown to contain an unapproved GM event (MON810, along with GA21) at a concentration well above the statutory labelling requirement.

CONCLUSION: Current legislation has restricted the penetration of GM maize into the Turkish food industry but not eliminated it, and the proliferation of different GM events is making monitoring increasingly complex. Our results indicate that labelling requirements are not being followed in some cases. (C) 2015 Society of Chemical Industry

Accession Number: WOS:000377203000030

PubMed ID: 27295429

ISSN: 0022-5142

eISSN: 1097-0010

Record 7 of 50

Title: Development of a qualitative real-time PCR method to detect 19 targets for identification of genetically modified organisms

Author(s): Peng, C (Peng, Cheng); Wang, PF (Wang, Pengfei); Xu, XL (Xu, Xiaoli); Wang, XF (Wang, Xiaofu); Wei, W (Wei, Wei); Chen, XY (Chen, Xiaoyun); Xu, JF (Xu, Junfeng)

Source: SPRINGERPLUS **Volume:** 5 **Article Number:** 889 **DOI:** 10.1186/s40064-016-2395-y **Published:** JUN 24 2016

Abstract: As the amount of commercially available genetically modified organisms (GMOs) grows recent years, the diversity of target sequences for molecular detection techniques are eagerly needed. Considered as the gold standard for GMO analysis, the real-time PCR technology was optimized to produce a high-throughput GMO screening method. With this method we can detect 19 transgenic targets. The specificity of the assays was demonstrated to be 100 % by the specific amplification of DNA derived from reference material from 20 genetically modified crops and 4 non modified crops. Furthermore, most assays showed a very sensitive detection, reaching the limit of ten copies. The 19 assays are the most frequently used genetic elements present in GM crops and theoretically enable the screening of the known GMO described in Chinese markets. Easy to use, fast and cost efficient, this method approach fits the purpose of GMO testing laboratories.

Accession Number: WOS:000378924900033

PubMed ID: 27386337

ISSN: 2193-1801

Record 8 of 50

Title: Biocontrol of the oriental armyworm, *Mythimna separata*, by the tachinid fly *Exorista civilis* is synergized by Cry1Ab protoxin

Author(s): Jiang, XF (Jiang, Xingfu); Zhang, L (Zhang, Lei); Yang, HX (Yang, Haixia); Sappington, TW (Sappington, Thomas W.); Cheng, YX (Cheng, Yunxia); Luo, LZ (Luo, Li Zhi)

Source: SCIENTIFIC REPORTS **Volume:** 6 **Article Number:** 26873 **DOI:** 10.1038/srep26873 **Published:** JUN 21 2016

Abstract: Tritrophic interactions between *Mythimna separata*, its tachinid parasite *Exorista civilis* and the Cry1Ab were examined. Although 6th instar *M. separata* mortality increased with increasing Cry1Ab concentration, some tolerance was evident. Likewise, parasitization by *E. civilis* resulted in only 18% host mortality. However, combination of Cry1Ab and *E. civilis* parasitization resulted in a significant Cry1Ab dose-dependent increase in mortality over that of either alone, including a 50-56% synergistic increase in efficacy at the two concentrations tested. Pupal weight, adult emergence and lifetime fecundity of *M. separata* derived from larvae surviving both agents were negatively affected. The ability of *E. civilis* to parasitize and subsequently develop on the host was not adversely influenced by Cry1Ab. Instead, pupation rate increased significantly among host larvae fed 3.125 µg/g Cry1Ab diet. Overall, our results demonstrate that use of Cry1Ab to control *M. separata* not only is compatible with the use of the tachinid parasitoid, but that the two methods can act synergistically to manage this destructive pest, provide support for the safety of transgenic Cry1Ab Bt plants in China. This example of two independent pest management strategies acting synergistically against a difficult pest offers a new perspective of broad significance in striving for agricultural sustainability.

Accession Number: WOS:000378244500001

PubMed ID: 27324469

ISSN: 2045-2322

Record 9 of 50

Title: Pure Bt-crop and mixed seed sowing strategies for optimal economic profit in the face of pest resistance to pesticides and Bt-corn

Author(s): Liang, JH (Liang, Juhua); Tang, SY (Tang, Sanyi); Cheke, RA (Cheke, Robert A.)

Source: APPLIED MATHEMATICS AND COMPUTATION **Volume:** 283 **Pages:** 6-21 **DOI:** 10.1016/j.amc.2016.02.023 **Published:** JUN 20 2016

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.

Accession Number: WOS:000373187400002

ISSN: 0096-3003

eISSN: 1873-5649

Record 10 of 50

Title: Performance and cross-crop resistance of Cry1F-maize selected *Spodoptera frugiperda* on transgenic Bt cotton: implications for resistance management

Author(s): Yang, F (Yang, Fei); Kerns, DL (Kerns, David L.); Brown, S (Brown, Sebe); Kurtz, R (Kurtz, Ryan); Dennehy, T (Dennehy, Tim); Braxton, B (Braxton, Bo); Head, G (Head, Graham); Huang, FN (Huang, Fangneng)

Source: SCIENTIFIC REPORTS **Volume:** 6 **Article Number:** 28059 **DOI:** 10.1038/srep28059 **Published:** JUN 15 2016

Abstract: Transgenic crops producing *Bacillus thuringiensis* (Bt) proteins have become a primary tool in pest management. Due to the intensive use of Bt crops, resistance of the fall armyworm, *Spodoptera frugiperda*, to Cry1F maize has occurred in Puerto Rico, Brazil, and some areas of the southeastern U.S. The sustainability of Bt crops faces a great challenge because the Cry1F-maize resistant *S. frugiperda* may also infest other Bt crops in multiple cropping ecosystems. Here we examined the survival and

plant injury of a *S. frugiperda* population selected with Cry1F maize on three single-gene and five pyramided Bt cotton products. Larvae of Cry1F-susceptible (SS), -heterozygous (RS), and -resistant (RR) genotypes of *S. frugiperda* were all susceptible to the pyramided cotton containing Cry1Ac/Cry2Ab, Cry1Ac/Cry1F/Vip3A, Cry1Ab/Cry2Ae, or Cry1Ab/Cry2Ae/Vip3A, and the single-gene Cry2Ae cotton. Pyramided cotton containing Cry1Ac/Cry1F was effective against SS and RS, but not for RR. These findings show that the Cry1F-maize selected *S. frugiperda* can cause cross-crop resistance to other Bt crops expressing similar insecticidal proteins. Resistance management and pest management programs that utilize diversify mortality factors must be implemented to ensure the sustainability of Bt crops. This is especially important in areas where resistance to single-gene Bt crops is already widespread.

Accession Number: WOS:000384605500001

PubMed ID: 27301612

Author Identifiers:

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

ISSN: 2045-2322

Record 11 of 50

Title: Broad-spectrum resistance to *Bacillus thuringiensis* toxins by western corn rootworm (*Diabrotica virgifera virgifera*)

Author(s): Jakka, SRK (Jakka, Siva R. K.); Shrestha, RB (Shrestha, Ram B.); Gassmann, AJ (Gassmann, Aaron J.)

Source: SCIENTIFIC REPORTS **Volume:** 6 **Article Number:** 27860 **DOI:** 10.1038/srep27860 **Published:** JUN 14 2016

Abstract: The evolution of resistance and cross-resistance threaten the sustainability of genetically engineered crops that produce insecticidal toxins derived from the bacterium *Bacillus thuringiensis* (Bt). Western corn rootworm, *Diabrotica virgifera virgifera* LeConte, is a serious pest of maize and has been managed with Bt maize since 2003. We conducted laboratory bioassays with maize hybrids producing Bt toxins Cry3Bb1, mCry3A, eCry3.1Ab, and Cry34/35Ab1, which represent all commercialized Bt toxins for management of western corn rootworm. We tested populations from fields where severe injury to Cry3Bb1 maize was observed, and populations that had never been exposed to Bt maize. Consistent with past studies, bioassays indicated that field populations were resistant to Cry3Bb1 maize and mCry3A maize, and that cross-resistance was present between these two types of Bt maize. Additionally, bioassays revealed resistance to eCry3.1Ab maize and cross-resistance among Cry3Bb1, mCry3A and eCry3.1Ab. However, no resistance or cross-resistance was detected for Cry34/35Ab1 maize. This broad-spectrum resistance illustrates the potential for insect pests to develop resistance rapidly to multiple Bt toxins when structural similarities are present among toxins, and raises concerns about the long-term durability of Bt crops for management of some insect pests.

Accession Number: WOS:000377824300001

PubMed ID: 27297953

ISSN: 2045-2322

Record 12 of 50

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

Author(s): Stenekamp, D (Stenekamp, Daleen); Pringle, K (Pringle, Ken); Addison, M (Addison, Matthew)

Source: FLORIDA ENTOMOLOGIST **Volume:** 99 **Special Issue:** 1 **Pages:** 200-205 **Published:** JUN 2016

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

Accession Number: WOS:000382249300023

ISSN: 0015-4040

eISSN: 1938-5102

Record 13 of 50

Title: Fluorescence Quenching Dynamics and Mechanism of Cry1Ab Toxin from *Bacillus thuringiensis* by Different Metal Ions

Author(s): Zhou, XY (Zhou, Xueyong); Zhang, JC (Zhang, Jiachen); She, CM (She, Chongmei); Liu, HF (Liu, Huifen)

Source: JOURNAL OF THE CHEMICAL SOCIETY OF PAKISTAN **Volume:** 38 **Issue:** 3 **Pages:** 524-532 **Published:** JUN 2016

Abstract: The reaction dynamics of Cry1Ab toxin from *Bacillus thuringiensis* with sodium, calcium and lead ions was studied by fluorescence quenching technique. Gradual quenching was observed by titration of Cry1Ab toxin with metal ions (Na⁺, Ca²⁺ or Pb²⁺). The quenched strength of these ions in the descending order was: lead ion > calcium ion > sodium ion. The quenching equilibrium of Cry1Ab toxin by metal ions reached within 60 min, and the quenching dynamics of Cry1Ab toxin could be expressed by the Elovich model. The toxin concentration, pH and temperature had influence on the quenching dynamics. The interaction between Cry1Ab toxin and metal ions is based on static quenching mechanism.

Accession Number: WOS:000381933700019

ISSN: 0253-5106

Record 14 of 50

Title: IPM Use With the Deployment of a Non-High Dose Bt Pyramid and Mitigation of Resistance for Western Corn Rootworm (*Diabrotica virgifera virgifera*)

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

Source: ENVIRONMENTAL ENTOMOLOGY **Volume:** 45 **Issue:** 3 **Pages:** 747-761 **DOI:** 10.1093/ee/nvw015 **Published:** JUN 2016

Abstract: Recent detection of western corn rootworm resistance to Bt (*Bacillus thuringiensis*) corn prompted recommendations for the use of integrated pest management (IPM) with planting refuges to prolong the durability of Bt technologies. We conducted a simulation experiment exploring the effectiveness of various IPM tools at extending durability of pyramided Bt traits. Results indicate that some IPM practices have greater merits than others. Crop rotation was the most effective strategy, followed by increasing the non-Bt refuge size from 5 to 20%. Soil-applied insecticide use for Bt corn did not increase the durability compared with planting Bt with refuges alone, and both projected lower durabilities. When IPM participation with randomly selected management tools was increased at the time of Bt commercialization, durability of pyramided traits increased as well. When non-corn rootworm expressing corn was incorporated as an IPM option, the durability further increased.

For corn rootworm, a local resistance phenomenon appeared immediately surrounding the resistant field (hotspot) and spread throughout the local neighborhood in six generations in absence of mitigation. Hotspot mitigation with random selection of strategies was ineffective at slowing resistance, unless crop rotation occurred immediately; regional mitigation was superior to random mitigation in the hotspot and reduced observed resistance allele frequencies in the neighborhood. As resistance alleles of mobile pests can escape hotspots, the scope of mitigation should extend beyond resistant sites. In the case of widespread resistance, regional mitigation was less effective at prolonging the life of the pyramid than IPM with Bt deployment at the time of commercialization.

Accession Number: WOS:000381910800026

ISSN: 0046-225X

eISSN: 1938-2936

Record 15 of 50

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

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

Source: BRITISH POULTRY SCIENCE **Volume:** 57 **Issue:** 3 **Pages:** 415-423 **DOI:** 10.1080/00071668.2016.1162281 **Published:** JUN 2016

Abstract: The hypothesis assumes that feed containing GMOs affects animal health and results in the transgene product accumulating in the body. Therefore, the objective of the study was to evaluate the impact of genetically modified (GM) ingredients used in poultry diets on aspects of bird health status and accumulation of transgenic DNA in eggs, breast muscle and internal organs. A total of 10 generations of Japanese quail were fed three types of diets: group A - containing GM soya (Roundup Ready) and non-GM maize, group B - containing GM maize (MON810) and non-GM soya, and group C - containing non-GM soya and maize. Bird performance traits were monitored

throughout the trial. In 17-week-old animals of each generation, health examination took place on birds from each group including post-mortem necropsy and histological organ evaluation. For the purpose of transgenic DNA detection, samples of selected important tissues were taken. A molecular screening method of PCR amplification was used. The analysis of the sectional examination of birds used in the current experiment did not indicate the existence of the pathological changes caused by pathogens, nutritional factors or of environmental nature. The histopathological changes occurred in all three dietary groups and there were no statistically significant differences between the groups. There was no transgene amplification - neither CaMV35S promoter sequence nor nos terminator sequence, in the samples derived from breast muscle, selected tissues and germinal discs (eggs). According to the obtained results, it was concluded that there was no negative effect of the use of GM soya or maize with regard to bird health status or to the presence of transgenic DNA in the final consumable product.

Accession Number: WOS:000380059900017

PubMed ID: 27095142

ISSN: 0007-1668

eISSN: 1466-1799

Record 16 of 50

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

Author(s): Coates, BS (Coates, Brad S.)

Source: CURRENT OPINION IN INSECT SCIENCE **Volume:** 15 **Pages:** 70-77 **DOI:** 10.1016/j.cois.2016.04.003 **Published:** JUN 2016

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

Accession Number: WOS:000378671000011

PubMed ID: 27436734

ISSN: 2214-5745

eISSN: 2214-5753

Record 17 of 50

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

Author(s): Gassmann, AJ (Gassmann, Aaron J.)

Source: CURRENT OPINION IN INSECT SCIENCE **Volume:** 15 **Pages:** 111-115 **DOI:** 10.1016/j.cois.2016.04.001 **Published:** JUN 2016

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

Accession Number: WOS:000378671000017

PubMed ID: 27436740

ISSN: 2214-5745

eISSN: 2214-5753

Record 18 of 50

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

Author(s): Velez, AM (Velez, Ana M.); Vellichirammal, NN (Vellichirammal, Neetha Nanoth); Jurat-Fuentes, JL (Jurat-Fuentes, Juan Luis); Siegfried, BD (Siegfried, Blair D.)

Source: CURRENT OPINION IN INSECT SCIENCE **Volume:** 15 **Pages:** 116-124 **DOI:** 10.1016/j.cois.2016.04.010 **Published:** JUN 2016

Abstract: The Cry1Fa protein from the bacterium *Bacillus thuringiensis* (Bt) is known for its potential to control lepidopteran pests, especially through transgenic expression in maize and cotton. The maize event TC1507 expressing the cry 1 Fa toxin gene became commercially available in the United States in 2003 for the management of key lepidopteran pests including the European corn borer, *Ostrinia nubilalis*, and the fall armyworm, *Spodoptera frugiperda*. A high-dose/refuge strategy has been widely adopted to delay evolution of resistance to event TC1507 and other transgenic Bt crops. Efficacy of this strategy depends on the crops expressing a high dose of the Bt toxin to targeted pests and adjacent refuges of non-Bt host plants serving as a source of abundant susceptible insects. While this strategy has proved effective in delaying *O. nubilalis* resistance, field-evolved resistance to event TC1507 has been reported in *S. frugiperda* populations in Puerto Rico, Brazil, and the southeastern United States. This paper examines available information on resistance to Cry1Fa in *O. nubilalis* and *S. frugiperda* and discusses how this information identifies opportunities to refine resistance management recommendations for Bt maize.

Accession Number: WOS:000378671000018

PubMed ID: 27436741

ISSN: 2214-5745

eISSN: 2214-5753

Record 19 of 50

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

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

Source: CURRENT OPINION IN INSECT SCIENCE **Volume:** 15 **Pages:** 131-138 **DOI:** 10.1016/j.cois.2016.04.012 **Published:** JUN 2016

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

Accession Number: WOS:000378671000020

PubMed ID: 27436743

Author Identifiers:

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

ISSN: 2214-5745

eISSN: 2214-5753

Record 20 of 50**Title:** Managing maize under pest species competition: Is Bt (*Bacillus thuringiensis*) maize the solution?**Author(s):** Catarino, R (Catarino, Rui); Ceddia, G (Ceddia, Graziano); Areal, F (Areal, Francisco); Parisey, N (Parisey, Nicolas); Park, J (Park, Julian)**Source:** ECOSPHERE **Volume:** 7 **Issue:** 6 **Article Number:** e01340 **DOI:** 10.1002/ecs2.1340 **Published:** JUN 2016

Abstract: Transgenic crops that contain Cry genes from Bt (*Bacillus thuringiensis*) have been adopted by farmers over the last 17 yr. Unlike traditional broad-spectrum chemical insecticides, Bt's toxicity spectrum is relatively narrow and selective, which may indirectly benefit secondary insects that may become important pests. The economic damage caused by the rise of secondary pests could offset some or all of the benefits associated with the use of Bt varieties. We develop a bioeconomic model to analyze the interactions between primary and secondary insect populations and the impact of different management options on insecticide use and economic impact over time. Results indicate that some of the benefits associated with the adoption of genetically engineered insect resistant crops may be eroded when taking into account ecological dynamics. It is suggested that secondary pests could easily become key insect pests requiring additional measures, such as insecticide applications or stacked traits, to keep their populations under the economic threshold.

Accession Number: WOS:000378523100017

ISSN: 2150-8925

Record 21 of 50**Title:** Evaluation of foliar damage by *Spodoptera frugiperda* (Lepidoptera: Noctuidae) to genetically modified corn (Poales: Poaceae) in Mexico**Author(s):** Aguirre, LA (Aguirre, Luis A.); Hernandez-Juarez, A (Hernandez-Juarez, Agustin); Flores, M (Flores, Mariano); Cerna, E (Cerna, Ernesto); Landeros, J (Landeros, Jeronimo); Frias, GA (Frias, Gustavo A.); Harris, MK (Harris, Marvin K.)**Source:** FLORIDA ENTOMOLOGIST **Volume:** 99 **Issue:** 2 **Pages:** 276-280 **Published:** JUN 2016

Abstract: The fall armyworm, *Spodoptera frugiperda* Smith & Abbot (Lepidoptera: Noctuidae), is a key pest of corn, *Zea mays* L. (Poales: Poaceae), in Mexico. The development of genetically modified (GM) corn hybrids for resistance to this insect, with the inclusion of several genes coding for proteins Cry1Ab, Vip3Aa20, and mCry3A of *Bacillus thuringiensis* Berliner (Bacillales: Bacillaceae) (Bt), offer an alternative to conventional insecticides to control this pest. Resistance to fall armyworms of the GM corn hybrids Agrisure 3000 GT, Agrisure Viptera 3110, and Agrisure Viptera 3111 was evaluated in 4 locations at Sinaloa for a 3 yr period. Damage evaluation showed that the maize hybrids with the Bt gene insertion were not affected by the fall armyworm as compared with their respective isolines, which were seriously damaged. The results reaffirm the insect control benefits provided by this technology and provide a baseline for resistance management.

Accession Number: WOS:000378163800018**Author Identifiers:**

Author	ResearcherID Number	ORCID Number
Hernandez Juarez, Agustin		0000-0001-7059-4471

ISSN: 0015-4040

eISSN: 1938-5102

Record 22 of 50**Title:** mCry3A-Selected Western Corn Rootworm (Coleoptera: Chrysomelidae) Colony Exhibits High Resistance and Has Reduced Binding of mCry3A to Midgut Tissue**Author(s):** Zhao, JZ (Zhao, Jian-Zhou); Oneal, MA (Oneal, Meghan A.); Richtman, NM (Richtman, Nina M.); Thompson, SD (Thompson, Stephen D.); Cowart, MC (Cowart, Miles C.); Nelson, ME (Nelson, Mark E.); Pan, ZQ (Pan, Zaiqi); Alves, AP (Alves, Analiza P.); Yamamoto, T (Yamamoto, Takashi)**Source:** JOURNAL OF ECONOMIC ENTOMOLOGY **Volume:** 109 **Issue:** 3 **Pages:** 1369-1377 **DOI:** 10.1093/jee/tow049 **Published:** JUN 2016

Abstract: Several Bt maize events expressing various insecticidal Cry protein genes have been commercialized for management of western corn rootworm, *Diabrotica virgifera virgifera* LeConte (Coleoptera: Chrysomelidae). We used high efficacy (> 99.7%) experimental maize events that express mCry3A for selections under laboratory conditions to develop a western corn rootworm colony resistant to mCry3A at higher levels than published results. The resistance ratio (RR) to mCry3A was > 97-fold based on LC50 values in diet-based bioassays after six generations of selections when compared to that of an unselected control colony. Using a sublethal seedling assay (SSA) method, we confirmed that the colony had no cross-resistance to maize event DAS-59122-7, which expresses Cry34/35Ab. Reciprocal crosses between the mCry3A-resistant colony and the susceptible colony were performed to test the inheritance of resistance. Larval survival and development evaluated by the SSA method indicated that resistance to mCry3A was inherited autosomally and was incompletely recessive ($h = 0.23-0.25$). Specific binding of mCry3A to brush border membrane vesicles of midgut tissue revealed reduced binding in the resistant colony when compared to binding in the susceptible colony. This is the first report where resistance in western corn rootworm has been shown to involve reduced binding of a Cry3-class protein in midgut tissue.

Accession Number: WOS:000378041400051

ISSN: 0022-0493

eISSN: 1938-291X

Record 23 of 50**Title:** Multiple Assays Indicate Varying Levels of Cross Resistance in Cry3Bb1-Selected Field Populations of the Western Corn Rootworm to mCry3A, eCry3.1Ab, and Cry34/35Ab1**Author(s):** Zukoff, SN (Zukoff, Sarah N.); Ostlie, KR (Ostlie, Kenneth R.); Potter, B (Potter, Bruce); Meihls, LN (Meihls, Lisa N.); Zukoff, AL (Zukoff, Anthony L.); French, L (French, Lee); Ellersieck, MR (Ellersieck, Mark R.); French, BW (French, B. Wade); Hibbard, BE (Hibbard, Bruce E.)**Source:** JOURNAL OF ECONOMIC ENTOMOLOGY **Volume:** 109 **Issue:** 3 **Pages:** 1387-1398 **DOI:** 10.1093/jee/tow073 **Published:** JUN 2016

Abstract: Minnesota populations of *Diabrotica virgifera virgifera* LeConte, the western corn rootworm, surviving Cry3Bb1-expressing corn in the field and western corn rootworm populations assumed to be susceptible to all Bt proteins were evaluated for susceptibility to Cry3Bb1, mCry3A, eCry3.1Ab, and Cry34/35Ab1 in diet assays and three different plant-based assays. Rootworm populations originating from Cry3Bb1 fields and that consistently experienced greater than expected damage had increased survival and larval growth compared to control populations assayed on Cry3Bb1 as well as mCry3A and eCry3.1Ab. Cross resistance was documented between Cry3Bb1 and both mCry3A and eCry3.1Ab as single toxins. Despite very high resistance ratios in some comparisons, cross resistance was not complete and also varied with the population being evaluated, the trait measured, and the susceptible rootworm population used for comparison. Regardless of resistance and cross resistance, all proteins, even Cry3Bb1, retained some efficacy in terms of either reducing rootworm larval growth, protecting plants from damage, or both, for all rootworm populations evaluated. For one Cry3Bb1-selected population, a resistance ratio of 9.1-fold was found to Cry34/35Ab1 when evaluating EC50 values relative to a susceptible control population; however, resistance to Cry34/35Ab1 was not evident in all assays in this population. The United States Environmental Protection Agency recently suggested eliminating diet assays as part of the Bt resistance monitoring process. However, given the variability of responses of western corn rootworm populations to different proteins in different assays, both plant and diet assays are needed as options for detecting and fully characterizing resistance.

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ISSN: 0022-0493

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Record 24 of 50**Title:** Field-Based Assessment of Resistance to Bt Corn by Western Corn Rootworm (Coleoptera: Chrysomelidae)**Author(s):** Shrestha, RB (Shrestha, Ram B.); Jakka, SRK (Jakka, Siva R. K.); French, BW (French, B. Wade); Gassmann, AJ (Gassmann, Aaron J.)**Source:** JOURNAL OF ECONOMIC ENTOMOLOGY **Volume:** 109 **Issue:** 3 **Pages:** 1399-1409 **DOI:** 10.1093/jee/tow087 **Published:** JUN 2016

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

terms of developing strategies for managing western corn rootworm with resistance to Cry3Bb1 and mCry3A, and delaying the additional evolution of Bt resistance by this pest.

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Record 25 of 50

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

Author(s): Lami, F (Lami, Francesco); Masetti, A (Masetti, Antonio); Neri, U (Neri, Ulderico); Lener, M (Lener, Matteo); Staiano, G (Staiano, Giovanni); Arpaia, S (Arpaia, Salvatore); Burgio, G (Burgio, Giovanni)

Source: BULLETIN OF INSECTOLOGY **Volume:** 69 **Issue:** 1 **Pages:** 49-57 **Published:** JUN 2016

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

Accession Number: WOS:000377642900008

ISSN: 1721-8861

Record 26 of 50

Title: Using intron sequence comparisons in the triose-phosphate isomerase gene to study the divergence of the fall armyworm host strains

Author(s): Nagoshi, RN (Nagoshi, R. N.); Meagher, RL (Meagher, R. L.)

Source: INSECT MOLECULAR BIOLOGY **Volume:** 25 **Issue:** 3 **Pages:** 324-337 **DOI:** 10.1111/imb.12223 **Published:** JUN 2016

Abstract: The noctuid moth *Spodoptera frugiperda* (the fall armyworm) is endemic to the Western Hemisphere and appears to be undergoing sympatric speciation to produce two subpopulations that differ in their choice of host plants. The 'rice strain' and 'corn strain' are morphologically indistinguishable, requiring the use of genetic markers for identification. Because fall armyworm is a major pest of corn and several other agricultural crops, characterizing the strains has important economic consequences. In this study, comparisons were made of the intron sequences from the triose-phosphate isomerase (Tpi) gene isolated from 85 fall armyworm specimens collected from two host plants. Sixteen new strain-specific haplotypes based on intron polymorphisms are described that can facilitate the characterization of fall armyworm populations associated with different host plants. Comparisons of genetic diversity within and between the strains provides evidence that the corn strain is undergoing active selection and supports the proposal of directional interstrain mating occurring in the wild. Comparisons of the polymorphisms indicate that each intron undergoes different patterns of mutation that in some cases corresponds to host plant preferences. The results confirm that intron sequence comparisons are an effective approach to study fall armyworm population genetics.

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PubMed ID: 26991678

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Record 27 of 50

Title: Genetically modified crops in Switzerland: implications for agrosystem sustainability evidenced by multi-criteria model

Author(s): Wohlfender-Buhler, D (Wohlfender-Buhler, Doris); Feusthuber, E (Feusthuber, Elisabeth); Wager, R (Wager, Robert); Mann, S (Mann, Stefan); Aubry, SJ (Aubry, Sylvain J.)

Source: AGRONOMY FOR SUSTAINABLE DEVELOPMENT **Volume:** 36 **Issue:** 2 **Article Number:** 33 **DOI:** 10.1007/s13593-016-0367-9 **Published:** JUN 2016

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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Author Identifiers:

Author	ResearcherID Number	ORCID Number
Aubry, Sylvain		0000-0002-7598-3609

ISSN: 1774-0746

eISSN: 1773-0155

Record 28 of 50

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

Author(s): Bernardi, D (Bernardi, Daniel); Bernardi, O (Bernardi, Oderlei); Horikoshi, RJ (Horikoshi, Renato Jun); Salmeron, E (Salmeron, Eloisa); Okuma, DM (Okuma, Daniela Miyuki); Omoto, C (Omoto, Celso)

Source: CIENCIA RURAL **Volume:** 46 **Issue:** 6 **Pages:** 1019-1024 **DOI:** 10.1590/0103-8478cr20150047 **Published:** JUN 2016

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

Accession Number: WOS:000375079100013

Author Identifiers:

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

ISSN: 0103-8478

eISSN: 1678-4596

Record 29 of 50

Title: Bacterial Vegetative Insecticidal Proteins (Vip) from Entomopathogenic Bacteria

Author(s): Chakroun, M (Chakroun, Maissa); Banyuls, N (Banyuls, Nuria); Bel, Y (Bel, Yolanda); Escriche, B (Escriche, Baltasar); Ferre, J (Ferre, Juan)

Source: MICROBIOLOGY AND MOLECULAR BIOLOGY REVIEWS **Volume:** 80 **Issue:** 2 **Pages:** 329-350 **DOI:** 10.1128/MMBR.00060-15 **Published:** JUN 2016

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

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Record 30 of 50

Title: Life-History Traits of Spodoptera frugiperda Populations Exposed to Low-Dose Bt Maize

Author(s): Sousa, FF (Sousa, Fernanda F.); Mendes, SM (Mendes, Simone M.); Santos-Amaya, OF (Santos-Amaya, Oscar F.); Araujo, OG (Araujo, Octavio G.); Oliveira, EE (Oliveira, Eugenio E.); Pereira, EJG (Pereira, Eliseu J. G.)

Source: PLOS ONE **Volume:** 11 **Issue:** 5 **Article Number:** e0156608 **DOI:** 10.1371/journal.pone.0156608 **Published:** MAY 31 2016

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

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PubMed ID: 27243977

Author Identifiers:

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

ISSN: 1932-6203

Record 31 of 50

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

Author(s): Andreassen, M (Andreassen, Monica); Bohn, T (Bohn, Thomas); Wikmark, OG (Wikmark, Odd-Gunnar); Bodin, J (Bodin, Johanna); Traavik, T (Traavik, Terje); Lovik, M (Lovik, Martinus); Nygaard, UC (Nygaard, Unni Cecilie)

Source: BMC IMMUNOLOGY **Volume:** 17 **Article Number:** 10 **DOI:** 10.1186/s12865-016-0148-x **Published:** MAY 4 2016

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

Accession Number: WOS:000375902200001

PubMed ID: 27141950

ISSN: 1471-2172

Record 32 of 50

Title: Sixteen Years of Bt Maize in the EU Hotspot: Why Has Resistance Not Evolved?

Author(s): Castanera, P (Castanera, Pedro); Farinos, GP (Farinos, Gema P.); Ortego, F (Ortego, Felix); Andow, DA (Andow, David A.)

Source: PLOS ONE **Volume:** 11 **Issue:** 5 **Article Number:** e0154200 **DOI:** 10.1371/journal.pone.0154200 **Published:** MAY 4 2016

Abstract: The majority of Bt maize production in the European Union (EU) is concentrated in northeast Spain, which is Europe's only hotspot where resistance might evolve, and the main target pest, Sesamia nonagrioides, has been exposed to Cry1Ab maize continuously since 1998. The cropping system in northeast Spain has some similar characteristics to those that probably led to rapid resistance failures in two other target noctuid maize pests. These include repeated cultivation of Bt maize in the same fields, low use of refuges, recurring exposure of larvae to non-high dose concentrations of Cry1Ab toxin during the first years of cultivation, low migratory potential, and production concentrated in an irrigated region with few alternative hosts. Available data reveal no evidence of resistance in S. nonagrioides after 16 years of use. We explore the possible reasons for this resistance management success using evolutionary models to consider factors expected to accelerate resistance, and those expected to delay resistance. Low initial adoption rates and the EU policy decision to replace Event 176 with MON 810 Bt maize were key to delaying resistance evolution. Model results suggest that if refuge compliance continues at the present 90%, Bt maize might be used sustainably in northeast Spain for at least 20 more years before resistance might occur. However, obtaining good estimates of the present R allele frequency and level of local assortative mating are crucial to reduce uncertainty about the future success of resistance management.

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PubMed ID: 27144535

Author Identifiers:

Author	ResearcherID Number	ORCID Number
Partearroyo, ClB-Biblioteca	L-3262-2014	0000-0002-1692-4481

ISSN: 1932-6203

Record 33 of 50

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

Author(s): dos Santos, CA (dos Santos, Christiane Almeida); Marucci, RC (Marucci, Rosangela Cristina); Barbosa, TAN (Nascimento Barbosa, Tatiane Aparecida); Araujo, OG (Araujo, Octavio Gabryel); Waquil, JM (Waquil, Jose Magid); Dias, AS (Dias, Aline Silvia); Hebach, FC (Hebach, Fabricio Carvalho); Mendes, SM (Mendes, Simone Martins)

Source: PESQUISA AGROPECUARIA BRASILEIRA **Volume:** 51 **Issue:** 5 **Pages:** 537-544 **DOI:** 10.1590/S0100-204X2016000500014 **Published:** MAY 2016

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

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Record 34 of 50

Title: Fitness index and lethal time of fall armyworm on Bt corn

Author(s): Waquil, MS (Waquil, Matheus Soares); Pereira, EJJ (Guedes Pereira, Eliseu Jose); Carvalho, SSD (de Sousa Carvalho, Samantha Stefannie); Pitta, RM (Pitta, Rafael Major); Waquil, JM (Waquil, Jose Magid); Mendes, SM (Mendes, Simone Martins)

Source: PESQUISA AGROPECUARIA BRASILEIRA **Volume:** 51 **Issue:** 5 **Pages:** 563-570 **DOI:** 10.1590/S0100-204X2016000500017 **Published:** MAY 2016

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

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ISSN: 0100-204X

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Record 35 of 50

Title: Development of a Model System Approach for Generating Fragments of the Cry1Ab Protein

Author(s): Albright, VC (Albright, Vurtice C., III); Hellmich, RL (Hellmich, Richard L.); Coats, JR (Coats, Joel R.)

Source: JOURNAL OF AOAC INTERNATIONAL **Volume:** 99 **Issue:** 3 **Pages:** 792-805 **DOI:** 10.5740/jaoacint.15-0229 **Published:** MAY-JUN 2016

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

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eISSN: 1944-7922

Record 36 of 50

Title: Long term tillage treatment effects on corn grain nutrient composition and yield

Author(s): Houx, JH (Houx, James H., III); Wiebold, WJ (Wiebold, William J.); Fritsch, FB (Fritsch, Felix B.)

Source: FIELD CROPS RESEARCH **Volume:** 191 **Pages:** 33-40 **DOI:** 10.1016/j.fcr.2016.04.002 **Published:** MAY 2016

Abstract: Corn (*Zea mays* L.) grain composition is important for human and livestock nutrition, when used as seed, and for ethanol production. However, few studies have evaluated the effects of common cultural practices on corn grain composition. This study was conducted to determine whether corn grain elemental composition is affected by tillage practices (tillage or no-tillage), and whether tillage affects grain, protein, and oil yield, and removal of elements from the field in grain. The concentration of protein, oil, P, K, Ca, Mg, Mn, Fe, Zn, Cu, and B, and grain yield were determined in years 20 and 22 of long-term tillage and no-tillage treatments. Tillage treatment did not affect any grain component across both years of sampling, but Cu concentrations were greater under no-tillage in one year. Grain, oil, and protein yield was not affected by tillage treatments across years, but was greater one year under tillage and one year under no-till. The removal of P and Fe was greater under tillage in 2010, and that of Ca and Mn was greater under no-till in 2012. Removal of Cu was greater one year under tillage and one year under no-tillage. Correlation and principle components analysis suggests that there are some differences in the relationships among the grain components between tillage treatments. However, results indicate that tillage is not a dominant factor affecting corn grain composition and removals of nutrients are dominated by grain yield and not the concentration in the grain. (C) 2016 Elsevier B.V. All rights reserved.

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Record 37 of 50

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

Author(s): Bohn, T (Bohn, Thomas); Rover, CM (Rover, Carina Macagnan); Semenchuk, PR (Semenchuk, Philipp Robert)

Source: FOOD AND CHEMICAL TOXICOLOGY **Volume:** 91 **Pages:** 130-140 **DOI:** 10.1016/j.fct.2016.03.009 **Published:** MAY 2016

Abstract: Cry-toxin genes originating from *Bacillus thuringiensis* are inserted into genetically modified (GM) plants, often called Bt-plants, to provide insect resistance to pests. Significant amounts of Bt-plant residues, and thus Cry-toxins, will be shed to soil and aquatic environments.

We exposed *Daphnia magna* to purified Cry1Ab and Cry2Aa toxins for the full life-span of the animals. We used single toxins in different doses and combinations of toxins and Roundup, another potential stressor on the rise in agricultural ecosystems.

Animals exposed to 4.5 mg/L (ppm) of Cry1Ab, Cry2Aa and the combination of both showed markedly higher mortality, smaller body size and very low juvenile production compared to controls. Animals exposed to 0.75 mg/L also showed a tendency towards increased mortality but with increased early fecundity compared to the controls. Roundup stimulated animals to strong early reproductive output at the cost of later rapid mortality.

We conclude that i) purified Cry-toxins in high concentrations are toxic to *D. magna*, indicating alternative modes-of-action for these Cry-toxins; ii) Cry-toxins act in combination, indicating that 'stacked events' may have stronger effects on non-target organisms; iii) further studies need to be done on combinatorial effects of multiple Cry-toxins and herbicides that co-occur in the environment. (C) 2016 Elsevier Ltd. All rights reserved.

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Record 38 of 50

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

Author(s): Jiao, YY (Jiao, Yaoyu); Yang, Y (Yang, Yan); Meissle, M (Meissle, Michael); Peng, YF (Peng, Yufa); Li, YH (Li, Yunhe)

Source: JOURNAL OF INVERTEBRATE PATHOLOGY **Volume:** 136 **Pages:** 95-99 **DOI:** 10.1016/j.jip.2016.03.010 **Published:** MAY 2016

Abstract: Transformation of rice with genes encoding insecticidal Cry proteins from *Bacillus thuringiensis* (Bt) should confer high resistance to target lepidopteran pests, such as *Chilo suppressalis*, and low toxicity to non-target organisms, such as silkworm *Bombyx mori*. Five purified Cry proteins that have been used for plant transformation were tested using dietary exposure assays. The susceptibility of *C. suppressalis* larvae to the five insecticidal proteins in the decreasing order was: Cry1Ca > Cry1Ab > Cry1Ac > Cry2Aa > Cry1Fa. However, the toxicities of the Cry proteins to *B. mori* were in the order: Cry1Fa > Cry1Ca > Cry2Aa > Cry1Ab > Cry1Ac. The Cry1Ca, Cry1Ab and Cry1Ac proteins exhibited relatively high toxicity to *C. suppressalis* larvae, with EC50 values of 16.4, 45.8 and 89.6 ng/g, respectively. The toxicities of the three Cry proteins to *B. mori* larvae were 8, 14, and 22 times lower, with EC50 values of 138.3, 628.4 and 1939.2 ng/g, respectively. The Cry1Fa and Cry2Aa proteins showed high toxicity to *B. mori* larvae, with EC50 values of 135.7 and 373.9 ng/g, respectively, but low toxicity to *C. suppressalis* larvae, with EC50 values of 6092.1 and 1208.5 ng/g, respectively. We thus conclude that Cry1Ab, Cry1Ac and Cry1Ca are appropriate for transforming rice to control lepidopteran rice pests. In contrast, Cry1Fa and Cry2Aa are not appropriate due to their high toxicity to silkworm larvae and low activity against the target pest. (C) 2016 Elsevier Inc. All rights reserved.

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Record 39 of 50

Title: Biomolecule-nanoparticle interactions: Elucidation of the thermodynamics by isothermal titration calorimetry

Author(s): Huang, RX (Huang, Rixiang); Lau, BLT (Lau, Boris L. T.)

Source: BIOCHIMICA ET BIOPHYSICA ACTA-GENERAL SUBJECTS **Volume:** 1860 **Issue:** 5 **Special Issue:** SI **Pages:** 945-956 **DOI:** 10.1016/j.bbagen.2016.01.027 **Published:** MAY 2016

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, Delta H, Delta S, and Delta G). 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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PubMed ID: 26851677

Author Identifiers:

Author	ResearcherID Number	ORCID Number
Huang, Rixiang	P-4151-2015	0000-0002-1843-710X

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Record 40 of 50

Title: Dominance of Cry1F resistance in *Spodoptera frugiperda* (Lepidoptera: Noctuidae) on TC1507 Bt maize in Brazil

Author(s): Farias, JR (Farias, Juliano R.); Andow, DA (Andow, David A.); Horikoshi, RJ (Horikoshi, Renato J.); Sorgatto, RJ (Sorgatto, Rodrigo J.); dos Santos, AC (dos Santos, Antonio C.); Omoto, C (Omoto, Celso)

Source: PEST MANAGEMENT SCIENCE **Volume:** 72 **Issue:** 5 **Pages:** 974-979 **DOI:** 10.1002/ps.4077 **Published:** MAY 2016

Abstract: BACKGROUND Dominance of resistance has been one of the major parameters affecting the rate of evolution of resistance to Bt crops. High dose is the capacity of Bt crops to kill heterozygous insects and has been an essential component of the most successful strategy to manage resistance to these crops. Experiments were conducted to evaluate directly and indirectly whether the TC1507 event is high dose to *Spodoptera frugiperda* (JE Smith).

RESULTS About 8% of heterozygote neonate larvae were able to survive, complete larval development and emerge as normal adults on TC1507 leaves, while susceptible larvae could not survive for 5 days. The estimated dominance of resistance was 0.150.09 and significantly higher than zero; therefore, the resistance to Cry1F expressed in TC1507 was not completely recessive. A 25-fold dilution of TC1507 maize leaf tissue in an artificial diet was able to cause a maximum mortality of only 37%, with growth inhibition of 82% at 7 days after larval infestation.

CONCLUSION Resistance to Cry1F in TC1507 maize is incompletely recessive in *S. frugiperda*. TC1507 maize is not high dose for *S. frugiperda*. Additional or alternative resistance management strategies, such as the replacement of single-trait Bt maize with pyramided Bt maize, which produces multiple proteins targeting the same insect pests, should be implemented wherever this technology is in use and *S. frugiperda* is the major pest. (c) 2015 Society of Chemical Industry

Accession Number: WOS:000373605000015

PubMed ID: 26172071

Author Identifiers:

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

ISSN: 1526-498X

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Record 41 of 50

Title: Current trends in Bt crops and their fate on associated microbial community dynamics: a review

Author(s): Singh, AK (Singh, Amit Kishore); Dubey, SK (Dubey, Suresh Kumar)

Source: PROTOPLASMA **Volume:** 253 **Issue:** 3 **Special Issue:** SI **Pages:** 663-681 **DOI:** 10.1007/s00709-015-0903-5 **Published:** MAY 2016

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.

Accession Number: WOS:000373578500005

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Record 42 of 50

Title: Frequency of *Bacillus thuringiensis* Cry1A.105 resistance alleles in field populations of the fall armyworm, *Spodoptera frugiperda*, in Louisiana and Florida
Author(s): Huang, FN (Huang, Fangneng); Qureshi, JA (Qureshi, Jawwad A.); Head, GP (Head, Graham P.); Price, PA (Price, Paula A.); Levy, R (Levy, Ronnie); Yang, F (Yang, Fei); Niu, Y (Niu, Ying)

Source: CROP PROTECTION **Volume:** 83 **Pages:** 83-89 **DOI:** 10.1016/j.cropro.2016.01.019 **Published:** MAY 2016

Abstract: Fall armyworm, *Spodoptera frugiperda* (J.E. Smith), is a major pest of many crops and a cross-crop target of transgenic maize, cotton, and soybean containing *Bacillus thuringiensis* (Bt) genes. Some of the current Bt maize products for controlling lepidopteran species contain the Bt event MON 89034. The objective of this study was to determine the frequency of resistance alleles in field populations of *S. frugiperda* collected from Louisiana and Florida, U.S. to Cry1A.105, one of the two Bt genes in MON 89034. A total of 150 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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Author Identifiers:

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

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Record 43 of 50

Title: Frequency of Cry1F Non-Recessive Resistance Alleles in North Carolina Field Populations of *Spodoptera frugiperda* (Lepidoptera: Noctuidae)

Author(s): Li, GP (Li, Guoping); Reising, D (Reising, Dominic); Miao, J (Miao, Jin); Gould, F (Gould, Fred); Huang, FN (Huang, Fangneng); Feng, HQ (Feng, Hongqiang)

Source: PLOS ONE **Volume:** 11 **Issue:** 4 **Article Number:** e0154492 **DOI:** 10.1371/journal.pone.0154492 **Published:** APR 27 2016

Abstract: Fall armyworm, *Spodoptera frugiperda* (J.E. Smith) (Lepidoptera: Noctuidae), is a target species of transgenic corn (*Zea mays* L.) that expresses single and pyramided *Bacillus thuringiensis* (Bt) toxin. In 2014, *S. frugiperda* were collected from a light trap in North Carolina, and a total of 212 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.

Accession Number: WOS:000374976200084

PubMed ID: 27119741

ISSN: 1932-6203

Record 44 of 50

Title: Transgenic Cabbage Expressing Cry1Ac1 Does Not Affect the Survival and Growth of the Wolf Spider, *Pardosa astrigera* L. Koch (Araneae: Lycosidae)

Author(s): Kim, YJ (Kim, Young-Joong); Lee, JH (Lee, Joon-Ho); Harn, CH (Harn, Chee Hark); Kim, CG (Kim, Chang-Gi)

Source: PLOS ONE **Volume:** 11 **Issue:** 4 **Article Number:** e0153395 **DOI:** 10.1371/journal.pone.0153395 **Published:** APR 7 2016

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.

Accession Number: WOS:000373608000128

PubMed ID: 27055120

ISSN: 1932-6203

Record 45 of 50

Title: The New Transgenic cry1Ab/vip3H Rice Poses No Unexpected Ecological Risks to Arthropod Communities in Rice Agroecosystems

Author(s): Lu, ZB (Lu, Zengbin); Dang, C (Dang, Cong); Han, NS (Han, Naishun); Shen, ZC (Shen, Zhicheng); Peng, YF (Peng, Yufa); Stanley, D (Stanley, David); Ye, GY (Ye, Gongyin)

Source: ENVIRONMENTAL ENTOMOLOGY **Volume:** 45 **Issue:** 2 **Pages:** 518-525 **DOI:** 10.1093/ee/nvv215 **Published:** APR 2016

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

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PubMed ID: 26721297

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eISSN: 1938-2936

Record 46 of 50

Title: Tolerance of eCry3.1Ab in Reciprocal Cross Offspring of eCry3.1Ab-Selected and Control Colonies of *Diabrotica virgifera virgifera* (Coleoptera: Chrysomelidae)

Author(s): Geisert, RW (Geisert, Ryan W.); Eilersieck, MR (Eilersieck, Mark R.); Hibbard, BE (Hibbard, Bruce E.)

Source: JOURNAL OF ECONOMIC ENTOMOLOGY **Volume:** 109 **Issue:** 2 **Pages:** 815-820 **DOI:** 10.1093/jeetov335 **Published:** APR 2016

Abstract: Two new insect colonies were created by separating virgin western corn rootworm, *Diabrotica virgifera virgifera* LeConte, males and females from both a selected laboratory colony that was being reared on eCry3.1Ab-expressing corn (*Zea mays* L.) and a control colony reared on its near-isoline corn. Females from the selected colony were paired with males of the control colony and vice versa to create both a selected female by control male colony (Sel female) and control female by selected male colony (Con female). Both colonies along with their parental colonies (eCry3.1Ab-selected and control) were evaluated on eCry3.1Ab-expressing corn and its near-isoline in seedling assays. Larvae from each colony were also used in diet toxicity experiments in order to determine the LC50 and EC50 values for the eCry3.1Ab toxin for each. Statistical analysis of seedling assay experiments did not indicate any significant colony x corn interaction but did show a significant main effect of corn type for both larval recovery and larval head capsule widths. Results from the diet toxicity assays showed the control colony to have a significantly lower LC50 value than the selected and cross colonies and a significantly lower EC50 than the selected and Con female colonies. Calculations of dominance values (*h*) of eCry3.1Ab resistance

traits from seedling assays indicated that the two reciprocal cross colonies have a dominance value (h) of similar to 1, suggesting dominance of the eCry3.1Ab resistance trait.

Accession Number: WOS:000374497000042

PubMed ID: 26628501

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Record 47 of 50

Title: Evolution of Resistance by *Helicoverpa zea* (Lepidoptera: Noctuidae) Infesting Insecticidal Crops in the Southern United States

Author(s): Pan, ZQ (Pan, Zaiqi); Onstad, D (Onstad, David); Crain, P (Crain, Philip); Crespo, A (Crespo, Andre); Hutchison, W (Hutchison, William); Buntin, D (Buntin, David); Porter, P (Porter, Pat); Catchot, A (Catchot, Angus); Cook, D (Cook, Don); Pilcher, C (Pilcher, Clint); Flexner, L (Flexner, Lindsey); Higgins, L (Higgins, Laura)

Source: JOURNAL OF ECONOMIC ENTOMOLOGY **Volume:** 109 **Issue:** 2 **Pages:** 821-831 **DOI:** 10.1093/jee/tov340 **Published:** APR 2016

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

Accession Number: WOS:000374497000043

PubMed ID: 26637533

ISSN: 0022-0493

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Record 48 of 50

Title: Near-Isogenic Cry1F-Resistant Strain of *Spodoptera frugiperda* (Lepidoptera: Noctuidae) to Investigate Fitness Cost Associated With Resistance in Brazil

Author(s): Horikoshi, RJ (Horikoshi, Renato J.); Bernardi, O (Bernardi, Oederlei); Bernardi, D (Bernardi, Daniel); Okuma, DM (Okuma, Daniela M.); Farias, JR (Farias, Juliano R.); Miraldo, LL (Miraldo, Leonardo L.); Amaral, FSA (Amaral, Fernando S. A.); Omoto, C (Omoto, Celso)

Source: JOURNAL OF ECONOMIC ENTOMOLOGY **Volume:** 109 **Issue:** 2 **Pages:** 854-859 **DOI:** 10.1093/jee/tov387 **Published:** APR 2016

Abstract: Field-evolved resistance to Cry1F maize in *Spodoptera frugiperda* (J.E. Smith) populations in Brazil was reported in 2014. In this study, to investigate fitness costs, we constructed a near-isogenic *S. frugiperda*-resistant strain (R-Cry1F) using Cry1F-resistant and Cry1F-susceptible strains sharing a close genetic background. A near-isogenic R-Cry1F strain was obtained by eight repeated backcrosses, each followed by sib-mating and selection among resistant and susceptible strains. Fitness cost parameters were evaluated by comparing the biological performance of resistant, susceptible, and heterozygous strains on artificial diet. Fitness parameters monitored included development time and survival rates of egg, larval, pupal, and egg-to-adult periods; sex ratio; adult longevity; timing of preoviposition, oviposition, and postoviposition; fecundity; and fertility. A fertility life table was also calculated. The near-isogenic R-Cry1F strain showed lower survival rate of eggs (32%), when compared with Sus and reciprocal crosses (41 and 55%, respectively). The number of R-Cry1F insects that completed the life cycle was reduced to similar to 25%, compared with the Sus strain with similar to 32% reaching the adult stage. The mean generation time (T) of R-Cry1F strain was similar to 2 d shorter than R-Cry1F male x Sus female and Sus strains. The reproductive parameters of R-Cry1F strain were similar to the Sus strain. However, fewer females were produced by R-Cry1F strain than R-Cry1F female x Sus male and more females than R-Cry1F male x Sus female. In summary, no relevant fitness costs are observed in a near-isogenic Cry1F-resistant strain of *S. frugiperda*, indicating stability of resistance to Cry1F protein in Brazilian populations of this species in the absence of selection pressure.

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PubMed ID: 26719594

Author Identifiers:

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

ISSN: 0022-0493

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Record 49 of 50

Title: Influence of Dual-Bt Protein Corn on Bollworm, *Helicoverpa zea* (Boddie), Survivorship on Bollgard II Cotton

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

Source: JOURNAL OF ECONOMIC ENTOMOLOGY **Volume:** 109 **Issue:** 2 **Pages:** 860-864 **DOI:** 10.1093/jee/tov401 **Published:** APR 2016

Abstract: Similar Cry proteins are expressed in both Bt corn, *Zea mays* L., and cotton, *Gossypium hirsutum* (L.), commercial production systems. At least one generation of corn earworm, *Helicoverpa zea* (Boddie), completes development on field corn in the Mid-South before dispersing across the landscape into other crop hosts like cotton. A concern is that Bt corn hybrids may result in selection for *H. zea* populations with a higher probability of causing damage to Bt cotton. The objective of this study was to determine the susceptibility of *H. zea* offspring from moths that developed on non-Bt and VT Triple Pro (VT3 PRO) field corn to lyophilized Bollgard II cotton tissue expressing Cry1Ac and Cry2Ab. Offspring of individuals reared on VT3 PRO expressing Cry1A.105 and Cry2Ab had a significantly higher LC50 two out of the three years this study was conducted. Excess larvae were placed on artificial diet and allowed to pupate to determine if there were any inheritable fitness costs associated with parental development on VT3 PRO corn. Offspring resulting from males collected from VT3 PRO had significantly lower pupal weight and longer pupal duration compared with offspring of individuals collected from non-Bt corn. However, offspring from females collected from VT3 PRO were not different from non-Bt offspring. Paternal influence on offspring in insects is not commonly observed, but illustrates the side effects of development on a transgenic plant expressing less than a high dose, 25 times the concentration needed to kill susceptible larvae.

Accession Number: WOS:000374497000048

PubMed ID: 26809264

ISSN: 0022-0493

eISSN: 1938-291X

Record 50 of 50

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

Author(s): Velez, AM (Velez, Ana Maria); Alves, AP (Alves, Analiza P.); Blankenship, EE (Blankenship, Erin E.); Siegfried, BD (Siegfried, Blair D.)

Source: ENTOMOLOGIA EXPERIMENTALIS ET APPLICATA **Volume:** 159 **Issue:** 1 **Pages:** 37-45 **DOI:** 10.1111/eea.12409 **Published:** APR 2016

Abstract: Understanding the behavior of pests targeted with *Bacillus thuringiensis* Berliner (Bt) crops is important to define resistance management strategies. Particularly the study of larval movement between plants is important to determine the feasibility of refuge configurations. Exposure to Bt maize, *Zea mays* L. (Poaceae), has been suggested to increase larval movement in lepidopteran species but few studies have examined the potential for resistance to interact with behavioral responses to Bt toxins. Choice and no-choice experiments were conducted with *Spodoptera frugiperda* (JE Smith) (Lepidoptera: Noctuidae) and *Ostrinia nubilalis* (Hubner) (Lepidoptera: Crambidae) to determine whether Cry1F resistance influences neonate movement. Leaf discs of Cry1F maize and the corresponding 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 7h. 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.

Accession Number: WOS:000373483300004

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Page 1 (Records 1 -- 50)

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Record 1 of 50**Title:** Can Pyramids and Seed Mixtures Delay Resistance to Bt Crops?**Author(s):** Carriere, Y (Carriere, Yves); Fabrick, JA (Fabrick, Jeffrey A.); Tabashnik, BE (Tabashnik, Bruce E.)**Source:** TRENDS IN BIOTECHNOLOGY **Volume:** 34 **Issue:** 4 **Pages:** 291-302 **DOI:** 10.1016/j.tibtech.2015.12.011 **Published:** APR 2016**Abstract:** The primary strategy for delaying the evolution of pest resistance to transgenic crops that produce insecticidal proteins from *Bacillus thuringiensis* (Bt) entails refuges of plants that do not produce Bt toxins and thus allow survival of susceptible pests. Recent advances include using refuges together with Bt crop 'pyramids' that make two or more Bt toxins effective against the same pest, and planting seed mixtures yielding random distributions of pyramided Bt and non-Bt corn plants within fields. We conclude that conditions often deviate from those favoring the success of pyramids and seed mixtures, particularly against pests with low inherent susceptibility to Bt toxins. For these problematic pests, promising approaches include using larger refuges and integrating Bt crops with other pest management tactics.**Accession Number:** WOS:000373655400005**PubMed ID:** 26774592**ISSN:** 0167-7799**Record 2 of 50****Title:** Sequential sampling plan for assessing corn rootworm (Coleoptera: Chrysomelidae) larval injury to Bt maize**Author(s):** Hong, BN (Hong, Bonnie); Nowatzki, TM (Nowatzki, Timothy M.); Sult, TS (Sult, Theresa S.); Owens, ED (Owens, Elizabeth D.); Pilcher, CD (Pilcher, Clinton D.)**Source:** CROP PROTECTION **Volume:** 82 **Pages:** 36-44 **DOI:** 10.1016/j.cropro.2016.01.001 **Published:** APR 2016**Abstract:** In-field product performance assessments are an essential component of corn rootworm (*Diabrotica* spp.; CRW) resistance management plans for transgenic maize (*Zea mays* L.) products expressing proteins derived from the bacterium *Bacillus thuringiensis* (Bt). The goal of a successful field sampling program is to accurately characterize in-field product performance while also minimizing resource demand, as collection of maize root samples to evaluate CRW injury can present resource challenges such as labor intensiveness, potential safety issues, and a limited time window available for sampling. A resource-efficient sequential sampling plan was developed that utilizes data-driven root injury threshold values derived from benchmark product performance data for both single and pyramided Bt maize traits for CRW control. This sequential sampling methodology incorporates unbiased sampling and controlled false positive and false negative error rates, enabling accurate assessment decisions to be made with efficient resource use. Our proposed approach enables systematic and effective classification of in-field Bt maize product performance, with applications to other CRW control technologies besides Bt maize products. (C) 2016 Pioneer Hi-Bred International, Inc. Published by Elsevier Ltd.**Accession Number:** WOS:000372689000006**ISSN:** 0261-2194**eISSN:** 1873-6904**Record 3 of 50****Title:** Single amino acid insertions in extracellular loop 2 of *Bombyx mori* ABCC2 disrupt its receptor function for *Bacillus thuringiensis* Cry1Ab and Cry1Ac but not Cry1Aa toxins**Author(s):** Tanaka, S (Tanaka, Shiho); Miyamoto, K (Miyamoto, Kazuhisa); Noda, H (Noda, Hiroaki); Endo, H (Endo, Haruka); Kikuta, S (Kikuta, Shingo); Sato, R (Sato, Ryoichi)**Source:** PEPTIDES **Volume:** 78 **Pages:** 99-108 **DOI:** 10.1016/j.peptides.2016.01.006 **Published:** APR 2016**Abstract:** In a previous report, seven Cry1Ab-resistant strains were identified in the silkworm, *Bombyx mori*; these strains were shown to have a tyrosine insertion at position 234 in extracellular loop 2 of the ABC transporter C2 (*BmABCC2*). This insertion was confirmed to destroy the receptor function of *BmABCC2* and confer the strains resistance against Cry1Ab and Cry1Ac. However, these strains were susceptible to Cry1Aa. In this report, we examined the mechanisms of the loss of receptor function of the transporter by expressing mutations in Sf9 cells. After replacement of one or two of the five amino acid residues in loop 2 of the susceptible *BmABCC2* gene [*BmABCC2_S*] with alanine, cells still showed susceptibility, retaining the receptor function. Five mutants with single amino acid insertions at position 234 in *BmABCC2* were also generated, resulting in loop 2 having six amino acids, which corresponds to replacing the tyrosine insertion in the resistant *BmABCC2* gene [*BmABCC2_R(+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 *BmABCC2R(+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 Published by Elsevier Inc.**Accession Number:** WOS:000372718700013**PubMed ID:** 26928903**Author Identifiers:**

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

ISSN: 0196-9781**eISSN:** 1873-5169**Record 4 of 50****Title:** The synergic and antagonistic activity of Cry1Ab and Cry2Aa proteins against lepidopteran pests**Author(s):** Azizoglu, U (Azizoglu, U.); Ayvaz, A (Ayvaz, A.); Yilmaz, S (Yilmaz, S.); Temizgul, R (Temizgul, R.)**Source:** JOURNAL OF APPLIED ENTOMOLOGY **Volume:** 140 **Issue:** 3 **Pages:** 223-227 **DOI:** 10.1111/jen.12241 **Published:** APR 2016**Abstract:** Cry1Ab and Cry2Aa were overexpressed in *Escherichia coli* BL21(DE3), and their proportions were determined for evaluating their synergic and antagonistic interactions on *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.**Accession Number:** WOS:000372278300007**ISSN:** 0931-2048**eISSN:** 1439-0418**Record 5 of 50****Title:** Selection of focal earthworm species as non-target soil organisms for environmental risk assessment of genetically modified plants**Author(s):** van Capelle, C (van Capelle, Christine); Schrader, S (Schrader, Stefan); Arpaia, S (Arpaia, Salvatore)**Source:** SCIENCE OF THE TOTAL ENVIRONMENT **Volume:** 548 **Pages:** 360-369 **DOI:** 10.1016/j.scitotenv.2015.12.165 **Published:** APR 1 2016**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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Author Identifiers:

Author	ResearcherID Number	ORCID Number
Schrader, Stefan		0000-0003-1647-9901

ISSN: 0048-9697

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Record 6 of 50

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

Author(s): Shen, PL (Shen, Peili); Geng, FZ (Geng, Fengzhen); Yu, Y (Yu, Yan); Zhang, YZ (Zhang, Yunzhe); Wang, ZX (Wang, Zhixin); Li, ZH (Li, Zhihui); Zhang, W (Zhang, Wei); Shu, CL (Shu, Changlong); Zhang, YJ (Zhang, Yongjun); Tan, JX (Tan, Jianxin)

Source: FOOD CONTROL **Volume:** 62 **Pages:** 357-364 **DOI:** 10.1016/j.foodcont.2015.10.035 **Published:** APR 2016

Abstract: Among the commercial genetically modified (GM) crops, the insect-resistant GM crops are the major cultivars that cry gene is introduced into. A 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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ISSN: 0956-7135

eISSN: 1873-7129

Record 7 of 50

Title: Using Ancient Traits to Convert Soil Health into Crop Yield: Impact of Selection on Maize Root and Rhizosphere Function

Author(s): Schmidt, JE (Schmidt, Jennifer E.); Bowles, TM (Bowles, Timothy M.); Gaudin, ACM (Gaudin, Amelie C. M.)

Source: FRONTIERS IN PLANT SCIENCE **Volume:** 7 **Article Number:** 373 **DOI:** 10.3389/fpls.2016.00373 **Published:** MAR 30 2016

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.

Accession Number: WOS:000372873000002

PubMed ID: 27066028

ISSN: 1664-462X

Record 8 of 50

Title: A Review of Cry Protein Detection with Enzyme-Linked Immunosorbent Assays

Author(s): Albright, VC (Albright, Vurtice C., III); Hellmich, RL (Hellmich, Richard L.); Coats, JR (Coats, Joel R.)

Source: JOURNAL OF AGRICULTURAL AND FOOD CHEMISTRY **Volume:** 64 **Issue:** 11 **Pages:** 2175-2189 **DOI:** 10.1021/acs.jafc.5b03766 **Published:** MAR 23 2016

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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PubMed ID: 26949828

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eISSN: 1520-5118

Record 9 of 50

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

Author(s): Liu, YM (Liu, Yanmin); Liu, QS (Liu, Qingsong); Wang, YA (Wang, Yanan); Chen, XP (Chen, Xiuping); Song, XY (Song, Xinyuan); Romeis, J (Romeis, Joerg); Li, YH (Li, Yunhe); Peng, YF (Peng, Yufa)

Source: SCIENTIFIC REPORTS **Volume:** 6 **Article Number:** 23507 **DOI:** 10.1038/srep23507 **Published:** MAR 23 2016

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.

Accession Number: WOS:000372607500001

PubMed ID: 27005950

ISSN: 2045-2322

Record 10 of 50

Title: Visual DNA Microarray Coupled with Multiplex-PCR for the Rapid Detection of Twelve Genetically Modified Maize

Author(s): Li, YJ (Li, Yongjin); Xiong, T (Xiong, Tao); Wu, HW (Wu, Huawei); Yang, YZ (Yang, Yazhen)

Source: BIOCHIP JOURNAL **Volume:** 10 **Issue:** 1 **Pages:** 42-47 **DOI:** 10.1007/s13206-016-0106-y **Published:** MAR 20 2016

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.

Accession Number: WOS:000372378500006

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eISSN: 2092-7843

Record 11 of 50

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

Author(s): Arias-Martin, M (Arias-Martin, Maria); Garcia, M (Garcia, Matias); Lucianez, MJ (Jose Lucianez, Ma); Ortego, F (Ortego, Felix); Castanera, P (Castanera, Pedro); Farinos, GP (Farinos, Gema P)

Source: AGRICULTURE ECOSYSTEMS & ENVIRONMENT **Volume:** 220 **Pages:** 125-134 **DOI:** 10.1016/j.agee.2015.09.007 **Published:** MAR 15 2016

Abstract: The impact of Cry1Ab-expressing Bt maize (event MON810) on non-target fauna has been a major concern since its deployment in Europe. In this paper, we have assessed the levels of Cry1Ab in rhizosphere soil samples from a Bt maize crop and evaluated the potential effects of Bt maize on soil microarthropods by a three-year trial in an experimental farm-scale field in Central Spain. The Cry1Ab toxin was detected in decaying soil organic matter (OM) from Bt maize plots up to three months after harvest, with values ranging between 0.10 and 0.18 ng Cry1Ab/mg OM, but it showed low insecticidal activity. The study focused on Acari and Collembola, the two major components of the soil microarthropod community. They accounted for 88% of the total specimens collected, and they were identified at the suborder and species level, respectively. Interestingly, Cry1Ab was detected for the first time in field collected collembolans, *Entomobrya* spp., demonstrating their exposure to the toxin. The abundance of mites and collembolans and the frequency of occurrence of the main collembolan species did not rely on the type of maize except for *Parisotoma notabilis*, more abundant and frequent in Bt maize plots. However, significant differences among years were common in both groups. Noticeably, we found higher values of species richness and diversity of collembolans in Cry1Ab-expressing Bt maize than in non-Bt plots, which could be explained under different scenarios. Our results suggest that continuous cultivation of Bt maize does not negatively affect soil microarthropods, indicating that Bt maize could be compatible with this community. (C) 2015 Elsevier B.V. All rights reserved.

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Author Identifiers:

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

ISSN: 0167-8809

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Record 12 of 50

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

Author(s): Fu, W (Fu, Wei); Wang, HY (Wang, Huiyu); Wang, CG (Wang, Chenguang); Mei, L (Mei, Lin); Lin, XM (Lin, Xiangmei); Han, XQ (Han, Xueqing); Zhu, SF (Zhu, Shuifang)

Source: BIOSENSORS & BIOELECTRONICS **Volume:** 77 **Pages:** 702-708 **DOI:** 10.1016/j.bios.2015.10.043 **Published:** MAR 15 2016

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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Record 13 of 50

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

Author(s): Zhou, DG (Zhou, Dinggang); Xu, LP (Xu, Liping); Gao, SW (Gao, Shiwu); Guo, JL (Guo, Jinlong); Luo, J (Luo, Jun); You, Q (You, Qian); Que, YX (Que, Youxiang)

Source: FRONTIERS IN PLANT SCIENCE **Volume:** 7 **Article Number:** 265 **DOI:** 10.3389/fpls.2016.00265 **Published:** MAR 8 2016

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.

Accession Number: WOS:000371399900001

PubMed ID: 27014291

ISSN: 1664-462X

Record 14 of 50

Title: Screening of new isolates of *Bacillus thuringiensis* for cry1 genes and testing of toxicity against *Dichocrocis punctiferalis* (Family: Pyralidae, Order: Lepidoptera)

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

Source: MICROBIOLOGY **Volume:** 85 **Issue:** 2 **Pages:** 191-197 **DOI:** 10.1134/S0026261716020144 **Published:** MAR 2016

Abstract: In order to identify the more toxic novel cry gene, the cry1 gene was screened in six indigenous isolates of Bt by PCR with degenerate primers showed amplification in all the Bt isolates. Subsequent screening of cry1 subfamily gene(s) by gene specific primer showed amplification of cry1A gene in the five Bt isolates, three out of the six cry1 positive isolates showed the presence of cry1Aa gene. One of the six Bt isolates showed the presence of cry1Ab gene. Five Bt isolates showed amplification for cry1Ac gene and a variation in size of amplification was observed in one of the Bt isolates Bt, T27. Further, SDS-PAGE analysis of a spore crystal mixture isolated from new isolates of Bt, T27 showed a single band of similar to 135 kDa indicating presence of cry1Ac gene. The toxicity analysis of Bt strain T27 against *Dichocrocis punctiferalis* showed 100 per cent mortality on the fifth day after treatment. The varied similar to 925 bp amplicon of cry1Ac gene of Bt, T27 was amplified and cloned in a T/A vector. Comparison of nucleotide sequence data generated from the cry1Ac (similar to 925 bp) gene showed 99 percent homology and two amino acid variation when comparison with its holotype sequence of Cry1Ac1.

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eISSN: 1608-3237

Record 15 of 50

Title: Field studies show no significant effect of a Cry1Ab/Ac producing transgenic cotton on the fungal community structure in rhizosphere soil

Author(s): Xie, M (Xie, Ming); Zhang, YJ (Zhang, Yan-Jun); Peng, DL (Peng, De-Liang); Wu, G (Wu, Gang); Xu, P (Xu, Peng); Zhao, JJ (Zhao, Jin-Jin); Zhang, ZR (Zhang, Zhao-Rong)

Source: EUROPEAN JOURNAL OF SOIL BIOLOGY **Volume:** 73 **Pages:** 69-76 **DOI:** 10.1016/j.ejsobi.2016.01.006 **Published:** MAR-APR 2016

Abstract: Transgenic cotton GK 12 expressing insecticidal Cry1Ab/1Ac gene can effectively control the lepidopteran pests in agriculture, however it may have unintended side-effects on soil fungal communities. Therefore, the fungal community size and structure in rhizosphere soil of Bt and non-Bt cottons were analyzed by real-time polymerase chain reaction (qPCR) and denaturing gradient gel electrophoresis (DGGE) at growth stages and three annual replications in an intensive conventional cultivation system. The Cry1Ab/1Ac protein was undetectable or occasionally detectable at a low level (<0.1 ng/g soil) at seedling and senescence, and that the concentration of Cry1Ab/Ac protein in soil extracts did not increase over time or repeated cultivations. No significant differences in fungal population size and structure in rhizosphere soil were found between Bt-cotton GK 12 and its near-isogenic comparator at all growth stages, but they were different between Bt-cotton GK 12 and conventional cotton DP 5415 at some growth stages. The fungal population size and structure was significantly influenced by variation in years and plant growth stages. Sequencing results from DGGE bands showed that the dominant fungi were not different between Bt-cotton GK 12 and its near-isogenic comparator. Thus, the data of this study do not indicate any significant effect of Bt-cotton GK 12 on the fungal community size and structure in rhizosphere soil during these three continuous years. (C) 2016 Elsevier Masson SAS. All rights reserved.

Accession Number: WOS:000373549800008

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Record 16 of 50

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

Author(s): Oyediran, I (Oyediran, Isaac); Dively, G (Dively, Galen); Huang, FN (Huang, Fangneng); Burd, T (Burd, Tony)

Source: CROP PROTECTION **Volume:** 81 **Pages:** 145-153 **DOI:** 10.1016/j.cropro.2015.12.008 **Published:** MAR 2016

Abstract: Blending *Bacillus thuringiensis* (Bt) corn and non-Bt corn seeds in the same bag is a convenient and easier compliance solution to satisfy refuge regulations. However, there has been considerable debate and concern about larval movement of the target insects in a seed blend because of its potential effect on the development of resistance. Reported here are studies to determine the larval movement of European corn borers, *Ostrinia nubilalis* (Hubner), in a seed blend compared to a structured refuge and their effects on survival, feeding injury and larval fitness. Also evaluated is the relative performance of a purple seeded corn hybrid as a surrogate host plant for tracking gene flow. Seed blend and structured refuge arrangements of Agrisure GT/CB/LL Bt corn expressing Cry1Ab and isoline plants were evaluated at two locations in 2013 and 2014 by manually infesting refuge plants with first and second generation corn borer larvae. The majority of leaf and stalk injury was recorded on the refuge plant, which amounted to 66-83% of the total tunnel length. In both refuge arrangements, plant injury and the number of larvae recovered significantly decreased on neighboring plants with increasing distance away from the refuge plant in the same row. The relative decline in injury was much more pronounced in the seed blend, with neighbor Bt plants experiencing very minor tunneling or no injury at all due to the high dose trait. Eighty-nine percent fewer live larvae were also found on neighbor Bt plants in the seed blend compared to those found in the structured refuge plots. Larvae that moved to Bt plants as well as older instars that were manually placed on Bt plants failed to complete development. Comparison of the number of tunnels and larvae recovered per refuge plant indicated that the seed blend may not produce as many susceptible individuals as those produced in a structured refuge arrangement. Although the purple seeded hybrid showed lower levels of ear and stalk injury, it could serve as an appropriate surrogate refuge plant to track gene flow. (C) 2015 Elsevier Ltd. All rights reserved.

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Record 17 of 50

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

Author(s): Santos-Amaya, OF (Santos-Amaya, Oscar F.); Tavares, CS (Tavares, Clebson S.); Monteiro, HM (Monteiro, Hugo M.); Teixeira, TPM (Teixeira, Thais P. M.); Guedes, RNC (Guedes, Raul N. C.); Alves, AP (Alves, Analiza P.); Pereira, EJG (Pereira, Eliseu J. G.)

Source: CROP PROTECTION **Volume:** 81 **Pages:** 154-162 **DOI:** 10.1016/j.cropro.2015.12.014 **Published:** MAR 2016

Abstract: Large-scale adoption of transgenic crops expressing genes from *Bacillus thuringiensis* (Bt) imposes high selection pressure for evolution of field-relevant resistance that can reduce pest control efficacy, such as reported for Cry1F maize (*Zea mays* L.) in populations of fall armyworm, *Spodoptera frugiperda* (J. E. Smith) (Lepidoptera: Noctuidae), of Puerto Rico, Brazil, and the United States. As part of our effort to improve fall armyworm resistance management to Bt crops, here we determined the genetic basis of Cry1F resistance in two *S. frugiperda* strains originated from field collections in different regions of Brazil and further selected in the laboratory for high levels of resistance to Cry1F maize. Continuous exposure to the TC1507 event for 11 generations resulted in more than 183-fold resistance to Cry1F in the two strains studied, and such a high resistance level enabled the insects to complete larval development on the Bt maize plants. Genetic analyses using concentration-response bioassays with progenies from reciprocal crosses between resistant and susceptible insects indicated that the inheritance of the resistance is autosomal, recessive and without maternal effects. Backcross of the 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.

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Author Identifiers:

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

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Record 18 of 50

Title: Development of leafroller resistant transgenic rice expressing cry2AX1 gene driven by green tissue-specific rbcS promoter

Author(s): Manikandan, R (Manikandan, R.); Balakrishnan, N (Balakrishnan, N.); Sudhakar, D (Sudhakar, D.); Udayasuriyan, V (Udayasuriyan, V.)

Source: WORLD JOURNAL OF MICROBIOLOGY & BIOTECHNOLOGY **Volume:** 32 **Issue:** 3 **Article Number:** 37 **DOI:** 10.1007/s11274-015-2006-z **Published:** MAR 2016

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 leafroller (*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 leafroller 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.

Accession Number: WOS:000371429200003

PubMed ID: 26867598

ISSN: 0959-3993

eISSN: 1573-0972

Record 19 of 50

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

Author(s): Steijven, K (Steijven, Karin); Steffan-Dewenter, I (Steffan-Dewenter, Ingolf); Hartel, S (Haertel, Stephan)

Source: APIDOLOGIE **Volume:** 47 **Issue:** 2 **Pages:** 216-226 **DOI:** 10.1007/s13592-015-0392-8 **Published:** MAR 2016

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

Accession Number: WOS:000371161500007

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eISSN: 1297-9678

Record 20 of 50

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

Author(s): Leite, NA (Leite, Natalia A.); Mendes, SM (Mendes, Simone M.); Santos-Amaya, OF (Santos-Amaya, Oscar F.); Santos, CA (Santos, Chritiane A.); Teixeira, TPM (Teixeira, Thais P. M.); Guedes, RNC (Guedes, Raul N. C.); Pereira, EJG (Pereira, Eliseu J. G.)

Source: ENTOMOLOGIA EXPERIMENTALIS ET APPLICATA **Volume:** 158 **Issue:** 3 **Pages:** 236-247 **DOI:** 10.1111/eea.12399 **Published:** MAR 2016

Abstract: Transgenic maize (*Zea mays* L., Poaceae) event TC1507, producing the Cry1F protein of *Bacillus thuringiensis* Berliner, has been used for management of the fall armyworm, *Spodoptera frugiperda* (JE Smith) (Lepidoptera: Noctuidae), in Brazil since 2009. A strain of *S. frugiperda*, obtained from field collections of larvae in TC1507 maize in Minas Gerais state in 2010, was selected in the laboratory for resistance to Cry1F using leaves of TC1507 maize in two selection regimes. Continuous exposure of larvae to Cry1F was more effective than exposure for 6, 8, and 10 days in the selection of resistant *S. frugiperda* individuals. With only four generations of laboratory selection, a strain with high levels of resistance to Cry1F was obtained, as indicated by the survival of insects reared on leaves of TC1507 maize plants and by the more than 300-fold resistance level measured in bioassays with the purified Cry1F protein. Importantly, reciprocal crosses between control and the Cry1F-selected strains revealed that the resistance is autosomal and incompletely recessive, and the response obtained in the backcross of the 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.

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Author Identifiers:

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

ISSN: 0013-8703

eISSN: 1570-7458

Record 21 of 50

Title: Field trials to evaluate the effects of transgenic cry1Ie maize on the community characteristics of arthropod natural enemies

Author(s): Guo, JF (Guo, Jingfei); He, KL (He, Kanglai); Hellmich, RL (Hellmich, Richard L.); Bai, SX (Bai, Shuxiong); Zhang, TT (Zhang, Tiantao); Liu, YJ (Liu, Yunjun); Ahmed, T (Ahmed, Tofael); Wang, ZY (Wang, Zhenying)

Source: SCIENTIFIC REPORTS **Volume:** 6 **Article Number:** 22102 **DOI:** 10.1038/srep22102 **Published:** FEB 26 2016

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.

Accession Number: WOS:000370927700002

PubMed ID: 26915985

ISSN: 2045-2322

Record 22 of 50

Title: A Comprehensive Assessment of the Effects of Transgenic Cry1Ac/Cry1Ab Rice Huahui 1 on Adult *Micraspis discolor* (Fabricius) (Coleoptera: Coccinellidae)

Author(s): Zhou, X (Zhou, Xia); Guo, YL (Guo, Yunling); Kong, H (Kong, Hua); Zuo, J (Zuo, Jiao); Huang, QX (Huang, Qixing); Jia, RZ (Jia, Ruizong); Guo, AP (Guo, Anping); Xu, L (Xu, Lin)

Source: PLOS ONE **Volume:** 11 **Issue:** 2 **Article Number:** e0142714 **DOI:** 10.1371/journal.pone.0142714 **Published:** FEB 25 2016

Abstract: *Micraspis discolor* (Fabricius) (Coleoptera: Coccinellidae) is a widely distributed coleoptera predator in southern Asia in rice ecosystem, and adult *M. discolor* feed on both rice pollen and soft-bodied arthropods. Bitrophic 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.

Accession Number: WOS:000371175700002

PubMed ID: 26914608

ISSN: 1932-6203

Record 23 of 50

Title: Development of an Amino Acid-Functionalized Fluorescent Nanocarrier to Deliver a Toxin to Kill Insect Pests

Author(s): Zheng, Y (Zheng, Yang); You, SS (You, Shusen); Ji, CD (Ji, Chendong); Yin, MZ (Yin, Meizhen); Yang, WT (Yang, Wantai); Shen, J (Shen, Jie)

Source: ADVANCED MATERIALS **Volume:** 28 **Issue:** 7 **Pages:** 1375-1380 **DOI:** 10.1002/adma.201504993 **Published:** FEB 17 2016

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.

Accession Number: WOS:000370192200003

PubMed ID: 26640174

Author Identifiers:

Author	ResearcherID Number	ORCID Number
shen, jie	H-9087-2016	

ISSN: 0935-9648

eISSN: 1521-4095

Record 24 of 50**Title:** Survival and development of spotted bollworm, *Earias vittella* (Fabricius) (Lepidoptera: Nolidae) on different transgenic Bt and isogenic non-Bt cotton genotypes**Author(s):** Shera, PS (Shera, P. S.); Arora, R (Arora, Ramesh)**Source:** PHYTOPARASITICA **Volume:** 44 **Issue:** 1 **Pages:** 99-113 **DOI:** 10.1007/s12600-016-0505-6 **Published:** FEB 2016

Abstract: Four Bt cotton hybrids, each with one of four different events, viz., MRC 6301 Bt (cry1Ac gene), JKCH 1947 Bt (modified cry1Ac gene), NCEH 6R Bt (fusion cry1Ac/cry1Ab gene) and MRC 7017 Bollgard II (cry1Ac and cry2Ab genes) were compared for survival and development of *Earias vittella* (Fabricius) along with their isogenic non-Bt genotypes. None of the neonates were able to complete the larval period and reach pupal stage on squares of 90, 120 and 150 days old crop of all Bt hybrids. Likewise, on bolls also, zero per cent larval survival was observed in all Bt hybrids except JKCH 1947 Bt where 0.67 per cent larvae could manage to reach prepupal stage at 120 and 150 days old crop but failed to form cocoon and enter pupal stage. The surviving larva took more development time (3.7 to 5.4 days) as compared to larvae fed on bolls of JKCH 1947 non-Bt. The average survival period (ASP) of larvae was in order of 150 > 120 > 90 days old crop among the crop ages; JKCH 1947 Bt > MRC 6301 Bt > NCEH 6 R Bt > MRC 7017 Bollgard II among Bt hybrids; and bolls > squares between fruiting bodies. However, reverse was true for speed index of toxic effect. The concentration of Cry toxin varied significantly in squares and bolls and also among the crop ages. The amount of Cry toxin in squares and bolls had significant negative correlation with ASP of the *E. vittella* larvae.

Accession Number: WOS:000378145100011

ISSN: 0334-2123

eISSN: 1876-7184

Record 25 of 50**Title:** Transportable data from non-target arthropod field studies for the environmental risk assessment of genetically modified maize expressing an insecticidal double-stranded RNA**Author(s):** Ahmad, A (Ahmad, Aqeel); Negri, I (Negri, Ignacio); Oliveira, W (Oliveira, Wladecir); Brown, C (Brown, Christopher); Asiiimwe, P (Asiiimwe, Peter); Sammons, B (Sammons, Bernard); Horak, M (Horak, Michael); Jiang, CJ (Jiang, Changjian); Carson, D (Carson, David)**Source:** TRANSGENIC RESEARCH **Volume:** 25 **Issue:** 1 **Pages:** 1-17 **DOI:** 10.1007/s11248-015-9907-3 **Published:** FEB 2016

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.

Accession Number: WOS:000371155500001**PubMed ID:** 26433587

ISSN: 0962-8819

eISSN: 1573-9368

Record 26 of 50**Title:** The interaction of two-spotted spider mites, *Tetranychus urticae* Koch, with Cry protein production and predation by *Amblyseius andersoni* (Chant) in Cry1Ac/Cry2Ab cotton and Cry1F maize**Author(s):** Guo, YY (Guo, Yan-Yan); Tian, JC (Tian, Jun-Ce); Shi, WP (Shi, Wang-Peng); Dong, XH (Dong, Xue-Hui); Romeis, J (Romeis, Joerg); Naranjo, SE (Naranjo, Steven E.); Hellmich, RL (Hellmich, Richard L.); Shelton, AM (Shelton, Anthony M.)**Source:** TRANSGENIC RESEARCH **Volume:** 25 **Issue:** 1 **Pages:** 33-44 **DOI:** 10.1007/s11248-015-9917-1 **Published:** FEB 2016

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

Accession Number: WOS:000371155500003**PubMed ID:** 26545599

ISSN: 0962-8819

eISSN: 1573-9368

Record 27 of 50**Title:** On-Plant Larval Movement and Feeding Behavior of Fall Armyworm (Lepidoptera: Noctuidae) on Reproductive Corn Stages**Author(s):** Pannuti, LER (Pannuti, L. E. R.); Baldin, ELL (Baldin, E. L. L.); Hunt, TE (Hunt, T. E.); Paula-Moraes, SV (Paula-Moraes, S. V.)**Source:** ENVIRONMENTAL ENTOMOLOGY **Volume:** 45 **Issue:** 1 **Pages:** 192-200 **DOI:** 10.1093/ee/nvv159 **Published:** FEB 2016

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.

Accession Number: WOS:000370271900024**PubMed ID:** 26476276

ISSN: 0046-225X

eISSN: 1938-2936

Record 28 of 50

Title: Early Detection and Mitigation of Resistance to Bt Maize by Western Corn Rootworm (Coleoptera: Chrysomelidae)

Author(s): Andow, DA (Andow, David A.); Pueppke, SG (Pueppke, Steven G.); Schaafsma, AW (Schaafsma, Arthur W.); Gassmann, AJ (Gassmann, Aaron J.); Sappington, TW (Sappington, Thomas W.); Meinke, LJ (Meinke, Lance J.); Mitche, PD (Mitche, Paul D.); Hurley, TM (Hurley, Terrance M.); Hellmich, RL (Hellmich, Richard L.); Porterl, RP (Porterl, R. Pat)

Source: JOURNAL OF ECONOMIC ENTOMOLOGY **Volume:** 109 **Issue:** 1 **Pages:** 1-12 **DOI:** 10.1093/jee/tov238 **Published:** FEB 2016

Abstract: Transgenic Bt maize that produces less than a high-dose has been widely adopted and presents considerable insect resistance management (IRM) challenges. Western corn rootworm, *Diabrotica virgifera virgifera* LeConte, has rapidly evolved resistance to Bt maize in the field, leading to local loss of efficacy for some corn rootworm Bt maize events. Documenting and responding to this resistance has been complicated by a lack of rapid diagnostic bioassays and by regulatory triggers that hinder timely and effective management responses. These failures are of great concern to the scientific and agricultural community. Specific challenges posed by western corn rootworm resistance to Bt maize, and more general concerns around Bt crops that produce less than a high-dose of Bt toxin, have caused uncertainty around current IRM protocols. More than 15 years of experience with IRM has shown that high-dose and refuge-based IRM is not applicable to Bt crops that produce less than a high-dose. Adaptive IRM approaches and pro-active, integrated IRM-pest management strategies are needed and should be in place before release of new technologies that produce less than a high-dose. We suggest changes in IRM strategies to preserve the utility of corn rootworm Bt maize by 1) targeting local resistance management earlier in the sequence of responses to resistance and 2) developing area-wide criteria to address widespread economic losses. We also favor consideration of policies and programs to counteract economic forces that are contributing to rapid resistance evolution.

Accession Number: WOS:000370273800001

PubMed ID: 26362989

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Record 29 of 50

Title: Survival of Corn Earworm (Lepidoptera: Noctuidae) on Bt Maize and Cross-Pollinated Refuge Ears From Seed Blends

Author(s): Crespo, ALB (Crespo, Andre Luiz Barreto); Alves, AP (Alves, Analiza Piovesan); Wang, YW (Wang, Yiwei); Hong, BN (Hong, Bonnie); Flexner, JL (Flexner, John Lindsey); Catchot, A (Catchot, Angus); Buntin, D (Buntin, David); Cook, D (Cook, Donald)

Source: JOURNAL OF ECONOMIC ENTOMOLOGY **Volume:** 109 **Issue:** 1 **Pages:** 288-298 **DOI:** 10.1093/jee/tov272 **Published:** FEB 2016

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.

Accession Number: WOS:000370273800039

PubMed ID: 26357846

ISSN: 0022-0493

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Record 30 of 50

Title: The Impact of Inter-Kernel Movement in the Evolution of Resistance to Dual-Toxin Bt-Corn Varieties in *Helicoverpa zea* (Lepidoptera: Noctuidae)

Author(s): Caprio, MA (Caprio, Michael A.); Martinez, JC (Martinez, Jeannette C.); Porter, PA (Porter, Patrick A.); Bynum, E (Bynum, Ed)

Source: JOURNAL OF ECONOMIC ENTOMOLOGY **Volume:** 109 **Issue:** 1 **Pages:** 307-319 **DOI:** 10.1093/jee/tov295 **Published:** FEB 2016

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.

Accession Number: WOS:000370273800041

PubMed ID: 26527792

ISSN: 0022-0493

eISSN: 1938-291X

Record 31 of 50

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

Author(s): Liu, YB (Liu, Yongbo); Li, JS (Li, Junsheng); Luo, ZL (Luo, Zunlan); Wang, HR (Wang, Huaru); Liu, F (Liu, Fang)

Source: ECOTOXICOLOGY AND ENVIRONMENTAL SAFETY **Volume:** 124 **Pages:** 455-459 **DOI:** 10.1016/j.ecoenv.2015.11.025 **Published:** FEB 2016

Abstract: Toxin proteins from transgenic crops entering into the environment are likely affect non-target organisms. To investigate the entry route and fate of fusion Cry1Ab/1Ac proteins from transgenic rice expressing insecticide toxins from *Bacillus thuringiensis* (Bt) in soil and water, we conducted greenhouse and field experiments in 2013 and 2014. Cry1Ab/1Ac proteins from Bt-transgenic rice in soil was found within a horizontal range of 25 cm, where most of plant roots distributed. Concentration of Cry1Ab/1Ac proteins was lower in water than in soil in the greenhouse experiment, and no Cry1Ab/1Ac protein was detected in field water. Cry1Ab/1Ac concentration from rice straws was higher in ditch water than in distilled water due to the existence of aquatic organisms in ditch water. Bt proteins from transgenic crops enter into soil ecosystems mainly through root exudates and into aquatic ecosystems through plant residues, which determines Bt fate in the environment. (C) 2015 Elsevier Inc. All rights reserved.

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PubMed ID: 26624932

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eISSN: 1090-2414

Record 32 of 50

Title: Field-Evolved Mode 1 Resistance of the Fall Armyworm to Transgenic Cry1Fa-Expressing Corn Associated with Reduced Cry1Fa Toxin Binding and Midgut Alkaline Phosphatase Expression

Author(s): Jakka, SRK (Jakka, Siva R. K.); Gong, L (Gong, Liang); Hasler, J (Hasler, James); Banerjee, R (Banerjee, Rahul); Sheets, JJ (Sheets, Joel J.); Narva, K (Narva, Kenneth); Blanco, CA (Blanco, Carlos A.); Jurat-Fuentes, JL (Jurat-Fuentes, Juan L.)

Source: APPLIED AND ENVIRONMENTAL MICROBIOLOGY **Volume:** 82 **Issue:** 4 **Pages:** 1023-1034 **DOI:** 10.1128/AEM.02871-15 **Published:** FEB 2016

Abstract: Insecticidal protein genes from the bacterium *Bacillus thuringiensis* (Bt) are expressed by transgenic Bt crops (Bt crops) for effective and environmentally safe pest control. The development of resistance to these insecticidal proteins is considered the most serious threat to the sustainability of Bt crops. Resistance in fall armyworm (*Spodoptera frugiperda*) populations from Puerto Rico to transgenic corn producing the Cry1Fa insecticidal protein resulted, for the first time in the United States, in practical resistance, and Bt corn was withdrawn from the local market. In this study, we used a field-collected Cry1Fa corn-resistant strain (456) of *S. frugiperda* to identify the mechanism responsible for field-evolved resistance. Binding assays detected reduced Cry1Fa, Cry1Ab, and Cry1Ac but not Cry1Ca toxin binding to midgut brush border membrane vesicles (BBMV) from the larvae of strain 456 compared to that from the larvae of a susceptible (Ben) strain. This binding phenotype is descriptive of

the mode I type of resistance to Bt toxins. A comparison of the transcript levels for putative Cry1 toxin receptor genes identified a significant downregulation (>90%) of a membrane-bound alkaline phosphatase (ALP), which translated to reduced ALP protein levels and a 75% reduction in ALP activity in BBMV from 456 compared to that of Ben larvae. We cloned and heterologously expressed this ALP from susceptible *S. frugiperda* larvae and demonstrated that it specifically binds with Cry1Fa toxin. This study provides a thorough mechanistic description of field-evolved resistance to a transgenic Bt crop and supports an association between resistance and reduced Cry1Fa toxin binding and levels of a putative Cry1Fa toxin receptor, ALP, in the midguts of *S. frugiperda* larvae.

Accession Number: WOS:000369375900005

ISSN: 0099-2240

eISSN: 1098-5336

Record 33 of 50

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

Author(s): Wang, YN (Wang, Ya-Nan); Ke, KQ (Ke, Kai-Qie); Li, YH (Li, Yun-He); Han, LZ (Han, Lan-Zhi); Liu, YM (Liu, Yan-Min); Hua, HX (Hua, Hong-Xia); Peng, YF (Peng, Yu-Fa)

Source: INSECT SCIENCE **Volume:** 23 **Issue:** 1 **Pages:** 78-87 **DOI:** 10.1111/1744-7917.12178 **Published:** FEB 2016

Abstract: Two transgenic rice lines (T2A-1 and T1C-19b) expressing cry2A and cry1C genes, respectively, were developed in China, targeting lepidopteran pests including *Chilo suppressalis* (Walker) (Lepidoptera: Crambidae). The seasonal expression of Cry proteins in different tissues of the rice lines and their resistance to *C. suppressalis* were assessed in comparison to a Bt rice line expressing a cry1Ab/Ac fusion gene, Huahui 1, which has been granted a biosafety certificate. In general, levels of Cry proteins were T2A-1 > Huahui 1 > T1C-19b among rice lines, and leaf > stem > root among rice tissues. The expression patterns of Cry protein in the rice line plants were similar: higher level at early stages than at later stages with an exception that high Cry1C level in T1C-19b stems at the maturing stage. The bioassay results revealed that the three transgenic rice lines exhibited significantly high resistance against *C. suppressalis* larvae throughout the rice growing season. According to Cry protein levels in rice tissues, the raw and corrected mortalities of *C. suppressalis* caused by each Bt rice line were the highest in the seedling and declined through the jointing stage with an exception for T1C-19b providing an excellent performance at the maturing stage. By comparison, T1C-19b exhibited more stable and greater resistance to *C. suppressalis* larvae than T2A-1, being close to Huahui 1. The results suggest cry1C is an ideal Bt gene for plant transformation for lepidopteran pest control, and T1C-19b is a promising Bt rice line for commercial use for tolerating lepidopteran rice pests.

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PubMed ID: 25284137

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Record 34 of 50

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

Author(s): Shao, ES (Shao, Ensi); Lin, L (Lin, Li); Chen, C (Chen, Chen); Chen, HZ (Chen, Hanze); Zhuang, HH (Zhuang, Haohan); Wu, SQ (Wu, Songqing); Sha, L (Sha, Li); Guan, X (Guan, Xiong); Huang, ZP (Huang, Zhipeng)

Source: SCIENTIFIC REPORTS **Volume:** 6 **Article Number:** 20106 **DOI:** 10.1038/srep20106 **Published:** FEB 1 2016

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.

Accession Number: WOS:000368996700003

PubMed ID: 26830331

ISSN: 2045-2322

Record 35 of 50

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

Author(s): Tumbalam, P (Tumbalam, Pavani); Thelen, KD (Thelen, Kurt D.); Adkins, A (Adkins, Andrew); Dale, B (Dale, Bruce); Balan, V (Balan, Venkatesh); Gunawan, C (Gunawan, Christa); Gao, J (Gao, Juan)

Source: BIOMASS & BIOENERGY **Volume:** 85 **Pages:** 119-125 **DOI:** 10.1016/j.biombioe.2015.12.004 **Published:** FEB 2016

Abstract: Literature values for glucose release from corn stover are highly variable which would likely result in tremendous variability in bio-refinery ethanol yield from corn stover feedstock. A relatively recent change in United States corn genetics is the inclusion of the *Bacillus thuringiensis* (Bt) trait, which now accounts for three-fourths of all US planted corn acreage. The objective of this study was to evaluate the effect of corn grain yield, inclusion of the Bt trait, and location environment on corn stover quality for subsequent ethanol conversion. Two hybrid pairs (each having a Bt and non-Bt near-isoline) were analyzed giving a total of 4 hybrids. In 2010 and 2011, field plots were located in Michigan at four latitudinal differing locations in four replicated plots at each location. Stover composition and enzymatic digestibility was analyzed and estimated ethanol yield (g g⁻¹) was calculated based on hydrolyzable 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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ISSN: 0961-9534

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Record 36 of 50

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

Author(s): Devos, Y (Devos, Y.); Alvarez-Alfageme, F (Alvarez-Alfageme, F.); Gennaro, A (Gennaro, A.); Mestdagh, S (Mestdagh, S.)

Source: JOURNAL OF APPLIED ENTOMOLOGY **Volume:** 140 **Issue:** 1-2 **Pages:** 1-10 **DOI:** 10.1111/jen.12248 **Published:** FEB 2016

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 stakeholders' views, mostly opposing EFSA's position on scientific grounds.

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Author Identifiers:

Author	ResearcherID Number	ORCID Number
Gennaro, Andrea	A-2774-2014	0000-0002-3020-2637

ISSN: 0931-2048

eISSN: 1439-0418

Record 37 of 50

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

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

Source: JOURNAL OF APPLIED ENTOMOLOGY **Volume:** 140 **Issue:** 1-2 **Pages:** 19-27 **DOI:** 10.1111/jen.12233 **Published:** FEB 2016

Abstract: The western corn rootworm, *Diabrotica virgifera virgifera* LeConte, is considered one of the most significant insect pests of maize in North America. Larvae of

other secondary subterranean pests such as grape colaspis, *Colaspis brunnea* (F.), and Japanese beetle, *Popillia japonica* Newman, can also injure maize seedlings and cause yield loss. In the past decade, maize hybrids containing Bt proteins have been used to manage the western corn rootworm; additionally, seeds are commonly treated with a 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.

Accession Number: WOS:000368144900003

ISSN: 0931-2048

eISSN: 1439-0418

Record 38 of 50

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

Author(s): Palinkas, Z (Palinkas, Zoltan); Zalai, M (Zalai, Mihaly); Szenasi, A (Szenasi, Agnes); Kadar, F (Kadar, Ferenc); Dorner, Z (Dorner, Zita); Balog, A (Balog, Adalbert)

Source: CROP PROTECTION **Volume:** 80 **Pages:** 87-93 **DOI:** 10.1016/j.cropro.2015.11.001 **Published:** FEB 2016

Abstract: This study investigated the effects of different GM maize crops on the abundances of rove beetles. It also investigated competition between rove beetles and other epigeic arthropod predatory groups (ground beetles and spiders). Altogether a total of 5926 rove beetle individuals belonging to 25 species were collected. Whilst the average number of rove beetle individuals per replicate per sampling date varied and, moreover, decreased each year, there were no observed differences in rove beetle abundance when compared between isogenic and GM maize plots within the study period. Furthermore, no clear trends on positive correlations between weed coverage and rove beetle abundances were detected. Altogether a total number of 76,070 ground beetle individuals and 11,126 spiders (including all Araneae) were collected with pitfall traps. Analyses revealed a strong negative relationship between rove beetles and the other two groups in each treatment and year. According to the results the effect of interspecific competition on rove beetle abundance in GM maize is much higher than the effects of treatments including both Bt toxins and extra glyphosate applications. (C) 2015 Elsevier Ltd. All rights reserved.

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Record 39 of 50

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

Author(s): Bortolotto, OC (Bortolotto, Orcial Ceolin); Mikami, AY (Mikami, Adriana Yatie); Bueno, AD (Bueno, Adeney de Freitas); Silva, GV (Silva, Gabriela Vieira); de Queiroz, AP (de Queiroz, Ana Paula)

Source: CIENCIA RURAL **Volume:** 46 **Issue:** 2 **Pages:** 254-259 **DOI:** 10.1590/0103-8478cr20150542 **Published:** FEB 2016

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 isolate. 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.

Accession Number: WOS:000367134300010

ISSN: 0103-8478

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Record 40 of 50

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

Author(s): Jachimska, B (Jachimska, Barbara); Tokarczyk, K (Tokarczyk, Karolina); Lapczynska, M (Lapczynska, Marta); Puciuł-Malinowska, A (Puciuł-Malinowska, Agnieszka); Zapotoczny, S (Zapotoczny, Szczepan)

Source: COLLOIDS AND SURFACES A-PHYSICOCHEMICAL AND ENGINEERING ASPECTS **Volume:** 489 **Pages:** 163-172 **DOI:** 10.1016/j.colsurfa.2015.10.033 **Published:** JAN 20 2016

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 x 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.

Accession Number: WOS:000366943200019

Author Identifiers:

Author	ResearcherID Number	ORCID Number
Jachimska, Barbara	G-1697-2015	
Tokarczyk, Karolina	G-6258-2014	
Zapotoczny, Szczepan	A-4987-2012	0000-0001-6662-7621

ISSN: 0927-7757

eISSN: 1873-4359

Record 41 of 50

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

Author(s): Armanious, A (Armanious, Antonius); Aeppli, M (Aeppli, Meret); Jacak, R (Jacak, Ronald); Refardt, D (Refardt, Dominik); Sigstam, T (Sigstam, Therese); Kohn, T (Kohn, Tamar); Sander, M (Sander, Michael)

Source: ENVIRONMENTAL SCIENCE & TECHNOLOGY **Volume:** 50 **Issue:** 2 **Pages:** 732-743 **DOI:** 10.1021/acs.est.5b04644 **Published:** JAN 19 2016

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, fr, GA, and Q 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.

Accession Number: WOS:000368563400024

PubMed ID: 26636722

Author Identifiers:

Author	ResearcherID Number	ORCID Number
Sander, Michael	J-7509-2012	0000-0003-3383-2041
Armanious, Antonius	J-3117-2014	0000-0002-8809-4659

ISSN: 0013-936X

eISSN: 1520-5851

Record 42 of 50**Title:** A high-throughput, in-vitro assay for *Bacillus thuringiensis* insecticidal proteins**Author(s):** Willcoxon, MI (Willcoxon, Michi Izumi); Dennis, JR (Dennis, Jaclyn R.); Lau, SI (Lau, Sabina I.); Xie, WP (Xie, Weiping); You, Y (You, You); Leng, S (Leng, Song); Fong, RC (Fong, Ryan C.); Yamamoto, T (Yamamoto, Takashi)**Source:** JOURNAL OF BIOTECHNOLOGY **Volume:** 217 **Pages:** 72-81 **DOI:** 10.1016/j.jbiotec.2015.10.021 **Published:** JAN 10 2016

Abstract: A high-throughput, in-vitro assay for *Bacillus thuringiensis* (Bt) insecticidal proteins designated as Cry was developed and evaluated for screening a large number of Cry protein variants produced by DNA shuffling. This automation-amenable assay exploits an insect cell line expressing a single receptor of Bt Cry proteins. The Cry toxin used to develop this assay is a variant of the Cry1Ab protein called IP1-88, which was produced previously by DNA shuffling. Cell mortality caused by the activated Bt Cry toxin was determined by chemical cell viability assay in 96/384-well microtiter plates utilizing CellTiter 96 (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.

Accession Number: WOS:000366757900010

ISSN: 0168-1656

eISSN: 1873-4863

Record 43 of 50**Title:** FUM Gene Expression Profile and Fumonisin Production by *Fusarium verticillioides* Inoculated in Bt and Non-Bt Maize**Author(s):** Rocha, LO (Rocha, Liliana O.); Barroso, VM (Barroso, Vinicius M.); Andrade, LJ (Andrade, Ludmila J.); Pereira, GHA (Pereira, Gustavo H. A.); Ferreira-Castro, FL (Ferreira-Castro, Fabiane L.); Duarte, AP (Duarte, Aildson P.); Michelotto, MD (Michelotto, Marcos D.); Correa, B (Correa, Benedito)**Source:** FRONTIERS IN MICROBIOLOGY **Volume:** 6 **Article Number:** 1503 **DOI:** 10.3389/fmicb.2015.01503 **Published:** JAN 6 2016

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

Accession Number: WOS:000367786300003

ISSN: 1664-302X

Record 44 of 50**Title:** Enzymatic Hydrolysis of Polyester Thin Films: Real-Time Analysis of Film Mass Changes and Dissipation Dynamics**Author(s):** Zumstein, MT (Zumstein, Michael Thomas); Kohler, HPE (Kohler, Hans-Peter E.); McNeill, K (McNeill, Kristopher); Sander, M (Sander, Michael)**Source:** ENVIRONMENTAL SCIENCE & TECHNOLOGY **Volume:** 50 **Issue:** 1 **Pages:** 197-206 **DOI:** 10.1021/acs.est.5b04103 **Published:** JAN 5 2016

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.

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PubMed ID: 26599203

Author Identifiers:

Author	ResearcherID Number	ORCID Number
Sander, Michael	J-7509-2012	0000-0003-3383-2041

ISSN: 0013-936X

eISSN: 1520-5851

Record 45 of 50**Title:** Grain and biomass nutrient uptake of conventional corn and their genetically modified isolines**Author(s):** Osborne, SL (Osborne, Shannon L.); Lehman, RM (Lehman, R. Michael); Rosentrater, KA (Rosentrater, Kurt A.)**Source:** JOURNAL OF PLANT NUTRITION **Volume:** 39 **Issue:** 14 **Pages:** 2047-2055 **DOI:** 10.1080/01904167.2016.1187753 **Published:** 2016

Abstract: The adoption of genetically engineered crops in the United States has increased dramatically over the past decade. Differences in agronomic characteristics and protein expression between genetically engineered plants and their naturally recombinant non-genetically modified (GM) counterparts are not well-understood. Experimental field plots were established in the spring of 2005 near Brookings, SD with 18 different commonly used corn hybrids including three conventional hybrids and their corresponding transgenic modifications. Specific research objectives were to evaluate in a side by side comparison, the impact of the genetic modifications on agronomic characteristics. Results show that glyphosate or insect resistance resulting from genetic modification, in the absence of significant insect pest or weed pressure and glyphosate application, were not likely to significantly alter productivity or nutrient composition of corn residue or grain. No significant differences were observed among the hybrids in average grain yield or above-ground biomass over the three years of the experiment.

Accession Number: WOS:000388009000006

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Record 46 of 50

Title: Genetic Technology and Food Security: Country Report - Germany

Author(s): Dederer, HG (Dederer, Hans-Georg)

Edited by: Norer R

Source: GENETIC TECHNOLOGY AND FOOD SAFETY **Book Series:** Ius Comparatum-Global Studies in Comparative Law **Volume:** 14 **Pages:** 73-124 **DOI:** 10.1007/978-3-319-23995-8_2 **Published:** 2016

Abstract: In 2013 and 2014, no GM plants were released into the environment in Germany, neither for research nor for commercial purposes. Political as well as legal grounds may have contributed to this development. In fact, the German public tends to be much more critical about agricultural biotechnology than the EU average. Politicians seem to have bowed to the public's distrust against GMOs. Both the executive and the legislature have exercised almost any margin of discretion left by EU law to the Member States in order to strangle GM plant cultivation. Examples include the Federal Ministry of Agriculture's order suspending the cultivation of the GM variety MON810 and strict liability provisions which prompted the German Farmers' Association to advise every farmer against GM crop cultivation.

Accession Number: WOS:000385439900003

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Record 47 of 50

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

Author(s): Raen, AZ (Raen, Akhtar Zunnu); Dang, C (Dang Cong); Wang, F (Wang Fang); Peng, YF (Peng Yu-fa); Ye, GY (Ye Gong-yin)

Source: JOURNAL OF INTEGRATIVE AGRICULTURE **Volume:** 15 **Issue:** 9 **Pages:** 2059-2069 **DOI:** 10.1016/S2095-3119(16)61414-4 **Published:** 2016

Abstract: Various rice lines have been genetically modified with genes from *Bacillus thuringiensis* (Bt) to continuously produce Bt insecticidal proteins against lepidopteran larvae. The Bt insecticidal protein constantly expresses in the plants to create an opportunity for non-target herbivores to acquire and convey the protein to their predators or parasitoids across trophic levels. This paper evaluates the effects of Bt rice (namely, Kemindao 1 (KMD1) and Kemindao 2 (KMD2)) expressing Cry1Ab as compared to its non-Bt control line, Xiushui 11 on non-target predator *Onus tantulus* (a generalist predatory anthocorid of thrips) under laboratory and field conditions. To measure several biological parameters such as total nymphal duration and fecundity of this bug, it was reared on thrips and pollens of KMD1 and KMD2 as compared to their control under laboratory conditions. By comparison with the control, Bt rice did not significantly affect main life-history characteristics (total nymphal duration, female adult longevity, oviposition period and fecundity) of this anthocorid preying on Bt rice-fed thrips along with Bt rice pollens, except that the fecundity of this predator for KMD1 was distinctly lower as compared with KMD2 or the control. Enzyme-linked immunosorbent assay (ELISA) results showed that no Cry1Ab protein was detected in this predator fed on thrips or rice pollen from Bt rice but was in Bt rice pollens. With the beat plate, plastic bag and color trap sampling methods, two-year field monitoring of *O. tantulus* abundance demonstrated that Bt rice had no significant detrimental effects on the population dynamics and seasonal average densities of this predatory anthocorid as compared with the control. Thus, it is suggested that growing our tested Bt rice (KMD1 and KMD2) producing Cry1Ab will pose a negligible risk to the anthocorid, *O. tantulus*.

Accession Number: WOS:000383411900013

ISSN: 2095-3119

Record 48 of 50

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

Author(s): Peterson, JA (Peterson, Julie A.); Obyrcki, JJ (Obyrcki, John J.); Harwood, JD (Harwood, James D.)

Source: BIOCONTROL SCIENCE AND TECHNOLOGY **Volume:** 26 **Issue:** 9 **Pages:** 1230-1248 **DOI:** 10.1080/09583157.2016.1193591 **Published:** 2016

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

Accession Number: WOS:000379754200005

ISSN: 0958-3157

eISSN: 1360-0478

Record 49 of 50

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

Author(s): Liu, RR (Liu Ran-ran); Zhao, GP (Zhao Gui-ping); Zheng, MQ (Zheng Mai-qing); Liu, J (Liu Jie); Zhang, JJ (Zhang Jing-jing); Li, P (Li Peng); Li, QH (Li Qing-he); Feng, JH (Feng Jing-hai); Zhang, MH (Zhang Min-hong); Wen, J (Wen Jie)

Source: JOURNAL OF INTEGRATIVE AGRICULTURE **Volume:** 15 **Issue:** 6 **Pages:** 1355-1363 **DOI:** 10.1016/S2095-3119(15)61281-3 **Published:** 2016

Abstract: The safety of feeding transgenic cry1Ab/cry1Ac rice (a genetically modified (GM) rice variety) to broilers was examined from an immunological perspective. Hatching Arbor Acres chickens (240) were assigned to two dietary treatments (diets containing GM or non-GM rice) with 12 replicates per group and 10 birds per replicate. Traits were measured on one randomly selected bird from each replicate at d 21 and 42. The 42-d feeding trial revealed that cry1Ab/cry1Ac rice had no significant effect relative to non-GM rice on body weight and the immune organ indices. No significant pathological lesion in the spleen and bursa of Fabricius was found in the GM rice group. There were no significant differences in serum concentrations of immunoglobulin Y (IgY), IgM, interleukin 4 (IL-4) and IL-6 between the two groups at d 21 or 42, except for IL-6 being higher ($P < 0.05$) in the GM-fed chickens at d 42. There were no differences in the T and B lymphocyte transformation rate and CD4(+)/CD8(+) ratio between the two groups at d 42. Additionally, there was no significant difference between the two diets in expression of relevant genes viz. the major histocompatibility complex class II beta chain (BLB2), interferon beta 1 (IFN beta), tumour necrosis factor alpha-like (TNF alpha) and toll-like receptor 4 (TLR4) in the spleen and bursa of Fabricius. All the data demonstrated that transgenic cry1Ab/cry1Ac rice had no adverse effect on these aspects of immune function of broilers during 42-d feeding trial. Transgenic rice was therefore indistinguishable from non-GM rice in terms of short-term feeding in chickens.

Accession Number: WOS:000378188600019

ISSN: 2095-3119

Record 50 of 50

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

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

Source: WORLD MYCOTOXIN JOURNAL **Volume:** 9 **Issue:** 3 **Pages:** 475-486 **DOI:** 10.3920/WMJ2015.1960 **Published:** 2016

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

Accession Number: WOS:000376604100013

ISSN: 1875-0710

eISSN: 1875-0796

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Record 1 of 9

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

Author(s): Resende, DC (Resende, Daniela Chaves); Mendes, SM (Mendes, Simone Martins); Marucci, RC (Marucci, Rosangela C.); Silva, AD (Silva, Alessandra de Carvalho); Campanha, MM (Campanha, Monica Matoso); Waquil, JM (Waquil, Jose Magid)

Source: REVISTA BRASILEIRA DE ENTOMOLOGIA **Volume:** 60 **Issue:** 1 **Pages:** 82-93 **DOI:** 10.1016/j.rbe.2015.12.001 **Published:** JAN-MAR 2016

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.

Accession Number: WOS:000372000100012

ISSN: 0085-5626

eISSN: 1806-9665

Record 2 of 9

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

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

Source: JOURNAL OF ENVIRONMENTAL BIOLOGY **Volume:** 37 **Issue:** 1 **Pages:** 121-127 **Published:** JAN 2016

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.

Accession Number: WOS:000370208700018

PubMed ID: 26930869

ISSN: 0254-8704

Record 3 of 9

Title: Current trends in the global market of transgenic plants and environmental safety issues

Author(s): Viktorov, AG (Viktorov, A. G.)

Source: RUSSIAN JOURNAL OF PLANT PHYSIOLOGY **Volume:** 63 **Issue:** 1 **Pages:** 38-45 **DOI:** 10.1134/S1021443716010179 **Published:** JAN 2016

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.

Accession Number: WOS:000370370300004

ISSN: 1021-4437

eISSN: 1608-3407

Record 4 of 9

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

Author(s): Zhang, FJ (Zhang, Fengjuan); Peng, DH (Peng, Donghai); Cheng, CS (Cheng, Chunsheng); Zhou, W (Zhou, Wei); Ju, SY (Ju, Shouyong); Wan, DF (Wan, Danfeng); Yu, ZQ (Yu, Ziqun); Shi, JW (Shi, Jianwei); Deng, YY (Deng, Yaoyao); Wang, FS (Wang, Fenshan); Ye, XB (Ye, Xiaobo); Hu, ZF (Hu, Zhenfei); Lin, J (Lin, Jian); Ruan, LF (Ruan, Lifang); Sun, M (Sun, Ming)

Source: PLOS PATHOGENS **Volume:** 12 **Issue:** 1 **Article Number:** e1005389 **DOI:** 10.1371/journal.ppat.1005389 **Published:** JAN 2016

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 Cry6Aa triggers necrosis represents a newly added necrosis paradigm in the *C. elegans*. Understanding this model could lead to new strategies for nematode control.

Accession Number: WOS:000369374500041

PubMed ID: 26795495

ISSN: 1553-7366

eISSN: 1553-7374

Record 5 of 9

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

Author(s): Zhang, L (Zhang, Li); Shen, WJ (Shen, Wenjing); Fang, ZX (Fang, Zhixiang); Liu, B (Liu, Biao)

Source: FRONTIERS IN BIOSCIENCE-LANDMARK **Volume:** 21 **Pages:** 447-454 **DOI:** 10.2741/4400 **Published:** JAN 1 2016

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.

Accession Number: WOS:000369078400015

PubMed ID: 26709785

ISSN: 1093-9946

eISSN: 1093-4715

Record 6 of 9

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

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

Source: NUTRIENT CYCLING IN AGROECOSYSTEMS **Volume:** 104 **Issue:** 1 **Pages:** 93-105 **DOI:** 10.1007/s10705-016-9761-6 **Published:** JAN 2016

Abstract: Better understanding of plant nutrition and nutrient interactions is of critical importance for developing best management practices in crop production. A three-

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

Accession Number: WOS:000369003700008

ISSN: 1385-1314

eISSN: 1573-0867

Record 7 of 9

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

Author(s): Deitloff, J (Deitloff, Jennifer); Dunbar, MW (Dunbar, Mike W.); Ingber, DA (Ingber, David A.); Hibbard, BE (Hibbard, Bruce E.); Gassmann, AJ (Gassmann, Aaron J.)

Source: PEST MANAGEMENT SCIENCE **Volume:** 72 **Issue:** 1 **Pages:** 190-198 **DOI:** 10.1002/ps.3988 **Published:** JAN 2016

Abstract: BACKGROUND *Diabrotica virgifera virgifera* LeConte is a major pest of corn and causes over a billion dollars of economic loss annually through yield reductions and management costs. Corn producing toxins derived from *Bacillus thuringiensis* (Bt) has been developed to help manage *D. v. virgifera*. However, previous studies have demonstrated the ability of this species to evolve resistance to Bt toxins in both laboratory and field settings.

RESULTS We used an experimental evolution approach to test the refuge strategies for delaying resistance of *D. v. virgifera* to corn producing Bt toxin Cry34/35Ab1. In the absence of refuges, *D. v. virgifera* developed resistance to Bt corn after three generations of selection. In some cases, non-Bt refuges reduced the level of resistance compared with the strain selected in the absence of refuges, but refuge strains did show reduced susceptibility to Bt corn compared with the unselected strain.

CONCLUSIONS In this study, non-Bt refuges delayed resistance to Bt corn by *D. v. virgifera* in some cases but not others. Combining the refuge strategy with pyramids of multiple Bt toxins and applying other pest management strategies will likely be necessary to delay resistance of *D. v. virgifera* to Bt corn. (c) 2015 Society of Chemical Industry

Accession Number: WOS:000368941400021

PubMed ID: 25652190

ISSN: 1526-498X

eISSN: 1526-4998

Record 8 of 9

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

Author(s): Li, JW (Li, Jing-Wei); Li, HH (Li, Hou-Hua); Wang, RR (Wang, Ren-Rui); Gao, XX (Gao, Xiao-Xia); Wang, QC (Wang, Qiao-Chun)

Source: ACTA PHYSIOLOGIAE PLANTARUM **Volume:** 38 **Issue:** 1 **Article Number:** 8 **DOI:** 10.1007/s11738-015-2028-z **Published:** JAN 2016

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.

Accession Number: WOS:000368015100008

ISSN: 0137-5881

eISSN: 1861-1664

Record 9 of 9

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

Author(s): Lombardo, L (Lombardo, Luca); Coppola, G (Coppola, Gerardo); Zelasco, S (Zelasco, Samanta)

Source: TRENDS IN BIOTECHNOLOGY **Volume:** 34 **Issue:** 1 **Pages:** 49-57 **DOI:** 10.1016/j.tibtech.2015.10.006 **Published:** JAN 2016

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.

Accession Number: WOS:000368205900006

PubMed ID: 26620971

ISSN: 0167-7799

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***Record 1 of 11.** Search terms matched: BORER(4); BORERS(1); BT(4); CORN(1); CRY1AB(2); LEPIDOPTERA(3); MAIZE(6); RESISTANT(1)

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

Authors: Erasmus, A; Marais, J; Van den Berg, J

Author Full Names: Erasmus, Annemie; Marais, Jaco; Van den Berg, Johnnie

Source: PEST MANAGEMENT SCIENCE, 72 (12):2287-2294; [10.1002/ps.4273](https://doi.org/10.1002/ps.4273) DEC 2016

Language: English

Abstract: BACKGROUNDProducts of plant biotechnology, for example genetically modified Bt maize, provide useful tools for pest management. The benefits provided by insect-resistant plants are, however, threatened by the evolution of resistance by target pest species. The high-dose/refuge insect resistance management strategy (IRM) as well as seed mixtures are globally used as IRM strategies. *Busseola fusca* (Lepidoptera: Noctuidae), the target stem borer of Bt maize in Africa, evolved resistance to Bt maize expressing Cry1Ab protein in South Africa. Owing to high larval mobility and subsequent sublethal exposure of larvae moving between non-Bt and Bt plants, more rapid resistance evolution has been proposed as a possibility with deployment of seed mixture strategies. RESULTSLaboratory and field studies were conducted to study *B. fusca* larval mobility. In the laboratory, different scenarios of *B. fusca* larval movement between single-gene (Cry1Ab) and stacked-trait (Cry1A.105 and Cry2Ab2) Bt maize were studied. Data on larval survival and mass over time indicated that Cry proteins do not kill larvae above certain developmental stages. A 2 year field study with the single gene and the stacked event was conducted using seed mixtures containing 5, 10, 15 and 20% non-Bt seed as well as a control treatment (non-Bt seed only). CONCLUSIONLarval movement continued for 5 weeks and resulted in a significant incidence of Bt and non-Bt damaged plants, indicating that the movement behaviour of *B. fusca* is of such a nature that seed mixtures as an IRM strategy may not be effective to delay resistance evolution. (c) 2016 Society of Chemical Industry

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Unique ID: WOS:000386927800011

PubMed ID: 26990107

***Record 2 of 11.** Search terms matched: BT(2); LEPIDOPTERA(2); MAIZE(6)

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

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

Title: Frequency of Cry1F resistance alleles in *Spodoptera frugiperda* (**Lepidoptera**: Noctuidae) in Brazil

Authors: Farias, JR; Andow, DA; Horikoshi, RJ; Bernardi, D; Ribeiro, RD; do Nascimento, ARB; dos Santos, AC; Omoto, C

Author Full Names: Farias, Juliano R.; Andow, David A.; Horikoshi, Renato J.; Bernardi, Daniel; Ribeiro, Rebeca da S.; do Nascimento, Antonio R. B.; dos Santos, Antonio C.; Omoto, Celso

Source: PEST MANAGEMENT SCIENCE, 72 (12):2295-2302; [10.1002/ps.4274](https://doi.org/10.1002/ps.4274) DEC 2016

Language: English

Abstract: BACKGROUND The frequency of resistance alleles is a major factor influencing the rate of resistance evolution. Here, we adapted the F-2 screen procedure for *Spodoptera frugiperda* (J. E. Smith) with a discriminating concentration assay, and extended associated statistical methods to estimate the frequency of resistance to Cry1F protein in *S. frugiperda* in Brazil when resistance was not rare. RESULTS We show that F-2 screen is efficient even when the resistance frequency is 0.250. It was possible to screen 517 isoparental lines from 12 populations sampled in five states of Brazil during the first half of 2012. Western Bahia had the highest allele frequency of Cry1F resistance, 0.192, with a 95% confidence interval (CI) between 0.163 and 0.220. All other states had a similar and lower frequency varying from 0.042 in Parana to 0.080 in Mato Grosso do Sul. CONCLUSION The high frequency in western Bahia may be related to year-round availability of maize, the high population density of *S. frugiperda*, the lack of refuges and the high adoption rate of Cry1F maize. Cry1F resistance alleles were not rare and occurred at frequencies that have already compromised the useful life of TC1507 maize in western Bahia. (c) 2016 Society of Chemical Industry

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IDS Number: EA8ZB

Unique ID: WOS:000386927800012

PubMed ID: 26990201

*Record 3 of 11. Search terms matched: BT(7); CORN(1); CRY1AB(7); MAIZE(9)

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

*Order Full Text []

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

Authors: Andow, DA; Zwahlen, C

Author Full Names: Andow, D. A.; Zwahlen, C.

Source: BIOLOGICAL CONTROL, 103 204-209; [10.1016/j.biocontrol.2016.09.009](https://doi.org/10.1016/j.biocontrol.2016.09.009) DEC 2016

Language: English

Abstract: Ground beetles are significant predators in agricultural habitats. While many studies have characterized effects of Bt maize on various carabid species, few have examined the potential acquisition of Cry toxins from live plants versus plant residue. In this study, we examined how live Bt maize and Bt maize residue affect acquisition of Cry1Ab in six species. Adult beetles were collected live from fields with either current-year Bt maize, one-year-old Bt maize residue, two-year-old Bt maize residue, or fields without any Bt crops or residue for the past two years, and specimens were analyzed using ELISA. Observed Cry1Ab concentrations in the beetles were similar to that reported in previously published studies. Only one specimen of *Cyclotrachelus iowensis* acquired Cry1Ab from two-year-old maize residue. Three species

acquired Cry1Ab from fields with either live plants or plant residue (*Cyclotrachelus iowensis*, *Poecilus lucublandus*, *Poecilus chalcites*), implying participation in both live-plant and residue-based food webs. Two species acquired toxin from fields with live plants, but not from fields with residue (*Bembidion quadrimaculatum*, *Elaphropus incurvus*), suggesting participation only in live plant-based food webs. One species did not acquire Cry1Ab from either live-plant or residue (*Scarites quadriceps*), suggesting that its food sources might not contain significant amounts of Cry1Ab. These results revealed significant differentiation among carabid species in their associations with live-plant and residue-based food webs in agricultural fields. (C) 2016 Elsevier Inc. All rights reserved.

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IDS Number: EA2ZZ

Unique ID: WOS:000386468300024

***Record 4 of 11.** Search terms matched: CRY1AB(2); LEPIDOPTERA(1)

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Title: Effects of Periplocoside P from *Periploca sepium* on the Midgut Transmembrane Potential of *Mythimna separata* Larvae

Authors: Wang, YY; Qi, ZJ; Qi, M; Hu, ZN; Wu, WJ

Author Full Names: Wang, YingYing; Qi, Zhijun; Qi, Meng; Hu, Zhaonong; Wu, Wenjun

Source: SCIENTIFIC REPORTS, 6 [10.1038/srep36982](https://doi.org/10.1038/srep36982) NOV 11 2016

Language: English

Abstract: Periplocoside P (PSP) isolated from the root bark of *Periploca sepium* contains a pregnane glycoside skeleton and possesses high insecticidal properties. Preliminary studies indicated that PSP disrupts epithelial functions in the midgut of lepidopteran larvae. In the present study, we examined the effects of PSP on the apical and basolateral membrane voltages, V-a and V-bl, respectively, of cells from (1) midguts isolated from the larvae of the oriental armyworm *Mythimna separata* that were in vitro incubated with toxins and (2) midguts isolated from *M. separata* larvae force-fed with PSP. We compared the effects of PSP with the effects of the *Bacillus thuringiensis* toxin Cry1Ab and inactive periplocoside E (PSE) on the midgut epithelial cells. The results showed that V-a rapidly decreased in the presence of PSP in a time- and dose-dependent manner, similar to the effects of Cry1Ab. By contrast, PSE did not affect the V-a and V-bl. Additionally, PSP did not influence the V-bl. Given these results, we speculate that PSP may modulate transport mechanisms at the apical membrane of the midgut epithelial cells by inhibiting the V-type H⁺ ATPase.

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Article Number: 36982

IDS Number: EB6EX

Unique ID: WOS:000387475300001

PubMed ID: 27833169

***Record 5 of 11.** Search terms matched: BORER(1); BT(4); CORN(1); MAIZE(7); OSTRINIA(2)

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

*Order Full Text []

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

Authors: Chen, HX; Yang, R; Yang, W; Zhang, L; Camara, I; Dong, XH; Liu, YQ; Shi, WP

Author Full Names: Chen, Hong-Xing; Yang, Rui; Yang, Wang; Zhang, Liu; Camara, Ibrahima; Dong, Xue-Hui; Liu, Yi-Qing; Shi, Wang-Peng

Source: ENVIRONMENTAL SCIENCE AND POLLUTION RESEARCH, 23 (21):21511-21516; [10.1007/s11356-016-7340-7](https://doi.org/10.1007/s11356-016-7340-7) NOV 2016

Language: English

Abstract: *Ostrinia furnacalis* (Guen,e) and *Helicoverpa armigera* (Hubner) are the most important pests of maize in China. A laboratory study and a 2-year field study on the efficacy of transgenic maize expressing the Cry1Ac protein BT38 against *O. furnacalis* and *H. armigera* were performed. We found that the husks, kernels, and silks of BT38 showed significant efficacy against larvae of *O. furnacalis* and *H. armigera*. In the field, when neonate larvae of *O. furnacalis* and *H. armigera* were on plants at different growth stages and when levels of leaf-damage or number of damaged silks were used to score efficacy, we found that BT38 showed significant insecticidal efficacy against *O. furnacalis* and *H. armigera*, but the non-Bt maize did not show significant efficacy against either pest. These results suggest that the insecticidal efficacy of Bt maize expressing the Cry1Ac protein could be useful in the integrated pest management of these key maize pests.

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IDS Number: EB7VQ

Unique ID: WOS:000387599600036

PubMed ID: 27510165

***Record 6 of 11.** Search terms matched: BORER(2); CORN(2); CRY1AB(1); MAIZE(5)

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

*Order Full Text []

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

Authors: Zhang, YW; Zhang, W; Liu, Y; Wang, JH; Wang, GY; Liu, YJ

Author Full Names: Zhang, Yuwen; Zhang, Wei; Liu, Yan; Wang, Jianhua; Wang, Guoying; Liu, Yunjun

Source: ANALYTICAL AND BIOANALYTICAL CHEMISTRY, 408 (28):8231-8239; [10.1007/s00216-016-9938-5](https://doi.org/10.1007/s00216-016-9938-5) NOV 2016

Language: English

Abstract: Cry1Ie is a kind of *Bacillus thuringiensis* (Bt) toxin protein which has a different action model than the Cry1Ab and Cry1Ac protein. The transgenic maize expressing Cry1Ie

might be commercially used in the near future and it is urgent to develop a method to detect Cry1Ie protein in transgenic plants and their products. To develop an ELISA method, Cry1Ie protein was expressed in Escherichia coli strain Transetta DE3, purified with the Ni-NTA spin columns, and then validated by sequencing. Bioassay results showed that the purified Cry1Ie protein was highly toxic to the Asian corn borer. The polyclonal antibody (pAb) and the specific monoclonal antibody (mAb) 1G(4)2D(6) were generated from rabbit and mice which were immunized with Cry1Ie protein, respectively. Western blotting of crude Cry1Ie protein extracts was established by employing mAb 1G(4)2D(6), whereas the mAb 1G(4)2D(6) negligibly recognized other Bt proteins. Sandwich ELISA against Cry1Ie protein was established by coating with pAb and detecting with mAb 1G(4)2D(6). The limit of detection (LOD), the limit of quantification (LOQ), and the quantification range of the assay in different matrices of maize plant were determined as 0.27-0.51, 0.29-0.78, and 0.45-15.71 ng/mL, respectively. Recoveries of Cry1Ie protein spiked in different maize tissues ranged from 75.1 to 99.5 %. The established sandwich ELISA was verified using transgenic maize overexpressing Cry1Ie. The results in this study suggested that the established ELISA method is effective for detecting Cry1Ie protein in transgenic plants.

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IDS Number: EA5VS

Unique ID: WOS:000386693000034

PubMed ID: 27659816

***Record 7 of 11.** Search terms matched: MAIZE(6); MON810(4)

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

*Order Full Text []

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

Authors: Zeljenkova, D; Alacova, R; Ondrejtkova, J; Amrusova, K; Bartusova, M; Kebis, A; Kovriznych, J; Rollerova, E; Szabova, E; Wimmerova, S; Cernak, M; Krivosikova, Z; Kuricova, M; Liskova, A; Spustova, V; Tulinska, J; Levkut, M; Revajova, V; Sevcikova, Z; Schmidt, K; Schmidtke, J; Schmidt, P; La Paz, JL; Corujo, M; Pla, M; Kleter, GA; Kok, EJ; Sharbati, J; Bohmer, M; Bohmer, N; Einspanier, R; Adel-Patient, K; Spok, A; Poting, A; Kohl, C; Wilhelm, R; Schiemann, J; Steinberg, P

Author Full Names: Zeljenkova, Dagmar; Alacova, Radka; Ondrejtkova, Julia; Amrusova, Katarina; Bartusova, Maria; Kebis, Anton; Kovriznych, Jevgenij; Rollerova, Eva; Szabova, Elena; Wimmerova, Sona; Cernak, Martin; Krivosikova, Zora; Kuricova, Miroslava; Liskova, Aurelia; Spustova, Viera; Tulinska, Jana; Levkut, Mikulas; Revajova, Viera; Sevcikova, Zuzana; Schmidt, Kerstin; Schmidtke, Joerg; Schmidt, Paul; La Paz, Jose Luis; Corujo, Maria; Pla, Maria; Kleter, Gijs A.; Kok, Esther J.; Sharbati, Jutta; Bohmer, Marc; Bohmer, Nils; Einspanier, Ralf; Adel-Patient, Karine; Spok, Armin; Poeting, Annette; Kohl, Christian; Wilhelm, Ralf; Schiemann, Joachim; Steinberg, Pablo

Source: ARCHIVES OF TOXICOLOGY, 90 (10):2531-2562; [10.1007/s00204-016-1798-4](https://doi.org/10.1007/s00204-016-1798-4)
OCT 2016

Language: English

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

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eISSN: 1432-0738

IDS Number: DZ2EH

Unique ID: WOS:000385654600014

PubMed ID: 27439414

***Record 8 of 11.** Search terms matched: BT(5); CORN(12); CORNFIELDS(3); MAIZE(1); ZEA MAYS(1)

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

*Order Full Text []

Title: Effects of Field History on **Corn** Root Injury and Adult Abundance of Northern and Western **Corn** Rootworm (Coleoptera: Chrysomelidae)

Authors: Dunbar, MW; O'Neal, ME; Gassmann, AJ

Author Full Names: Dunbar, Mike W.; O'Neal, Matthew E.; Gassmann, Aaron J.

Source: JOURNAL OF ECONOMIC ENTOMOLOGY, 109 (5):2096-2104;

[10.1093/jee/tow163](#) OCT 2016

Language: English

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

management inputs for *Diabrotica* spp.; however, its effects on resistance evolution remain undetermined.

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IDS Number: DZ8QU

Unique ID: WOS:000386136700018

PubMed ID: 27498115

***Record 9 of 11.** Search terms matched: BORER(2); BT(1); CORN(4); MAIZE(1); TOLERANT(1); YIELD(1)

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

*Order Full Text []

Title: Integrating Insect, Resistance, and Floral Resource Management in Weed Control Decision-Making

Authors: DiTommaso, A; Averill, KM; Hoffmann, MP; Fuchsberg, JR; Losey, JE

Author Full Names: DiTommaso, Antonio; Averill, Kristine M.; Hoffmann, Michael P.; Fuchsberg, Jeffrey R.; Losey, John E.

Source: WEED SCIENCE, 64 (4):743-756; [10.1614/WS-D-16-00052.1](https://doi.org/10.1614/WS-D-16-00052.1) OCT-DEC 2016

Language: English

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

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IDS Number: DZ7OH

Unique ID: WOS:000386055100021

***Record 10 of 11.** Search terms matched: BORER(2); BT(3); CORN(14); LEPIDOPTERA(1); OSTRINIA(4); ZEA MAYS(1)

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

*Order Full Text []

Title: Estimating E-Race European **Corn Borer (Lepidoptera: Crambidae)** Adult Activity in Snap Bean Fields Based on **Corn** Planting Intensity and Their Activity in **Corn** in New York Agroecosystems

Authors: Schmidt-Jeffris, RA; Huseeth, AS; Nault, BA

Author Full Names: Schmidt-Jeffris, Rebecca A.; Huseeth, Anders S.; Nault, Brian A.

Source: JOURNAL OF ECONOMIC ENTOMOLOGY, 109 (5):2210-2214;

[10.1093/jee/tow149](https://doi.org/10.1093/jee/tow149) OCT 2016

Language: English

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

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IDS Number: DZ8QU

Unique ID: WOS:000386136700032

***Record 11 of 11.** Search terms matched: BT(1); CORN(4); MAIZE(1); YIELD(1)

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

*Order Full Text []

Title: Grain and biomass nutrient uptake of conventional **corn** and their genetically modified isolines

Authors: Osborne, SL; Lehman, RM; Rosentrater, KA

Author Full Names: Osborne, Shannon L.; Lehman, R. Michael; Rosentrater, Kurt A.

Source: JOURNAL OF PLANT NUTRITION, 39 (14):2047-2055;

[10.1080/01904167.2016.1187753](https://doi.org/10.1080/01904167.2016.1187753) 2016

Language: English

Abstract: The adoption of genetically engineered crops in the United States has increased dramatically over the past decade. Differences in agronomic characteristics and protein expression between genetically engineered plants and their naturally recombinant non-genetically modified (GM) counterparts are not well-understood. Experimental field plots were established in the spring of 2005 near Brookings, SD with 18 different commonly used corn hybrids including three conventional hybrids and their corresponding transgenic modifications. Specific research objectives were to evaluate in a side by side comparison, the impact of the genetic modifications on agronomic characteristics. Results show that glyphosate or insect resistance resulting from genetic modification, in the absence of significant insect pest or weed pressure and glyphosate application, were not likely to significantly alter productivity or nutrient composition of corn residue or grain. No significant differences were observed among the hybrids in average grain yield or above-ground biomass over the three years of the experiment.

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IDS Number: EC3ER

Unique ID: WOS:000388009000006

***Record 1 of 8.** Search terms matched: BORER(1); BT(2); CORN(8); CRY1AB(5); LEPIDOPTERA(3); MAIZE(1); TOLERANT(1)

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

*Order Full Text []

Title: Field-Evolved Resistance in **Corn** Earworm to Cry Proteins Expressed by Transgenic Sweet **Corn**

Authors: Dively, GP; Venugopal, PD; Finkenbinder, C

Author Full Names: Dively, Galen P.; Venugopal, P. Dilip; Finkenbinder, Chad

Source: PLOS ONE, 11 (12):[10.1371/journal.pone.0169115](https://doi.org/10.1371/journal.pone.0169115) DEC 30 2016

Language: English

Abstract: Background Transgenic corn engineered with genes expressing insecticidal toxins from the bacterium *Bacillus thuringiensis* (Berliner) (Bt) are now a major tool in insect pest management. With its widespread use, insect resistance is a major threat to the sustainability of the Bt transgenic technology. For all Bt corn expressing Cry toxins, the high dose requirement for resistance management is not achieved for corn earworm, *Helicoverpa zea* (Boddie), which is more tolerant to the Bt toxins. Methodology/Major Findings We present field monitoring data using Cry1Ab (1996-2016) and Cry1A.105+Cry2Ab2 (2010-2016) expressing sweet corn hybrids as in-field screens to measure changes in field efficacy and Cry toxin susceptibility to *H. zea*. Larvae successfully damaged an increasing proportion of ears, consumed more kernel area, and reached later developmental stages (4th - 6th instars) in both types of Bt hybrids

(Cry1Ab-event Bt11, and Cry1A.105+Cry2Ab2-event MON89034) since their commercial introduction. Yearly patterns of *H. zea* population abundance were unrelated to reductions in control efficacy. There was no evidence of field efficacy or tissue toxicity differences among different Cry1Ab hybrids that could contribute to the decline in control efficacy. Supportive data from laboratory bioassays demonstrate significant differences in weight gain and fitness characteristics between the Maryland *H. zea* strain and a susceptible strain. In bioassays with Cry1Ab expressing green leaf tissue, Maryland *H. zea* strain gained more weight than the susceptible strain at all concentrations tested. Fitness of the Maryland *H. zea* strain was significantly lower than that of the susceptible strain as indicated by lower hatch rate, longer time to adult eclosion, lower pupal weight, and reduced survival to adulthood.

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

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Unique ID: WOS:000391229300056

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

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

*Order Full Text []

Title: INTERACTIONS BETWEEN Bt CROPS AND AQUATIC ECOSYSTEMS: A REVIEW

Authors: Venter, HJ; Bohn, T

Author Full Names: Venter, Hermoine J.; Bohn, Thomas

Source: ENVIRONMENTAL TOXICOLOGY AND CHEMISTRY, 35 (12):2891-2902;
[10.1002/etc.3583](https://doi.org/10.1002/etc.3583) DEC 2016

Language: English

Abstract: The term Bt crops collectively refers to crops that have been genetically modified to include a gene (or genes) sourced from *Bacillus thuringiensis* (Bt) bacteria. These genes confer the ability to produce proteins toxic to certain insect pests. The interaction between Bt crops and adjacent aquatic ecosystems has received limited attention in research and risk assessment, despite the fact that some Bt crops have been in commercial use for 20 yr. Reports of effects on aquatic organisms such as *Daphnia magna*, *Elliptio complanata*, and *Chironomus dilutus* suggest that some aquatic species may be negatively affected, whereas other reports suggest that the decreased use of insecticides precipitated by Bt crops may benefit aquatic communities. The present study reviews the literature regarding entry routes and exposure pathways by which aquatic organisms may be exposed to Bt crop material, as well as feeding trials and field surveys that have investigated the effects of Bt-expressing plant material on such organisms.

The present review also discusses how Bt crop development has moved past single-gene events, toward multigene stacked varieties that often contain herbicide resistance genes in addition to multiple Bt genes, and how their use (in conjunction with co-technology such as glyphosate/Roundup) may impact and interact with aquatic ecosystems. Lastly, suggestions for further research in this field are provided. (C) 2016 SETAC

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Unique ID: WOS:000391031400001

PubMed ID: 27530353

***Record 3 of 8.** Search terms matched: CRY1AB(2); MAIZE(1)

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

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

Title: ENZYME-LINKED IMMUNOSORBENT ASSAY DETECTION AND BIOACTIVITY OF CRY1AB PROTEIN FRAGMENTS

Authors: Albright, VC; Hellmich, RL; Coats, JR

Author Full Names: Albright, Vurtice C., III; Hellmich, Richard L.; Coats, Joel R.

Source: ENVIRONMENTAL TOXICOLOGY AND CHEMISTRY, 35 (12):3101-3112;
[10.1002/etc.3497](https://doi.org/10.1002/etc.3497) DEC 2016

Language: English

Abstract: The continuing use of transgenic crops has led to an increased interest in the fate of insecticidal crystalline (Cry) proteins in the environment. Enzyme-linked immunosorbent assays (ELISAs) have emerged as the preferred detection method for Cry proteins in environmental matrices. Concerns exist that ELISAs are capable of detecting fragments of Cry proteins, which may lead to an overestimation of the concentration of these proteins in the environment. Five model systems were used to generate fragments of the Cry1Ab protein, which were then analyzed by ELISAs and bioassays. Fragments from 4 of the model systems were not detectable by ELISA and did not retain bioactivity. Fragments from the proteinase K model system were detectable by ELISA and retained bioactivity. In most cases, ELISAs appear to provide an accurate estimation of the amount of Cry proteins in the environment, as detectable fragments retained bioactivity and nondetectable fragments did not retain bioactivity. (C) 2016 SETAC

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IDS Number: EG4RM

Unique ID: WOS:000391031400022

PubMed ID: 27206791

***Record 4 of 8.** Search terms matched: BT(1); CORN(1)

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

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

Title: Understanding fungal reservoirs: Tracking *Aspergillus* populations in air, soil, crop debris and the reproductive organs of Bt and non-Bt corn

Authors: Abbas, H; Weaver, M; Accinelli, C; Shier, W; Zablutowicz, R

Author Full Names: Abbas, H.; Weaver, M.; Accinelli, C.; Shier, W.; Zablutowicz, R.

Source: PHYTOPATHOLOGY, 106 (12):98-99; S DEC 2016

Language: English

ISSN: 0031-949X

eISSN: 1943-7684

IDS Number: EF6WM

Unique ID: WOS:000390471900513

***Record 5 of 8.** Search terms matched: CRY1AB(1)

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

*Order Full Text []

Title: Identification of zebrafish magnetoreceptor and cryptochrome homologs

Authors: Zhou, ZQ; Peng, XY; Chen, JB; Wu, XS; Wang, YQ; Hong, YH

Author Full Names: Zhou, Zuoqiong; Peng, Xiyang; Chen, Jianbin; Wu, Xiushan; Wang, Yuequn; Hong, Yunhan

Source: SCIENCE CHINA-LIFE SCIENCES, 59 (12):1324-1331; [10.1007/s11427-016-0195-x](https://doi.org/10.1007/s11427-016-0195-x)
DEC 2016

Language: English

Abstract: Magnetoreception is essential for magnetic orientation in animal migration. The molecular basis for magnetoreception has recently been elucidated in fruitfly as complexes between the magnetic receptor magnetoreceptor (MagR) and its ligand cryptochrome (Cry). MagR and Cry are present in the animal kingdom. However, it is unknown whether they perform a conserved role in diverse animals. Here we report the identification and expression of zebrafish MagR and Cry homologs towards understanding their roles in lower vertebrates. A single magr gene and 7 cry genes are present in the zebrafish genome. Zebrafish has four cry1 genes (cry1aa, cry1ab, cry1ba and cry1bb) homologous to human CRY1 and a single ortholog of human CRY2 as well as 2 cry-like genes (cry4 and cry5). By RT-PCR, magr exhibited a high level of ubiquitous RNA expression in embryos and adult organs, whereas cry genes displayed differential embryonic and adult expression. Importantly, magr depletion did not produce apparent abnormalities in organogenesis. Taken together, magr and cry2 exist as a single copy gene, whereas cry1 exists as multiple gene duplicates in zebrafish. Our result suggests that magr may play a dispensable role in organogenesis and predicts a possibility to generate magr mutants for analyzing its role in zebrafish.

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IDS Number: EF9SA

Unique ID: WOS:000390669100015

***Record 6 of 8.** Search terms matched: BT(1); CORN(1); CRY1AB(1); MAIZE(2); OSTRINIA(1); RESISTANT(1)

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

*Order Full Text []

Title: Bt CryIIe Toxin Does Not Impact the Survival and Pollen Consumption of Chinese Honey Bees, *Apis cerana cerana* (Hymenoptera, Apidae)

Authors: Dai, PL; Jia, HR; Jack, CJ; Geng, LL; Liu, F; Hou, CS; Diao, QY; Ellis, JD

Author Full Names: Dai, Ping-Li; Jia, Hui-Ru; Jack, Cameron J.; Geng, Li-Li; Liu, Feng; Hou, Chun-Sheng; Diao, Qing-Yun; Ellis, James D.

Source: JOURNAL OF ECONOMIC ENTOMOLOGY, 109 (6):2259-2263;
[10.1093/jee/tow204](https://doi.org/10.1093/jee/tow204) DEC 2016

Language: English

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

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IDS Number: EF4WU

Unique ID: WOS:000390333500002

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

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

*Order Full Text []

Title: SELECTION AND CHARACTERIZATION OF *Bacillus thuringiensis* ISOLATES WITH A HIGH INSECTICIDAL ACTIVITY AGAINST *Spodoptera frugiperda* (**Lepidoptera**: Noctuidae)

Authors: Cerqueira, FB; Alves, GB; Correa, RFT; Martins, ES; Barbosa, LCB; do Nascimento, IR; Monnerat, RG; Ribeiro, BM; Aguiar, RWD

Author Full Names: Cerqueira, Fernando Barnabe; Alves, Giselly Batista; Teixeira Correa, Roberto Franco; Martins, Erica Soares; Bertucci Barbosa, Luiz Carlos; do Nascimento, Ildon Rodrigues; Monnerat, Rose Gomes; Ribeiro, Bergmann Morais; de Souza Aguiar, Raimundo Wagner

Source: BIOSCIENCE JOURNAL, 32 (6):1522-1536; NOV-DEC 2016

Language: English

Abstract: *Spodoptera frugiperda* (SMITH, 1797) (Lepidoptera: Noctuidae) affects diverse crops of great economic interest, for instance, it can cause severe yield losses in maize, rice and sorghum. In this study, a selection and characterization of *Bacillus thuringiensis* (BERLINER, 1911) isolates with a high insecticidal activity against *S. frugiperda* was performed. Fifty-two crystal-forming *B. thuringiensis* isolates that were identified from 3384 *Bacillus*-like colonies were examined and screened by PCR for the presence cry genes (cry1, cry1Aa, cry1Ab, cry1Ac, cry1D, cry2 and cry2Ab). Four isolates that showed high toxicity towards *S. frugiperda* were shown to harbor cry2 genes. The crystals were analyzed by electron microscopy and showed bipyramidal and cuboidal shapes. Furthermore, these four isolates had lethal concentration (LC50) values of 44.5 ng/cm(2) (SUFT01), 74.0 ng/cm(2) (SUFT02), 89.0 ng/cm(2) (SUFT03) and 108 ng/cm(2) (SUFT 04) to neonate *S. frugiperda* larvae. An ultrastructural analysis of midgut cells from *S. frugiperda* incubated with the SUFT01 spore-crystal complex showed disruptions in cellular integrity and in the microvilli of the midgut columnar cells. The isolates characterized in this work are good candidates for the control of *S. frugiperda*, and could be used for the formulation of new bioinsecticides.

ISSN: 1981-3163

IDS Number: EG6BL

Unique ID: WOS:000391128700010

***Record 8 of 8.** Search terms matched: MAIZE(2); MON810(1); RESISTANT(1)

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

*Order Full Text []

Title: Body size inequality in ground beetle (Coleoptera: Carabidae) assemblages as a potential method to monitor crops

Authors: Di Grumo, D; Lovei, GL

Author Full Names: Di Grumo, Davide; Lovei, Gabor L.

Source: PERIODICUM BIOLOGORUM, 118 (3):223-230; [10.18054/pb.2016.118.3.3921](https://doi.org/10.18054/pb.2016.118.3.3921) SEP 2016

Language: English

Abstract: Background and Purpose: Despite the obligatory post-market environmental monitoring of genetically modified (GM) plants, there are no available methodological guidelines or standards. Our aim was to examine the suitability of carabid body size inequality as a method for environmental monitoring. Material and Methods: We used carabids collected by pitfall traps in both insect-resistant (IR) (expressing *Bacillus thuringiensis* toxin) and isogenic maize plots at Flakkebjerg (Denmark), within the framework of the AMIGA Project. Results: A total of 6339 carabids belonging to 38 species were captured and identified. The analysis detected differences in body size inequality between months, indicating the larger number of individuals of smaller-sized species later in the season, but no significant differences in mean body size were found between the assemblages in GM vs. isogenic maize plots. Conclusions: We conclude that body size inequality was sensitive to subtle changes in the structure of the carabid assemblages, and this method had the potential to detect the unanticipated environmental effects of GM plants.

ISSN: 0031-5362

IDS Number: EF8IH

Unique ID: WOS:000390572000009

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

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

*Order Full Text []

Title: How well will stacked transgenic pest/herbicide resistances delay pests from evolving resistance?

Authors: Gressel, J; Gassmann, AJ; Owen, MDK

Author Full Names: Gressel, Jonathan; Gassmann, Aaron J.; Owen, Micheal D. K.

Source: PEST MANAGEMENT SCIENCE, 73 (1):22-34; [10.1002/ps.4425](https://doi.org/10.1002/ps.4425) JAN 2017

Language: English

Abstract: Resistance has evolved to single transgenic traits engineered into crops for arthropod and herbicide resistance, but the more recently introduced pathogen resistances. Combining transgenes against the same target pest is being used as a solution to this problem. This solution will work if used pre-emptively, but where resistance has evolved to one member of a stack, the second gene in most cases. We propose and elaborate criteria that could be used to evaluate the value of stacked partners. Stacked partners must: target the same pest species; be in a tandem construct to preclude segregation; target same tissues; have similar tissue persistence; target pest species that are still susceptible to at least two stacked partners; must not be degraded in the same manner, and there should be a lack of cross-resistance to stacked transgenes. For herbicide resistance transgenes, both herbicides must be used and have the same persistence. If these criteria are met, management practices, resistance may be considerably delayed. (c) 2016 Society of Chemical Industry

ISSN: 1526-498X

eISSN: 1526-4998

IDS Number: EE2IT

Unique ID: WOS:000389408100004

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

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

*Order Full Text []

Title: Monitoring changes in the actinobacterial field communities present in the rhizosphere soil of a transgenic cotton

Authors: Zhang, YJ; Xie, M; Li, Q; Zhang, XL; Zhang, ZR

Author Full Names: Zhang, Yan-Jun; Xie, Ming; Li, Qian; Zhang, Xiao-Lin; Zhang, Zhao-Rong

Source: CROP PROTECTION, 91 1-7; [10.1016/j.cropro.2016.09.013](https://doi.org/10.1016/j.cropro.2016.09.013) JAN 2017

Language: English

Abstract: Transgenic cotton GK 12 producing Cry1Ab/Ac proteins can effectively control lepidopteran pests in the field, but that GK 12 has unintended side-effects on actinobacterial communities in the soil. Actinobacterial communities were analyzed by real-time PCR (qPCR) and denaturing gradient gel electrophoresis (DGGE) at different growth stages and under different conditions. Population sizes and community structures of Actino-bacteria were markedly affected by natural variation between cultivars. No significant differences were found in population sizes (excepting at budding in 2009), community structure of Actinobacteria (excepting at budding in 2010) between the GK 12 and its non-transgenic parent Simian 3, although there were differences between GK 12 and the conventional cotton DP 5415. Phylogenetic analysis of DGGE band sequences indicated that *Cetobacterium* sp. only occurred in the GK 12 and the Simian 3. The dominant Actinobacteria did not differ between the GK 12 and DP 5415. The overall impacts of the GK 12 on actinobacterial communities in the rhizosphere soil, based on qPCR and DGGE analysis, were stable in continuous years in northern China. (C) 2016 Elsevier Ltd. All rights reserved.

ISSN: 0261-2194

eISSN: 1873-6904

IDS Number: ED3YB

Unique ID: WOS:000388783300001

***Record 3 of 6.** Search terms matched: BORER(4); BORERS(2); BT(1); CORN(2); LEPIDOPTERA(4); MAIZE(1)

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

*Order Full Text []

Title: Susceptibility of Genetically Modified **Maize** Hybrids to Sugarcane **Borer**, *Diatraea saccharalis* (F.)(1), and

Authors: Flores, M; Hernandez-Juarez, A; Aguirre, LA; Cerna, E; Landeros, J; Frias, GA; Ochoa, Y

Author Full Names: Flores, Mariano; Hernandez-Juarez, Agustin; Aguirre, Luis A.; Cerna, Ernesto; Landeros, Yisa

Source: SOUTHWESTERN ENTOMOLOGIST, 41 (4):991-997; DEC 2016

Language: English

Abstract: Use of genetically modified hybrids of maize, *Zea mays* L., is a pest management tool with special significance. The sugarcane borer, *Diatraea saccharalis* (F.) (Lepidoptera: Crambidae), becomes less responsive to conventional control methods. Two maize hybrids 'Agrisure (TM) 3000 GT' and 'Agrisure (R) Viptera (TM) 3111' were evaluated against stalk borer damage in maize hybrids with or without insecticide. During evaluation, few borers were found, especially during the first year (2015). Larval density was less in Agrisure (TM) 3000 GT and Agrisure (R) Viptera (TM) 3111 than in their conventional isolines. The pest and even treated conventional maize was damaged. Use of Agrisure (TM) 3000 GT and Agrisure (R) Viptera (TM) 3111 as a pest management tool to prevent damage by sugarcane borer in maize.

ISSN: 0147-1724

eISSN: 2162-2647

IDS Number: ED3FB

Unique ID: WOS:000388733700009

***Record 4 of 6.** Search terms matched: BT(1); MAIZE(1)

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

*Order Full Text []

Title: Do genetically modified plants affect adversely on soil microbial communities?

Authors: Guan, ZJ; Lu, SB; Huo, YL; Guan, ZP; Liu, BA; Wei, W

Author Full Names: Guan, Zheng-jun; Lu, Shun-bao; Huo, Yan-lin; Guan, Zheng-Ping; Liu, Biao; Wei, Wei

Source: AGRICULTURE ECOSYSTEMS & ENVIRONMENT, 235 289-305; [10.1016/j.agee.2016.10.026](https://doi.org/10.1016/j.agee.2016.10.026) NCI

Language: English

Abstract: With the increase in the number of commercial applications and larger cultivation areas of genetically modified (GM) plants, the impact of GM plants on soil microorganisms has become a controversial issue. The effects on the diversity and abundance of soil microorganisms are one of the main concerns in the evaluation of the biosafety risks of GM plants. So far, no definite conclusions have been drawn about whether GM plants affect soil microorganisms. In this review, we discuss the advances that have been made in recent years in the research into the effects of GM plants on soil microbial communities. It has been argued that foreign gene products that are released from the residue of GM plants may affect soil microbial communities. Moreover, foreign genes may change the genetic and functional properties of soil microorganisms. The advantages and disadvantages of various detection technologies from classical culture-dependent methods to modern molecular biology techniques are reviewed here. To accurately and comprehensively evaluate the effects of GM plants on microorganisms, more attention should be considered in the assessment of risks of GM plants for soil microorganisms (e.g., foreign proteins, marker genes, and other factors), as well as the problems and prospects related to biosafety assessment platforms for GM plants. (C) 2017 Elsevier B.V.

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eISSN: 1873-2305

IDS Number: EE0VJ

Unique ID: WOS:000389296700028

***Record 5 of 6.** Search terms matched: BORERS(1); BT(2); LEPIDOPTERA(1); MAIZE(6); OSTRINIA(1); F
YIELD(1)

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

*Order Full Text []

Title: Development of Bt Rice and **Bt Maize** in China and Their Efficacy in Target Pest Control

Authors: Liu, QS; Hallerman, E; Peng, YF; Li, YH

Author Full Names: Liu, Qingsong; Hallerman, Eric; Peng, Yufa; Li, Yunhe

Source: INTERNATIONAL JOURNAL OF MOLECULAR SCIENCES, 17 (10):[10.3390/ijms17101561](https://doi.org/10.3390/ijms17101561) OCT

Language: English

Abstract: Rice and maize are important cereal crops that serve as staple foods, feed, and industrial material in C production of both crops, among which insect pests are an important one. Lepidopteran pests cause enormous y to control these pests, China plays an active role in development and application of genetic engineering (GE) to maize lines expressing insecticidal proteins from the soil bacterium *Bacillus thuringiensis* (Bt) have been devel environmental release, field testing, and preproduction testing, and laboratory and field experiments have show lines developed in China exhibited effective control of major target lepidopteran pests on rice (*Chilo suppressal* *Cnaphalocrocis medinalis*) and maize (*Ostrinia furnacalis*), demonstrating bright prospects for application. How commercially planted through this writing in 2016. Challenges and perspectives for development and applicatio discussed. This article provides a general context for colleagues to learn about research and development of Bt future work in this field.

ISSN: 1422-0067

Article Number: 1561

IDS Number: EC0DO

Unique ID: WOS:000387768300043

***Record 6 of 6.** Search terms matched: CRY1AB(1); LEPIDOPTERA(2)

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

*Order Full Text []

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

Authors: Shera, PS; Arora, R

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

Source: PHYTOPARASITICA, 44 (4):447-457; [10.1007/s12600-016-0540-3](https://doi.org/10.1007/s12600-016-0540-3) SEP 2016

Language: English

Abstract: The quality of food consumed by the insect is the key factor determining the utilization of food, thus development, and longevity. Genetically modified plants with genes from soil inhabiting spore forming bacteriu produces delta-endotoxin, which target the gut of insect, so food intake and its utilization are likely to be affecte of four events, viz. MRC 6301 Bt (*cry1Ac* gene), JKCH 1947 Bt (modified *cry1Ac* gene), NCEH 6R Bt (*cry1A*

II (cry1Ac and cry2Ab genes) were compared for nutritional indices of spotted bollworm, *Earias vittella* (Fabricius) on isogenic non-Bt genotypes. Various consumption and utilization indices, viz. consumption index (CI), relative growth rate (RGR), conversion of ingested food (ECI) and efficiency of conversion of digested food (ECD) were worked out. The Bt cotton significantly reduced CI, RGR, ECI and ECD of 4th instar *E. vittella* larvae as compared to their isogenic non-Bt cotton bolls of 90, 120 and 150 days crop age. Further, the Bollgard II genotype MRC 7017 BG II was found to be more superior than other Bt cotton values for all the above given indices. Despite the fact that, the differences between Bt and their isogenic non-Bt cotton of the crop but still Bt cotton hybrids were significantly inferior as insect food as compared to the non-Bt ones of the crop. The amount of Cry1Ac toxin in squares and bolls of Bt cotton had a significant negative correlation with food consumption of *E. vittella* larvae. The studies thus indicated that Bt toxin has a substantial impact on the nutritional performance of

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IDS Number: ED3DJ

Unique ID: WOS:000388729200003

***Record 1 of 11.** Search terms matched: BT(4); CORN(7); CRY1AB(5); LEPIDOPTERA(1); MAIZE(1); MON810(1)

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

*Order Full Text []

Title: Responses of the cutworm *Spodoptera litura* (**Lepidoptera: Noctuidae**) to two **Bt corn** hybrids expressing

Authors: Shu, YH; Du, Y; Chen, J; Wei, JX; Wang, JW

Author Full Names: Shu Yinghua; Du Yan; Chen Jin; Wei Jiayi; Wang Jianwu

Source: SCIENTIFIC REPORTS, 7 [10.1038/srep41577](https://doi.org/10.1038/srep41577) FEB 10 2017

Language: English

Abstract: To examine the responses of the secondary lepidopteran pest *Spodoptera litura* to two *Bacillus thuringiensis* (*Bt*11), 5422CBCL (MON810)] expressing Cry1Ab, larval bioassays with Cry1Ab toxin, corn leaves or kernels were conducted. The results showed that larvae displayed a similar performance when fed kernels, but not leaves of 5422CBCL or isogenic non-Bt corn (5422). Significantly higher Cry1Ab amounts were detected in larvae fed leaves than kernels of 5422CBCL. Molecular weights of protein band in plants (72 and 90 kDa for 5422Bt1 and 5422CBCL, respectively), gut contents and histology indicated that larvae had lower ingestion, higher degradation and excretion of Cry1Ab when fed kernels not leaves of 5422CBCL. Levels of cadherin-like receptors and alkaline phosphatase transcripts were detected in larvae fed leaves than kernels of 5422CBCL. Superoxide dismutase and glutathione-S-transferase activities in larvae fed 5422Bt1 leaves were significantly higher than those of 5422CBCL. Therefore, *S. litura* had low susceptibility to 5422Bt1 and 5422CBCL when larvae fed kernels not leaves of Bt cotton. 5422CBCL had much stronger tolerance to 5422CBCL than 5422Bt1.

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Article Number: 41577

IDS Number: EK1AO

Unique ID: WOS:000393658400001

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

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

*Order Full Text []

Title: Variation among conventional cultivars could be used as a criterion for environmental safety assessment of Bt rice on nontarget arthropods

Authors: Wang, F; Dang, C; Chang, XF; Tian, J; Lu, ZB; Chen, Y; Ye, GY

Author Full Names: Wang, Fang; Dang, Cong; Chang, Xuefei; Tian, Junce; Lu, Zengbin; Chen, Yang; Ye, Gongyin

Source: SCIENTIFIC REPORTS, 7 [10.1038/srep41918](https://doi.org/10.1038/srep41918) FEB 7 2017

Language: English

Abstract: The current difficulty facing risk evaluations of *Bacillus thuringiensis* (Bt) crops on nontarget arthropods (NTAs) is the lack of criteria for determining what represents unacceptable risk. In this study, we investigated the biological parameters in the laboratory and field population abundance of *Nilaparvata lugens* (Hemiptera: Delphacidae) on two Bt rice lines and the non-Bt parent, together with 14 other conventional rice cultivars. Significant differences were found in nymphal duration and fecundity of *N. lugens* fed on Bt rice KMD2, as well as field population density on 12 October, compared with non-Bt parent. However, compared with the variation among conventional rice cultivars, the variation of each parameter between Bt rice and the non-Bt parent was much smaller, which can be easily seen from low-high bar graphs and also the coefficient of variation value (C.V). The variation among conventional cultivars is proposed to be used as a criterion for the safety assessment of Bt rice on NTAs, particularly when statistically significant differences in several parameters are found between Bt rice and its non-Bt parent. Coefficient of variation is suggested as a promising parameter for ecological risk judgement of IRGM rice on NTAs.

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Article Number: 41918

IDS Number: EJ8FM

Unique ID: WOS:000393460700001

PubMed ID: 28167821

***Record 3 of 11.** Search terms matched: MAIZE(2); MON810(1)

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

*Order Full Text []

Title: Semi-Quantification of GM **Maize** Using Ready-To-Use RTi-PCR Plates

Authors: Gatto, F; Bassani, N; Rosa, SF; Lievens, A; Brustio, R; Kreysa, J; Querci, M

Author Full Names: Gatto, Francesco; Bassani, Niccolo; Rosa, Sabrina Francesca; Lievens, Antoon; Brustio, Roberta; Kreysa, Joachim; Querci, Maddalena

Source: FOOD ANALYTICAL METHODS, 10 (2):549-558; [10.1007/s12161-016-0609-0](https://doi.org/10.1007/s12161-016-0609-0) FEB 2017

Language: English

Abstract: European Union (EU) legislation foresees that food and feed are labelled for their genetically modified organism (GMO) content when the ingredients contain authorised GMOs in a proportion higher than 0.9 %. Non-authorised GMOs are not allowed on the EU market. Exception is made for feed materials containing traces of GM events lawfully placed on the market in non-EU countries and for which an authorisation is pending in the EU or expired: in these cases, a minimum required performance limit (MRPL) of 0.1 % is applied. Considering that the number of GMOs placed on the EU market is constantly growing, laboratories need to expand their capacity accordingly to be able to identify and, if necessary, quantify any GM material. To this purpose, our laboratory had previously developed a multi-target ready-to-use

system, also known as a pre-spotted plate (PSP), which allows the qualitative detection of up to 44 GM events in one single real-time (RTi) PCR experiment. Should any event be detected, the laboratory would proceed with its quantification. This study evaluates the possibility to use the data generated by the PSP system in a semi-quantitative manner, allowing a categorisation of the GM quantity in the sample. Delta Cq values were calculated and modelled via linear regression to estimate limits indicating whether the GM content is (1) above, (2) below or (3) near a defined quantity and thus requires further quantification. Identifying the GM events present in a sample and simultaneously discriminating whether it needs or not further quantification would offer to testing laboratories a valuable gain in time and resources. Six maize GM events frequently found in food and feed were selected for this evaluation (Bt11, MON810, MON88017, MON89034, NK603 and TC1507). The feasibility of the approach was successfully verified in-house using spiked and proficiency test samples.

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IDS Number: EI3HC

Unique ID: WOS:000392379600030

***Record 4 of 11.** Search terms matched: CORN(1); CRY1AB(1); MAIZE(1); RESISTANT(1)

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

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

Title: Establishment of a sensitive time-resolved fluoroimmunoassay for detection of *Bacillus thuringiensis* Cry1Ie toxin based nanobody from a phage display library

Authors: Xu, CX; Liu, XQ; Zhang, CZ; Zhang, X; Zhong, JF; Liu, Y; Hu, XD; Lin, MM; Liu, XJ

Author Full Names: Xu, Chongxin; Liu, Xiaoqin; Zhang, Cunzheng; Zhang, Xiao; Zhong, Jianfeng; Liu, Yuan; Hu, Xiaodan; Lin, Manman; Liu, Xianjin

Source: ANALYTICAL BIOCHEMISTRY, 518 53-59; [10.1016/j.ab.2016.11.006](https://doi.org/10.1016/j.ab.2016.11.006) FEB 1 2017

Language: English

Abstract: Cry1Ie toxin was an insect-resistant protein used in genetically modified crops (GMC). In this study, a large human VH gene nanobodies phage displayed library was employed to select anti-Cry1Ie toxin antibody by affinity panning. After 5 rounds of panning, total 12 positive monoclonal phage particles were obtained. One of the identified positive phage nanobody was expressed in *E.coli* BL21 and the purified protein was indicated as a molecular mass of approximately 20 kDa by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE). Then a sensitive indirect competitive time-resolved fluoroimmunoassay (IC-TRFIA) was established for detection of Cry1Ie toxin by the purified protein. The working range of detection for Cry1Ie toxin standards in the IC-TRFIA were 0.08-6.44 ng mL⁻¹ and the medium inhibition of control (IC₅₀) was 0.73 ng mL⁻¹. It showed a weak cross-reactivity with Cry1Ab toxin (at 5.6%), but did not recognize Cry1B, Cry1C, Cry1F, and Cry2A toxins (were <0.1%). The average recoveries of Cry1Ie toxin from respectively spiked in rice, corn and soil samples were in the range of 83.5%-96.6% and with a coefficient of variation (CV) among 2.0%-8.6%. These results showed the IC-TRFIA was promising for detection of Cry1Ie toxin in agricultural and environmental samples. (C) 2016 Elsevier Inc. All rights reserved.

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IDS Number: EI4JX

Unique ID: WOS:000392461000007

PubMed ID: 27838242

***Record 5 of 11.** Search terms matched: BT(1); CORN(1); MAIZE(3)

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

*Order Full Text []

Title: No effect of Bt Cry1Ie toxin on bacterial diversity in the midgut of the Chinese honey bees, *Apis cerana cerana* (Hymenoptera, Apidae)

Authors: Jia, HR; Dai, PL; Geng, LL; Jack, CJ; Li, YH; Wu, YY; Diao, QY; Ellis, JD

Author Full Names: Jia, Hui-Ru; Dai, Ping-Li; Geng, Li-Li; Jack, Cameron J.; Li, Yun-He; Wu, Yan-Yan; Diao, Qing-Yun; Ellis, James D.

Source: Scientific Reports, 7 [10.1038/srep41688](https://doi.org/10.1038/srep41688) JAN 31 2017

Language: English

Abstract: Cry1Ie protein derived from *Bacillus thuringiensis* (Bt) has been proposed as a promising candidate for the development of a new Bt-maize variety to control maize pests in China. We studied the response of the midgut bacterial community of *Apis cerana cerana* to Cry1Ie toxin under laboratory conditions. Newly emerged bees were fed one of the following treatments for 15 and 30 days: three concentrations of Cry1Ie toxin (20 ng/mL, 200 ng/mL, and 20 µg/mL) in sugar syrup, pure sugar syrup as a negative control and 48 ng/mL imidacloprid as a positive control. The relative abundance of 16S rRNA genes was measured by Quantitative Polymerase Chain Reaction and no apparent differences were found among treatments for any of these counts at any time point. Furthermore, the midgut bacterial structure and compositions were determined using high-throughput sequencing targeting the V3-V4 regions of the 16S rDNA. All core honey bee intestinal bacterial genera such as *Lactobacillus*, *Bifidobacterium*, *Snodgrassella*, and *Gilliamella* were detected, and no significant changes were found in the species diversity and richness for any bacterial taxa among treatments at different time points. These results suggest that Cry1Ie toxin may not affect gut bacterial communities of Chinese honey bees.

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Article Number: 41688

IDS Number: EJ3EC

Unique ID: WOS:000393094400001

PubMed ID: 28139751

***Record 6 of 11.** Search terms matched: CRY1AB(1)

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

*Order Full Text []

Title: Molecular Mechanisms of Interface Interactions between Nanomaterials and Proteins

Authors: Hou, JF; Yang, YL; Wang, C

Author Full Names: Hou Jing-Fei; Yang Yan-Lian; Wang Chen

Source: ACTA PHYSICO-CHIMICA SINICA, 33 (1):63-79; [10.3866/PKU.WHXB201608233](https://doi.org/10.3866/PKU.WHXB201608233)
JAN 15 2017

Language: Chinese

Abstract: Nanomaterials have excellent properties and have been used widely in chemical engineering, electronics, mechanics, environment, energy, aerospace, and many other fields in recent years. Besides, nanomaterials have attracted increasing attention in the biomedical field. The interactions between nanomaterials and protein molecules are not only significant to the basic science of the biomedical field, but also crucial for the evaluation of biomedical applications and biosafety of nanomaterials. The interfacial interactions between proteins and nanomaterials could induce a series of changes to the structures and functions of proteins, such as the transformation of protein conformations, and the modulation of aggregation states, which would influence the functions of the protein molecules. Interfacial interactions can also influence the physicochemical features of nanomaterials, including morphology, size, hydrophilicity/hydrophobicity, and surface charge density. In this review we explained the molecular level mechanisms for the interactions between nanomaterials and proteins at the interface based on the detection technologies, and discussed the changes in physical and chemical features, structures, and functions. We envision this review could be helpful for the deeper understanding of the complicated interactions between nanomaterials and proteins, and could be beneficial for promoting the healthy, safe, and sustainable development and application of nanomaterials in the biological and medical fields.

ISSN: 1000-6818

IDS Number: EI5TC

Unique ID: WOS:000392556700005

*Record 7 of 11. Search terms matched: CRY1AB(5)

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

*Order Full Text []

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

Authors: Portugal, L; Munoz-Garay, C; de Castro, DLM; Soberon, M; Bravo, A

Author Full Names: Portugal, Leivi; Munoz-Garay, Carlos; Martinez de Castro, Diana L.; Soberon, Mario; Bravo, Alejandra

Source: INSECT BIOCHEMISTRY AND MOLECULAR BIOLOGY, 80 21-31;
[10.1016/j.ibmb.2016.11.004](https://doi.org/10.1016/j.ibmb.2016.11.004) JAN 2017

Language: English

Abstract: *Bacillus thuringiensis* (Bt) bacteria produce Cry toxins that are able to kill insect pests. Different models explaining the mode of action of these toxins have been proposed. The pore formation model proposes that the toxin creates pores in the membrane of the larval midgut cells after interaction with different receptors such as cadherin, aminopeptidase N and alkaline phosphatase and that this pore formation activity is responsible for the toxicity of these proteins. The alternative model proposes that interaction with cadherin receptor triggers an intracellular cascade response involving protein G, adenylate cyclase (AC) and protein kinase A (PKA). In addition, it was shown that Cry toxins induce a defense response in the larvae involving the activation of mitogen-activated kinases such as MAPK p38 in different insect

orders. Here we analyzed the mechanism of action of Cry1Ab and Cry1Ac toxins and a collection of mutants from these toxins in the insect cell line CF1 from *Choristoneura fumiferana*, that is naturally sensitive to these toxins. Our results show that both toxins induced permeability of K⁺ ions into the cells. The initial response after intoxication with Cry1Ab and Cry1Ac toxins involves the activation of a defense response that involves the phosphorylation of MAPK p38. Analysis of activation of PRA and AC activities indicated that the signal transduction involving PKA, AC and cAMP was not activated during Cry1Ab or Cry1Ac intoxication. In contrast we show that Cry1Ab and Cry1Ac activate apoptosis. These data indicate that Cry toxins can induce an apoptotic death response not related with AC/PKA activation. Since Cry1Ab and Cry1Ac toxins affected K⁺ ion permeability into the cells, and that mutant toxins affected in pore formation are not toxic to CF1, we propose that pore formation activity of the toxins is responsible of triggering cell death response in CF1 cells. (C) 2016 Elsevier Ltd. All rights reserved.

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eISSN: 1879-0240

IDS Number: EI5TN

Unique ID: WOS:000392557800003

PubMed ID: 27867074

***Record 8 of 11.** Search terms matched: BORER(2); BT(6); CORN(8); OSTRINIA(2); PROTECT(1); RESISTANT(2)

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

*Order Full Text []

Title: Evaluation of **Bt Corn** with Pyramided Genes on Efficacy and Insect Resistance Management for the Asian **Corn Borer** in China

Authors: Jiang, F; Zhang, TT; Bai, SX; Wang, ZY; He, KL

Author Full Names: Jiang, Fan; Zhang, Tiantao; Bai, Shuxiong; Wang, Zhenying; He, Kanglai

Source: PLoS One, 11 (12):[10.1371/journal.pone.0168442](https://doi.org/10.1371/journal.pone.0168442) DEC 22 2016

Language: English

Abstract: A Bt corn hybrid (Acle) with two Bt genes (cry1 le and cry1 Ac) was derived by breeding stack from line expressing Cry1 le and a line expressing Cry1 Ac. Efficacy of this pyramided Bt corn hybrid against the Asian corn borer (ACB), *Ostrinia furnacalis*, was evaluated. We conducted laboratory bioassays using susceptible and resistant ACB strains fed on artificial diet or fresh plant tissues. We also conducted field trials with artificial infestations of ACB neonates at the V6 and silk stages. The toxin -diet bioassay data indicated that mixtures of Cry1 Ac and Cry1 le proteins had synergistic insecticidal efficacy. The plant tissue bioassay data indicated that Bt corn hybrids expressing either a single toxin (Cry1 Ac or Cry1 le) or two toxins had high efficacy against susceptible ACB. Damage ratings in the field trials indicated that the Bt corn hybrids could effectively protect against 1st and the 2' generation ACB in China. The hybrid line with two Bt genes showed a higher efficacy against ACB larvae resistant to Cry1 Ac or Cry1 le than the hybrid containing one Bt gene, and the two gene hybrid would have increased potential for managing or delaying the evolution of ACB resistance to Bt corn plants.

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Article Number: e0168442

IDS Number: EI9QH

Unique ID: WOS:000392843200051

PubMed ID: 28006032

***Record 9 of 11.** Search terms matched: BT(1); CORN(5); MAIZE(6); RESISTANT(1); ZEA MAYS(1)

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

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

Title: Quantifying rates of random mating in western **corn** rootworm emerging from Cry3Bb1-expressing and refuge **maize** in field cages

Authors: Taylor, SV; Smith, SJ; Krupke, CH

Author Full Names: Taylor, Sally V.; Smith, Steven J.; Krupke, Christian H.

Source: ENTOMOLOGIA EXPERIMENTALIS ET APPLICATA, 161 (3):203-212;

[10.1111/eea.12513](https://doi.org/10.1111/eea.12513) DEC 2016

Language: English

Abstract: The western corn rootworm (WCR), *Diabrotica virgifera virgifera* LeConte (Coleoptera: Chrysomelidae), is the most significant pest of field maize, *Zea mays* L. (Poaceae), in the USA. Maize plants expressing Bt toxins targeting the corn rootworm complex have been widely adopted and are the primary insecticidal control measure for this pest in North America. Insect resistance management tactics using various refuge structures have been adopted to ensure Bt products will retain durability. An assumption of the refuge strategy is that males and females emerging from Bt and refuge plantings mate randomly; this has not been tested in the field. We conducted cage studies using field populations of WCR in Indiana, USA, to generate empirical field data on mating rates between beetles emerging from Cry3Bb1-expressing Bt and refuge maize plants. Two refuge configurations were tested; all refuge plants were labeled using the stable isotope N-15. This mark persists in adult beetles after eclosion, allowing for collection and analysis of isotopic ratios of all beetles. Additional data collected included adult emergence rates, timing and sex ratios for each of the treatments, and head capsule size and dry weights of beetles collected. Treatment had a significant effect on dry weight; mean dry weight decreased in Bt-only treatments. Fisher's exact test of proportions of mating pairs of refuge and Bt insects indicated that mating was not random in 20% strip refuges and 5% seed blend treatments. We found high percentages of beetles that fed on Bt-expressing plants as larvae, suggesting that mating between resistant beetles may not be rare even if random mating did occur.

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IDS Number: EH7JK

Unique ID: WOS:000391948800006

***Record 10 of 11.** Search terms matched: BT(1); CORN(3); LEPIDOPTERA(3); MAIZE(1); TOLERANT(1)

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

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

Title: Susceptibility of *Spodoptera frugiperda* (**Lepidoptera**: Noctuidae) field populations to the Cry1F *Bacillus thuringiensis* insecticidal protein

Authors: Da Silva, KF; Spencer, TA; Crespo, ALB; Siegfried, BD

Author Full Names: Da Silva, Karen F.; Spencer, Terence A.; Crespo, Andre L. B.; Siegfried, Blair D.

Source: FLORIDA ENTOMOLOGIST, 99 (4):629-633; DEC 2016

Language: English

Abstract: The fall armyworm, *Spodoptera frugiperda* (Smith & Abbot) (Lepidoptera: Noctuidae), is a polyphagous insect pest affecting multiple crops. Fall armyworm in corn is managed with insecticides and corn hybrids expressing insecticidal proteins derived from *Bacillus thuringiensis* Berliner (Bt). The early detection of insect resistance is important for making appropriate management decisions and for implementing integrated pest management and insect resistance management recommendations. The objective of this study was to estimate susceptibility of fall armyworm populations to the Cry1F Bt insecticidal protein, emphasizing collections from locations where fall armyworm overwinters in the U.S. Fall armyworm neonates were exposed to artificial diet treated with increasing Cry1F concentrations, and mortality and growth inhibition were evaluated after 7 d. Differences in Cry1F susceptibility between the most susceptible and the most tolerant field populations were 2- and 6-fold for 2012 and 2013, respectively. These results are consistent with other susceptibility studies of Bt toxicity in other species although reduced susceptibility in one population collected from Florida may suggest resistance development.

ISSN: 0015-4040

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IDS Number: EH1KO

Unique ID: WOS:000391525700007

***Record 11 of 11.** Search terms matched: BORER(1); BT(7); CORN(1); CRY1AB(1); MAIZE(15)

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

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

Title: Effects of transgenic cry1Ie **maize** on non-lepidopteran pest abundance, diversity and community composition

Authors: Guo, JF; He, KL; Bai, SX; Zhang, TT; Liu, YJ; Wang, FX; Wang, ZY

Author Full Names: Guo, Jingfei; He, Kanglai; Bai, Shuxiong; Zhang, Tiantao; Liu, Yunjun; Wang, Fuxin; Wang, Zhenying

Source: TRANSGENIC RESEARCH, 25 (6):761-772; [10.1007/s11248-016-9968-y](https://doi.org/10.1007/s11248-016-9968-y) DEC 2016

Language: English

Abstract: Non-lepidopteran pests are exposed to, and may be influenced by, Bt toxins when feeding on Bt maize that express insecticidal Cry proteins derived from *Bacillus thuringiensis* (Bt). In order to assess the potential effects of transgenic cry1Ie maize on nonlepidopteran pest

species and ecological communities, a 2-year field study was conducted to compare the nonlepidopteran pest abundance, diversity and community composition between transgenic cry1Ie maize (Event IE09S034, Bt maize) and its near isoline (Zong 31, non-Bt maize) by whole plant inspections. Results showed that Bt maize had no effects on non-lepidopteran pest abundance and diversity (ShannonWiener diversity index, Simpson's diversity index, species richness, and Pielou's index). There was a significant effect of year and sampling time on those indices analyzed. Redundancy analysis indicated maize type, sampling time and year totally explained 20.43 % of the variance in the non-lepidopteran pest community composition, but no association was presented between maize type (Bt maize and non-Bt maize) and the variance. Nonmetric multidimensional scaling analysis showed that sampling time and year, rather than maize type had close relationship with the non-lepidopteran pest community composition. These results corroborated the hypothesis that, at least in the short-term, the transgenic cry1Ie maize had negligible effects on the non-lepidopteran pest abundance, diversity and community composition.

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eISSN: 1573-9368

IDS Number: EJ5AQ

Unique ID: WOS:000393229300001

PubMed ID: 27344564

***Record 1 of 8.** Search terms matched: BT(3); LEPIDOPTERA(1); MAIZE(12); RESISTANT(1)

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

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

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

Authors: Bernardi, D; Bernardi, O; Horikoshi, RJ; Salmeron, E; Okuma, DM; Farias, JR; do Nascimento, ARB; Omoto, C

Author Full Names: Bernardi, Daniel; Bernardi, Oderlei; Horikoshi, Renato J.; Salmeron, Eloisa; Okuma, Daniela M.; Farias, Juliano R.; do Nascimento, Antonio R. B.; Omoto, Celso

Source: CROP PROTECTION, 94 64-68; [10.1016/j.cropro.2016.11.026](https://doi.org/10.1016/j.cropro.2016.11.026) APR 2017

Language: English

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

adult period, 9% reduction in the survival rate until adult stage, and similar to 35% lower reproductive rate than SS and heterozygous strains. In summary, our results showed that the resistance of FAW to MON 89034 x TC1507 x NK603 maize is functionally recessive and associated with relevant fitness costs. Therefore, the adoption of refuge areas as a resistance management strategy can prolong the lifetime of MON 89034 x TC1507 x NK603 maize in Brazil. (C) 2016 Elsevier Ltd. All rights reserved.

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eISSN: 1873-6904

IDS Number: EK1XA

Unique ID: WOS:000393719900009

***Record 2 of 8.** Search terms matched: BT(1); CRY1AB(7); MAIZE(1)

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

*Order Full Text []

Title: A Novel Impedimetric Microfluidic Analysis System for Transgenic Protein **Cry1Ab** Detection

Authors: Jin, SR; Ye, ZZ; Wang, YX; Ying, YB

Author Full Names: Jin, Shunru; Ye, Zunzhong; Wang, Yixian; Ying, Yibin

Source: SCIENTIFIC REPORTS, 7 [10.1038/srep43175](https://doi.org/10.1038/srep43175) MAR 2 2017

Language: English

Abstract: Impedimetric analysis method is an important tool for food safety detection. In this work, a novel impedimetric microfluidic analysis system consisted of a printed gold electrode chip and a microfluidic flow cell was developed for sensitive and selective detection of transgenic protein Cry1Ab. AntiCry1Ab aptamer coated magnetic beads were used to recognize transgenic protein Cry1Ab and form Cry1Ab-aptamer modified magnetic beads. After separation, the obtained Cry1Ab-aptamer modified magnetic beads were dissolved in 0.01 M mannitol and followed by injection into the microfluidic flow cell for impedimetric measurement. At the frequency of 358.3 Hz, the impedance signal shows a good linearity with the concentrations of Cry1Ab protein at a range from 0 to 0.2 nM, and the detection limit is 0.015 nM. The results demonstrate that the impedimetric microfluidic analysis system provides an alternative way to enable sensitive, rapid and specific detection of transgenic protein Cry1Ab.

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IDS Number: EM5RK

Unique ID: WOS:000395369900001

PubMed ID: 28251986

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

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

*Order Full Text []

Title: Fall armyworm migration across the Lesser Antilles and the potential for genetic exchanges between North and South American populations

Authors: Nagoshi, RN; Fleischer, S; Meagher, RL; Hay-Roe, M; Khan, A; Murua, MG; Silvie, P; Vergara, C; Westbrook, J

Author Full Names: Nagoshi, Rodney N.; Fleischer, Shelby; Meagher, Robert L.; Hay-Roe, Mirian; Khan, Ayub; Murua, M. Gabriela; Silvie, Pierre; Vergara, Clorinda; Westbrook, John

Source: PLOS ONE, 12 (2):[10.1371/journal.pone.0171743](https://doi.org/10.1371/journal.pone.0171743) FEB 6 2017

Language: English

Abstract: The fall armyworm, *Spodoptera frugiperda* (J.E. Smith)(Lepidoptera: Noctuidae), is an important agricultural pest of the Western Hemisphere noted for its broad host range, long distance flight capabilities, and a propensity to develop resistance to pesticides that includes a subset of those used in genetically modified corn varieties. These characteristics exacerbate the threat fall armyworm poses to agriculture, with the potential that a resistance trait arising in one geographical location could rapidly disseminate throughout the hemisphere. A region of particular concern is the Caribbean, where a line of islands that extends from Florida to Venezuela provides a potential migratory pathway between populations from North and South America that could allow for consistent and substantial genetic interactions. In this study, surveys of populations from Peru, Bolivia, Paraguay, and Trinidad & Tobago expand on previous work in South America that indicates a generally homogeneous population with respect to haplotype markers. This population differs from that found in most of the Lesser Antilles where a combination of genetic and meteorological observations is described that indicate fall armyworm migration from Puerto Rico to as far south as Barbados, but does not support significant incursion into Trinidad & Tobago and South America. Air transport projections demonstrate that the wind patterns in the Caribbean region are not conducive to consistent flight along the north-south orientation of the Lesser Antilles, supporting the conclusion that such migration is minor and sporadic, providing few opportunities for genetic exchanges. The implications of these findings on the dissemination of deleterious traits between the two Western Hemisphere continents are discussed.

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IDS Number: EK1QH

Unique ID: WOS:000393700100069

PubMed ID: 28166292

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

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

*Order Full Text []

Title: Minnesota field population of western **corn** rootworm (Coleoptera: Chrysomelidae) shows incomplete resistance to Cry34Ab1/Cry35Ab1 and Cry3Bb1

Authors: Ludwick, DC; Meihls, LN; Ostlie, KR; Potter, BD; French, L; Hibbard, BE

Author Full Names: Ludwick, D. C.; Meihls, L. N.; Ostlie, K. R.; Potter, B. D.; French, L.; Hibbard, B. E.

Source: JOURNAL OF APPLIED ENTOMOLOGY, 141 (1-2):28-40; [10.1111/jen.12377](https://doi.org/10.1111/jen.12377) FEB 2017

Language: English

Abstract: In the United States of America, the western corn rootworm, *Diabrotica virgifera virgifera* LeConte (Coleoptera: Chrysomelidae), is commonly managed with transgenic corn (*Zea mays* L.) expressing insecticidal proteins from the bacteria *Bacillus thuringiensis* Berliner (Bt). Colonies of this pest have been selected in the laboratory on each commercially available transformation event and several resistant field populations have also been identified; some field populations are also resistant. In this study, progeny of a western corn rootworm population collected from a Minnesota corn field planted to SmartStax (R) corn were evaluated for resistance to corn hybrids expressing Cry3Bb1 (event MON88017) or Cry34/35Ab1 (event DAS-59122-7) and to the individual constituent proteins in diet-overlay bioassays. Results from these assays suggest that this population is resistant to Cry3Bb1 and is incompletely resistant to Cry34/35Ab1. In diet toxicity assays, larvae of the Minnesota (MN) population had resistance ratios of 4.71 and >13.22 for Cry34/35Ab1 and Cry3Bb1 proteins, respectively, compared with the control colonies. In all on-plant assays, the relative survival of the MN population on the DAS-59122-7 and MON88017 hybrids was significantly greater than the control colonies. Larvae of the MN population had inhibited development when reared on DAS-59122-7 compared with larvae reared on the non-Bt hybrid, indicating resistance was incomplete. Overall, these results document resistance to Cry3Bb1 and an incomplete resistance to Cry34/35Ab1 in a population of WCR from a SmartStax (R) performance problem field.

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eISSN: 1439-0418

IDS Number: EK4FO

Unique ID: WOS:000393882700004

***Record 5 of 8.** Search terms matched: BORER(2); BT(2); CORN(3); LEPIDOPTERA(2); MAIZE(6); OSTRINIA(2); RESISTANT(4)

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

*Order Full Text []

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

Authors: Petzold-Maxwell, JL; Siegfried, BD; Hellmich, RL; Abel, CA; Coates, BS; Spencer, TA; Horikoshi, RJ; Gassmann, AJ

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

Source: JOURNAL OF APPLIED ENTOMOLOGY, 141 (1-2):67-79; [10.1111/jen.12356](https://doi.org/10.1111/jen.12356) FEB 2017

Language: English

Abstract: Crops producing insecticidal toxins derived from the bacterium *Bacillus thuringiensis* (Bt) are widely planted to manage insect pests. Bt crops can provide an effective tool for pest management; however, the evolution of Bt resistance can diminish this benefit. The European corn borer, *Ostrinia nubilalis* Hubner, is a significant pest of maize and is widely managed with Bt maize in the Midwest of the United States. When Bt crops are grown in conjunction with

non-Bt refuges, fitness costs of Bt resistance can delay the evolution of resistance. Importantly, fitness costs often vary with ecological factors, including host-plant genotype and diapause. In this study, we examined fitness costs associated with Cry1F resistance in *O. nubilalis* when insects were reared on three maize lines. Fitness costs were tested in two experiments. One experiment assessed the fitness costs when Cry1F-resistant and Cry1F-susceptible insects were reared on plants as larvae and experienced diapause. The second experiment tested resistant, susceptible and F1 heterozygotes that were reared on plants but did not experience diapause. Despite some evidence of greater adult longevity for Cry1F-resistant insects, these insects produced fewer fertile eggs than Cry1F-susceptible insects, and this occurred independent of diapause. Reduced fecundity was not detected among heterozygous individuals, which indicated that this fitness cost was recessive. Additionally, maize lines did not affect the magnitude of this fitness cost. The lower fitness of Cry1F-resistant *O. nubilalis* may contribute to the maintenance of Cry1F susceptibility in field populations more than a decade after Cry1F maize was commercialized.

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eISSN: 1439-0418

IDS Number: EK4FO

Unique ID: WOS:000393882700008

***Record 6 of 8.** Search terms matched: BT(3); CORN(3); MAIZE(7); PROTECTION(1); RESISTANT(3); ZEA MAYS(1)

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

*Order Full Text []

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

Authors: Schrader, PM; Estes, RE; Tinsley, NA; Gassmann, AJ; Gray, ME

Author Full Names: Schrader, P. M.; Estes, R. E.; Tinsley, N. A.; Gassmann, A. J.; Gray, M. E.

Source: JOURNAL OF APPLIED ENTOMOLOGY, 141 (1-2):41-52; [10.1111/jen.12329](https://doi.org/10.1111/jen.12329) FEB 2017

Language: English

Abstract: The transgenic maize (*Zea mays* L.) event MON 88017 produces the *Bacillus thuringiensis* Berliner (Bt) toxin Cry3Bb1 to provide protection from western corn rootworm (*Diabrotica virgifera virgifera* LeConte) larval feeding. In response to reports of reduced performance of Cry3Bb1-expressing maize at two locations in Illinois, we conducted a two-year experiment at these sites to characterize suspected resistance, as well as to evaluate root injury and adult emergence. Single-plant bioassays were performed on larvae from each population that was suspected to be resistant. Results indicate that these populations had reduced mortality on Cry3Bb1-expressing maize relative to susceptible control populations. No evidence of cross-resistance between Cry3Bb1 and Cry34/35Ab1 was documented for the Cry3Bb1-resistant populations. Field studies were conducted that included treatments with commercially available rootworm Bt hybrids and their corresponding non-Bt near-isolines. When compared with their near-isolines, larval root injury and adult emergence were typically reduced for hybrids expressing Cry34/35Ab1 either alone or in a pyramid. In many instances, larval root injury and

adult emergence were not significantly different for hybrids expressing mCry3A or Cry3Bb1 alone when compared with their non-Bt near-isolines. These findings suggest that Cry34/35Ab1-expressing Bt maize may represent a valuable option for maize growers where Cry3Bb1 resistance is either confirmed or suspected. Consistent trends in adult size (head capsule width and dry mass) for individuals recovered from emergence cages were not detected during either year of this experiment. Because of the global importance of transgenic crops for managing insect pests, these results suggest that improved decision-making for insect resistance management is needed to ensure the durability of Bt maize.

ISSN: 0931-2048

eISSN: 1439-0418

IDS Number: EK4FO

Unique ID: WOS:000393882700005

***Record 7 of 8.** Search terms matched: CRY1AB(4)

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

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

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

Authors: Wang, J; Peng, YD; Xiao, KF; Wei, BY; Hu, JL; Wang, Z; Song, QS; Zhou, XG

Author Full Names: Wang, Juan; Peng, Yuande; Xiao, Kaifu; Wei, Baoyang; Hu, Jilin; Wang, Zhi; Song, Qisheng; Zhou, Xuguo

Source: BMC BIOTECHNOLOGY, 17 [10.1186/s12896-016-0325-2](https://doi.org/10.1186/s12896-016-0325-2) JAN 18 2017

Language: English

Abstract: Background: *Bacillus thuringiensis* (Bt) toxin produced in Cry1-expressing genetically modified rice (Bt rice) is highly effective to control lepidopteran pests, which reduces the needs for synthetic insecticides. Non-target organisms can be exposed to Bt toxins through direct feeding or trophic interactions in the field. The wolf spider *Pardosa pseudoannulata*, one of the dominant predators in South China, plays a crucial role in the rice agroecosystem. In this study, we investigated transcriptome responses of the 5th instar spiders fed on preys maintained on Bt- and non-Bt rice. Results: Comparative transcriptome analysis resulted in 136 differentially expressed genes (DEGs) between spiderlings preying upon *N. lugens* fed on Bt- and non-Bt rice (Bt- and non-Bt spiderlings). Functional analysis indicated a potential impact of Bt toxin on the formation of new cuticles during molting. GO and KEGG enrichment analyses suggested that GO terms associated with chitin or cuticle, including "chitin binding", "chitin metabolic process", "chitin synthase activity", "cuticle chitin biosynthetic process", "cuticle hydrocarbon biosynthetic process", and "structural constituent of cuticle", and an array of amino acid metabolic pathways, including "alanine, aspartate and glutamate metabolism", "glycine, serine and threonine metabolism", "cysteine and methionine metabolism", "tyrosine metabolism", "phenylalanine metabolism and phenylalanine", and "tyrosine and tryptophan biosynthesis" were significantly influenced in response to Cry1Ab. Conclusions: The Cry1Ab may have a negative impact on the formation of new cuticles during molting, which is contributed to the delayed development of spiderlings. To validate these transcriptomic responses, further examination at the translational level will be warranted.

ISSN: 1472-6750

Article Number: 7

IDS Number: EK1TX

Unique ID: WOS:000393709800001

***Record 8 of 8.** Search terms matched: BORER(2); BT(2); CORN(1); CRY1AB(4); LEPIDOPTERA(3); MAIZE(5); MON810(1); MON 810(1); RESISTANT(4); ZEA MAYS(1)

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

*Order Full Text []

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

Authors: Yang, GQ; Niu, Y; Head, GP; Price, PA; Huang, FN

Author Full Names: Yang, Guoqing; Niu, Ying; Head, Graham P.; Price, Paula A.; Huang, Fangneng

Source: ENTOMOLOGIA EXPERIMENTALIS ET APPLICATA, 162 (1):51-59;

[10.1111/eea.12502](https://doi.org/10.1111/eea.12502) JAN 2017

Language: English

Abstract: A seed mix strategy has been used to provide refuge to susceptible insects for resistance management in planting transgenic maize expressing *Bacillus thuringiensis* Berliner (Bt) proteins. To determine whether larval movement in a seed mix planting creates favorable conditions for resistant heterozygotes of a target pest, performance of Cry1Ab-susceptible (SS) and-heterozygous resistant (RS) populations of the sugarcane borer, *Diatraea saccharalis* (Fabricius) (Lepidoptera: Crambidae), was evaluated in sequential feeding on non-Bt and Cry1Ab (event MON810) maize plant tissue. For each insect population, nine feeding sequences were employed. SS and RS feeding on non-Bt plants for their entire larval stages survived well and > 60% of the adult pairs produced viable eggs, with an average of 269 progeny per female, whereas none of the two populations on Bt maize plants survived to the pupal stage. SS larvae could not develop to adults if the larvae fed on non-Bt plants for ≤ 15 days and then moved to Bt plants. In contrast, 4.2-29.2% of RS larvae that fed on non-Bt plants for ≥ 9 days and then moved to Bt plants developed to adults, and 63.6% of pairs of these adults produced viable eggs, with an average of 185 progeny per female. For SS larvae that fed on Bt plants for 1 or 2 days and then moved to non-Bt plants, few larvae developed to adults with varied emergence times, whereas 28.1 and 13.5% RS larvae feeding on Bt plants for 1 and 2 days, respectively, successfully developed to adults; 43.8% of pairs of these adults produced viable eggs, with an average of 220 progeny per female. For the case of the single Bt gene maize plants (event MON 810), the results suggest that RS insects may have advantages in survival and reproduction over SS if RS larvae hatch and feed on Bt plants during the first 1 or 2 days and then move to non-Bt plants. This advantage is less for RS larvae that hatch and feed on non-Bt plants first and then move to Bt plants, unless the larval movement occurs in the later stages (e.g., fourth or fifth instars).

ISSN: 0013-8703

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IDS Number: EL7EL

Unique ID: WOS:000394783800007

***Record 1 of 21.** Search terms matched: BORER(3); BORERS(1); BT(1); CORN(2); LEPIDOPTERA(1); MAIZE(2); RESISTANT(2)

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

*Order Full Text []

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

Authors: Campagne, P; Capdevielle-Dulac, C; Pasquet, R; Cornell, SJ; Kruger, M; Silvain, JF; LeRu, B; Van den Berg, J

Author Full Names: Campagne, P.; Capdevielle-Dulac, C.; Pasquet, R.; Cornell, S. J.; Kruger, M.; Silvain, J-F; LeRu, B.; Van den Berg, J.

Source: HEREDITY, 118 (4):330-339; [10.1038/hdy.2016.104](https://doi.org/10.1038/hdy.2016.104) APR 2017

Language: English

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

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eISSN: 1365-2540

IDS Number: EN3IL

Unique ID: WOS:000395902100003

PubMed ID: 27782120

***Record 2 of 21.** Search terms matched: BT(1); MAIZE(2); ZEA-MAYS(1)

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

*Order Full Text []

Title: Assessing environmental impacts of genetically modified plants on non-target organisms: The relevance of in planta studies

Authors: Arpaia, S; Birch, ANE; Kiss, J; van Loon, JJA; Messean, A; Nuti, M; Perry, JN; Sweet, JB; Tebbe, CC

Author Full Names: Arpaia, Salvatore; Birch, A. Nicholas E.; Kiss, Jozsef; van Loon, Joop J. A.; Messean, Antoine; Nuti, Marco; Perry, Joe N.; Sweet, Jeremy B.; Tebbe, Christoph C.

Source: SCIENCE OF THE TOTAL ENVIRONMENT, 583 123-132;
[10.1016/j.scitotenv.2017.01.039](https://doi.org/10.1016/j.scitotenv.2017.01.039) APR 1 2017

Language: English

Abstract: In legal frameworks worldwide, genetically modified plants (GMPs) are subjected to pre-market environmental risk assessment (ERA) with the aim of identifying potential effects on the environment. In the European Union, the EFSA Guidance Document introduces the rationale that GMPs, as well as their newly produced metabolites, represent the potential stressor to be evaluated during ERA. As a consequence, during several phases of ERA for cultivation purposes, it is considered necessary to use whole plants or plant parts in experimental protocols. The importance of in planta studies as a strategy to address impacts of GMPs on non-target organisms is demonstrated, to evaluate both effects due to the intended modification in plant phenotype (e.g. expression of Cry proteins) and effects due to unintended modifications in plant phenotype resulting from the transformation process (e.g. due to somaclonal variations or pleiotropic effects). In planta tests are also necessary for GMPs in which newly expressed metabolites cannot easily be studied in vitro. This paper reviews the scientific literature supporting the choice of in planta studies as a fundamental tool in ERA of GMPs in cultivation dossiers; the evidence indicates they can realistically mimic the ecological relationships occurring in their receiving environments and provide important insights into the biology and sustainable management of GMPs. (C) 2017 Elsevier B.V. All rights reserved.

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IDS Number: EL3YK

Unique ID: WOS:000394556400014

PubMed ID: 28095991

***Record 3 of 21.** Search terms matched: BT(10); CORN(1); CRY1AB(2); MAIZE(11); MON810(1)

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

*Order Full Text []

Title: Effects of Cry1 Ab Bt maize straw return on bacterial community of earthworm *Eisenia fetida*

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

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

Source: CHEMOSPHERE, 173 1-13; [10.1016/j.chemosphere.2017.01.023](https://doi.org/10.1016/j.chemosphere.2017.01.023) APR 2017

Language: English

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

Bt maize straw return had significant effects on soil nutrients, especially for available nitrogen (N). The significant differences were shown in soil bacterial community between Bt and non-Bt maize treatments on the 75th and 90th d, which was closely correlated with soil available N, P and K rather than CryIAb protein. There was no statistically significant difference in the bacterial community of earthworm gut contents between Bt and non-Bt maize treatments. The significant differences in the bacterial community of earthworm casts were found among three maize varieties treatments, which were closely correlated with CryIAb protein and N levels. The differentiated bacterial species in earthworm casts mainly belonged to Proteobacteria, including *Brevundimonas*, *Caulobacter*, *Pseudomonas*, *Stenotrophomonas*, *Methylobacterium*, *Asticcacaulis* and *Achromobacter* etc., which were associated with the mineralization, metabolic process and degradation of plants residues. Therefore, Bt maize straw return caused changes in the bacterial community of *E. fetida* casts, which was possibly caused by the direct (CryIAb protein) and non-expected effects (N levels) of Bt maize straw. (C) 2017 Elsevier Ltd. All rights reserved.

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IDS Number: EM3KN

Unique ID: WOS:000395213700001

PubMed ID: 28104475

***Record 4 of 21.** Search terms matched: BT(4); LEPIDOPTERA(1); MAIZE(8)

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

*Order Full Text []

Title: Consumption of **Bt Maize** Pollen Containing CryI_{Ie} Does Not Negatively Affect *Propylea japonica* (Thunberg) (Coleoptera: Coccinellidae)

Authors: Li, Y; Liu, Y; Yin, X; Romeis, J; Song, X; Chen, X; Geng, L; Peng, Y; Li, Y

Author Full Names: Li, Yonghui; Liu, Yanmin; Yin, Xinming; Romeis, Joerg; Song, Xinyuan; Chen, Xiuping; Geng, Lili; Peng, Yufa; Li, Yunhe

Source: TOXINS, 9 (3):[10.3390/toxins9030108](https://doi.org/10.3390/toxins9030108) MAR 2017

Language: English

Abstract: *Propylea japonica* (Thunberg) (Coleoptera: Coccinellidae) are prevalent predators and pollen feeders in East Asian maize fields. They are therefore indirectly (via prey) and directly (via pollen) exposed to Cry proteins within Bt-transgenic maize fields. The effects of CryI_{Ie}-producing transgenic maize pollen on the fitness of *P. japonica* was assessed using two dietary-exposure experiments in the laboratory. In the first experiment, survival, larval developmental time, adult fresh weight, and fecundity did not differ between ladybirds consuming Bt or non-Bt maize pollen. In the second experiment, none of the tested lethal and sublethal parameters of *P. japonica* were negatively affected when fed a rapeseed pollen-based diet containing CryI_{Ie} protein at 200 g/g dry weight of diet. In contrast, the larval developmental time, adult fresh weight, and fecundity of *P. japonica* were significantly adversely affected when fed diet containing the positive control compound E-64. In both experiments, the bioactivity of the CryI_{Ie} protein in the food sources was confirmed by bioassays with a CryI_{Ie}-sensitive lepidopteran species. These results indicated that *P. japonica* are not affected by the consumption of CryI_{Ie}-expressing maize pollen and are not sensitive to

the Cry1Ie protein, suggesting that the growing of Bt maize expressing Cry1Ie protein will pose a negligible risk to *P. japonica*.

ISSN: 2072-6651

Article Number: 108

IDS Number: ER3UR

Unique ID: WOS:000398725400035

***Record 5 of 21.** Search terms matched: BORER(1); BT(15); CORN(1); CRY1AB(1); LEPIDOPTERA(2); MAIZE(16); MON810(3); RESISTANT(1)

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

*Order Full Text []

Title: Monitoring resistance to **Bt maize** in field populations of *Busseola fusca* (Fuller) (**Lepidoptera**: Noctuidae) from smallholder farms in the Eastern Cape Province of South Africa

Authors: Kotey, DA; Obi, A; Assefa, Y; Erasmus, A; Van den Berg, J

Author Full Names: Kotey, D. A.; Obi, A.; Assefa, Y.; Erasmus, A.; Van den Berg, J.

Source: AFRICAN ENTOMOLOGY, 25 (1):200-209; [10.4001/003.025.0200](#) MAR 2017

Language: English

Abstract: Post-release monitoring of transgenic Bt maize fields for resistant pest populations is an important activity that will contribute to early identification and mitigation of resistance evolution by target pests. An effective Bt maize pest resistance monitoring programme relies on well-established baseline susceptibility data. The target pest of Bt maize in South Africa, *Busseola fusca* (Fuller) (Lepidoptera: Noctuidae), has evolved resistance to Bt maize expressing Cry1Ab proteins, with numerous reports of resistance from the highveld region of the country. Although Bt maize has been cultivated in the Eastern Cape province since 2001, no data exist on the resistance status of field populations of *B. fusca* to Bt maize in this region. In view of this, *B. fusca* larvae were collected from fields in two Bt maize cultivating areas and a non-Bt maize cultivating area of the Eastern Cape for laboratory assays to determine the level of susceptibility of *B. fusca* to Bt maize. Rearing colonies of each population were established and neonate larvae from each population were used to infest non-Bt maize plants, and Bt maize of events MON810 and MON89034. All larvae maintained on MON89034 died within seven days of infestation. Survival of all *B. fusca* populations maintained on MON810 declined rapidly during the first seven days and was significantly ($P < 0.001$) lower than larval survival on non-Bt maize. Similarly, mass of surviving larvae of all populations on MON810 from the first two weeks to the 21st day was significantly ($P < 0.001$) lower than the mass of larvae on non-Bt maize. These results indicate that fieldcollected populations screened in this study are still susceptible to Bt maize.

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eISSN: 1026-4914

IDS Number: ER5KP

Unique ID: WOS:000398840900020

***Record 6 of 21.** Search terms matched: BT(1); CORN(5); LEPIDOPTERA(2); MAIZE(3); MON810(1)

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

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

Title: Attack and defense movements involved in the interaction of *Spodoptera frugiperda* and *Helicoverpa zea* (**Lepidoptera**: Noctuidae)

Authors: Bentivenha, JPF; Baldin, ELL; Montezano, DG; Hunt, TE; Paula-Moraes, SV

Author Full Names: Bentivenha, Jose P. F.; Baldin, Edson L. L.; Montezano, Debora G.; Hunt, Thomas E.; Paula-Moraes, Silvana V.

Source: JOURNAL OF PEST SCIENCE, 90 (2):433-445; [10.1007/s10340-016-0802-3](https://doi.org/10.1007/s10340-016-0802-3) MAR 2017

Language: English

Abstract: The fall armyworm, *Spodoptera frugiperda* (J. E. Smith) and the corn earworm, *Helicoverpa zea* (Boddie) are among the main pests of maize. Both species exhibit cannibalistic behavior and quite often share the same feeding guild in maize (maize ears), which can result in several interspecific and intraspecific interactions. Paired interaction scenarios of intraspecific and interspecific larvae were assessed in arenas in the presence and absence of food to characterize movements resulting from interactions of these insects. There was a difference in the frequency of behavioral movements in all the interactions, except for *S. frugiperda* in the presence of food. Head touching and recoiling were the predominant movements in most of the interaction scenarios. *Spodoptera frugiperda* exhibited a predominance of defensive movements when competing against *H. zea* in the same instars. Cannibalism and predation occurred frequently in interactions involving 6th instar of *H. zea* against opponents in 4th instar. Larvae of *H. zea* show a higher aggressive movement than *S. frugiperda*. The larvae of *S. frugiperda* take advantage during the interactions, although they present more defensive movements compared to *H. zea*. This study provides relevant information regarding the interaction of these species and intraguild interaction, which might influence the population dynamics and the competitive displacement of pest species that share the same ecological niche.

ISSN: 1612-4758

eISSN: 1612-4766

IDS Number: EM7SQ

Unique ID: WOS:000395513000003

***Record 7 of 21.** Search terms matched: CRY1AB(2); YIELD(3)

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

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

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

Authors: Jiang, Y; Ling, L; Zhang, LL; Domingo, A; Cai, ML; Li, CF; Zhan, M; Wang, JP; Cao, CG

Author Full Names: Jiang, Yang; Ling, Lin; Zhang, Lingli; Domingo, Abigail; Cai, Mingli; Li, Chengfang; Zhan, Ming; Wang, Jinping; Cao, Cougui

Source: ACTA PHYSIOLOGIAE PLANTARUM, 39 (3):[10.1007/s11738-017-2384-y](https://doi.org/10.1007/s11738-017-2384-y) MAR 2017

Language: English

Abstract: Transgenic *Bacillus thuringiensis* (Bt) rice have been reported to acquire effective resistance against the target pests; however, the insertion and expression of alien Bt genes may have some unintended effects on the growth characteristics of rice. A screen-house experiment was conducted and repeated twice to investigate the growth characteristics and Bt protein expressions in two Bt rice lines [MH63 (Cry2A*) and MH63 (Cry1Ab/Ac)], which had different Bt protein expression levels in leaves, under zero nitrogen (N0) and recommended nitrogen (NR) fertilizer applications. Compared to the counterpart MH63, MH63 (Cry2A*) under N0 experienced accelerated leaf senescence and a lower internal N use efficiency (IEN), resulting in a 23.2% decrease in grain yield and a lower accumulated biomass. These variations were revealed to be correlated to the higher ratio of the Bt protein content to the soluble protein content (BTC/SPC) with a maximum value of 4.3 parts per thousand in MH63 (Cry2A*) leaves in the late growth stage. Under NR, no differences in growth characteristics between MH63 (Cry2A*) and MH63 were found. The growth characteristics of MH63 (Cry1Ab/Ac), with a lower BTC/SPC in the late growth stage compared to MH63 (Cry2A*), were identical to those of MH63 under the two N applications. Results show that the transgenic Bt rice MH63 (Cry2A*), with a relatively higher Bt protein expression in the late growth stage, had an inferior adaptation to nitrogen deficiency compared to its non-Bt counterpart. And this inferior adaptation was found to be correlated with the higher BTC/SPC in MH63 (Cry2A*) leaves in the late growth stage.

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eISSN: 1861-1664

Article Number: 89

IDS Number: EN6KJ

Unique ID: WOS:000396112600024

***Record 8 of 21.** Search terms matched: CRY1AB(1)

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

*Order Full Text []

Title: Identification of medaka magnetoreceptor and cryptochromes

Authors: Wang, YZ; Chen, JB; Zhu, F; Hong, YH

Author Full Names: Wang, Yunzhi; Chen, Jianbin; Zhu, Feng; Hong, Yunhan

Source: SCIENCE CHINA-LIFE SCIENCES, 60 (3):271-278; [10.1007/s11427-016-0266-5](https://doi.org/10.1007/s11427-016-0266-5)
MAR 2017

Language: English

Abstract: Magnetoreception is a hallmark ability of animals for orientation and migration via sensing and utilizing geomagnetic fields. Magnetoreceptor (MagR) and cryptochromes (Cry) have recently been identified as the basis for magnetoreception in *Drosophila*. However, it has remained unknown whether MagR and Cry have conserved roles in diverse animals. Here we report the identification and expression of *magr* and *cry* genes in the fish medaka (*Oryzias latipes*). Cloning and sequencing identified a single *magr* gene, four *cry* genes and one *cry*-like gene in medaka. By sequence alignment, chromosomal synteny and gene structure analysis, medaka *cry2* and *magr* were found to be the orthologs of human *Cry2* and *Magr*, with *cry1aa* and *cry1ab* being coorthologs of human *Cry1*. Therefore, *magr* and *cry2* have remained as single copy genes, whereas *cry1* has undergone two rounds of gene duplication in medaka.

Interestingly, magr and cry genes were detected in various stages throughout embryogenesis and displayed ubiquitous expression in adult organs rather than specific or preferential expression in neural organs such as brain and eye. Importantly, magr knockdown by morpholino did not produce visible abnormality in developing embryos, pointing to the possibility of producing viable magr knockouts in medaka as a vertebrate model for magnet biology.

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IDS Number: EO7LB

Unique ID: WOS:000396871100006

PubMed ID: 27858334

***Record 9 of 21.** Search terms matched: CORN(1); CRY1AB(1)

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

*Order Full Text []

Title: AQUATIC FATE OF A DOUBLE-STRANDED RNA IN A SEDIMENT-WATER SYSTEM FOLLOWING AN OVER-WATER APPLICATION

Authors: Fischer, JR; Zapata, F; Dubelman, S; Mueller, GM; Uffman, JP; Jiang, CJ; Jensen, PD; Levine, SL

Author Full Names: Fischer, Joshua R.; Zapata, Fatima; Dubelman, Samuel; Mueller, Geoffrey M.; Uffman, Joshua P.; Jiang, Changjian; Jensen, Peter D.; Levine, Steven L.

Source: ENVIRONMENTAL TOXICOLOGY AND CHEMISTRY, 36 (3):727-734; [10.1002/etc.3585](https://doi.org/10.1002/etc.3585) MAR 2017

Language: English

Abstract: Determining the rate of biodegradation of double-stranded RNA (dsRNA) in the environment is an essential element of a comprehensive risk assessment of an RNA-based agricultural product. This information is used during problem formulation to define relevant routes and durations of environmental exposure for in planta-expressed dsRNA. Although exposure to biotechnology-derived crops expressing dsRNA traits in the aquatic environment is predicted to be minimal, little is known regarding the fate of dsRNA in these environments. To assess exposure to aquatic environments, a study was conducted to measure the rate of biodegradation of DvSnf7 dsRNA in aerobic water-sediment systems. Aquatic systems containing natural water and sediments that varied in physical and chemical characteristics were treated with dsRNA by applying DvSnf7 dsRNA directly to the water column. In the present study, DvSnf7 dsRNA dissipated rapidly from the water phase and was undetectable within 7 d as measured by QuantiGene (Affymetrix) and a sensitive insect bioassay in these diverse systems. Degradation kinetics estimated a half-life (time to 50% dissipation [DT50]) of less than 3 d and a time to 90% dissipation of approximately 4 d. Further analysis indicated that DvSnf7 dsRNA had DT50 values of less than 6 d in both sediment-free systems containing natural water and systems with only sediment. Taken together, the results of the present study indicate that dsRNA-based agricultural products rapidly degrade and consequently are unlikely to persist in aquatic environments. (C) 2016 SETAC

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IDS Number: EL5YX

Unique ID: WOS:000394698700006

PubMed ID: 27530554

***Record 10 of 21.** Search terms matched: CORN(2); MAIZE(1); MON810(1)

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

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

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

Authors: Castan, M; Ben Ali, SE; Hochegger, R; Ruppitsch, W; Haslberger, AG; Brandes, C

Author Full Names: Castan, Magali; Ben Ali, Sina-Elisabeth; Hochegger, Rupert; Ruppitsch, Werner; Haslberger, Alexander G.; Brandes, Christian

Source: EUROPEAN FOOD RESEARCH AND TECHNOLOGY, 243 (3):353-365;

[10.1007/s00217-016-2749-2](https://doi.org/10.1007/s00217-016-2749-2) MAR 2017

Language: English

Abstract: The examination of transgenic loci is an integral part of biosafety legislation in the European Union (EU). The EU directive 2001/18/EC requires any genetically modified (GM) event to be stable. Mutations in the nucleotide sequence of GM events must be avoided in the production and use of seeds. In the present work, an F1 and an F2 generation of the corn event NK603 were studied in stacked varieties (NK603 x MON810). The central aspect of this work was to utilize high-resolution melting analysis, real-time PCR, and Sanger sequencing for the examination of genetic stability of the entire construct of NK603 as well as in the regions flanking NK603. To perform such screening, it was necessary to develop specific PCR primers for the NK603 insert. Twenty-five specific primer pairs and PCR reactions were used to screen a total number of 340 samples. In addition to the screening, the NK603 zygosity was determined by a PCR-based testing method. Differences to the published patent sequence occurring in all samples were detected in two locations of the transgenic DNA sequence. These differences were also found in certified NK603 reference material.

ISSN: 1438-2377

eISSN: 1438-2385

IDS Number: EL2QA

Unique ID: WOS:000394463300001

***Record 11 of 21.** Search terms matched: CRY1AB(11); MAIZE(1)

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

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

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

Authors: Dong, S; Zhang, X; Liu, Y; Zhang, CZ; Xie, YJ; Zhong, JF; Xu, CX; Liu, XJ

Author Full Names: Dong, Sa; Zhang, Xiao; Liu, Yuan; Zhang, Cunzheng; Xie, Yajing; Zhong, Jianfeng; Xu, Chongxin; Liu, Xianjin

Source: ANALYTICAL AND BIOANALYTICAL CHEMISTRY, 409 (8):1985-1994; [10.1007/s00216-016-0146-0](https://doi.org/10.1007/s00216-016-0146-0) MAR 2017

Language: English

Abstract: Cry1Ab toxin is commonly expressed in genetically modified crops in order to control chewing pests. At present, the detection method with enzyme-linked immunosorbent assay (ELISA) based on monoclonal antibody cannot specifically detect Cry1Ab toxin for Cry1Ab's amino acid sequence and spatial structure are highly similar to Cry1Ac toxin. In this study, based on molecular design, a novel hapten polypeptide was synthesized and conjugated to keyhole limpet hemocyanin (KLH). Then, through animal immunization with this antigen, a monoclonal antibody named 2C12, showing high affinity to Cry1Ab and having no cross reaction with Cry1Ac, was produced. The equilibrium dissociation constant (K (D)) value of Cry1Ab toxin with MAb 2C12 was 1.947×10^{-8} M. Based on this specific monoclonal antibody, a sandwich enzyme-linked immunosorbent assay (DAS-ELISA) was developed for the specific determination of Cry1Ab toxin and the LOD and LOQ values were determined as 0.47 ± 0.11 and 2.43 ± 0.19 ng mL⁻¹, respectively. The average recoveries of Cry1Ab from spiked rice leaf and rice flour samples ranged from 75 to 115%, with coefficient of variation (CV) less than 8.6% within the quantitation range (2.5-100 ng mL⁻¹), showing good accuracy for the quantitative detection of Cry1Ab toxin in agricultural samples. In conclusion, this study provides a new approach for the production of high specific antibody and the newly developed DAS-ELISA is a useful method for Cry1Ab monitoring in agriculture products.

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IDS Number: EM1DE

Unique ID: WOS:000395057500003

PubMed ID: 28078413

***Record 12 of 21.** Search terms matched: BT(10); CRY1AB(4); LEPIDOPTERA(1); MAIZE(12); RESISTANT(1)

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

*Order Full Text []

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

Authors: Zhang, B; Yang, Y; Zhou, X; Shen, P; Peng, YF; Li, YH

Author Full Names: Zhang, Bing; Yang, Yan; Zhou, Xiang; Shen, Ping; Peng, Yufa; Li, Yunhe

Source: ENVIRONMENTAL POLLUTION, 222 94-100; [10.1016/j.envpol.2016.12.079](https://doi.org/10.1016/j.envpol.2016.12.079) MAR 2017

Language: English

Abstract: The common soil arthropod *Folsomia candida* can survive well when fed only maize pollen and thus may be exposed to insecticidal proteins by ingesting insect-resistant genetically engineered maize pollen containing *Bacillus thuringiensis* (Bt) proteins when being released

into the soil. Laboratory experiments were conducted to assess the potential effects of Cry1Ab/Cry2Aj-producing transgenic Bt maize (Shuangkang 12-5) pollen on *F. candida* fitness. Survival, development, and the reproduction were not significantly reduced when *F. candida* fed on Bt maize pollen rather than on non-Bt maize pollen, but these parameters were significantly reduced when *F. candida* fed on non-Bt maize pollen containing the protease inhibitor E-64 at 75 $\mu\text{g/g}$ pollen. The intrinsic rate of increase ($r(m)$) was not significantly reduced when *F. candida* fed on Bt maize pollen but was significantly reduced when *F. candida* fed on non-Bt maize pollen containing E-64. The activities of antioxidant-related enzymes in *F. candida* were not significantly affected when *F. candida* fed on Bt maize pollen but were significantly increased when *F. candida* fed on non-Bt pollen containing E-64. The results demonstrate that consumption of Bt maize pollen containing Cry1Ab/Cry2Aj has no lethal or sublethal effects on *F. candida*. (C) 2017 Elsevier Ltd. All rights reserved.

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IDS Number: EM5OJ

Unique ID: WOS:000395360900011

PubMed ID: 28082132

***Record 13 of 21.** Search terms matched: CRY1AB(1)

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

*Order Full Text []

Title: Effects of the consecutive cultivation and periodic residue incorporation of *Bacillus thuringiensis* (Bt) cotton on soil microbe-mediated enzymatic properties

Authors: Chen, ZH; Wei, K; Chen, LJ; Wu, ZJ; Luo, JY; Cui, JJ

Author Full Names: Chen, Zhenhua; Wei, Kai; Chen, Lijun; Wu, Zhijie; Luo, Junyu; Cui, Jinjie

Source: AGRICULTURE ECOSYSTEMS & ENVIRONMENT, 239 154-160;

[10.1016/j.agee.2017.01.017](https://doi.org/10.1016/j.agee.2017.01.017) FEB 15 2017

Language: English

Abstract: Risk assessments of insecticidal Cry proteins from *Bacillus thuringiensis* (Bt) cotton in soils have been mainly based on microcosm and short-term experiments. There is a lack of longer-term field results, especially when Bt-cotton residues are incorporated into the soil. In this study, we used a six-year field trial to evaluate how cultivation duration and Cry1Ac-inputted modes of Bt-cotton affect the persistence of Cry1Ac proteins and soil microbe-mediated enzymatic properties. The results showed that the persistence of Cry1Ac proteins increased with cultivation duration and periodic residue incorporation of the transgenic Bt-cotton variety ZM41. Moreover, temporal residue incorporation had a relatively larger contribution to the persistence of Cry1Ac proteins in the soil than their release in the growth period. Regardless of Bt-cotton cultivation or residue incorporation, soil microbial biomass was significantly suppressed. However, the dehydrogenase activity was significantly stimulated in Bt-cotton cultivation but suppressed in residue incorporation. The activities of beta-glucosidase, nitrate reductase, phosphomonoesterase and arylsulfatase were significantly stimulated in soils with Bt-cotton residue incorporation. Based on a structural equation model analysis, the change

in enzymatic activity of these four enzymes was attributed to both a direct effect from Cry1Ac proteins and an indirect effect via dehydrogenase. (C) 2017 Elsevier B.V. All rights reserved.

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IDS Number: EP7HY

Unique ID: WOS:000397550100015

***Record 14 of 21.** Search terms matched: BT(1); CORN(1); MAIZE(7); ZEA-MAYS(1)

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

***Order Full Text []**

Title: No adverse effects of transgenic **maize** on population dynamics of endophytic *Bacillus subtilis* strain B916-gfp

Authors: Sun, CS; Geng, LL; Wang, ML; Shao, GX; Liu, YF; Shu, CL; Zhang, J

Author Full Names: Sun, Chongsi; Geng, Lili; Wang, Meiling; Shao, Gaoxiang; Liu, Yongfeng; Shu, Changlong; Zhang, Jie

Source: MICROBIOLOGYOPEN, 6 (1):[10.1002/mbo3.404](https://doi.org/10.1002/mbo3.404) FEB 2017

Language: English

Abstract: Endophytic bacterial communities play a key role in promoting plant growth and combating plant diseases. However, little is known about their population dynamics in plant tissues and bulk soil, especially in transgenic crops. This study investigated the colonization of transgenic maize harboring the *Bacillus thuringiensis* (Bt) cry1Ah gene by *Bacillus subtilis* strain B916-gfp present in plant tissues and soil. Bt and nontransgenic maize were inoculated with B916-gfp by seed soaking, or root irrigation under both laboratory greenhouse and field conditions. During the growing season, B916-gfp colonized transgenic as well as nontransgenic plants by both inoculation methods. No differences were observed in B916-gfp population size between transgenic and nontransgenic plants, except at one or two time points in the roots and stems that did not persist over the examination period. Furthermore, planting transgenic maize did not affect the number of B916-gfp in bulk soil in either laboratory or field trials. These results indicate that transgenic modification of maize with the cry1Ah gene has no influence on colonization by the endophytic bacteria B916-gfp present in the plant and in bulk soil.

ISSN: 2045-8827

Article Number: UNSP e00404

IDS Number: EM0HG

Unique ID: WOS:000394998800012

***Record 15 of 21.** Search terms matched: CORN(1); MAIZE(7); MON 810(3)

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

***Order Full Text []**

Title: Determination of Mycotoxin Production of *Fusarium* Species in Genetically Modified **Maize** Varieties by Quantitative Flow Immunocytometry

Authors: Banati, H; Darvas, B; Feher-Toth, S; Czeh, A; Szekacs, A

Author Full Names: Banati, Hajnalka; Darvas, Bela; Feher-Toth, Szilvia; Czeh, Arpad; Szekacs, Andras

Source: TOXINS, 9 (2):[10.3390/toxins9020070](https://doi.org/10.3390/toxins9020070) FEB 2017

Language: English

Abstract: Levels of mycotoxins produced by *Fusarium* species in genetically modified (GM) and near-isogenic maize, were determined using multi-analyte, microbead-based flow immunocytometry with fluorescence detection, for the parallel quantitative determination of fumonisin B1, deoxynivalenol, zearalenone, T-2, ochratoxin A, and aflatoxin B1. Maize varieties included the genetic events MON 810 and DAS-59122-7, and their isogenic counterparts. Cobs were artificially infested by *F. verticillioides* and *F. proliferatum* conidia, and contained *F. graminearum* and *F. sporotrichoides* natural infestation. The production of fumonisin B1 and deoxynivalenol was substantially affected in GM maize lines: *F. verticillioides*, with the addition of *F. graminearum* and *F. sporotrichoides*, produced significantly lower levels of fumonisin B1 (similar to 300 mg.kg(-1)) in DAS-59122-7 than in its isogenic line (similar to 580 mg.kg(-1)), while *F. proliferatum*, in addition to *F. graminearum* and *F. sporotrichoides*, produced significantly higher levels of deoxynivalenol (similar to 18 mg.kg(-1)) in MON 810 than in its isogenic line (similar to 5 mg.kg(-1)). *Fusarium verticillioides*, with *F. graminearum* and *F. sporotrichoides*, produced lower amounts of deoxynivalenol and zearalenone than *F. proliferatum*, with *F. graminearum* and *F. sporotrichoides*. T-2 toxin production remained unchanged when considering the maize variety. The results demonstrate the utility of the Fungi-Plex T quantitative flow immunocytometry method, applied for the high throughput parallel determination of the target mycotoxins.

ISSN: 2072-6651

Article Number: 70

IDS Number: EM6VM

Unique ID: WOS:000395450500027

***Record 16 of 21.** Search terms matched: BORER(8); CORN(17); LEPIDOPTERA(3); OSTRINIA(3); PROTECT(1)

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

*Order Full Text []

Title: Can the Use of *Trichogramma ostriniae* (Hymenoptera: Trichogrammatidae) to Control *Ostrinia nubilalis* (Lepidoptera: Crambidae) Be Economically Sustainable for Processing Sweet Corn?

Authors: Gagnon, AE; Audette, C; Duval, B; Boisclair, J

Author Full Names: Gagnon, Annie-Eve; Audette, Carolane; Duval, Brigitte; Boisclair, Josee

Source: JOURNAL OF ECONOMIC ENTOMOLOGY, 110 (1):59-66; [10.1093/jee/tow293](https://doi.org/10.1093/jee/tow293) FEB 2017

Language: English

Abstract: European corn borer, *Ostrinia nubilalis* (Hubner) (Lepidoptera: Crambidae), is the main pest causing damage to sweet corn in North America. Conventional management with multiple use of insecticides is a common practice for processing sweet corn. In Canada, the use of *Trichogramma* spp. began in the 1990s, but the adoption of this approach for European corn

borer management is still limited to the fresh market of sweet corn. *Trichogramma ostrinae* (Peng & Chen) has great potential as a biological control agent for large areas such as in processing sweet corn. The objective of this study was to evaluate an economically and environmentally sustainable alternative to insecticides for controlling European corn borer populations in processing sweet corn. During the growing season, the mean number of larvae decreased after insecticide (0.07 +/- 0.04) and *Trichogramma* (1.32 +/- 0.59) treatments compared with the control (2.4260.72). At harvest, damages associated with European corn borer were similar after *Trichogramma* (1.0 +/- 0.7%) and insecticide (1.0 +/- 0.6%) treatments, but significantly lower than the control (8.7 +/- 3.3%). This study showed that the use of *T. ostrinae* can significantly decrease the pressure exerted by European corn borer and its damage on corn ears. This outcome is particularly interesting considering that it was achieved with lower doses of *Trichogramma*, a lower number of releases, and on large crop areas, compared with what is actually done to protect fresh market corn from European corn borer. Under these conditions, the use of *Trichogramma* is an economically and competitive alternative to insecticide applications.

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IDS Number: EO7ZY

Unique ID: WOS:000396909800008

PubMed ID: 28039428

***Record 17 of 21.** Search terms matched: BORER(6); BORERS(2); BT(5); CORN(1); LEPIDOPTERA(3); MAIZE(6); RESISTANT(1); SESAMIA(1)

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

*Order Full Text []

Title: Insect Resistance Management in **Bt Maize:** Wild Host Plants of Stem **Borers** Do Not Serve as Refuges in Africa

Authors: Van den Berg, J

Author Full Names: Van den Berg, J.

Source: JOURNAL OF ECONOMIC ENTOMOLOGY, 110 (1):221-229; [10.1093/jee/tow276](https://doi.org/10.1093/jee/tow276)
FEB 2017

Language: English

Abstract: Resistance evolution by target pests threatens the sustainability of Bt maize in Africa where insect resistance management (IRM) strategies are faced by unique challenges. The assumptions, on which current IRM strategies for stem borers are based, are not all valid for African maize stem borer species. The high dose-refuge strategy which is used to delay resistance evolution relies heavily on the presence of appropriate refuges (non-Bt plants) where pests are not under selection pressure and where sufficient numbers of Bt-susceptible individuals are produced to mate with possible survivors on the Bt maize crop. Misidentification of stem borer species and inaccurate reporting on wild host plant diversity over the past six decades created the perception that grasses will contribute to IRM strategies for these pests in Africa. Desired characteristics of refuge plants are that they should be good pest hosts, implying that larval survival is high and that it produces sufficient numbers of high-quality moths. Refuge plants should also have large cover abundance in areas where Bt maize is planted. While wild

host plants may suffice in IRM strategies for polyphagous pests, this is not the case with stenophagous pests. This review discusses data of ecological studies and stem borer surveys conducted over the past decade and shows that wild host plants are unsuitable for development and survival of sufficient numbers of stem borer individuals. These grasses rather act as dead-end-trap plants and do not comply with refuge requirements of producing 500 susceptible individuals for every one resistant individual that survives on Bt maize.

ISSN: 0022-0493

eISSN: 1938-291X

IDS Number: EO7ZY

Unique ID: WOS:000396909800028

PubMed ID: 28007833

***Record 18 of 21.** Search terms matched: BORER(3); CORN(7); CRY1AB(9); LEPIDOPTERA(1); MON810(1); OSTRINIA(3); RESISTANT(4)

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

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

Title: Comparisons of Transcriptional Profiles of Gut Genes between **Cry1Ab-Resistant** and Susceptible Strains of **Ostrinia nubilalis** Revealed Genes Possibly Related to the Adaptation of **Resistant** Larvae to Transgenic **Cry1Ab Corn**

Authors: Yao, JX; Zhu, YC; Lu, NY; Buschman, LL; Zhu, KY

Author Full Names: Yao, Jianxiu; Zhu, Yu-Cheng; Lu, Nanyan; Buschman, Lawrent L.; Zhu, Kun Yan

Source: INTERNATIONAL JOURNAL OF MOLECULAR SCIENCES, 18 (2):[10.3390/ijms18020301](#) FEB 2017

Language: English

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

ISSN: 1422-0067

Article Number: 301

IDS Number: EM6YD

Unique ID: WOS:000395457700070

***Record 19 of 21.** Search terms matched: BORER(2); CRY1AB(8)

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

*Order Full Text []

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

Authors: Wang, XY; Du, LX; Liu, CX; Gong, L; Han, LZ; Peng, YF

Author Full Names: Wang, X. Y.; Du, L. X.; Liu, C. X.; Gong, L.; Han, L. Z.; Peng, Y. F.

Source: JOURNAL OF INVERTEBRATE PATHOLOGY, 143 1-10;

[10.1016/j.jip.2016.11.004](https://doi.org/10.1016/j.jip.2016.11.004) FEB 2017

Language: English

Abstract: The striped stem borer, *Chilo suppressalis*, is a major target pest of transgenic rice expressing the Cry1Ab protein from the bacterium *Bacillus thuringiensis* (Bt) in China. Evolution of resistance in this pest is a major threat to the durability of Bt rice. Since Bt exerts its activity through binding to specific receptors in the midgut of target insects, identification of functional Cry1Ab receptors in the midgut of *C. suppressalis* larvae is crucial to evaluate potential resistance mechanisms and develop effective strategies for delaying insect resistance. In this work, we identified the putative Cry1Ab toxin-binding protein, aminopeptidase-N (APN), in the midgut of *C. suppressalis* by ligand blot and mass spectrometry. After cloning the full-length cDNAs encoding APN isoforms from the *C. suppressalis* larval midgut, we studied their spatiotemporal expression in different gut tissues and developmental stages. Furthermore, RNA interference (RNAi) against *C. suppressalis* aminopeptidases (CsAPNs) was employed to illustrate a functional role for CsAPNs in Cry1Ab toxicity to *C. suppressalis* larvae using injection and oral delivery of Stealth (TM) siRNA. Down-regulating the expression of CsAPNs by RNAi was closely associated with reduced susceptibility of *C. suppressalis* to Cry1Ab. These data provide the first direct evidence that CsAPNs participate in the mode of Cry1Ab action and may act as the functional receptor of Cry1A in *C. suppressalis* larvae. (C) 2016 Published by Elsevier Inc.

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IDS Number: EM3PU

Unique ID: WOS:000395227900001

PubMed ID: 27823898

***Record 20 of 21.** Search terms matched: CRY1AB(1); LEPIDOPTERA(1)

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

*Order Full Text []

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

Authors: Liu, LP; Gao, MJ; Yang, S; Liu, SY; Wu, YD; Carriere, Y; Yang, YH

Author Full Names: Liu, Laipan; Gao, Meijing; Yang, Song; Liu, Shaoyan; Wu, Yidong; Carriere, Yves; Yang, Yihua

Source: EVOLUTIONARY APPLICATIONS, 10 (2):170-179; [10.1111/eva.12438](https://doi.org/10.1111/eva.12438) FEB 2017

Language: English

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

ISSN: 1752-4571

IDS Number: EL4EE

Unique ID: WOS:000394573700005

PubMed ID: 28127393

***Record 21 of 21.** Search terms matched: BT(1); CORN(6); PROTECTION(1)

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

*Order Full Text []

Title: Discovery of a novel insecticidal protein from *Chromobacterium piscinae*, with activity against Western **Corn** Rootworm, *Diabrotica virgifera virgifera*

Authors: Sampson, K; Zaitseva, J; Stauffer, M; Vande Berg, B; Guo, R; Tomso, D; McNulty, B; Desai, N; Balasubramanian, D

Author Full Names: Sampson, Kimberly; Zaitseva, Jelena; Stauffer, Maria; Vande Berg, Brian; Guo, Rong; Tomso, Daniel; McNulty, Brian; Desai, Nalini; Balasubramanian, Deepa

Source: JOURNAL OF INVERTEBRATE PATHOLOGY, 142 34-43; SI

[10.1016/j.jip.2016.10.004](https://doi.org/10.1016/j.jip.2016.10.004) JAN 2017

Language: English

Abstract: Western corn rootworm (WCR), *Diabrotica virgifera virgifera*, is one of the most significant pests of corn in the United States. Although transgenic solutions exist, increasing resistance concerns make the discovery of novel solutions essential. In order to find a novel protein with high activity and a new mode of action, a large microbial collection was surveyed for toxicity to WCR using in vitro bioassays. Cultures of strain ATX2024, identified as *Chromobacterium piscinae*, had very high activity against WCR larvae. The biological activity from the strain was purified using chromatographic techniques and fractions were tested against WCR larvae. Proteins in the final active fraction were identified by mass spectrometry and N-

terminal sequencing and matched to the genome of ATX2024. A novel 58.9 kDa protein, identified by this approach, was expressed in a recombinant expression system and found to have specific activity against WCR. Transgenic corn events containing this gene showed good protection against root damage by WCR, with average scores ranging between 0.01 and 0.04 on the Iowa State node injury scale. Sequence analysis did not reveal homology to any known insecticidal toxin, suggesting that this protein may act in a novel way to control WCR. The new WCR active protein is named GNIP1Aa, for Gram Negative Insecticidal Protein. (C) 2016 Elsevier Inc. All rights reserved.

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IDS Number: EL9EK

Unique ID: WOS:000394922200007

PubMed ID: 27983944

***Record 1 of 11.** Search terms matched: CRY 1AB(1); TOLERANCE(1); TOLERANT(1)

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

***Order Full Text []**

Title: A temperature-**tolerant** multiplex elements and genes screening system for genetically modified organisms based on dual priming oligonucleotide primers and capillary electrophoresis

Authors: Fu, W; Wei, S; Wang, CG; Du, ZX; Zhu, PY; Wu, XY; Wu, G; Zhu, SF

Author Full Names: Fu, Wei; Wei, Shuang; Wang, Chenguang; Du, Zhixin; Zhu, Pengyu; Wu, Xiyang; Wu, Gang; Zhu, Shuifang

Source: FOOD CHEMISTRY, 229 396-402; [10.1016/j.foodchem.2017.02.088](https://doi.org/10.1016/j.foodchem.2017.02.088) AUG 15 2017

Language: English

Abstract: High throughput screening systems are the preferred solution to meet the urgent requirement of increasing number of genetically modified organisms (GMOs). In this study, we have successfully developed a multiplex GMO element screening system with dual priming oligonucleotide (DPO) primers. This system can detect the cauliflower mosaic virus 35S (CaMV 35S), terminator of nopaline synthase gene (NOS), figwort mosaic virus 35S (FMV 35S) promoter, neomycin phosphotransferaseII (NPTII), Bt Cry 1Ab, phosphinothricin acetyltransferase genes (bar) and Streptomyces viridochromogenes (pat) simultaneously, which covers more than 90% of all authorized GMO species worldwide. This system exhibits a high tolerance to annealing temperatures, high specificity and a limit of detection equal to conventional PCR. A total of 214 samples from markets, national entry-exit agencies, the Institute for Reference Materials and Measurement (IRMM) and the American Oil Chemists' Society (AOCS) were also tested for applicability. This screening system is therefore suitable for GMO screening. (C) 2017 Elsevier Ltd. All rights reserved.

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IDS Number: ET1MH

Unique ID: WOS:000400033000050

PubMed ID: 28372191

***Record 2 of 11.** Search terms matched: BT(1); CORN(2); CRY1AB(8); MAIZE(3)

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

*Order Full Text []

Title: Occurrence, leaching, and degradation of **Cry1Ab** protein from transgenic **maize** detritus in agricultural streams

Authors: Griffiths, NA; Tank, JL; Royer, TV; Rosi, EJ; Shogren, AJ; Frauendorf, TC; Whiles, MR

Author Full Names: Griffiths, Natalie A.; Tank, Jennifer L.; Royer, Todd V.; Rosi, Emma J.; Shogren, Ariel J.; Frauendorf, Therese C.; Whiles, Matt R.

Source: SCIENCE OF THE TOTAL ENVIRONMENT, 592 97-105;

[10.1016/j.scitotenv.2017.03.065](https://doi.org/10.1016/j.scitotenv.2017.03.065) AUG 15 2017

Language: English

Abstract: The insecticidal Cry1Ab protein expressed by transgenic (Bt) maize can enter adjacent water bodies via multiple pathways, but its fate in stream ecosystems is not as well studied as in terrestrial systems. In this study, we used a combination of field sampling and laboratory experiments to examine the occurrence, leaching, and degradation of soluble Cry1Ab protein derived from Bt maize in agricultural streams. We surveyed 11 agricultural streams in northwestern Indiana, USA, on 6 dates that encompassed the growing season, crop harvest, and snowmelt/spring flooding, and detected Cry1Ab protein in the water column and in flowing subsurface tile drains at concentrations of 3-60 ng/L. In a series of laboratory experiments, submerged Bt maize leaves leached Cry1Ab into stream water with 1% of the protein remaining in leaves after 70 d. Laboratory experiments suggested that dissolved Cry1Ab protein degraded rapidly in microcosms containing water-column microorganisms, and light did not enhance breakdown by stimulating assimilatory uptake of the protein by autotrophs. The common detection of Cry1Ab protein in streams sampled across an agricultural landscape, combined with laboratory studies showing rapid leaching and degradation, suggests that Cry1Ab may be pseudo-persistent at the watershed scale due to the multiple input pathways from the surrounding terrestrial environment. (C) 2017 Elsevier B. V. All rights reserved.

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eISSN: 1879-1026

IDS Number: ET2EN

Unique ID: WOS:000400082100012

PubMed ID: 28314135

***Record 3 of 11.** Search terms matched: MAIZE(4); MON810(1)

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

*Order Full Text []

Title: Application of molecular biology in the studies towards genetically modified organisms used in feed in Poland

Authors: Sieradzki, Z; Mazur, M; Krol, B; Kwiatek, K

Author Full Names: Sieradzki, Zbigniew; Mazur, Malgorzata; Krol, Beata; Kwiatek, Krzysztof

Source: MEDYCYNA WETERYNARYJNA-VETERINARY MEDICINE-SCIENCE AND PRACTICE, 73 (5):299-302; [10.21521/mw.5691](https://doi.org/10.21521/mw.5691) MAY 2017

Language: Polish

Abstract: Genetically modified organisms are increasingly used in the production of feed and food, which has met with opposition from consumers. The aim of the study was the use of molecular biology methods with particular emphasis on techniques of real-time PCR in the research in the detection and identification of genetically modified feed. The research materials were samples of feed taken from feed produced and used in animal nutrition in Poland in the years 2004-2015. The applied research methods included PCR and real-time PCR techniques, and consisted in the detection and determination of the DNA content of genetically modified plants. Cascade methods used in this study included the screening method of detection of GMOs, the method of identifying the type of GMO, and methods of quantitative analysis of GMO content. As part of the research task in the years 2004-2015 a total of 1435 samples of feed towards GMOs were examined. A positive result was found in 559 cases (39%). Most frequently the positive samples were found the presence of genetically modified soybeans (531, 37%). Moreover, within the years 2014-2015 an increase in the number of positive GM rape samples was observed (56, 4%). GM maize contained the least positive samples (38, 2.6%). GMO content above the legislative threshold 0.9% was found in the vast majority of samples containing GM soy, while for maize and rapeseed the number of samples containing more than 0.9% GMO was respectively 12 and 8. Analysis of the feed market in Poland indicates that the soybean plant is the most common genetically modified crop. Analysis of the origin of sources of GM rapeseed showed that the reasons for this should be sought in batches of rapeseed imported from third countries. It has been observed with regard to the situation of GM maize for the feed market in Poland that from 2013 the situation changed radically as a result of the Decree of the Ministry of Agriculture issued prohibiting the cultivation of MON810 maize on Polish fields. The result of our study showed that the proportion of genetically modified feed on the feed market in Poland is very similar to other EU countries. The source of GMOs in feed on the Polish market is feed materials imported into Poland as a source of feed protein.

ISSN: 0025-8628

IDS Number: EU0TP

Unique ID: WOS:000400724700008

*Record 4 of 11. Search terms matched: CRY1AB(1); LEPIDOPTERA(2); RESISTANT(4)

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

*Order Full Text []

Title: Bacillus thuringiensis Vip3Aa Toxin Resistance in *Heliothis virescens* (**Lepidoptera:** Noctuidae)

Authors: Pickett, BR; Gulzar, A; Ferre, J; Wright, DJ

Author Full Names: Pickett, Brian R.; Gulzar, Asim; Ferre, Juan; Wright, Denis J.

Source: APPLIED AND ENVIRONMENTAL MICROBIOLOGY, 83 (9):[10.1128/AEM.03506-16](https://doi.org/10.1128/AEM.03506-16) MAY 2017

Language: English

Abstract: Laboratory selection with Vip3Aa of a field-derived population of *Heliothis virescens* produced >2,040-fold resistance in 12 generations of selection. The Vip3Aa-selected

(Vip-Sel)-resistant population showed little cross-resistance to Cry1Ab and no cross-resistance to Cry1Ac. Resistance was unstable after 15 generations without exposure to the toxin. F-1 reciprocal crosses between Vip3Aa-unselected (Vip-Unsel) and Vip-Sel insects indicated a strong paternal influence on the inheritance of resistance. Resistance ranged from almost completely recessive (mean degree of dominance [h] = 0.04 if the resistant parent was female) to incompletely dominant (mean h = 0.53 if the resistant parent was male). Results from bioassays on the offspring from backcrosses of the F-1 progeny with Vip-Sel insects indicated that resistance was due to more than one locus. The results described in this article provide useful information for the insecticide resistance management strategies designed to overcome the evolution of resistance to Vip3Aa in insect pests. **IMPORTANCE** *Heliothis virescens* is an important pest that has the ability to feed on many plant species. The extensive use of *Bacillus thuringiensis* (Bt) crops or spray has already led to the evolution of insect resistance in the field for some species of Lepidoptera and Coleoptera. The development of resistance in insect pests is the main threat to Bt crops. The effective resistance management strategies are very important to prolong the life of Bt plants. Lab selection is the key step to test the assumption and predictions of management strategies prior to field evaluation. Resistant insects offer useful information to determine the inheritance of resistance and the frequency of resistance alleles and to study the mechanism of resistance to insecticides.

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Article Number: UNSP e03506-16

IDS Number: ES5GM

Unique ID: WOS:000399566400020

***Record 5 of 11.** Search terms matched: BT(1); CORN(2); MAIZE(4)

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

*Order Full Text []

Title: *Fusarium verticillioides* and fumonisin contamination in Bt and non-Bt maize cultivated in Brazil

Authors: Barroso, VM; Rocha, LO; Reis, TA; Reis, GM; Duarte, AP; Michelotto, MD; Correa, B

Author Full Names: Barroso, Vinicius M.; Rocha, Liliana O.; Reis, Tatiana A.; Reis, Gabriela M.; Duarte, Aildson P.; Michelotto, Marcos D.; Correa, Benedito

Source: MYCOTOXIN RESEARCH, 33 (2):121-127; [10.1007/s12550-017-0271-4](https://doi.org/10.1007/s12550-017-0271-4) MAY 2017

Language: English

Abstract: *Fusarium verticillioides* is one of the main pathogens of maize, causing ear and stalk rots. This fungus is also able to produce high levels of fumonisins, which have been linked to various illnesses in humans and animals. Previous studies have shown that maize hybrids genetically modified with the cry genes from the bacterium *Bacillus thuringiensis* (Bt) presented lower incidence of *F. verticillioides* and fumonisin levels, presumably through the reduction of insects, which could act as vectors of fungi. The aim of this study was to assess the incidence of *F. verticillioides* and the concentration of fumonisins in Bt and isogenic non-Bt hybrids (2B710Hx, 30F35YG, 2B710, and 30F35, respectively). The samples of 2B710Hx and 30F35YG presented lower *F. verticillioides* frequency than 2B710 and 30F35 samples.

However, there was no statistical difference between fumonisin contamination when Bt and non-Bt samples were compared ($P > 0.05$). The results suggest that other environmental parameters could possibly trigger fumonisin production during plant development in the field; consequently, other management strategies should be applied to aid controlling fumonisin contamination in maize.

ISSN: 0178-7888

eISSN: 1867-1632

IDS Number: ES6ZH

Unique ID: WOS:000399698800005

PubMed ID: 28265970

***Record 6 of 11.** Search terms matched: BT(1); MAIZE(1)

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

***Order Full Text []**

Title: The Prediction of a New CLCuD Epidemic in the Old World

Authors: Sattar, MN; Iqbal, Z; Tahir, MN; Ullah, S

Author Full Names: Sattar, Muhammad N.; Iqbal, Zafar; Tahir, Muhammad N.; Ullah, Sami

Source: FRONTIERS IN MICROBIOLOGY, 8 [10.3389/fmicb.2017.00631](https://doi.org/10.3389/fmicb.2017.00631) APR 19 2017

Language: English

Abstract: Cotton leaf curl disease (CLCuD), the most complex disease of cotton, is a major limiting biotic factor to worldwide cotton productivity. Several whitefly-transmitted monopartite begomoviruses causing CLCuD have been characterized and designated as CLCuD-associated begomoviruses. Despite of being reported over 100 years ago in Africa, CLCuD became economically pandemic causing massive losses to cotton production in Pakistan and India during past couple of decades. In Asia, cotton has faced two major epidemics during this period viz. "Multan epidemic" and "Burewala epidemic." The "Multan epidemic" era was 1988-1999 after which the virus remained calm until 2002 when "Burewala epidemic" broke into the cotton fields in Indo-Pak subcontinent, till 2013-2014. However, both the epidemics were caused by monopartite begomovirus complex. Similarly in Africa, Cotton leaf curl Gezira virus with associated DNA-satellites causes CLCuD. Quite recently, in the Old World (both Asia and Africa), bipartite begomoviruses have started appearing in the areas under cotton cultivation. Under such aggravated circumstances, it seems we are heading toward another epidemic of CLCuD in the Old World. Here we articulate the causes and potential emergence of the third epidemic of CLCuD in Asia. The current situation of CLCuD in Asia and Africa is also discussed.

ISSN: 1664-302X

Article Number: 631

IDS Number: ES4TA

Unique ID: WOS:000399526400001

PubMed ID: 28469604

***Record 7 of 11.** Search terms matched: BT(1); CORN(1); MAIZE(4); RESISTANT(3); TOLERANT(2); ZEA MAYS(1)

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

*Order Full Text []

Title: Effects of genetically modified **maize** events expressing Cry34Ab1, Cry35Ab1, Cry1F, and CP4 EPSPS proteins on arthropod complex food webs

Authors: Palinkas, Z; Kiss, J; Zalai, M; Szenasi, A; Dorner, Z; North, S; Woodward, G; Balog, A

Author Full Names: Palinkas, Zoltan; Kiss, Jozsef; Zalai, Mihaly; Szenasi, Agnes; Dorner, Zita; North, Samuel; Woodward, Guy; Balog, Adalbert

Source: ECOLOGY AND EVOLUTION, 7 (7):2286-2293; [10.1002/ece3.2848](https://doi.org/10.1002/ece3.2848) APR 2017

Language: English

Abstract: Four genetically modified (GM) maize (*Zea mays* L.) hybrids (coleopteran resistant, coleopteran and lepidopteran resistant, lepidopteran resistant and herbicide tolerant, coleopteran and herbicide tolerant) and its non-GM control maize stands were tested to compare the functional diversity of arthropods and to determine whether genetic modifications alter the structure of arthropods food webs. A total number of 399,239 arthropod individuals were used for analyses. The trophic groups' number and the links between them indicated that neither the higher magnitude of Bt toxins (included resistance against insect, and against both insects and glyphosate) nor the extra glyphosate treatment changed the structure of food webs. However, differences in the average trophic links/trophic groups were detected between GM and non-GM food webs for herbivore groups and plants. Also, differences in characteristic path lengths between GM and non-GM food webs for herbivores were observed. Food webs parameterized based on 2-year in-field assessments, and their properties can be considered a useful and simple tool to evaluate the effects of Bt toxins on non-target organisms.

ISSN: 2045-7758

IDS Number: ES7OD

Unique ID: WOS:000399738700026

PubMed ID: 28405292

***Record 8 of 11.** Search terms matched: BT(5); MAIZE(12); MON810(1)

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

*Order Full Text []

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

Authors: Mashiane, RA; Ezeokoli, OT; Adeleke, RA; Bezuidenhout, CC

Author Full Names: Mashiane, Ramadimetja A.; Ezeokoli, Obinna T.; Adeleke, Rasheed A.; Bezuidenhout, Cornelius C.

Source: WORLD JOURNAL OF MICROBIOLOGY & BIOTECHNOLOGY, 33 (4):[10.1007/s11274-017-2249-y](https://doi.org/10.1007/s11274-017-2249-y) APR 2017

Language: English

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

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***Record 9 of 11.** Search terms matched: MAIZE(5); MON810(2)

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

*Order Full Text []

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

Authors: Schmidt, K; Schmidtke, J; Schmidt, P; Kohl, C; Wilhelm, R; Schiemann, J; van der Voet, H; Steinberg, P

Author Full Names: Schmidt, Kerstin; Schmidtke, Joerg; Schmidt, Paul; Kohl, Christian; Wilhelm, Ralf; Schiemann, Joachim; van der Voet, Hilko; Steinberg, Pablo

Source: ARCHIVES OF TOXICOLOGY, 91 (4):1977-2006; [10.1007/s00204-016-1857-x](https://doi.org/10.1007/s00204-016-1857-x) APR 2017

Language: English

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

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

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***Record 10 of 11.** Search terms matched: BT(1); CORN(1); CRY1AB(2); LEPIDOPTERA(2); MAIZE(3); YIELD(1); ZEA MAYS(1)

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

*Order Full Text []

Title: Efficacy of transgenic maize insecticide treatment to control fall armyworm in late-season **maize** in Sao Paulo state, Brazil

Authors: Michelotto, MD; Neto, JC; Pirota, MZ; Duarte, AP; de Feitas, RS; Finoto, EL

Author Full Names: Michelotto, Marcos Doniseti; Neto, Jacob Crosariol; Pirota, Melina Zacarelli; Duarte, Aildson Pereira; de Feitas, Rogerio Soares; Finoto, Everton Luis

Source: CIENCIA E AGROTECNOLOGIA, 41 (2):128-138; [10.1590/1413-70542017412020816](https://doi.org/10.1590/1413-70542017412020816) MAR-APR 2017

Language: English

Abstract: Several genetically modified maize events expressing insecticidal proteins from *Bacillus thuringiensis* (Bt) have been commercially available in Brazil, intended to control of fall armyworm, *Spodoptera frugiperda* (Lepidoptera: Noctuidae). The objective of this study was to evaluate the efficiency of transgenic (Bt) and conventional (non-Bt) hybrids in the control of fall armyworm, treated or not with insecticides throughout three late growing seasons. To this end, trials were conducted at three locations in the state of Sao Paulo, in a randomized complete block design, in factorial arrangements with 5x4, 5x4 and 8x4 factors, respectively. The first factor consisted of the number of commercial hybrids of different companies. The second factor was represented by the different control managements of insect (non-Bt hybrid with and without insecticide; Bt hybrid with and without insecticide). The damage caused by fall armyworm was evaluated on a visual 1-9 scale, from score 0 (no

damage) to 9 (totally destroyed whorl), and grain yield (kg ha⁻¹). The data were analyzed by analysis of variance and the means compared by the Tukey test at 5% probability for each parameter evaluated at each location. For the Bt hybrids, the damage scores attributed to fall armyworm were lower and the proteins Cry 1F, Cry 1A105 and VIP3Aa20 were the most efficient in reducing leaf damage. Insecticide applications proved efficient in reducing leaf damage caused by the pest. Application of insecticides to Bt hybrids generally reduced leaf damage, especially for Cry1Ab-producing hybrids, which were the least effective in reducing pest damage without insecticides.

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

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

*Order Full Text []

Title: Terahertz spectroscopy detection of genetically modified sugar beets containing the Xa21 gene based on chemometrics methods

Authors: Liu, JJ

Author Full Names: Liu, Jianjun

Source: JOURNAL OF OPTICAL TECHNOLOGY, 83 (10):627-631; [10.1364/JOT.83.000627](https://doi.org/10.1364/JOT.83.000627)
OCT 1 2016

Language: English

Abstract: Because traditional detection of genetically modified organisms (GMOs) has the disadvantages of being costly, time consuming, and awkward to perform, a novel method for the detection of GMOs based on terahertz spectroscopy combined with chemometrics methods is proposed. In this work, terahertz spectrum data of a genetically modified sugar beet and its parents are pretreated by using principal component analysis and then using the weighted discriminant analysis model, which is an improved discriminant analysis that applies a weighted algorithm to the detection of a genetically modified sugar beet and its parents. It is found from the experimental results that the samples are expressed by the zonation of saline minerals. By analyzing this phenomenon, it is easy to identify these genetically modified sugar beets. By combining terahertz spectroscopy with chemometrics methods, this paper provides a precise, fast, convenient, and nondestructive method for the detection of GMOs. (C) 2017 Optical Society of America

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