Appendix 5.4 MON 810 Literature Review – List of all hits (June 2015 – May 2016) – Cabi Cab Abstracts® database

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FN Thomson Reuters Web of Science™
VR 1.0

PT J
AU Bernardi, D.
   Bernardi, O.
   Horikoshi, R. J.
   Salmeron, E.
   Okuma, D. M.
   Omoto, C.
TI Biological activity of Bt proteins expressed in different structures of
   transgenic corn against  Spodoptera frugiperda.
SO Ciencia Rural
VL 46
IS 6
PS 1019-1024
PY 2016
AB 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.
UT CABI:20163150699
SN 0103-8478
DI 10.1590/0103-8478cr20150047
ER

PT J
AU Velez, A. M.
   Alves, A. P.
   Blankenship, E. E.
   Siegfried, B. D.
TI Effect of Cry1F maize on the behavior of susceptible and resistant
   Spodoptera frugiperda and  Ostrinia nubilalis.
SO Entomologia Experimentalis et Applicata
VL 159
IS 1
PS 37-45
PY 2016
AB 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
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   configurations. Exposure to Bt maize,  Zea mays L. (Poaceae), has been
   suggested to increase larval movement in lepidopteran species but few
   studies have examined the potential for resistance to interact with
   behavioral responses to Bt toxins. Choice and no-choice experiments were
   conducted with  Spodoptera frugiperda (JE Smith) (Lepidoptera:
   Noctuidae) and  Ostrinia nubilalis (Hubner) (Lepidoptera: Crambidae) to
   determine whether Cry1F resistance influences neonate movement. Leaf
   discs of Cry1F maize and the corresponding isoline were used to
   characterize behavioral responses. In both experiments, the location (on
   or off of plant tissues) and mortality of susceptible and Cry1F
   resistant neonates was recorded for 5 days, but the analysis of larvae
   location was performed until 7 h. Our results indicated no strong
   difference between resistant and susceptible phenotypes in  S.
   frugiperda and  O. nubilalis, although a small percentage of susceptible
   neonates in both species abandoned maize tissue expressing Cry1F.
   However, significant behavioral differences were observed between
   species.  Ostrinia nubilalis exhibited increased movement between leaf
   discs, whereas  S. frugiperda selected plant tissue within the first 30
   min and remained on the chosen plant regardless of the presence of
   Cry1F.  Spodoptera frugiperda reduced larval movement may have
   implications to refuge configuration. This study represents the first
   step toward understanding the effects of Cry1F resistance on Lepidoptera
   larval behavior. Information regarding behavioral differences between
   species could aid in developing better and more flexible resistance
   management strategies.
UT CABI:20163137911
SN 0013-8703
DI 10.1111/eea.12409
ER

PT J
AU Schenkelaars, P.
   Wesseler, J.
BE Wesseler, J.
   Punt, M.
TI Farm-level GM coexistence policies in the EU: context, concepts and
   developments.
SO Eurochoices
VL 15
IS 1
PS 5-11
PY 2016
AB Many EU MS have implemented coexistence policies to govern the
   cultivation of GM crops on their territory but only one GM crop, the Bt
   maize event MON810, is currently cultivated in the EU. From a practical
   point of view, a combination of paper traceability and implementation of
   isolation distances between GM and non-GM maize are considered as being
   the most effective way of segregating both types of materials. In
   general, infringements will however only become apparent after
   harvesting the crops. Liability issues will then be invoked late in the
   process restricting or at least limiting flexibility in the marketing of
   the materials in an appropriate way. Nevertheless, following the general
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   guidelines for coexistence developed by the European Commission, EU
   Member States are progressively regulating coexistence at the national
   level. The policies in the EU governing coexistence can be
   differentiated into  ex-ante regulations and  ex-post liability rules.
   This differentiation is useful as the economic implications between the
   two differ. With regard to maize, studies show that the costs of
   complying with the given threshold values for GM content at farm level
   range from zero to 2 per cent of the total growing costs for both
   conventional and organic production.
UT CABI:20163148849
SN 1478-0917
DI 10.1111/1746-692X.12112
ER

PT J
AU Zhou Xia
   Guo YunLing
   Kong Hua
   Zuo Jiao
   Huang QiXing
   Jia RuiZong
   Guo AnPing
   Xu Lin
TI A comprehensive assessment of the effects of transgenic Cry1Ac/Cry1Ab
   rice Huahui 1 on adult  Micraspis discolor (Fabricius) (Coleoptera:
   Coccinellidae).
SO PLoS ONE
VL 11
IS 2
PS e0142714
PY 2016
AB 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 life-table parameters tested between Cry
   protein-containing and pure diet. Artificial diet containing E-64
   (N-(trans-Epoxysuccinyl)-L-leucine 4-guanidinobutylamide) was included
   as a positive control. In contrast, the pre-oviposition and fecundity of
   M. discolor were significantly adversely affected by feeding on
   E-64-containing diet. In both bioassays, the uptakes of Cry protein by
   adult  M. discolor were tested by ELISA measurements. These results
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   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.
UT CABI:20163140868
SN 1932-6203
DI 10.1371/journal.pone.0142714
ER

PT J
AU Tanaka, S.
   Miyamoto, K.
   Noda, H.
   Endo, H.
   Kikuta, S.
   Sato, R.
TI 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.
SO Peptides
VL 78
PS 99-108
PY 2016
AB In a previous report, seven Cry1Ab-resistant strains were identified in
   the silkworm,  Bombyx mori; these strains were shown to have a tyrosine
   insertion at position 234 in extracellular loop 2 of the ABC transporter
   C2 (BmABCC2). This insertion was confirmed to destroy the receptor
   function of BmABCC2 and confer the strains resistance against Cry1Ab and
   Cry1Ac. However, these strains were susceptible to Cry1Aa. In this
   report, we examined the mechanisms of the loss of receptor function of
   the transporter by expressing mutations in Sf9 cells. After replacement
   of one or two of the five amino acid residues in loop 2 of the
   susceptible  BmABCC2 gene [ BmABCC2_S] with alanine, cells still showed
   susceptibility, retaining the receptor function. Five mutants with
   single amino acid insertions at position 234 in BmABCC2 were also
   generated, resulting in loop 2 having six amino acids, which corresponds
   to replacing the tyrosine insertion in the resistant  BmABCC2 gene [
   BmABCC2_R(+ 234Y)] with another amino acid. All five mutants exhibited
   loss of function against Cry1Ab and Cry1Ac. These results suggest that
   the amino acid sequence in loop 2 is less important than the loop size
   (five vs. six amino acids) or loop structure for Cry1Ab and Cry1Ac
   activity. Several domain-swapped mutant toxins were then generated among
   Cry1Aa, Cry1Ab, and Cry1Ac, which are composed of three domains. Swapped
   mutants containing domain II of Cry1Ab or Cry1Ac did not kill Sf9 cells
   expressing BmABCC2_R(+ 234Y), suggesting that domain II of the Cry toxin
   is related to the interaction with the receptor function of BmABCC2.
   This also suggests that different reactions against Bt-toxins in some
   B. mori strains, that is, Cry1Ab resistance or Cry1Aa susceptibility,
   are attributable to structural differences in domain II of Cry1A toxins.

UT CABI:20163132494
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SN 0196-9781
DI 10.1016/j.peptides.2016.01.006
ER

PT J
AU Carriere, Y.
   Fabrick, J. A.
   Tabashnik, B. E.
TI Can pyramids and seed mixtures delay resistance to Bt crops?
SO Trends in Biotechnology
VL 34
IS 4
PS 291-302
PY 2016
AB 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.
UT CABI:20163133070
SN 0167-7799
DI 10.1016/j.tibtech.2015.12.011
ER

PT J
AU Huang FangNeng
   Qureshi, J. A.
   Head, G. P.
   Price, P. A.
   Levy, R.
   Yang Fei
   Niu Ying
TI Frequency of  Bacillus thuringiensis Cry1A.105 resistance alleles in
   field populations of the fall armyworm,  Spodoptera frugiperda, in
   Louisiana and Florida.
SO Crop Protection
VL 83
PS 83-89
PY 2016
AB 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
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   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.
UT CABI:20163122805
SN 0261-2194
DI 10.1016/j.cropro.2016.01.019
ER

PT J
AU Hong, B.
   Nowatzki, T. M.
   Sult, T. S.
   Owens, E. D.
   Pilcher, C. D.
TI Sequential sampling plan for assessing corn rootworm (Coleoptera:
   Chrysomelidae) larval injury to Bt maize.
SO Crop Protection
VL 82
PS 36-44
PY 2016
AB 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
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   in-field Bt maize product performance, with applications to other CRW
   control technologies besides Bt maize products.
UT CABI:20163122788
SN 0261-2194
DI 10.1016/j.cropro.2016.01.001
ER

PT J
AU Xie Ming
   Zhang YanJun
   Peng DeLiang
   Wu Gang
   Xu Peng
   Zhao JinJin
   Zhang ZhaoRong
TI Field studies show no significant effect of a Cry1Ab/Ac producing
   transgenic cotton on the fungal community structure in rhizosphere soil.
SO European Journal of Soil Biology
VL 73
PS 69-76
PY 2016
AB 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.
UT CABI:20163121123
SN 1164-5563
ER

PT J
AU Farias, J. R.
   Andow, D. A.
   Horikoshi, R. J.
   Sorgatto, R. J.
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   Santos, A. C. dos
   Omoto, C.
TI Dominance of Cry1F resistance in  Spodoptera frugiperda (Lepidoptera:
   Noctuidae) on TC1507  Bt maize in Brazil.
SO Pest Management Science
VL 72
IS 5
PS 974-979
PY 2016
AB 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.
UT CABI:20163126064
SN 1526-498X
DI 10.1002/ps.4077
ER

PT J
AU Leite, N. A.
   Mendes, S. M.
   Santos-Amaya, O. F.
   Santos, C. A.
   Teixeira, T. P. M.
   Guedes, R. N. C.
   Pereira, E. J. G.
TI Rapid selection and characterization of Cry1F resistance in a Brazilian
   strain of fall armyworm.
SO Entomologia Experimentalis et Applicata
VL 158
IS 3
PS 236-247
PY 2016
AB Transgenic maize ( Zea mays L., Poaceae) event TC1507, producing the
   Cry1F protein of  Bacillus thuringiensis Berliner, has been used for
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   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.
UT CABI:20163112002
SN 0013-8703
DI 10.1111/eea.12399
ER

PT J
AU Arias-Martin, M.
   Garcia, M.
   Lucianez, M. J.
   Ortego, F.
   Castanera, P.
   Farinos, G. P.
TI Effects of three-year cultivation of Cry1Ab-expressing Bt maize on soil
   microarthropod communities.
SO Agriculture, Ecosystems & Environment
VL 220
PS 125-134
PY 2016
AB 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
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   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.
UT CABI:20163106076
RI Ortego, Felix/F-9402-2011
SN 0167-8809
DI 10.1016/j.agee.2015.09.007
ER

PT J
AU Rocha, L. O.
   Barroso, V. M.
   Andrade, L. J.
   Pereira, G. H. A.
   Ferreira-Castro, F. L.
   Duarte, A. P.
   Michelotto, M. D.
   Correa, B.
TI FUM gene expression profile and fumonisin production by  Fusarium
   verticillioides inoculated in  Bt and non- Bt maize.
SO Frontiers in Microbiology
VL 7
IS January
PS 01503
PY 2016
AB 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 (FB 1 and FB
   2) production and  FUM1, FUM3, FUM6, FUM7, FUM8, FUM13, FUM14, FUM15,
   and  FUM19 expression. 2B710 Hx and 30F35 YG kernel samples were
   virtually intact when compared to the non- Bt hybrids that came from the
   field. Statistical analysis showed that FB 1 production was
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   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 FB 2
   production ( P >0.05). The kernel injuries observed in the non- Bt
   samples have possibly facilitated  F. verticillioides penetration and
   promoted FB 1 production under controlled conditions.  FUM genes were
   expressed by  F. verticillioides in all of the samples. However, there
   was indication of lower expression of a few  FUM genes in the  Bt
   hybrids; and a weak association between FB 1 production and the relative
   expression of some of the  FUM genes were observed in the 30F35 YG
   hybrid.
UT CABI:20163106740
SN 1664-302X
ER

PT J
AU Steijven, K.
   Steffan-Dewenter, I.
   Hartel, S.
TI Testing dose-dependent effects of stacked Bt maize pollen on in
   vitro-reared honey bee larvae.
SO Apidologie
VL 47
IS 2
PS 216-226
PY 2016
AB 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).
UT CABI:20163096774
SN 0044-8435
ER

PT J
AU Jakka, S. R. K.
   Gong Liang
   Hasler, J.
   Rahul Banerjee
   Sheets, J. J.
   Narva, K.
   Blanco, C. A.
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   Jurat-Fuentes, J. L.
TI 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.
SO Applied and Environmental Microbiology
VL 82
IS 4
PS 1023-1034
PY 2016
AB Insecticidal protein genes from the bacterium  Bacillus thuringiensis
   (Bt) are expressed by transgenic Bt crops (Bt crops) for effective and
   environmentally safe pest control. The development of resistance to
   these insecticidal proteins is considered the most serious threat to the
   sustainability of Bt crops. Resistance in fall armyworm ( Spodoptera
   frugiperda) populations from Puerto Rico to transgenic corn producing
   the Cry1Fa insecticidal protein resulted, for the first time in the
   United States, in practical resistance, and Bt corn was withdrawn from
   the local market. In this study, we used a field-collected Cry1Fa
   corn-resistant strain (456) of  S. frugiperda to identify the mechanism
   responsible for field-evolved resistance. Binding assays detected
   reduced Cry1Fa, Cry1Ab, and Cry1Ac but not Cry1Ca toxin binding to
   midgut brush border membrane vesicles (BBMV) from the larvae of strain
   456 compared to that from the larvae of a susceptible (Ben) strain. This
   binding phenotype is descriptive of the mode 1 type of resistance to Bt
   toxins. A comparison of the transcript levels for putative Cry1 toxin
   receptor genes identified a significant downregulation (>90%) of a
   membrane-bound alkaline phosphatase (ALP), which translated to reduced
   ALP protein levels and a 75% reduction in ALP activity in BBMV from 456
   compared to that of Ben larvae. We cloned and heterologously expressed
   this ALP from susceptible  S. frugiperda larvae and demonstrated that it
   specifically binds with Cry1Fa toxin. This study provides a thorough
   mechanistic description of field-evolved resistance to a transgenic Bt
   crop and supports an association between resistance and reduced Cry1Fa
   toxin binding and levels of a putative Cry1Fa toxin receptor, ALP, in
   the midguts of  S. frugiperda larvae.
UT CABI:20163101472
SN 0099-2240
DI 10.1128/AEM.02871-15
ER

PT J
AU Oyediran, I.
   Dively, G.
   Huang, F.
   Burd, T.
TI Evaluation of European corn borer  Ostrinia nubilalis (Lepidoptera:
   Crambidae) larval movement and survival in structured and seed blend
   refuge plantings.
SO Crop Protection
VL 81
PS 145-153
PY 2016
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AB 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.

UT CABI:20163099767
SN 0261-2194
DI 10.1016/j.cropro.2015.12.008
ER

PT J
AU Santos-Amaya, O. F.
Tavares, C. S.
Monteiro, H. M.
Teixeira, T. P. M.
Guedes, R. N. C.
Alves, A. P.
Pereira, E. J. G.
TI Genetic basis of Cry1F resistance in two Brazilian populations of fall armyworm, Spodoptera frugiperda.
SO Crop Protection
VL 81
PS 154-162
PY 2016
AB Large-scale adoption of transgenic crops expressing genes from Bacillus thuringiensis (Bt) imposes high selection pressure for evolution of

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   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.
UT CABI:20163099768
RI Pereira, Eliseu/C-5365-2015
OI Pereira, Eliseu/0000-0002-8957-6465
SN 0261-2194
DI 10.1016/j.cropro.2015.12.014
ER

PT J
AU Azizoglu, U.
   Ayvaz, A.
   Yilmaz, S.
   Temizgul, R.
TI The synergic and antagonistic activity of Cry1Ab and Cry2Aa proteins
   against lepidopteran pests.
SO Journal of Applied Entomology
VL 140
IS 3
PS 223-227
PY 2016
AB 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
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   Cry1Ab:Cry2Aa should be avoided in control programmes for these larvae.
UT CABI:20163096193
SN 0931-2048
DI 10.1111/jen.12241
ER

PT J
AU Ma, B. L.
   Zheng, Z. M.
   Morrison, M. J.
   Gregorich, E. G.
TI Nitrogen and phosphorus nutrition and stoichiometry in the response of
   maize to various N rates under different rotation systems.
SO Nutrient Cycling in Agroecosystems
VL 104
IS 1
PS 93-105
PY 2016
AB 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.
UT CABI:20163088534
SN 1385-1314
DI 10.1007/s10705-016-9761-6
ER

PT J
AU Willcoxon, M. I.
   Dennis, J. R.
   Lau, S. I.
   Xie WeiPing
   You You
   Leng Song
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   Fong, R. C.
   Yamamoto, T.
TI A high-throughput, in-vitro assay for  Bacillus thuringiensis
   insecticidal proteins.
SO Journal of Biotechnology
VL 217
PS 72-81
PY 2016
AB A high-throughput, in-vitro assay for  Bacillus thuringiensis (Bt)
   insecticidal proteins designated as Cry was developed and evaluated for
   screening a large number of Cry protein variants produced by DNA
   shuffling. This automation-amenable assay exploits an insect cell line
   expressing a single receptor of Bt Cry proteins. The Cry toxin used to
   develop this assay is a variant of the Cry1Ab protein called IP1-88,
   which was produced previously by DNA shuffling. Cell mortality caused by
   the activated Bt Cry toxin was determined by chemical cell viability
   assay in 96/384-well microtiter plates utilizing CellTiter 96 obtained
   from Promega. A widely-accepted mode-of-action theory of certain Bt Cry
   proteins suggests that the activated toxin binds to one or more
   receptors and forms a pore through the insect gut epithelial cell apical
   membrane. A number of insect proteins such as cadherin-like protein
   (Cad), aminopeptidase-N (APN), alkaline phosphatase (ALP) and ABC
   transporter (ABCC) have been identified as the receptors of Bt Cry
   toxins. In this study, Bt Cry toxin receptors  Ostrinia nubilalis
   (European corn borer) cadherin-like protein (On-Cad) and
   aminopeptidase-N 1 and 3 (On-APN1, On-APN3) and  Spodoptera frugiperda
   (fall armyworm) cadherin-like protein (Sf-Cad) were cloned in an insect
   cell line, Sf21, and a mammalian cell line, Expi293F. It was observed by
   ligand blotting and immunofluorescence microscopy that trypsin-activated
   IP1-88 bound to On-Cad and On-APN1, but not Sf-Cad or On-APN3. In
   contrast, IP1-88 bound only to APN1 in BBMV (Brush Border Membrane
   Vesicles) prepared from the third and fourth-instar  O. nubilalis larval
   midgut. The sensitivity of the recombinant cells to the toxin was then
   tested. IP1-88 showed no toxicity to non-recombinant Sf21 and Expi293F.
   Toxicity was observed only when the On-Cad gene was cloned and
   expressed. Sf-Cad and On-APN1 were not able to make those cells
   sensitive to the toxin. Since the expression of On-Cad alone was
   sufficient to make both insect and mammalian cells sensitive to the
   IP1-88 toxin, it is not likely that a secondary receptor, which may
   exist specifically in the Sf21 insect cell but not in the Expi293F cell,
   is involved in the cytotoxicity of IP1-88.
UT CABI:20163080318
SN 0168-1656
ER

PT J
AU Shera, P. S.
   Ramesh Arora
TI Survival and development of spotted bollworm,  Earias vittella
   (Fabricius) (Lepidoptera: Nolidae) on different transgenic  Bt and
   isogenic non- Bt cotton genotypes.
SO Phytoparasitica
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VL 44
IS 1
PS 99-113
PY 2016
AB Four  Bt cotton hybrids, each with one of four different events,  viz.,
   MRC 6301  Bt ( cry1Ac gene), JKCH 1947  Bt (modified  cry1Ac gene), NCEH
   6R  Bt (fusion  cry1Ac/cry1Ab gene) and MRC 7017 Bollgard II ( cry1Ac
   and  cry2Ab genes) were compared for survival and development of  Earias
   vittella (Fabricius) along with their isogenic non- Bt genotypes. None
   of the neonates were able to complete the larval period and reach pupal
   stage on squares of 90, 120 and 150 days old crop of all  Bt hybrids.
   Likewise, on bolls also, zero per cent larval survival was observed in
   all  Bt hybrids except JKCH 1947  Bt where 0.67 per cent larvae could
   manage to reach pre-pupal stage at 120 and 150 days old crop but failed
   to form cocoon and enter pupal stage. The surviving larva took more
   development time (3.7 to 5.4 days) as compared to larvae fed on bolls of
   JKCH 1947 non- Bt. The average survival period (ASP) of larvae was in
   order of 150 > 120 > 90 days old crop among the crop ages; JKCH 1947  Bt
   > MRC 6301  Bt > NCEH 6 R  Bt > MRC 7017 Bollgard II among  Bt hybrids;
   and bolls > squares between fruiting bodies. However, reverse was true
   for speed index of toxic effect. The concentration of Cry toxin varied
   significantly in squares and bolls and also among the crop ages. The
   amount of Cry toxin in squares and bolls had significant negative
   correlation with ASP of the  E. vittella larvae.
UT CABI:20163084441
SN 0334-2123
DI 10.1007/s12600-016-0505-6
ER

PT J
AU Guo YanYan
   Tian JunCe
   Shi WangPeng
   Dong XueHui
   Romeis, J.
   Naranjo, S. E.
   Hellmich, R. L.
   Shelton, A. M.
TI 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.
SO Transgenic Research
VL 25
IS 1
PS 33-44
PY 2016
AB 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:
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   Phytoseiidae) is a cosmopolitan predator of the two-spotted spider mite,
   Tetranychus urticae (Acari: Tetranychidae), a significant pest of cotton
   and maize. Tri-trophic studies were conducted to assess the potential
   effects of Cry1Ac/Cry2Ab cotton and Cry1F maize on life history
   parameters (survival rate, development time, fecundity and egg hatching
   rate) of  A. andersoni. We confirmed that these Bt crops have no effects
   on the biology of  T. urticae and, in turn, that there were no
   differences in any of the life history parameters of  A. andersoni when
   it fed on  T. urticae feeding on Cry1Ac/Cry2Ab or non-Bt cotton and
   Cry1F or non-Bt maize. Use of a susceptible insect assay demonstrated
   that  T. urticae contained biologically active Cry proteins. Cry
   proteins concentrations declined greatly as they moved from plants to
   herbivores to predators and protein concentration did not appear to be
   related to mite density. Free-choice experiments revealed that  A.
   andersoni had no preference for Cry1Ac/Cry2Ab cotton or Cry1F
   maize-reared  T. urticae compared with those reared on non-Bt cotton or
   maize. Collectively these results provide strong evidence that these
   crops can complement other integrated pest management tactics including
   biological control.
UT CABI:20163077149
SN 0962-8819
ER

PT J
AU Tumbalam, P.
   Thelen, K. D.
   Adkins, A.
   Dale, B.
   Balan, V.
   Gunawan, C.
   Gao, J.
TI Corn stover ethanol yield as affected by grain yield, Bt trait, and
   environment.
SO Biomass and Bioenergy
VL 85
PS 119-125
PY 2016
AB 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
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   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.
UT CABI:20163069703
SN 0961-9534
DI 10.1016/j.biombioe.2015.12.004
ER

PT J
AU Abbas, H. K.
   Bellaloui, N.
   Bruns, H. A.
TI Investigating transgenic corn hybrids as a method for mycotoxin control.
SO Food and Nutrition Sciences
VL 7
IS 1
PS 44-54
PY 2016
AB Transgenic Bt corn hybrids have been available for more than 10 years
   and are known to control specific insects. More recently, so-called
   "stacked-gene" hybrids, have been released with multiple insect
   resistance genes and genes for herbicide resistance, resulting in up to
   6 traits per plant. Because insect damage can lead to increased levels
   of mycotoxins, such as aflatoxins and fumonisin, we designed a study to
   compare ten commercially available corn hybrids, two non-transgenic,
   four with both herbicide and insect tolerance (stacked-gene) and four
   with glyphosate tolerance only to determine if any hybrid class had the
   advantage of reduced mycotoxin contamination. The experiment was carried
   out in the Mississippi State University Delta Research Extension fields
   in Stoneville, MS for two years in fine sandy loam and clay soil. Rows
   were either inoculated at the V10 stage of growth with toxigenic
   Aspergillus flavus K54 (NRRL 58987, isolated from corn kernels in
   Mississippi), grown on wheat, and applied at a rate of 22.42 kg/ha or
   allowed to become naturally infected with disease-producing fungi,
   including various  Fusarium and other  Aspergillus spp. Mycotoxin
   production differed according to the soil type with lower levels
   detected in the hybrids planted in clay soil vs. sandy soil. However, no
   significant differences in mycotoxin production were found amongst the
   hybrid classes. More research is needed to identify conditions under
   which transgenic hybrids might produce higher yields and lower mycotoxin
   levels. Presently, selection of transgenic hybrids will not replace
   integrated strategies of biocontrol, host plant resistance, or good crop
   management practices for achieving adequate mycotoxin control in corn.
UT CABI:20163068687
SN 2157-944X
DI 10.4236/fns.2016.71006
ER
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PT J
AU Wang YaNan
   Ke KaiQie
   Li YunHe
   Han LanZhi
   Liu YanMin
   Hua HongXia
   Peng YuFa
TI Comparison of three transgenic  Bt rice lines for insecticidal protein
   expression and resistance against a target pest,  Chilo suppressalis
   (Lepidoptera: Crambidae).
SO Insect Science
VL 23
IS 1
PS 78-87
PY 2016
AB 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.
UT CABI:20163075200
SN 1672-9609
DI 10.1111/1744-7917.12178
ER

PT J
AU Shen PeiLi
   Geng FengZhen
   Yu Yan
   Zhang YunZhe
   Wang ZhiXin
   Li ZhiHui
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   Zhang Wei
   Shu ChangLong
   Zhang YongJun
   Tan JianXin
TI A rapid loop-mediated isothermal amplification method for detection of
   the modified GM  cry1A gene in transgenic insect-resistant cotton and
   rice.
SO Food Control
VL 62
PS 357-364
PY 2016
AB 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°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.
UT CABI:20163052844
SN 0956-7135
DI 10.1016/j.foodcont.2015.10.035
ER

PT J
AU Shera, P. S.
   Ramesh Arora
TI Comparative study on oviposition and larval preference of spotted
   bollworm,  Earias vittella on Bt and non-Bt cotton.
SO Journal of Environmental Biology
VL 37
IS 1
PS 121-127
PY 2016
AB 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
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   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.
UT CABI:20163056907
SN 0254-8704
ER

PT J
AU Estes, R. E.
   Tinsley, N. A.
   Gray, M. E.
TI Evaluation of soil-applied insecticides with Bt maize for managing corn
   rootworm larval injury.
SO Journal of Applied Entomology
VL 140
IS 1/2
PS 19-27
PY 2016
AB The western corn rootworm,  Diabrotica virgifera virgifera LeConte, is
   considered one of the most significant insect pests of maize in North
   America. Larvae of other secondary subterranean pests such as grape
   colaspis,  Colaspis brunnea (F.), and Japanese beetle,  Popillia
   japonica Newman, can also injure maize seedlings and cause yield loss.
   In the past decade, maize hybrids containing Bt proteins have been used
   to manage the western corn rootworm; additionally, seeds are commonly
   treated with a neonicotinoid and fungicide combination to control
   secondary pests. Recently, soil-applied insecticides have been used in
   conjunction with rootworm Bt hybrids (and seed-applied insecticides) in
   areas with perceived risk for increased rootworm larval or secondary
   pest damage. We conducted a series of trials from 2009 to 2011 that
   examined multiple rootworm Bt hybrids and their near-isolines, along
   with two soil-applied insecticides, to determine whether the Bt plus
   insecticide combination resulted in an increased level of efficacy or
   yield. We also sampled for Japanese beetle and grape colaspis larvae to
   determine their potential for reducing yield. Densities of secondary
   pests in our trials were low and likely had no effect on maize yield.
   The addition of a soil-applied insecticide to rootworm Bt hybrids
   improved efficacy only once across 17 location-years, when overall corn
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   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.
UT CABI:20163032656
SN 0931-2048
ER

PT J
AU Li JingWei
   Li HouHua
   Wang RenRui
   Gao XiaoXia
   Wang QiaoChun
TI Cryopreservation for retaining morphology, genetic integrity, and
   foreign genes in transgenic plants of  Torenia fournieri.
SO Acta Physiologiae Plantarum
VL 38
IS 1
PS 8
PY 2016
AB 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.
UT CABI:20163024674
SN 0137-5881
ER

PT J
AU Palinkas, Z.
   Zalai, M.
   Szenasi, A.
   Kadar, F.
   Dorner, Z.
   Balog, A.
TI Rove beetles (Coleoptera Staphylinidae) - their abundance and
   competition with other predatory groups in Bt maize expressing Cry34Ab1,
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   Cry35Ab1, Cry1F and CP4 EPSPS proteins.
SO Crop Protection
VL 80
PS 87-93
PY 2016
AB 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.
UT CABI:20163025173
SN 0261-2194
ER

PT J
AU Deitloff, J.
   Dunbar, M. W.
   Ingber, D. A.
   Hibbard, B. E.
   Gassmann, A. J.
TI Effects of refuges on the evolution of resistance to transgenic corn by
   the western corn rootworm,  Diabrotica virgifera virgifera LeConte.
SO Pest Management Science
VL 72
IS 1
PS 190-198
PY 2016
AB 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
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   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.
UT CABI:20163022223
SN 1526-498X
DI 10.1002/ps.3988
ER

PT J
AU Liu YongBo
   Li JunSheng
   Luo ZunLan
   Wang HuaRu
   Liu Fang
TI The fate of fusion Cry1Ab/1Ac proteins from  Bt-transgenic rice in soil
   and water.
SO Ecotoxicology and Environmental Safety
VL 124
PS 455-459
PY 2016
AB Toxin proteins form 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.
UT CABI:20153446166
SN 0147-6513
ER

PT J
AU Xu XueLiang
   Xiao YeQing
   Ji XiangYun
   Liu ZiRong
   Chen LianSheng
   Jiang JieXian
   Chen DaZhou
   Hu LanXiang
   Yao YingJuan
TI Effect of the transgenic Bt rice variety "Ganlv 1" on the feeding,
   oviposition behavior and development of  Nilaparvata lugens (Stal).
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SO Chinese Journal of Applied Entomology
VL 52
IS 4
PS 977-982
PY 2015
AB Objectives: To assess the potential impact of the transgenic  cry1Ab/Ac
   rice variety "Ganlv 1" on the brown planthopper (BPH). Methods: The
   resistance of "Ganlv 1" and non-transgenic control rice to BPH was
   compared using the Standard Seedbox Screening Technique (SST). The
   feeding and oviposition behavior of BPH on "Ganlv 1" and control rice
   were measured by conducting a feeding and oviposition selectivity
   experiment. The effects of "Ganlv 1" on development (nymph duration and
   adult weight) and reproduction (number of offspring) of BPH were
   evaluated by feeding five successive BPH generations on this variety.
   Results: Both "Ganlv 1" and non-transgenic rice showed moderate
   resistance to BPH at the seedling stage. There were no significant
   differences in the feeding or oviposition preferences of BPH for "Ganlv
   1" vs the non-transgenic strain. No significant differences in nymph
   duration, adult weight and number of 2nd and 5th generation offspring
   were found between BPH fed on "Ganlv 1" and the non-transgenic strain,
   except that the duration of the 3rd instar of the 2nd generation fed on
   "Ganlv 1" was shorter than that fed on non-transgenic rice. Conclusion:
   There was no obvious adverse effect on the resistance of seedlings to
   BPH between the transgenic Bt rice "Ganlv 1" and a non-transgenic
   strain, nor were there significant differences in the feeding and
   oviposition preferences, or development, of BPH fed on "Ganlv 1"
   compared to those fed on the non-transgenic strain.
UT CABI:20163105932
SN 2095-1353
ER

PT J
AU Cayabyab, B. F.
   Alcantara, E. P.
   Sumalde, A. C.
   Gonzales, P. G.
   Cuaterno, W. R.
   Siegfried, B. D.
   Malenab, M. C.
   Belen, J. M.
   Ardez, K.
TI F 2 screening for rare resistance alleles of Asian Corn Borer,  Ostrinia
   furnacalis Guenee (Lepidoptera: Crambidae) in the Philippines.
SO Journal of ISSAAS (International Society for Southeast Asian
   Agricultural Sciences)
VL 21
IS 2
PS 1-7
PY 2015
AB Ostrinia furnacalis Guenee commonly known as Asian Corn Borer (ACB) is
   the major pest of corn in the Philippines. This study attempted to
   determine the frequency of Cry1Ab resistance alleles in ACB that will
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   serve as quantitative baseline data for monitoring ACB resistance in Bt
   corn in the Philippines. The initial frequency of Cry1Ab resistance
   alleles in ACB collected from corn farms in Lubao, Pampanga, Philippines
   was studied using the F2 screen method from March 2006 to December 2008.
   A total of 2,606 females of ACB were used to establish 800 isofemale
   lines. From these isofemale lines, 37,702 larvae from the F2 screen were
   susceptible to the toxin, Cry1Ab protein. The mortality rate for all the
   isofemale lines peaked during the first seven days of exposure to
   Cry1Ab. Two hundred fifty three (253) isofemale lines or 10% were
   observed to be partially positive to the toxin wherein four (4)
   isofemale lines (15, 19, 116, and 121) have survivors and successfully
   reached adult stage. However, due to the low survival of ACB larvae of
   each isolines, unsynchronized adult emergence and high percentage of
   male moth emergence, the re-testing of resistance to the isofemale lines
   were unsuccessful. Furthermore, an equal number of ACB larvae (37,702)
   were used for the control. A total of one thousand twenty seven (1,027)
   or 2.88% mortality was observed. This small percentage mortality from
   the control can be attributed to mechanical injury from handling. The
   calculated frequency of resistance alleles (E [ pR]) was 3.12*10 -4.
   This shows that the resistance allele is rare.
UT CABI:20163105339
SN 0859-3132
ER

PT J
AU Bernardi, O.
   Bernardi, D.
   Amado, D.
   Sousa, R. S.
   Fatoretto, J.
   Medeiros, F. C. L.
   Conville, J.
   Burd, T.
   Omoto, C.
TI Resistance risk assessment of  Spodoptera frugiperda (Lepidoptera:
   Noctuidae) and  Diatraea saccharalis (Lepidoptera: Crambidae) to
   Vip3Aa20 insecticidal protein expressed in corn.
SO Journal of Economic Entomology
VL 108
IS 6
PS 2711-2719
PY 2015
AB Transgenic Agrisure Viptera 3 corn that expresses Cry1Ab, Vip3Aa20, and
   EPSPS proteins and Agrisure Viptera expressing Vip3Aa20 are used for
   control of  Spodoptera frugiperda (J.E. Smith) and  Diatraea saccharalis
   (F.) in Brazil. To support a resistance management program, resistance
   risk assessment studies were conducted to characterize the dose
   expression of Vip3Aa20 protein and level of control against these
   species. The Vip3Aa20 expression in Agrisure Viptera 3 and Agrisure
   Viptera decreased from V6 to V10 stage of growth. However, Vip3Aa20
   expression in Agrisure Viptera 3 at V6 and V10 stages was 13- and
   16-fold greater than Cry1Ab, respectively. The Vip3Aa20 expression in
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   lyophilized tissue of Agrisure Viptera 3 and Agrisure Viptera diluted
   25-fold in an artificial diet caused complete larval mortality of  S.
   frugiperda and  D. saccharalis. In contrast, lyophilized tissue of Bt11
   at the same dilution does not provide complete mortality of these
   species. Agrisure Viptera 3 and Agrisure Viptera also caused a high
   level of mortality against  S. frugiperda and  D. saccharalis. Moreover,
   100% mortality was observed for  S. frugiperda larvae (neonates through
   fifth-instar larvae) when fed in corn with the Vip trait technology.
   Viptera corn achieves a high level of control against  S. frugiperda and
   D. saccharalis providing a high dose, which is an important
   determination to support the refuge strategy for an effective resistance
   management program.
UT CABI:20163077925
RI Omoto, Celso/D-9794-2012
OI Omoto, Celso/0000-0002-6432-830X
SN 0022-0493
DI 10.1093/jee/tov219
ER

PT J
AU Burkness, E. C.
   Cira, T. M.
   Moser, S. E.
   Hutchison, W. D.
TI Bt maize seed mixtures for  Helicoverpa zea (Lepidoptera: Noctuidae):
   larval movement, development, and survival on non-transgenic maize.
SO Journal of Economic Entomology
VL 108
IS 6
PS 2761-2769
PY 2015
AB In 2012 and 2013, field trials were conducted near Rosemount, MN, to
   assess the movement and development of  Helicoverpa zea (Boddie) larvae
   on non-Bt refuge corn plants within a seed mixture of non-Bt and Bt
   corn. The Bt corn hybrid expressed three Bt toxins - Cry1Ab, Cry1F, and
   Vip3A. As the use of seed mixtures for insect resistance management
   (IRM) continues to be implemented, it is necessary to further
   characterize how this IRM approach impacts resistance development in
   ear-feeding Lepidopteran pests. The potential for Bt pollen movement and
   cross pollination of the non-Bt ears in a seed mixture may lead to Bt
   toxin exposure to larvae developing on those refuge ears. Larval
   movement and development by  H. zea, feeding on non-Bt refuge plants
   adjacent to either transgenic Bt or non-Bt plants, were measured to
   investigate the potential for unintended Bt exposure. Non-Bt plants were
   infested with  H. zea eggs and subplots were destructively sampled twice
   per week within each treatment to assess larval development, location,
   and kernel injury. Results indicate that  H. zea larval movement between
   plants is relatively low, ranging from 2-16% of larvae, and occurs
   mainly after reaching the second instar. Refuge plants in seed mixtures
   did not produce equivalent numbers of  H. zea larvae, kernel injury, and
   larval development differed as compared with a pure stand of non-Bt
   plants. This suggests that there may be costs to larvae developing on
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   refuge plants within seed mixtures and additional studies are warranted
   to define potential impacts.
UT CABI:20163077931
SN 0022-0493
DI 10.1093/jee/tov253
ER

PT J
AU Sebastiao, I.
   Lemes, A. R. N.
   Figueiredo, C. S.
   Polanczyk, R. A.
   Desiderio, J. A.
   Lemos, M. V. F.
TI Toxicity and binding capacity of Cry1 proteins to  Helicoverpa armigera
   (Lepidoptera: Noctuidae) intestine receptors.
TI Toxicidade e capacidade de ligacao de proteinas cry1 a receptores
   intestinais de  Helicoverpa armigera (Lepidoptera: Noctuidae).
SO Pesquisa Agropecuaria Brasileira
VL 50
IS 11
PS 999-1005
PY 2015
AB The objective of this work was to evaluate the toxicity and the binding
   capacity of the Cry1Aa, Cry1Ab, Cry1Ac, and Cry1Ca proteins, from
   Bacillus thuringiensis, to  Helicoverpa armigera intestine receptors.
   Binding analysis of the activated proteins to the brush-border membrane
   vesicles (BBMV) in the midgut of  H. armigera, besides heterologous
   competition assays to evaluate their binding capacity, was performed.
   Cry1Ac stood out as the most toxic protein, followed by Cry1Ab and
   Cry1Aa. The Cry1Ca protein had no toxicity to the caterpillars and,
   therefore, it was not possible to evaluate its LC 50 and LC 90 toxicity
   parameters. The Cry1Aa, Cry1Ab, and Cry1Ac proteins are able to bind
   themselves to the same receptor in the midgut membrane, which increases
   the risk of developing cross-resistance. Therefore, the use of these
   proteins together should be avoided.
UT CABI:20163062546
SN 0100-204X
DI 10.1590/S0100-204X2015001100002
ER

PT J
AU Zeng HuiLan
   Tan FengXiao
   Shu YingHua
   Zhang YanYan
   Feng YuanJiao
   Wang JianWu
TI The Cry1Ab protein has minor effects on the arbuscular mycorrhizal
   fungal communities after five seasons of continuous Bt maize
   cultivation.
SO PLoS ONE
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VL 10
IS 12
PS e0146041
PY 2015
AB The cultivation of genetically modified plants (GMP) has raised concerns
   regarding the plants' ecological safety. A greenhouse experiment was
   conducted to assess the impact of five seasons of continuous Bt (
   Bacillus thuringiensis) maize cultivation on the colonisation and
   community structure of the non-target organisms arbuscular mycorrhizal
   fungi (AMF) in the maize roots, bulk soils and rhizospheric soils using
   the terminal restriction fragment length polymorphism (T-RFLP) analysis
   of the 28S ribosomal DNA and sequencing methods. AMF colonisation was
   significantly higher in the two Bt maize lines that express Cry1Ab,
   5422Bt1 (event Bt11) and 5422CBCL (MON810) than in the non-Bt isoline
   5422. No significant differences were observed in the diversity of the
   AMF community between the roots, bulk soils and rhizospheric soils of
   the Bt and non-Bt maize cultivars. The AMF genus  Glomus was dominant in
   most of the samples, as detected by DNA sequencing. A clustering
   analysis based on the DNA sequence data suggested that the sample types
   (i.e., the samples from the roots, bulk soils or rhizospheric soils)
   might have greater influence on the AMF community phylotypes than the
   maize cultivars. This study indicated that the Cry1Ab protein has minor
   effects on the AMF communities after five seasons of continuous Bt maize
   cultivation.
UT CABI:20163064834
SN 1932-6203
DI 10.1371/journal.pone.0146041
ER

PT J
AU Xing ZhenJuan
   Bai ShuXiong
   He KangLai
   Wang ZhenYing
TI Degradation dynamics of Cry1Ab insecticidal protein within transgenic
   Bacillus thuringiensis corn plant debris under different conditions.
SO Acta Phytophylacica Sinica
VL 42
IS 6
PS 1025-1029
PY 2015
AB In order to clarify the degradation dynamics of Cry1Ab insecticidal
   protein in the plant debris of  cry1Ab transgenic corn under different
   conditions, the contents of Cry1Ab protein in the  cry1Ab transgenic
   corn MON810 and Bt11 were quantified by using enzyme-linked
   immunosorbent essay (ELISA) method. The results showed that there were
   significant differences in the degradation rates of Cry1Ab insecticidal
   protein of MON810 and Bt11 under different conditions and sampling
   times. The degradation rate of Cry1Ab insecticidal protein in the whole
   plant was slower than that in the smashed plant debris. The degradation
   rate of the Cry1Ab insecticidal protein in the smashed stalks buried in
   the winter wheat field was faster than the other treatments. The
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   degradation rate of the Cry1Ab insecticidal protein in MON810 was slower
   than that of Bt11. The DT 50 of the Cry1Ab insecticidal protein in
   MON810 and Btll were 10.2-207.8, 13.6-124.0 d, and the DT 90 values were
   185.1-368.3, 45.2-224.0 d, respectively. The degradation rates of Cry1Ab
   insecticidal protein were different under different conditions. In four
   treatments, the degradation rate of Cry1Ab insecticidal protein in the
   smashed stalks buried in winter wheat field was the highest, followed by
   the smashed stalks buried in after-harvest corn field, in the smashed
   stalks placed on the surface of the soil, and in whole corn plants on
   the ground.
UT CABI:20163055003
SN 0577-7518
ER

PT J
AU Ye ShuiFeng
   Gao Xiang
TI Excavating abiotic stress-related gene resources of terrestrial
   macroscopic cyanobacteria for crop genetic engineering: dawn and
   challenge.
SO Bioengineered
VL 6
IS 6
PS 313-315
PY 2015
AB Genetically engineered (GE) crops with resistance to environmental
   stresses are one of the most important solutions for future food
   security. Numerous genes associated to plant stress resistance have been
   identified and characterized. However, the current reality is that only
   a few transgenic crops expressing prokaryotic genes are successfully
   applied in field conditions. These few prokaryotic genes include
   Agrobacterium strain CP4  EPSPS gene,  Bacillus thuringiensis Cry1Ab
   gene and a bacterial chaperonin gene. Thus, the excavation of
   potentially critical genes still remains an arduous task for crop
   engineering. Terrestrial macroscopic cyanobacteria,  Nostoc commune and
   Nostoc flagelliforme, which exhibit extreme resistance to desiccation
   stress, may serve as new prokaryotic bioresources for excavating
   critical genes. Recently, their marker gene  wspA was heterologously
   expressed in  Arabidopsis plant and the transgenics exhibited more
   flourishing root systems than wild-type plants under osmotic stress
   condition. In addition, some new genes associated with drought response
   and adaptation in  N. flagelliforme are being uncovered by our ongoing
   RNA-seq analysis. Although the relevant work about the terrestrial
   macroscopic cyanobacteria is still underway, we believe that the
   prospect of excavating their critical genes for application in GE crops
   is quite optimistic.
UT CABI:20163041184
SN 2165-5979
ER

PT J
AU Wang Fang
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   Ning Duo
   Chen Yang
   Dang Cong
   Han NaiShun
   Liu Yu'e
   Ye GongYin
TI Comparing gene expression profiles between Bt and non-Bt rice in
   response to brown planthopper infestation.
SO Frontiers in Plant Science
VL 6
IS December
PS 1181
PY 2015
AB Bt proteins are the most widely used insecticidal proteins in transgenic
   crops for improving insect resistance. We previously observed longer
   nymphal developmental duration and lower fecundity in brown planthopper
   (BPH) fed on Bt rice line KMD2, although Bt insecticidal protein Cry1Ab
   could rarely concentrate in this non-target rice pest. In the present
   study, we performed microarray analysis in an effort to detect
   Bt-independent variation, which might render Bt rice more defensive
   and/or less nutritious to BPH. We detected 3834 and 3273 differentially
   expressed probe-sets in response to BPH infestation in non-Bt parent
   Xiushui 11 and Bt rice KMD2, respectively, only 439 of which showed
   significant differences in expression between rice lines. Our analysis
   revealed a shift from growth to defense responses in response to BPH
   infestation, which was also detected in many other studies of plants
   suffering biotic and abiotic stresses. Chlorophyll biosynthesis and
   basic metabolism pathways were inhibited in response to infestation. IAA
   and GA levels decreased as a result of the repression of
   biosynthesis-related genes or the induction of inactivation-related
   genes. In accordance with these observations, a number of IAA-, GA-,
   BR-signaling genes were downregulated in response to BPH. Thus, the
   growth of rice plants under BPH attack was reduced and defense related
   hormone signaling like JA, SA and ET were activated. In addition,
   growth-related hormone signaling pathways, such as GA, BR, and auxin
   signaling pathways, as well as ABA, were also found to be involved in
   BPH-induced defense. On the other side, 51 probe-sets (represented 50
   genes) that most likely contribute to the impact of Bt rice on BPH were
   identified, including three early nodulin genes, four lipid metabolic
   genes, 14 stress response genes, three TF genes and genes with other
   functions. Two transcription factor genes,  bHLH and  MYB, together with
   lipid transfer protein genes  LTPL65 and early nodulin gene  ENOD93, are
   the most likely candidates for improving herbivore resistance in plants.

UT CABI:20163047085
SN 1664-462X
ER

PT J
AU Sartowska, K. E.
   Korwin-Kossakowska, A.
   Sender, G.
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TI Genetically modified crops in a 10-generation feeding trial on Japanese
   quails - evaluation of its influence on birds' performance and body
   composition.
SO Poultry Science
VL 94
IS 12
PS 2909-2916
PY 2015
AB The effect of genetically modified (GM) feed components comprising soya
   bean meal and maize on the performance indices (reproduction, survival
   rate, growth, egg production, relative weight of chosen internal organs,
   and basic chemical composition of breast muscle and egg yolk) of
   Japanese quails was investigated during a 10-generation trial. A total
   number of 8,438 healthy quail chicks were used in the course of the
   trial. In each generation, birds were maintained in 3 experimental
   groups differing in the main feed components, i.e. (1) GM soya (Roundup
   Ready) and non-GM maize, (2) GM maize (MON810) and non-GM soya, and (3)
   non-GM soya and maize. The different feeds used did not influence any of
   the biological hatch indices, survival rate, or BW of young or adult
   quails. With regard to egg-laying performance, the GM maize group showed
   a better laying percentage and a higher egg mass production compared to
   the other groups; the GM soya group showed reduced average egg mass
   compared to the other groups, whereas the overall egg production level
   was the same as in the control group. Results showed a higher relative
   weight of breast muscle and gizzard in birds fed GM maize compared to
   the control group, whereas live BW and the relative weights of liver and
   heart were not different among groups. Meat from the GM soya group
   showed higher protein and lower fat levels compared to the control
   group. In the case of egg yolk, its chemical composition in the
   experimental groups did not differ from the control group. Even though
   some differences were found among the feeding groups, none could be
   judged as a negative influence of GM maize or GM soya in feed on the
   birds or final consumer products over 10 generations of Japanese quails.
UT CABI:20163025783
RI Sender, Grazyna/K-2589-2012
SN 0032-5791
DI 10.3382/ps/pev271
ER

PT J
AU Bzowska-Bakalarz, M.
   Trendak, A.
   Marszalek, D.
   Pniak, M.
   Bagar, M.
   Czarnigowski, J.
BE Huyghebaert, B.
   Lorencowicz, E.
   Uziak, J.
TI Aerial method of plant protection with the use of an autogyro for
   sustainable agriculture.
SO Agriculture and Agricultural Science Procedia
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VL 7
PS 54-58
PY 2015
AB Despite the limitations in the use of aerial applications resulting from
   Directive 2009/128/EC of the European Parliament and of the Council and
   the Plant Protection Agents Act (OJ L item 455. 2013), scientific
   progress in engineering enables the development of new, environmentally
   safe technologies to expand the use of agroaviation. This paper proposes
   an innovative method of biological protection of corn against  Ostrinia
   nubilalis with the use of an autogyro and presents the results of these
   operations. An autogyro adaptation for forest applications is proposed,
   and the preliminary results of a spray uniformity assessment are
   presented. Based on a two-year study (542.5 ha), the introduction of the
   Tricholet preparation against  Ostrinia nubilalis was found to be highly
   effective (73.55%), which is a positive indication for the innovative
   autogyro method for introducing  Trichogramma evanescens. Similarly,
   positive results were obtained for a liquid agent application using an
   autogyro-mounted installation: an even coverage of the area was achieved
   across the entire spray path width while maintaining the required dosing
   of the plant protection agent.
UT CABI:20163016864
CT 7th International Scientific Symposium on Farm Machinery and Processes
   Management in Sustainable Agriculture, Gembloux, Belgium, 25-27 November
   2015.
SN 2210-7843
DI 10.1016/j.aaspro.2015.12.031
ER

PT J
AU Niedmann L., L.
TI Control of tomato moth ( Tuta absoluta M.) using a truncated  cry1Ab
   gene of a native delta-endotoxin of  Bacillus thuringiensis.
TI Control de la polilla del tomate ( Tuta absoluta M.) utilizando un gen
   truncado  Cry1ab de una delta-endotoxina nativa de  Bacillus
   thuringiensis.
SO Chilean Journal of Agricultural & Animal Sciences, ex Agro-Ciencia
VL 31
IS 3
PS 197-210
PY 2015
AB The tomato moth ( Tuta absoluta Meyrick) is the most devastating pest of
   tomato ( Solanum lycopersicum) in Chile, causing losses of 60 to 100% in
   fields not treated with insecticides. In addition, it has been found
   that a significant number of insects present levels of resistance to one
   or more chemical insecticides commonly used, while the number of insects
   doubles every six years. At present, this concern stimulates interest in
   the use of so-called 'biopesticides' which, unlike chemical pesticides,
   are environment-friendly and innocuous for other living beings. A great
   number of known species with insecticidal properties belongs to the
   genus  Bacillus, especially to the species  Bacillus thuringiensis (
   Bt). The insect comes in contact with the toxin when it eats the leaf
   tissue of plants previously sprayed with a suspension of  Bt. but there
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   are leaf miners, such as the larvae of tomato moth. The generation of
   transgenic plants that express the gene for a delta-endotoxin selected
   can avoid this problem. In this study, the lines transformed with the
   cry gene presented less damage compared to those untransformed (p<0.05;
   n=3).
UT CABI:20163011390
SN 0719-3882
ER

PT J
AU Ingber, D. A.
   Gassmann, A. J.
TI Inheritance and fitness costs of resistance to Cry3Bb1 corn by western
   corn rootworm (Coleoptera: Chrysomelidae).
SO Journal of Economic Entomology
VL 108
IS 5
PS 2421-2432
PY 2015
AB Transgenic crops that produce insecticidal toxins derived from the
   bacterium  Bacillus thuringiensis (Bt) are widely planted to manage pest
   insects. One of the primary pests targeted by Bt corn in the United
   States is western corn rootworm,  Diabrotica virgifera virgifera LeConte
   (Coleoptera: Chrysomelidae). Cry3Bb1 corn for management of western corn
   rootworm was commercialized in 2003, and beginning in 2009, populations
   of western corn rootworm with field-evolved resistance to Cry3Bb1 corn
   were found in Iowa. Here we quantify the magnitude, inheritance, and
   fitness costs of resistance to Cry3Bb1 corn in two strains (Hopkinton
   and Cresco) derived from field populations that evolved resistance to
   Cry3Bb1 corn. For Hopkinton, we found evidence for complete resistance
   to Cry3Bb1 corn and nonrecessive inheritance. Additionally, no fitness
   costs of Cry3Bb1 resistance were detected for Hopkinton. For Cresco,
   resistance was incomplete and recessive, and we detected fitness costs
   affecting developmental rate, survival to adulthood, and fecundity.
   These results suggest that variation may exist among field populations
   in both the inheritance and accompanying fitness costs of resistance. To
   the extent that field populations exhibit nonrecessive inheritance and a
   lack of fitness cost, this will favor more rapid evolution of resistance
   than would be expected when resistance is functionally recessive and is
   accompanied by fitness costs.
UT CABI:20163006963
SN 0022-0493
ER

PT J
AU Bannikova, M. A.
TI Detection of stress resistance genes in transgenic maize by multiplex
   and touchdown polymerase chain reaction.
SO Biopolymers and Cell
VL 31
IS 5
PS 362-370
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PY 2015
AB To develop a methodology for detection of the genes of resistance to the
   stress factors in transgenic maize by multiplex (mPCR) and touchdown
   polymerase chain reactions. Methods. Isolation of total DNA by CTAB
   method, purification of DNA from RNA and proteins, electrophoresis of
   total DNA and amplification products in agarose gel, polymerase chain
   reaction. Results. The protocol of multiplex and touchdown polymerase
   chain reactions has been developed for simultaneous verification of the
   quality of total DNA extracted from the studied maize plant samples and
   detection of the genes that determine resistance to the stress factors
   in the transgenic maize and maize transformation events: BT176, MON810,
   MON88017, DAS1507, DAS59122, MIR604, GA21, NK603 (mPCR), Bt11, MON863,
   MON89034, T25 (touchdown PCR). The multiplex PCR and touchdown PCR were
   developed using the reference samples. Conclusions. The proposed
   protocol of mPCR and touchdown PCR reactions can be used for mass
   analysis of maize samples to detect the genes of tolerance/resistance to
   herbicides and genes of resistance to insects reliably, authentically,
   quickly and cheaply.
UT CABI:20163004833
SN 0233-7657
DI 10.7124/bc.0008F8
ER

PT J
AU Gui FangYan
   Liu YuFang
   Mo ShuYin
   Sun LiChuan
   Liu WenHai
   Ge Feng
TI Ecological safety of transgenic  Cry1Ab/Ac rice on zoobenthos community
   in paddy fields.
SO Acta Phytophylacica Sinica
VL 42
IS 5
PS 715-723
PY 2015
AB To investigate the ecological safety of transgenic  Bt rice on the
   aquatic organisms in paddy fields, the effects of transgenic  Bt rice on
   zoobenthos community in paddy fields in Xiangtan, Hunan Province were
   studied by using community methodology. In this study, the transgenic
   Cry1Ab/Ac rice, Huahui No. 1 (HH1 for short) was the  Bt rice, while the
   non-transgenic parental rice Minghui 63 (MH63 for short) was used as
   control and benthic animal community in paddy fields was used as a
   bioindicator. The results in 2012 showed that 37 and 38 species of
   benthic animal were collected in paddy fields of HH1 and MH63 rice,
   respectively, with 31 species in common. The similarity of all species
   and that of dominant species in HH1 and MH63 fields was 0.8267 and
   0.8235, respectively. In 2013, 40 and 41 species of benthic animal were
   collected in paddy fields of HH1 and MH63 rice, respectively, with 33
   species in common. The similarity of all species and that of dominant
   species was 0.8148 and 0.9231, respectively. The temporal dynamics of
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   community parameters such as species richness, number of individuals,
   indexes of diversity, evenness and dominant concentration in HH1 and
   MH63 habitats in 2012 and 2013 showed the same trends and no significant
   difference were found. These results indicated that there were no
   significant adverse effects of transgenic  Cry1Ab/Ac rice on benthic
   animal community.
UT CABI:20153443393
SN 0577-7518
ER

PT J
AU Lang, A.
   Oehen, B.
   Ross, J. H.
   Bieri, K.
   Steinbrich, A.
TI Potential exposure of butterflies in protected habitats by  Bt maize
   cultivation: a case study in Switzerland.
SO Biological Conservation
VL 192
PS 369-377
PY 2015
AB Transgenic  Bt maize can produce insecticidal Cry proteins toxic to
   butterflies and moths (Lepidoptera). In protected habitats near maize
   fields,  Bt maize pollen containing the toxin can be drifted by wind
   onto host plants of Lepidoptera, and inadvertently harm lepidopteran
   larvae feeding on these host plants. For a heterogeneous, agricultural
   landscape in Switzerland, we investigated the butterfly community of
   protected habitats and their potential exposure to possible cultivation
   of  Bt maize, recorded the densities of maize pollen deposited on a
   butterfly host plant, simulated the effect of different pollen dispersal
   ranges and  Bt maize adoption rates on the exposure of protected
   habitats, and explored the consequences of different buffer zones around
   protected habitats. On average, the 49 recorded butterfly species showed
   a temporal overlap of larvae of 50.10%30.09% with the maize pollen
   shedding period. Mean maize pollen density on nettles ( Urtica dioica)
   was 6.4913.58 pollen/cm 2 (range: 0-100). Most of the pollen was
   deposited close to maize fields less than 30 m distance, but pollen also
   drifted onto host plants as far as 500 m away. In simulations, protected
   habitats were highly exposed to  Bt maize pollen deposition even at low
   adoption rates of  Bt maize, given that maize pollen is distributed to
   larger distances. The conflict between species conservation and  Bt
   maize cultivation could be minimised by establishing buffer zones around
   protected habitats, where non- Bt maize is grown. The results and the
   known sensitivities of lepidopteran larvae to  Bt suggest at least 50
   m-100 m broad buffer zones, and case-specific risk assessments for
   distances above 100 m.
UT CABI:20153445548
SN 0006-3207
DI 10.1016/j.biocon.2015.10.006
ER
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PT J
GA EFSA Panel on Genetically Modified Organisms
TI Revised annual post-market environmental monitoring (PMEM) report on the
   cultivation of genetically modified maize MON 810 in 2013 from Monsanto
   Europe S.A.
SO EFSA Journal
VL 13
IS 11
PS 4295
PY 2015
AB Following a request from the European Commission, the Panel on
   Genetically Modified Organisms of the European Food Safety Authority
   (EFSA GMO Panel) assessed the results of the general surveillance
   activities contained in the revised annual post-market environmental
   monitoring (PMEM) report for the 2013 growing season of maize MON 810
   provided by Monsanto Europe S.A. The supplied data do not indicate any
   unanticipated adverse effects on human and animal health or the
   environment arising from the cultivation of maize MON 810 cultivation in
   2013. Similar methodological shortcomings to those observed in previous
   annual PMEM reports were identified in the analysis of farmer
   questionnaires and the conduct of the literature review. The EFSA GMO
   Panel therefore strongly reiterates its previous recommendations to
   improve the methodology of future annual PMEM reports on maize MON 810.
   The EFSA GMO Panel urges the applicant to consider how to make best use
   of the information recorded in national registers in order to optimise
   sampling for farmer questionnaires, reiterates its previous
   recommendations on insect resistance monitoring and continued screening,
   and requests to continue reviewing and discussing relevant scientific
   publications on possible adverse effects of maize MON 810 on rove
   beetles. Also, the EFSA GMO Panel encourages relevant parties to
   continue developing a methodological framework to use existing networks
   in the broader context of environmental monitoring.
UT CABI:20153439637
SN 1831-4732
ER

PT J
AU Bernardi, D.
   Salmeron, E.
   Horikoshi, R. J.
   Bernardi, O.
   Dourado, P. M.
   Carvalho, R. A.
   Martinelli, S.
   Head, G. P.
   Omoto, C.
TI Cross-resistance between Cry1 proteins in fall armyworm ( Spodoptera
   frugiperda) may affect the durability of current pyramided Bt maize
   hybrids in Brazil.
SO PLoS ONE
VL 10
IS 10
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PS e0140130
PY 2015
AB Genetically modified plants expressing insecticidal proteins from
   Bacillus thuringiensis (Bt) offer valuable options for managing insect
   pests with considerable environmental and economic benefits. Despite the
   benefits provided by Bt crops, the continuous expression of these
   insecticidal proteins imposes strong selection for resistance in target
   pest populations. Bt maize ( Zea mays) hybrids have been successful in
   controlling fall armyworm ( Spodoptera frugiperda), the main maize pest
   in Brazil since 2008; however, field-evolved resistance to the protein
   Cry1F has recently been reported. Therefore it is important to assess
   the possibility of cross-resistance between Cry1F and other Cry proteins
   expressed in Bt maize hybrids. In this study, an F 2 screen followed by
   subsequent selection on MON 89034 maize was used to select an  S.
   frugiperda strain (RR) able to survive on the Bt maize event MON 89034,
   which expresses the Cry1A.105 and Cry2Ab2 proteins. Field-collected
   insects from maize expressing the Cry1F protein (event TC1507)
   represented most of the positive (resistance allele-containing)
   (iso)families found. The RR strain showed high levels of resistance to
   Cry1F, which apparently also conferred high levels of cross resistance
   to Cry1A.105 and Cry1Ab, but had only low-level (10-fold) resistance to
   Cry2Ab2. Life history studies to investigate fitness costs associated
   with the resistance in RR strain revealed only small reductions in
   reproductive rate when compared to susceptible and heterozygous strains,
   but the RR strain produced 32.2% and 28.4% fewer females from each
   female relative to the SS and RS (pooled) strains, respectively.
   Consistent with the lack of significant resistance to Cry2Ab2, MON 89034
   maize in combination with appropriate management practices continues to
   provide effective control of  S. frugiperda in Brazil. Nevertheless, the
   occurrence of Cry1F resistance in  S. frugiperda across Brazil, and the
   cross-resistance to Cry1Ab and Cry1A.105, indicates that current
   Cry1-based maize hybrids face a challenge in managing  S. frugiperda in
   Brazil and highlights the importance of effective insect resistance
   management for these technologies.
UT CABI:20153441046
RI Omoto, Celso/D-9794-2012
OI Omoto, Celso/0000-0002-6432-830X
SN 1932-6203
ER

PT J
AU Leenaars, J. G. B.
   Hengl, T.
   Gonzalez, M. R.
   Jesus, J. S. M. de
   Heuvelink, G. B. M.
   Wolf, J.
   Bussel, L. G. J. van
   Claessens, L.
   Yang, H.
   Cassman, K. G.
TI Root zone plant-available water holding capacity of the Sub-Saharan
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   Africa soil: gridded functional soil information (dataset RZ-PAWHC SSA
   version 1.0).
SO Report - ISRIC World Soil Information
IS 2015/02
PS 109 pp.
PY 2015
AB The objective of this project is to produce a robust, quantitative
   framework, which is updateable and spatially explicit, to generate and
   maintain functional soil information on root zone depth and associated
   plant available soil water holding capacity for a major rainfed staple
   food crop (maize) in Sub-Saharan Africa. In most cases, the rootable
   soil depth is considered to be an intrinsic soil property because it is
   difficult to modify the soil physical and chemical traits that restrict
   root growth, including high acidity or alkalinity, subsoil compaction,
   cemented layers, abrupt textural transitions, and bedrock. To achieve
   the project's objective, a collaborative project was established among
   the Africa Soil Information Service (AfSIS) project and the Global Yield
   Gap and Water Productivity Atlas (GYGA) project, both funded by the Bill
   and Melinda Gates Foundation. Partners in the AfSIS project
   (www.africasoils.net) are Columbia Global Centers, ICRAF and ISRIC.
   Partners in the GYGA project (www.yieldgap.org) are the University of
   Nebraska, Wageningen University, ICRISAT, and participating institutes
   and universities in ten Sub-Saharan countries. The collaborative project
   was led by ISRIC - World Soil Information. All soil data (field
   observations and laboratory measurements) and relevant covariate data (1
   km-250 m resolution imagery), as generated by the AfSIS project and
   publicly available, are used to assess and map the plant-available water
   holding capacity of the effective root zone depth of maize. Maps of
   primary soil properties are interpreted for producing maps of functional
   soil properties, including soil moisture retention characteristics
   derived by pedotransfer functions and root zone depth derived from rules
   and thresholds as developed for this study. The resulting functional
   soil information for Sub-Saharan Africa is publicly available as a
   gridded dataset at 1 km resolution, referred to as version 1.0 of the
   Root Zone Plant-Available Water Holding Capacity dataset (RZ-PAWHC SSA
   v.1.). The dataset is used by the GYGA project as input to simulation of
   crop yield potentials under water-limited (i.e. rainfed) production,
   including temporal variation, to estimate yield gaps in ten Sub-Saharan
   countries. Summarizing, the collaborative work developed a consistent
   and updateable high-resolution soil information framework for agronomic
   modelling in support of both long- and short-term goals of smallholder
   farmers in SSA.
UT CABI:20153438350
ER

PT J
AU Takacs, E.
   Nagy, A.
   Gelencser, E.
   Szekacs, A.
TI Internal Quality Control of an enzyme-linked immunoassay for Cry1Ab
   toxin detection applied in animal tissues.
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SO Acta Alimentaria (Budapest)
VL 44
IS 4
PS 593-600
PY 2015
AB Reliable determination of microbial or transgenic Cry toxins is an
   essential issue in food and feed analyses, and enzyme-linked
   immunosorbent assays (ELISAs) are the method of choice for quantifying
   these toxins currently in food and environmental analysis. Internal
   Quality Control (IQC) is an indispensable method to assess accuracy,
   precision, and reproducibility of analytical measurements. To assess the
   utility of the ELISA method, IQC was performed on EnviroLogix
   Cry1Ab/Cry1Ac QualiPlate ELISA with manufacturer supplied analytical
   standards. Applicability of negative and positive controls (C- and C+)
   was examined by Shewhart Control Charts for bias and Control Chart of
   the Range of Duplicates for precision. Linear regression (up to 5 ng ml
   -1 Cry1Ab concentration) of the commercial ELISA kit was compared to
   sigmoid calibration (up to 60 ng ml -1 Cry1Ab concentration). For
   immunoassay optimization process, possible matrix effects in different
   liquid and solid vertebrate tissues were examined by determination of
   the limit of detection values in these matrices.
UT CABI:20153423335
SN 0139-3006
DI 10.1556/066.2015.44.0032
ER

PT J
AU Hoss, S.
   Reiff, N.
   Ottermanns, R.
   Pagel-Wieder, S.
   Dohrmann, A. B.
   Tebbe, C. C.
   Traunspurger, W.
TI Risk assessment of the cultivation of a stacked Bt-maize variety
   (MON89034 * MON88017) for nematode communities.
SO Soil Biology & Biochemistry
VL 91
PS 109-118
PY 2015
AB Genetically modified Bt-maize MON89034 * MON88017 contains three
   different genes derived from  Bacillus thuringiensis (Bt) which enable
   protection against insect pests, due to expression of three different
   insecticidal crystal proteins (Cry proteins), i.e., Cry1A.105 and
   Cry2Ab2 against the European corn borer and Cry3Bb1 against the Western
   corn root worm. Nematodes are important organisms in agricultural soil
   ecosystems, and on fields with Bt-maize cultivation they will be exposed
   to Cry proteins released into the soil from roots or plant residues. The
   objective of this study was to analyze in a field experiment the effect
   of Bt-maize MON89034 * MON88017 on nematodes as non-target organisms.
   Nematode communities from soil planted with the Bt-maize were compared
   to those from soil planted with the near-isogenic cultivar (with and
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   without chemical insecticide treatment) and two conventional maize
   cultivars. The experimental field consisted of 40 plots in a completely
   randomized block design (eight plots for each treatment), which were
   monitored over two growing seasons (2008 and 2009) at six sampling dates
   for nematode diversity at the genus level in the rhizosphere soil.
   Physicochemical soil properties and Cry protein concentrations were also
   analyzed. Nematodes showed very high abundances, as well as a high
   diversity of taxa and functional guilds, indicating the relevance of
   maize fields as their habitat. Neither Bt-maize cultivation, nor
   insecticide treatment adversely affected abundance or community
   structure of nematode assemblages in field plots compared to several
   non-Bt cultivars including a near-isogenic cultivar. This confirmed the
   risk estimations based on the analyzed soil concentrations of
   extractable Cry protein, not exceeding 4.8 ng g -1 soil dry weight and
   thus revealing a safe toxicity-exposure ratio of >20.
UT CABI:20153419525
SN 0038-0717
ER

PT J
AU Liu Xin
   Zhang JiWen
   Zhang CuiCui
   Wang LiangChao
   Chen Hao
   Zhu ZengRong
   Tu JuMin
TI Development of photoperiod- and thermo-sensitive male sterility rice
   expressing transgene  Bacillus thuringiensis.
SO Breeding Science
VL 65
IS 4
PS 333-339
PY 2015
AB Stem borers and leaffolders are the main pests that cause severe damage
   in rice ( Oryza sativa L.) production worldwide. We developed the first
   photoperiod- and thermo-sensitive male sterility (PTSMS) rice 208S with
   the  cry1Ab/1Ac Bacillus thuringiensis ( Bt) gene, through sexual
   crossing with Huahui 1 (elite line with the  cry1Ab/1Ac gene). The novel
   208S and its hybrids presented high and stable resistance to stem borers
   and leaffolders, and the content of Cry1Ab/1Ac protein in chlorophyllous
   tissues achieved the identical level as donor and showed little
   accumulation in non-chlorophyllous tissue. No dominant dosage effect in
   the  Bt gene was observed in 208S and its derived hybrids. An analysis
   of fertility transition traits indicated that 208S was completely
   sterile under long day length/high temperature, but partially fertile
   under short day length/low temperature. With fine grain quality and
   favorable combining ability, 208S had no observed negative effects on
   fertility and agronomic traits from  Bt ( cry1Ab/1Ac). Additionally,
   208S as a male sterile line showed no fertility decrease caused by  Bt
   transgenic process, as it is the case in Huahui 1. Thus, 208S has great
   application value in two-line hybrid production for insect resistance,
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   and can also be used as a bridge material in rice  Bt transgenic
   breeding.
UT CABI:20153409844
SN 1344-7610
ER

PT J
AU Chen Yang
   Lai FengXiang
   Sun YanQun
   Hong LiYing
   Tian JunCe
   Zhang ZhiTao
   Fu Qiang
TI CrylAb rice does not impact biological characters and functional
   response of  Cyrtorhinus lividipennis preying on  Nilaparvata lugens
   eggs.
SO Journal of Integrative Agriculture
VL 14
IS 10
PS 2011-2018
PY 2015
AB One concern about the use of transgenic plants is their potential risk
   to natural enemies. In this study, using the eggs of the rice brown
   planthopper,  Nilaparvata lugens, as a food source, we investigated the
   effects of Cry1Ab rice on the biological characteristics and functional
   response of an important predator  Cyrtorhinus lividipennis. The results
   showed that the survival ability (adult emergence rate and egg hatching
   rate), development (egg duration, nymphal developmental duration), adult
   fresh weight, adult longevity and fecundity of  C. lividipennis on Bt
   rice plants were not significantly different compared to those on non-Bt
   rice plants. Furthermore, two important parameters of functional
   response (instantaneous search rate and handling time) were not
   significantly affected by Bt rice. In conclusion, the tested Cry1Ab rice
   does not adversely impact the biological character and functional
   response of  C. lividipennis.
UT CABI:20153412630
SN 2095-3119
DI 10.1016/S2095-3119(14)60978-3
ER

PT J
AU Welch, K. L.
   Unnithan, G. C.
   Degain, B. A.
   Wei JiZhen
   Zhang Jie
   Li XianChun
   Tabashnik, B. E.
   Carriere, Y.
TI Cross-resistance to toxins used in pyramided Bt crops and resistance to
   Bt sprays in  Helicoverpa zea.
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SO Journal of Invertebrate Pathology
VL 132
PS 149-156
PY 2015
AB To delay evolution of resistance by insect pests, farmers are rapidly
   increasing their use of transgenic crops producing two or more  Bacillus
   thuringiensis (Bt) toxins that kill the same pest. A key condition
   favoring durability of these "pyramided" crops is the absence of
   cross-resistance between toxins. Here we evaluated cross-resistance in
   the major lepidopteran pest  Helicoverpa zea (Boddie) to Bt toxins used
   in pyramids. In the laboratory, we selected a strain of this pest with
   Bt toxin Cry1Ac followed by selection with MVP II, a formulation
   containing a hybrid protoxin that is identical to Cry1Ac in the active
   portion of the toxin and 98.5% identical overall. We calculated the
   resistance ratio as the EC 50 (concentration causing mortality or
   failure to develop beyond the first instar of 50% of larvae) for the
   laboratory-selected strain divided by the EC 50 for its field-derived
   parent strain that was not selected in the laboratory. The resistance
   ratio was 20.0-33.9 (mean=27.0) for MVP II, 57.0 for Cry1Ac, 51.3 for
   Cry1A.105, 22.4 for Cry1Ab, 3.3 for Cry2Ab, 1.8 for Cry1Fa, and 1.6 for
   Vip3Aa. Resistance ratios were 2.9 for DiPel ES and 2.0 for Agree VG,
   which are commercial Bt spray formulations containing Cry1Ac, other Bt
   toxins, and Bt spores. By the conservative criterion of non-overlap of
   95% fiducial limits, the EC 50 was significantly higher for the selected
   strain than its parent strain for MVP II, Cry1Ac, Cry1A.105, Cry1Ab,
   Cry2Ab and DiPel ES. For Cry1Fa, Vip3Aa, and Agree VG, significantly
   lower susceptibility to a high concentration indicated low
   cross-resistance. The resistance ratio for toxins other than Cry1Ac was
   associated with their amino acid sequence similarity to Cry1Ac in domain
   II. Resistance to Cry1Ac and the observed cross-resistance to other Bt
   toxins could accelerate evolution of  H. zea resistance to currently
   registered Bt sprays and pyramided Bt crops.
UT CABI:20153411570
SN 0022-2011
ER

PT J
AU Dai PingLi
   Zhou Wei
   Zhang Jie
   Lang ZhiHong
   Zhou Ting
   Wang Qiang
   Cui HongJuan
   Jiang WeiYu
   Wu YanYan
TI Effects of Bt  cry1Ah corn pollen on immature worker survival and
   development of  Apis cerana cerana.
SO Journal of Apicultural Research
VL 54
IS 1
PS 72-76
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PY 2015
AB The honey bee may be exposed to insecticidal proteins from transgenic
   plants via pollen. An assessment of the impact of such exposures on the
   honey bee is an essential part of the risk assessment process for
   transgenic  Bacillus thuringiensis (Bt) corn. The effects of dietary
   transgenic Bt corn pollen on honey bee immature workers of  Apis cerana
   cerana were examined by feeding trials in colonies. Four- to six-day-old
   honey bee worker larvae were fed various pollens ( cry1Ah corn pollen,
   regular corn pollen, mixed bee pollen and control) and then sampled to
   record their survival and development. There were no significant
   differences in capping rate, emergence rate and immature stage among
   treatments. Our studies suggest that  cry1Ah corn pollen carries no risk
   for the survival and development of  A. c. cerana immature workers.
UT CABI:20153404602
SN 0021-8839
ER

PT J
AU Yang Fei
   Kerns, D.
   Huang FangNeng
TI Refuge-in-the-bag strategy for managing insect resistance to Bt maize.
SO Outlooks on Pest Management
VL 26
IS 5
PS 226-228
PY 2015
UT CABI:20153376006
SN 1743-1026
DI 10.1564/v26_oct_10
ER

PT J
AU Li ZeYang
   Gao Yang
   Zhang MinHong
   Feng JingHai
   Xiong YanDan
TI Effects of a diet containing genetically modified rice expressing the
   Cry1 Ab/1 Ac protein ( Bacillus thuringiensis toxin) on broiler
   chickens.
SO Archives of Animal Nutrition
VL 69
IS 6
PS 487-498
PY 2015
AB The aim of this study was to evaluate the effect of feeding  Bacillus
   thuringiensis ( Bt) rice expressing the  Cry1 Ab/1 Ac protein on broiler
   chicken. The genetically modified (GM)  Bt rice was compared with the
   corresponding non-GM rice regarding performance of feeding groups, their
   health status, relative organ weights, biochemical serum parameters and
   occurrence of  Cry1 Ab/1 Ac gene fragments. One hundred and eighty
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   day-old Arbor Acres female broilers with the same health condition were
   randomly allocated to the two treatments (6 replicate cages with 15
   broilers in each cage per treatment). They received diets containing GM
   rice (GM group) or its parental non-GM rice (non-GM group) at 52-57% of
   the air-dried diet for 42 days. The results show that the transgenic
   rice had a similar nutrient composition as the non-GM rice and had no
   adverse effects on chicken growth, biochemical serum parameters and
   necropsy during the 42-day feeding period. In birds fed the GM rice, no
   transgenic gene fragments were detected in the samples of blood, liver,
   kidneys, spleen, jejunum, ileum, duodenum and muscle tissue. In
   conclusion, the results suggest that  Bt rice expressing  Cry1 Ab/1 Ac
   protein has no adverse effects on broiler chicken. Therefore, it can be
   considered as safe and used as feed source for broiler chicken.
UT CABI:20153396773
SN 1745-039X
ER

PT J
AU Lee JinSeok
   Jung TaeWook
   Son BeomYoung
   Shin SeongHyu
   Kim JungTae
   Bae HwanHee
   Baek SeongBum
   Ku JaHwan
   Hwang JongJin
   Kim SunLim
   Kim SungKook
   Kwon YoungUp
   Lee JeomHo
TI A white waxy corn hybrid with lodging tolerance, 'Hayanchal95'.
SO Korean Journal of Breeding Science
VL 47
IS 3
PS 306-311
PY 2015
AB A 'Hayanchal95', a new waxy corn hybrid, is a single cross hybrid
   developed by the maize breeding team at the National Institute of Crop
   Science (NICS), Rural Development Administration (RDA) in 2011. This
   hybrid was made by crossing between seed parent KW44 and pollen parent
   KW35. Days to silking of Hayanchal95 was three days earlier than
   Ilmichal, a check hybrid. Ear length and diameter of Hayanchal95 were
   18.3 cm and 4.1 cm, respectively. The ratio of kernel set length to ear
   length was 90% and lower than Ilmichal. Its quality characteristics like
   amylopectin content, hardness of kernels, and value of sensory
   evaluation were not significantly different from Ilmichal except grain
   length. Resistance to corn borer and lodging tolerance of Hayanchal95
   were better than Ilmichal. The number of fresh ears was similar to those
   of Ilmichal and weight of fresh ears was lower than Ilmichal in regional
   yield trials (RYT) from 2009 to 2011. Although flowering time of its
   parent lines was good match during crossing between the seed and pollen
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   parents, seed production was low. It is adaptable to the whole country.
   Plant variety protection right of 'Hayanchal95' was registered in July
   2014, and its grant number is 5110.
UT CABI:20153395281
SN 0250-3360
ER

PT J
AU Zhao Can
   Jurat-Fuentes, J. L.
   Abdelgaffar, H. M.
   Pan HongYu
   Song FuPing
   Zhang Jie
TI Identification of a new  cry1I-type gene as a candidate for gene
   pyramiding in corn to control  Ostrinia species larvae.
SO Applied and Environmental Microbiology
VL 81
IS 11
PS 3699-3705
PY 2015
AB Pyramiding of diverse  cry toxin genes from  Bacillus thuringiensis with
   different modes of action is a desirable strategy to delay the evolution
   of resistance in the European corn borer ( Ostrinia nubilalis).
   Considering the dependency of susceptibility to Cry toxins on toxin
   binding to receptors in the midgut of target pests, a diverse mode of
   action is commonly defined as recognition of unique binding sites in the
   target insect. In this study, we present a novel  cry1Ie toxin gene (
   cry1Ie2) as a candidate for pyramiding with Cry1Ab or Cry1Fa in corn to
   control  Ostrinia species larvae. The new toxin gene encodes an 81-kDa
   protein that is processed to a protease-resistant core form of
   approximately 55 kDa by trypsin digestion. The purified protoxin
   displayed high toxicity to  Ostrinia furnacalis and  O. nubilalis larvae
   but low to no activity against  Spodoptera or heliothine species or the
   coleopteran  Tenebrio molitor. Results of binding assays with
   125I-labeled Cry1Ab toxin and brush border membrane vesicles from  O.
   nubilalis larvae demonstrated that Cry1Ie2 does not recognize the Cry1Ab
   binding sites in that insect. Reciprocal competition binding assays with
   biotin-labeled Cry1Ie2 confirmed the lack of shared sites with Cry1Ab or
   Cry1Fa in  O. nubilalis brush border membrane vesicles. These data
   support Cry1Ie2 as a good candidate for pyramiding with Cry1Ab or Cry1Fa
   in corn to increase the control of  O. nubilalis and reduce the risk of
   resistance evolution.
UT CABI:20153387856
OI Jurat-Fuentes, Juan Luis/0000-0002-8945-1814
SN 0099-2240
ER

PT J
AU Garcia, M.
   Ortego, F.
   Hernandez-Crespo, P.
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   Farinos, G. P.
   Castanera, P.
TI Inheritance, fitness costs, incomplete resistance and feeding
   preferences in a laboratory-selected MON810-resistant strain of the true
   armyworm  Mythimna unipuncta.
SO Pest Management Science
VL 71
IS 12
PS 1631-1639
PY 2015
AB BACKGROUND: The low efficacy of MON810 maize against  Mythimna unipuncta
   represents a scenario of non-compliance with the 'high-dose' strategy,
   raising concerns about potential resistance development and outbreaks of
   this secondary pest. The present study offers insight into the different
   components related to resistance in a laboratory-selected
   MON810-resistant (MR) strain of  M. unipuncta. RESULTS: The resistance
   in the MR strain is autosomal and inherited as a partially dominant
   trait. We have found a lack of fitness costs in this strain for
   essential life history traits, reproductive potential and most of the
   population growth parameters analysed, the only exception being an
   increment in the mean generation time. Larvae of the MR strain reared on
   Bacillus thuringiensis ( Bt) maize took longer to develop, presented a
   high adult cumulative emergence time and had lower growth rate than
   those reared on non- Bt maize, suggesting the existence of incomplete
   resistance. Feeding preference assays reveal a low discrimination
   between  Bt and conventional maize. CONCLUSION: Both resistant and
   heterozygous larvae of  M. unipuncta survive the Cry1Ab toxin expressed
   on  Bt maize, with a weak fitness cost for the homozygous larvae,
   indicating the potential risk of field-evolved resistance and its
   relevance to resistance monitoring.
UT CABI:20153388855
RI Ortego, Felix/F-9402-2011; Pedro, Hernandez-Crespo/H-9937-2015;
OI Pedro, Hernandez-Crespo/0000-0001-9350-3640; GARCIA,
   MATIAS/0000-0003-1428-9733
SN 1526-498X
DI 10.1002/ps.3971
ER

PT J
AU Reisig, D. D.
   Reay-Jones, F. P. F.
TI Inhibition of  Helicoverpa zea (Lepidoptera: Noctuidae) growth by
   transgenic corn expressing Bt toxins and development of resistance to
   Cry1Ab.
SO Environmental Entomology
VL 44
IS 4
PS 1275-1285
PY 2015
AB Transgenic corn,  Zea mays L., that expresses the  Bacillus
   thuringiensis (Bt) toxin Cry1Ab is only moderately toxic to  Helicoverpa
   zea (Boddie) and has been planted commercially since 1996. Growth and
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   development of  H. zea was monitored to determine potential changes in
   susceptibility to this toxin over time. Small plots of corn hybrids
   expressing Cry1F, Cry1F * Cry1Ab, Cry1Ab * Cry3Bb1, Cry1A.105 * Cry2Ab2
   * Cry3Bb1, Cry1A.105 * Cry2Ab2, and Vip3Aa20 * Cry1Ab * mCry3A were
   planted in both 2012 and 2013 in North and South Carolina with paired
   non-Bt hybrids from the same genetic background.  H. zea larvae were
   sampled on three time periods from ears and the following factors were
   measured: kernel area injured (cm 2) by  H. zea larvae, larval number
   per ear, larval weight, larval length, and larval head width. Pupae were
   sampled on a single time period and the following factors recorded:
   number per ear, weight, time to eclosion, and the number that eclosed.
   There was no reduction in larval weight, number of insect entering the
   pupal stadium, pupal weight, time to eclosion, and number of pupae able
   to successfully eclose to adulthood in the hybrid expressing Cry1Ab
   compared with a non-Bt paired hybrid. As Cry1Ab affected these in 1996,
   H. zea may be developing resistance to Cry1Ab in corn, although these
   results are not comprehensive, given the limited sampling period, size,
   and geography. We also found that the negative impacts on larval growth
   and development were greater in corn hybrids with pyramided traits
   compared with single traits.
UT CABI:20153375148
SN 0046-225X
DI 10.1093/ee/nvv076
ER

PT J
AU Hitchon, A. J.
   Smith, J. L.
   French, B. W.
   Schaafsma, A. W.
TI Impact of the Bt corn proteins Cry34/35Ab1 and Cry3Bb1, alone or
   pyramided, on western corn rootworm (Coleoptera: Chrysomelidae) beetle
   emergence in the field.
SO Journal of Economic Entomology
VL 108
IS 4
PS 1986-1993
PY 2015
AB Western corn rootworm,  Diabrotica virgifera virgifera LeConte, is a
   major pest of corn,  Zea mays L. The effect of the Bt proteins
   Cry34/35Ab1 and Cry3Bb1, alone or pyramided in corn hybrids on  D. v.
   virgifera adult emergence was evaluated in field experiments for 3 yr.
   Experiments were infested artificially with 2,500 viable  D. v.
   virgifera eggs per row meter of corn. The reduction in beetle emergence
   compared with non-Bt controls, from Cry34/35Ab1, Cry3Bb1, and the
   pyramided hybrids ranged from 64.3 to 97.4%, 91.1 to 95.2%, and 98.1 to
   99.6%, respectively. The sex ratio of emerged beetles was usually
   female-biased from the Cry3Bb1 and pyramided treatments, but not from
   Cry34/35Ab1 treatment alone. Emergence from all Bt hybrids was delayed
   compared with the control, with the delay longest from the pyramided
   hybrid. In 2013, three egg infestation levels were tested, with
   densitydependent mortality observed at 1,250 viable eggs per row meter.
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   The effect of Bt proteins on the emergence timing and sex ratio of  D.
   v. virgifera may impact the suitability of resistance management plans,
   specifically the effectiveness of the refuge strategy. Susceptible males
   emerging from refuge might not be synchronized to mate with potentially
   resistant females emerging later from Bt corn hybrids.
UT CABI:20153368981
SN 0022-0493
DI 10.1093/jee/tov125
ER

PT J
AU Grohmann, L.
   Reiting, R.
   Made, D.
   Uhlig, S.
   Simon, K.
   Frost, K.
   Randhawa, G. J.
   Zur, K.
TI Collaborative trial validation of cry1Ab/Ac and Pubi-cry TaqMan-based
   real-time PCR assays for detection of DNA derived from genetically
   modified Bt plant products.
SO Accreditation and Quality Assurance
VL 20
IS 2
PS 85-96
PY 2015
AB Presence of genetic modifications in rice products originating from
   China and imported to the European Union market is detected since 2006.
   Neither these products from China nor any other genetically modified
   rice lines are approved as food or feed in the EU. The transgenic rice
   varieties identified contain genetic elements and constructs coding for
   insect-resistance genes from  Bacillus thuringiensis (Bt) coding for
   insecticidal crystal (cry) proteins. In particular, DNA sequences coding
   for codon-optimised or fused cry1Ab/c genes and constructs driven by the
   maize ubiquitin promoter (P-ubiZM1) were identified. For improved
   screening and identification of genetic modifications present in Asian
   rice products, two TaqMan-based real-time PCR assays targeting
   codon-optimised cry1Ab/Ac and the Pubi-cry construct have been
   developed. These assays have been validated in an international
   collaborative trial with 17 participants from 10 countries. Based on a
   new mathematical-statistical model and an adjusted experimental set-up
   of the collaborative trial, a close examination of the limit of
   detection ( LOD95%) and the probability of detection of the qualitative
   PCR assays was conducted. The evaluation of the method performance
   characteristics and results of the collaborative trial validation are
   presented.
UT CABI:20153361815
SN 0949-1775
DI 10.1007/s00769-015-1108-5
ER
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PT J
AU Lang, A.
   Otto, M.
TI Feeding behaviour on host plants may influence potential exposure to  Bt
   maize pollen of  Aglais urticae larvae (Lepidoptera, Nymphalidae).
SO Insects
VL 6
IS 3
PS 760-771
PY 2015
AB Non-target butterfly larvae may be harmed by feeding on host plants
   dusted with  Bt maize pollen. Feeding patterns of larvae and their
   utilization of host plants can affect the adverse  Bt impact because the
   maize pollen is distributed unequally on the plant. In a field study, we
   investigated the feeding of larvae of the Small Tortoiseshell,  Aglais
   urticae, on nettles,  Urtica dioica. Young larvae used smaller host
   plants than older larvae. In general, the position of the larvae was in
   the top part of the host plant, but older larvae showed a broader
   vertical distribution on the nettles. Leaf blades and leaf tips were the
   plant parts most often consumed. Leaf veins were consumed but midribs
   were fed on to a lesser extent than other plant veins, particularly by
   young larvae. The feeding behavior of the larvae may increase possible
   exposure to  Bt maize pollen because pollen densities are expected to be
   higher on the top parts and along leaf veins of nettles.
UT CABI:20153360842
SN 2075-4450
DI 10.3390/insects6030760
ER

PT J
AU Gui FangYan
   Liu YuFang
   Mo ShuYin
   Sun LiChuan
   Sun YuanDong
   Liu WenHai
   Ge Feng
TI Effects of transgenic  Cry1Ab/Ac rice on zoobenthos communities in paddy
   fields.
SO Zhongguo Shengtai Nongye Xuebao / Chinese Journal of Eco-Agriculture
VL 23
IS 9
PS 1178-1184
PY 2015
AB Transgenic  Bt rice has been developed successfully and has provided an
   effective and economical control on lepidopterous pests in rice field.
   Zoobenthos in paddy fields is an important non-target organism for
   transgenic  Bt rice. To understand the safety of transgenic  Bt rice on
   zoobenthos community in paddy fields, the effects of transgenic
   Cry1Ab/Ac rice on zoobenthos community were studied in paddy fields
   using the community method. The experiment was conducted in
   2-consecutive-year field of transgenic  Cry1Ab/Ac rice 'Huahui No. 1'
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   (HH1 for short) in Nanchang, Jiangxi Province. The non-transgenic parent
   rice 'Minghui 63' (MH63 for short) was used as control treatment.
   Benthic animal community in paddy fields was used as bio-indicator. In
   2012, some 22 and 25 species of benthic animals were respectively
   collected in HH1 and MH63 paddy fields. There were 19 species in common
   and 7 dominant species in zoobenthos communities in HH1 and MH63 paddy
   fields. The similarity of all the species and the dominant species of
   zoobenthos communities in HH1 and MH63 habitats were 0.808 5 and 0.833
   3, respectively. In 2013, 26 and 28 species of benthic animals were
   collected in paddy fields planted respectively with HH1 and MH63,
   comprising of 22 common and 6 dominant species. The similarity of all
   the species and the dominant species of zoobenthos communities in HH1
   and MH63 paddy fields were respectively 0.814 8 and 1.000 0. Analyses of
   both total and temporal dynamics of community parameters such as the
   indexes of species richness, individual number, diversity, evenness and
   dominance in HH1 and MH63 paddy fields in 2012 and 2013 displayed
   similar rates and trends and with no observed significant difference.
   Analysis of HH1 field (with 2 consecutive years of cultivation) in
   Nanchang suggested that transgenic  Cry1Ab/Ac rice had no obvious
   adverse effect on benthic animal community.
UT CABI:20153360108
SN 1671-3990
ER

PT J
AU Szenasi, A.
   Marko, V.
TI Flea beetles (Coleoptera: Chrysomelidae, Alticinae) in Bt- (MON810) and
   near isogenic maize stands: species composition and activity densities
   in Hungarian fields.
SO Crop Protection
VL 77
PS 38-44
PY 2015
AB Flea beetles (Chrysomelidae, Alticinae) were collected with Pherocon AM
   yellow sticky traps in maize plots to compare the assemblages from
   transgenic Bt- (genetic event MON810, producing Cry1Ab protein effective
   against lepidopteran pests) and near isogenic maize in Hungary.
   Altogether, 51,348 flea beetle individuals from 26 species were
   collected. The dominant species were  Phyllotreta atra (F.) and
   Phyllotreta vittula (Redtenbacher). Their abundances along with other
   (non- P. atra and non- P. vittula) flea beetle species showed no
   significant differences between Bt- and isogenic maize plots. Similarly,
   no difference was found between Bt maize and isogenic maize plots in the
   species richness of the flea beetle assemblages.
UT CABI:20153352041
SN 0261-2194
DI 10.1016/j.cropro.2015.07.008
ER

PT J
AU Rahman, M.
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   Muhammad Zaman
   Tayyaba Shaheen
   Samra Irem
   Yusuf Zafar
TI Safe use of  Cry genes in genetically modified crops.
SO Environmental Chemistry Letters
VL 13
IS 3
PS 239-249
PY 2015
AB Genomic technologies have been used to improve cultivated crop species.
   For example,  Bt genes such as  Cry1Ac,  Cry2Ab,  Cry1F and  Cry3Bb1 are
   derived from  Bacillus thuringiensis, a soil bacterium. Such genes
   provide protection against lepidopteran insect pests.  Bt genes have
   been introduced in corn, cotton, soybean, rice, potato and canola.
   Genetically modified (GM)-cotton, containing the  Cry1Ac gene, was
   released for cultivation in the mid-1990s in the USA and later in 28
   countries including China and India. Potential harmful effects of the
   Bt-crops on non-targets were assessed before release into the
   environment. Most commonly, cultivation of the Bt-crops was found safe.
   Safety was tested using various experiments including: the insertional
   impact of transgene and its regulatory elements on plant phenotype and
   agronomic performance; effect on non-target organisms; and nutritional
   impacts on multiple experimental models, albeit the studies were
   conducted for limited durations. However, skeptics always claim for
   conducting extensive clinical as well as field trials and also cast
   doubt on methods and procedures of calculating the ecological risks.
   This debate got further momentum especially after the publication of
   reports on substantial reduction in monarch butterfly caterpillars when
   exposed to Bt-maize pollen - though later nullified - and detection of
   traces of transgene in various tissues of experimental animals. It is
   generally accepted that procedures, methods and protocols for evaluating
   the potential risks of GM-crops and foods should be standardized for
   building confidence of all stakeholders. Efforts should be exerted in
   deploying genes of interest, marker genes and regulatory sequences
   invoking no or little issues of potential risks to the ecosystem.
UT CABI:20153351177
SN 1610-3653
DI 10.1007/s10311-015-0508-4
ER

PT J
AU Aguirre, L. A.
   Hernandez, A.
   Flores, M.
   Frias, G. A.
   Cerna, E.
   Landeros, J.
   Harris, M. K.
TI Genetically modified maize resistant to corn earworm (Lepidoptera:
   Noctuidae) in Sinaloa, Mexico.
SO Florida Entomologist
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VL 98
IS 3
PS 821-826
PY 2015
AB Helicoverpa zea (Boddie) (Lepidoptera: Noctuidae), the corn earworm, is
   a key pest causing damage to corn  Zea mays L. (Poales: Poaceae). The
   development of hybrids expressing Cry1Ab, Vip3Aa20, and mCry3A protein
   of  Bacillus thuringiensis Berliner (Bt) (Bacillales: Bacillaceae) is an
   option to control this insect. Corn hybrids Agrisure TM 3000 GT,
   Agrisure Viptera TM 3110, and Agrisure Viptera TM 3111 were tested for
   corn earworm suppression in the agricultural region of Sinaloa during
   the 2011, 2012, and 2013 autumn-winter growing seasons, and compared
   with their respective isolines. Gallery length on the ear and the number
   of damaged ears were evaluated. The genetically modified hybrids
   demonstrated the effectiveness of inserted proteins to confer resistance
   to the corn earworm by killing the pest or reducing its growth and
   damage to the ear. Based on the results, Agrisure 3000 GT, Agrisure
   Viptera TM 3110, and Agrisure Viptera TM 3111 are useful elements for an
   integrated pest management program on corn in Sinaloa, Mexico.
UT CABI:20153348192
SN 0015-4040
ER

PT J
AU Bhupendra Koul
   Reena Yadav
   Indraneel Sanyal
   Amla, D. V.
TI Comparative performance of modified full-length and truncated  Bacillus
   thuringiensis-cry1Ac genes in transgenic tomato.
SO SpringerPlus
VL 4
IS 203
PS (30 April 2015)
PY 2015
AB Background: Bt- cry1Ac gene has been reputedly effective against
   Helicoverpa armigera a notorious lepidopteran pest. Reports on the
   expression of full-length and truncated  cry1Ac genes in plants for
   effective resistance against  Helicoverpa sp. have been documented
   however, their performance is still ambiguous. Moreover, the question
   remains to be addressed that truncation of 3′ end of the native gene was
   documented and suggested for active insecticidal toxin production while
   the most successful transgenic event(s) of commercialized-cotton are
   based on full-length of the  cry gene. Therefore, we performed a
   comparative study on the efficacy of the two versions of  cry1Ac genes
   (full-length: 3,510 bp and truncated: 1,845 bp) in T 0 and T 1
   transgenic tomato plants and analyzed the extent of protection against
   H. armigera and also compared the results with our previous findings
   related to a successful transgenic tomato line Ab25E, expressing  cry1Ab
   gene. The integration of  cry1Ac gene(s) in T 0 transgenic plants and
   its inheritance in T 1 progeny was observed by PCR, RT-PCR and Southern
   blot hybridization analysis while, the toxin integrity, expression and
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   toxicity was monitored by Western immunoassay, DAS-ELISA and insect
   bioassay respectively. Results: An average transformation frequency and
   Bt-Cry protein content of 16.932.10 and 0.0020-0.0128% of total soluble
   protein (TSP) was obtained with pRD400 vector (Tr cry1Ac) while, a much
   lower value of 9.302.041 and 0.0001-0.0026% of TSP was observed with
   pNBRI-1 vector (Fl cry1Ac), respectively. The promising Tr cry1Ac T 0
   transgenic plants and their T 1 progeny gave full protection from  H.
   armigera. Although Flcry1Ac gene showed lower transformation frequency
   and lower expression, it showed higher toxicity to  H. armigera when
   compared with truncated Tr cry1Ac gene. Conclusions: The full-length
   cry1Ac gene can be redesigned for higher expression and performance in
   dicots or a hybrid gene could be designed having a blend of strong
   receptor binding and stable expression characteristics for enhanced
   efficacy and toxicity to the susceptible insects.
UT CABI:20153346033
SN 2193-1801
ER

PT J
AU Huang, F. N.
   Chen, M.
   Gowda, A.
   Clark, T. L.
   McNulty, B. C.
   Yang, F.
   Niu, Y.
TI Identification, inheritance, and fitness costs of Cry2Ab2 resistance in
   a field-derived population of sugarcane borer,  Diatraea saccharalis
   (F.) (Lepidoptera: Crambidae).
SO Journal of Invertebrate Pathology
VL 130
PS 116-123
PY 2015
AB The sugarcane borer,  Diatraea saccharalis (F.), is one of the major
   target pests of transgenic maize,  Zea mays, expressing  Bacillus
   thuringiensis (Bt) proteins in South America and mid-southern region of
   the U.S. The MON89034 maize expresses Cry2Ab2 and Cry1A.105 Bt proteins
   and it was developed to provide better control of key lepidopteran pests
   of maize including  D. saccharalis. The objectives of this study were to
   select and characterize the resistance of  D. saccharalis to Cry2Ab2
   using a non-commercial Cry2Ab2 single gene Bt maize line. A
   Cry2Ab2-resistant strain (Cry2Ab2-RR) of  D. saccharalis was established
   from 28 two-parent families collected from fields in northeast
   Louisiana, U.S. The Cry2Ab2-RR showed a high level of resistance to
   Cry2Ab2 in both diet-incorporated and whole maize plant bioassays. The
   Cry2Ab2 resistance in  D. saccharalis was likely inherited as a single
   or a few tightly linked autosomal genes. The resistance was
   non-recessive and not associated with fitness costs. The results should
   provide valuable information in resistance monitoring, assessing
   resistance risk, and developing effective management strategies for the
   sustainable use of Bt maize technology for managing maize stalk borers.
UT CABI:20153317630
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SN 0022-2011
DI 10.1016/j.jip.2015.07.007
ER

PT J
AU Holderbaum, D. F.
   Cuhra, M.
   Wickson, F.
   Orth, A. I.
   Nodari, R. O.
   Bohn, T.
TI Chronic responses of  Daphnia magna under dietary exposure to leaves of
   a transgenic (event MON810) Bt-maize hybrid and its conventional
   near-isoline.
SO Journal of Toxicology and Environmental Health. Part A
VL 78
IS 15
PS 993-1007
PY 2015
AB Insect resistance is the second most common trait globally in cultivated
   genetically modified (GM) plants. Resistance is usually obtained by
   introducing into the plant's genome genes from the bacterium  Bacillus
   thuringiensis (Bt) coding for insecticidal proteins (Cry proteins or
   toxins) that target insect pests. The aim of this study was to examine
   the hypothesis that a chronic, high-dose dietary exposure to leaves of a
   Bt-maize hybrid (GM event MON810, expressing a transgenic or recombinant
   Cry1Ab toxin), exerted no adverse effects on fitness parameters of the
   aquatic nontarget organism  Daphnia magna (water flea) when compared to
   an identical control diet based on leaves of the non-GM near-isoline.
   Cry1Ab was immunologically detected and quantified in GM maize leaf
   material used for  Daphnia feed. A 69-kD protein near Bt's active
   core-toxin size and a 34-kD protein were identified. The  D. magna
   bioassay showed a resource allocation to production of resting eggs and
   early fecundity in  D. magna fed GM maize, with adverse effects for body
   size and fecundity later in life. This is the first study to examine
   GM-plant leaf material in the  D. magna model, and provides of negative
   fitness effects of a MON810 maize hybrid in a nontarget model organism
   under chronic, high dietary exposure. Based upon these results, it is
   postulated that the observed transgenic proteins exert a nontarget
   effect in  D. magna and/or unintended changes were produced in the maize
   genome/metabolome by the transformation process, producing a nutritional
   difference between GM-maize and non-GM near-isoline.
UT CABI:20153318653
RI Nodari, Rubens/B-7006-2014;
OI Nodari, Rubens/0000-0002-8884-2426; Cuhra, Marek/0000-0003-0127-1569
SN 1528-7394
ER

PT J
AU Li Bo
   Xu YangYang
   Han Cao
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   Han LanZhi
   Hou MaoLin
   Peng YuFa
TI Chilo suppressalis and  Sesamia inferens display different
   susceptibility responses to Cry1A insecticidal proteins.
SO Pest Management Science
VL 71
IS 10
PS 1433-1440
PY 2015
AB BACKGROUND:  Chilo suppressalis and  Sesamia inferens are important
   lepidopteran rice pests that occur concurrently in rice-growing areas of
   China. The development of transgenic rice expressing Cry1A insecticidal
   proteins has provided a useful strategy for controlling these pests.
   RESULTS: This study evaluated the baseline susceptibilities of  C.
   suppressalis and  S. inferens to Cry1A, as well as their responses to
   selection with Cry1A. Wide geographic variation in susceptibility was
   observed across all field populations. Within a given population, the LC
   50 of both Cry1Ab and Cry1Ac against  S. inferens was drastically higher
   than that of  C. suppressalis. Large LC 50 differences (74.6-fold) were
   detected between the two species for Cry1Ab in the Poyang population,
   while small differences (3.6-fold) were detected for Cry1Ac in the
   Changsha population. The Cry1Ac LC 50 of  C. suppressalis and  S.
   inferens increased 8.4- and 4.4-fold after 21 and eight selection
   generations respectively. Additionally, the estimated realised
   heritabilities ( h2) of Cry1Ac tolerance were 0.11 in  C. suppressalis
   and 0.292 in  S. inferens. CONCLUSIONS:  S. inferens exhibited a
   significantly lower susceptibility and more rapidly evolved resistance
   to Cry1A compared with  C. suppressalis. Therefore,  S. inferens is more
   likely to evolve increased resistance, which threatens the
   sustainability of rice expressing Cry1A protein.
UT CABI:20153317350
SN 1526-498X
ER

PT J
AU Valldor, P.
   Miethling-Graff, R.
   Martens, R.
   Tebbe, C. C.
TI Fate of the insecticidal Cry1Ab protein of GM crops in two agricultural
   soils as revealed by  14C-tracer studies.
SO Applied Microbiology and Biotechnology
VL 99
IS 17
PS 7333-7341
PY 2015
AB Insecticidal delta-endotoxins of  Bacillus thuringiensis are among the
   most abundant recombinant proteins released by genetically modified (GM)
   crops into agricultural soils worldwide. However, there is still
   controversy about their degradation and accumulation in soils. In this
   study,  14C-labelled Cry1Ab protein was applied to soil microcosms at
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   two concentrations (14 and 50 g g -1 soil) to quantify the
   mineralization of Cry1Ab, its incorporation into the soil microbial
   biomass, and its persistence in two soils which strongly differed in
   their texture but not in silt or pH. Furthermore, ELISA was used to
   quantify Cry1Ab and its potential immunoreactive breakdown products in
   aqueous soil extracts. In both soils,  14CO 2-production was initially
   very high and then declined during a total monitoring period of up to
   135 days. A total of 16 to 23% of the  14C activity was incorporated
   after 29 to 37 days into the soil microbial biomass, indicating that
   Cry1Ab protein was utilized by microorganisms as a growth substrate.
   Adsorption in the clay-rich soil was the most important factor limiting
   microbial degradation; as indicated by higher degradation rates in the
   more sandy soil, extremely low concentrations of immunoreactive Cry1Ab
   molecules in the soils' aqueous extracts and a higher amount of  14C
   activity bound to the soil with more clay. Ecological risk assessments
   of Bt-crops should therefore consider that the very low concentrations
   of extractable Cry1Ab do not reflect the actual elimination of the
   protein from soils but that, on the other hand, desorbed proteins
   mineralize quickly due to efficient microbial degradation.
UT CABI:20153309597
SN 0175-7598
DI 10.1007/s00253-015-6655-5
ER

PT J
AU Fu JianMei
   Fang ZhiXiang
   Guo RuQing
   Liu Biao
TI Ecological fitness of transgenic  cry1Ab/c rice in nutrient-deficient
   soils.
SO Journal of Ecology and Rural Environment
VL 31
IS 4
PS 528-533
PY 2015
AB In a simulated nutrient-deficient soil (without fertilizer application
   or target insect stress), transgenic  cry1Ab/c rice HH1 (Bt rice) and
   its non-transgenic parental cultivar (CK rice) were planted for
   comparison of the two rice cultivars in ecological fitness. Results show
   that the Bt rice planted in either the simulated soil or the field
   followed a similar basic rule of  cry1Ab/c gene expression but the
   expression level of Bt protein was much lower in the former case. Bt
   rice showed significantly higher fitness benefits in plant height,
   chlorophyll content, leaf shape and root system development in most
   developmental stages than CK rice, and apparent positive effects of
   ecological fitness, as well, on reproductive parameters such as seed
   number per plant, seed number per spike, seed weight per plant and total
   weight per 1 000 seeds. All these findings suggest that Bt rice might
   exceed CK rice in survivability and reproductibility in nature, and
   hence it may pose some environmental risks.
UT CABI:20153306083
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SN 1673-4831
ER

PT J
AU Zhang Li
   Hu WenJun
   Sheng WenJing
   Fang ZhiXiang
   Liu Biao
TI Residue of Cry1Ab/c protein in soil and water of paddy field cultivated
   with Bt-SY63 rice for years in a row.
SO Journal of Ecology and Rural Environment
VL 31
IS 4
PS 534-539
PY 2015
AB Field investigations were conducted during the rice growing season to
   monitor residues of Cry1Ab/c protein in water and soil of paddy fields
   cultivated with Bt-shanyou63 (Bt-SY63) rice for years in a row, 4 years
   in Wuhan, 3 years in Suizhou, 3 years in Wuxue and 2 years in Xiaogan of
   Hubei and 3 years in Dezhou of Shandong, using the enzyme-linked
   immunosorbent assay (ELISA) method. Results show that no significant
   differences were found in concentration of Cry1Ab/c protein in water
   between the fields cultivated with Bt-SY63 rice for 2-4 years and those
   with SY63 rice ( P>0.05), and the highest residue of Cry1Ab/c protein
   was measured to be 0.373 ng.mL -1 only. Similar to residue in the water,
   residue of the protein in the soil, regardless of growth stage, was
   found below the detection limit of the testing kit (0.25 ng.g -1) in all
   the paddy fields, except for the field in Suizhou where 0.261 ng.g -1
   was detected in the soil at the seedling stage, and the field in Dezhou
   where 0.540 and 0.361 ng.g -1 was at the jointing and blooming stages,
   respectively, forming significant difference from the control fields.
   Besides, no significant difference was detected in residue of Cry1Ab/c
   protein in soil and water between fields different in Bt-SY63’s
   cultivation history. It is, therefore, held that Bt-SY63 rice may
   release only a trace amount of Cry1Ab/c protein into the water and soil
   of the field after 2, 3 or 4 years of cultivation of the crop in a row.
   However, the amount is so low that it would not result in accumulation
   of Cry1Ab/c protein in the water and soil of the field.
UT CABI:20153306084
SN 1673-4831
ER

PT J
AU Shu YingHua
   Zhang YanYan
   Cheng MiaoMiao
   Zeng HuiLan
   Wang JianWu
TI Multilevel assessment of Cry1Ab Bt-maize straw return affecting the
   earthworm  Eisenia fetida.
SO Chemosphere
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VL 137
PS 59-69
PY 2015
AB Non-target effects of two varieties of  Bacillus thuringiensis
   (Bt)-maize straw (5422Bt1 [event Bt11] and 5422CBCL [MON810]) return on
   the  Eisenia fetida were investigated by using multilevel assessments,
   compared to near-isogenic non-Bt-maize (5422). 5422Bt1 straw return had
   no deleterious effects on adult earthworms and had significantly
   positive effects on juveniles over three generations. Negative, no, and
   positive effects on adults treated with 5422CBCL straw were observed in
   the 1st, 2nd and 3rd generation, respectively. Negative and positive
   effects were observed on juveniles produced from the 1st- and
   2nd-generation adults treated with 5422CBCL straw, respectively.
   Glutathione peroxidase activity of earthworms from Bt-maize treatments
   was significantly higher than that of control on the 90th d.
   Translationally controlled tumour protein (TCTP) and superoxide
   dismutase (SOD) genes were down-regulated, while annetocin (ANN)
   expression was up-regulated in 5422Bt1 treatments. TCTP and SOD genes
   were up-regulated, while ANN and heat shock protein 70 were
   down-regulated in  E. fetida from 5422CBCL treatments. Enzyme-linked
   immunosorbent assay revealed that Cry1Ab released from 5422Bt1 and
   5422CBCL straw degraded rapidly on the 15th and 30th d and had a slow
   decline in the rest testing time. Cry1Ab concentrations in the soil,
   casts and guts of earthworm significantly decreased over the course of
   the experiment. This study was the first to evaluate generational
   effects of Bt-maize straw return on earthworms under laboratory
   conditions. The responses of enzymes activity and genes expression may
   contribute to better understand above different effects of Bt-maize
   straw return on earthworms from the 1st generation.
UT CABI:20153300934
SN 0045-6535
ER

PT J
AU Yang YanHua
   Dai Li
   Zhu KeMing
   Xia HengChuan
   Chen Liang
   Liu HaiLong
   Chen KePing
TI Foreign protein detection in transgenic rice revealed by comparative
   proteomic analysis.
SO Crop Science
VL 55
IS 5
PS 2225-2233
PY 2015
AB To investigate whether the foreign protein in transgenic rice ( Oryza
   sativa L.) can be detected and then characterize the different proteins
   between transgenic rice and nontransgenic rice, we employed proteomic
   tools including two-dimensional electrophoresis (2-DE) and mass
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   spectrometry (MS) to globally identify different proteins between
   Bt-'Minghui 63' (MH63) (with the fused  Cry1Ab-Cry1Ac gene) and its
   nontransgenic control MH63. In all, 37 statistically different proteins
   between  Bt-MH63 and MH63 were successfully identified, including six
   unique proteins in  Bt-MH63. Gene ontology analysis showed that these
   six unique proteins were mainly involved in metabolic, catalytic,
   binding, and antioxidant process. Among these six unique proteins, two
   non-rice source proteins, phosphinothricin- N-acetyltransferase, were
   only expressed in germinating seed and seedling of  Bt-MH63, but not in
   MH63, which were further confirmed by matrix-assisted laser
   desorption-ionization time of flight (MALDI-TOF) MS-MS analysis. Our
   work suggests that a comparative proteomic approach may be feasible for
   identifying foreign proteins and genes in rice.
UT CABI:20153299988
SN 0011-183X
DI 10.2135/cropsci2014.11.0799
ER

PT J
AU Datukishvili, N.
   Kutateladze, T.
   Gabriadze, I.
   Bitskinashvili, K.
   Vishnepolsky, B.
TI New multiplex PCR methods for rapid screening of genetically modified
   organisms in foods.
SO Frontiers in Microbiology
VL 6
IS July
PS 757
PY 2015
AB We present novel multiplex PCR methods for rapid and reliable screening
   of genetically modified organisms (GMOs). New designed PCR primers
   targeting four frequently used GMO specific sequences permitted
   identification of new DNA markers, in particular 141 bp fragment of
   cauliflower mosaic virus (CaMV) 35S promoter, 224 bp fragment of
   Agrobacterium tumefaciens nopaline synthase (NOS) terminator, 256 bp
   fragment of 5-enolppyruvylshikimate-phosphate synthase ( epsps) gene and
   258 bp fragment of Cry1Ab delta-endotoxin ( cry1Ab) gene for GMO
   screening. The certified reference materials containing Roundup Ready
   soybean (RRS) and maize MON 810 were applied for the development and
   optimization of uniplex and multiplex PCR systems. Evaluation of
   amplification products by agarose gel electrophoresis using negative and
   positive controls confirmed high specificity and sensitivity at 0.1% GMO
   for both RRS and MON 810. The fourplex PCR was developed and optimized
   that allows simultaneous detection of three common transgenic elements,
   such as: CaMV 35S promoter, NOS terminator,  epsps gene together with
   soybean-specific lectin gene. The triplex PCR developed enables
   simultaneous identification of transgenic elements, such as: 35S
   promoter and  cry1Ab gene together with maize zein gene. The analysis of
   different processed foods demonstrated that multiplex PCR methods
   developed in this study are useful for accurate and fast screening of GM
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   food products.
UT CABI:20153303586
SN 1664-302X
ER

PT J
AU Bumunang, E. W.
   Jordaan, K.
   Barros, E.
   Bezuidenhout, C.
   Babalola, O. O.
TI Analysis of rhizobacterial community in field grown GM and non-GM maize
   soil samples using PCR-DGGE.
SO International Journal of Agricultural Technology
VL 11
IS 4
PS 831-838
PY 2015
AB This study assessed the impact of  Bacillus thuriengensis genetically
   modified maize (GM Bt maize) on functional community of rhizobacteria.
   Denaturing gradient gel electrophoresis technique (DGGE) was used.
   Results indicated that band patterns of GM and non-GM samples were
   similar to each other at 30 days after sowing (DAS) and 1 day after
   harvest (DAH). Sequence analysis showed that uncultured bacteria,
   Actinobacterium,  Bradyrhizobium spp., and  Sphingomonas spp., were
   common in the soil samples indicating that these were a stable community
   and species. These findings showed that the GM maize did not alter the
   soil microbial community which is significant in the assessment of the
   impact of GM maize on rhizobacteria.
UT CABI:20153288357
SN 1686-9141
ER

PT J
AU Silva, M. C.
   Siqueira, H. A. A.
   Silva, L. M.
   Marques, E. J.
   Barros, R.
TI Cry proteins from  Bacillus thuringiensis active against diamondback
   moth and fall armyworm.
SO Neotropical Entomology
VL 44
IS 4
PS 392-401
PY 2015
AB Biopesticides based on  Bacillus thuringiensis and genetically modified
   plants with genes from this bacterium have been used to control
   Plutella xylostella (L.) and  Spodoptera frugiperda (J.E. Smith).
   However, the selection pressure imposed by these technologies may
   undermine the efficiency of this important alternative to synthetic
   insecticides. Toxins with different modes of action allow a satisfactory
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   control of these insects. The purpose of this study was to characterize
   the protein and gene contents of 20  B. thuringiensis isolates from soil
   and insect samples collected in several areas of Northeast Brazil which
   are active against  P. xylostella and  S. frugiperda. Protein profiles
   were obtained by sodium dodecyl sulfate polyacrylamide gel
   electrophoresis (SDS-PAGE). Polymerase chain reaction assays were used
   to determine toxin genes present within bacterial isolates. The protein
   profile of the majority of the isolates produced bands of approximately
   130 kDa, suggesting the presence of Cry1, Cry8 and Cry9 proteins. The
   gene content of the isolates of  B. thuringiensis investigated showed
   different gene profiles. Isolates LIIT-4306 and LIIT-4311 were the most
   actives against both species, with LC 50 of 0.03 and 0.02*10 8 spores mL
   -1, respectively, for  P. xylostella, and LC 50 of 0.001*10 8 spores mL
   -1 for  S. frugiperda. These isolates carried the  cry1,  cry1Aa,
   cry1Ab,  cry1Ac,  cry1B,  cry1C,  cry1D,  cry1F,  cry2,  cry2A,  cry8,
   and  cry9C genes. The obtained gene profiles showed great potential for
   the control of  P. xylostella and  S. frugiperda, primarily because of
   the presence of several  cry1A genes, which are found in isolates of  B.
   thuringiensis active against these insects.
UT CABI:20153283424
RI Siqueira, Herbert/C-6062-2013
OI Siqueira, Herbert/0000-0002-8802-8977
SN 1519-566X
ER

PT J
AU Guo ShuaiShuai
   Xiao HongMei
TI Study on degradation of endogenous and exogenous genes in  Bt transgenic
   rice during food processing.
SO Journal of Nanjing Agricultural University
VL 38
IS 4
PS 667-675
PY 2015
AB Objectives: The aim of this study is to assess the degradation of
   endogenous and exogenous genes during food processing. Methods:
   Genetically modified (GM) rice ('Huahui 1') with  Cry1Ab/Ac (TT51-1) and
   non-GM rice ('Minghui 63') was used as raw material to produce different
   processed foods, including boiled rice (boiling for 10, 15, 20, 25 and
   30 min), autoclaving treated rice (autoclaving for 20, 25 and 30 min),
   rice crackers (boiling, 1st drying, 2nd drying, microwaving, baking and
   frying), and sweet rice wine (boiling, and fermenting for 1-4 day).
   Different amplified fragments-size PCR primers were designed by Primer
   Premier 5.0 software according to the endogenous gene  SPS, and
   exogenous genes or elements actin1 promoter,  Cry1Ab/Ac, event-specific
   3’ junction sequence, and NOS terminator. 23 pairs of primers in all
   were used in this experiment, including 6 pairs of primers for SPS gene,
   5 pairs of primers for actin1 promoter, 6 pairs of primers for
   Cry1Ab/Ac gene, 4 pairs of primers for event-specific 3’ junction
   sequence, and 2 pairs of primers for NOS terminator. The amplifications
   by PCR were analyzed by agarose gel electrophoresis. Results: For boiled
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   rice and autoclaving treated rice, autoclaving processing had more
   effect on the degradation of endogenous and exogenous genes of GM rice,
   compared to boiling processing. For rice crackers, boiling, 1st drying
   and 2nd drying contributed to the initial degradation of endogenous and
   exogenous genes of GM rice, and frying was the most severe procedure,
   followed by baking and microwaving. In the preparation of sweet rice
   wine, after boiling step which resulted in the marked degradation of
   endogenous and exogenous genes of GM rice, and there was no further
   degradation during fermenting for 1 to 4 days. Also, all fragments less
   than 200 bp had high stability in the processing. Conclusions: The test
   showed that different food procedures had diverse degrees of effect on
   the degradation of endogenous and exogenous genes of genetically
   modified rice.
UT CABI:20153276552
SN 1000-2030
ER

PT J
AU Bumunang, E. W.
   Jordaan, K.
   Barros, E.
   Bezuidenhout, C.
   Babalola, O. O.
TI Analysis of rhizobacterial community in field grown GM and non-GM maize
   soil samples using PCR-DGGE.
SO International Journal of Agricultural Technology
VL 11
IS 5
PS 1109-1117
PY 2015
AB This study assessed the impact of  Bacillus thuriengensis genetically
   modified maize (GM Bt maize) on functional community of rhizobacteria.
   Denaturing gradient gel electrophoresis technique (DGGE) was used.
   Results indicated that band patterns of GM and non-GM samples were
   similar to each other at 30 days after sowing (DAS) and 1 day after
   harvest (DAH). Sequence analysis showed that uncultured bacteria,
   Actinobacterium,  Bradyrhizobium spp., and  Sphingomonas spp., were
   common in the soil samples indicating that these were a stable community
   and species. These findings showed that the GM maize did not alter the
   soil microbial community which is significant in the assessment of the
   impact of GM maize on rhizobacteria.
UT CABI:20153272876
SN 1686-9141
ER

PT J
AU Gutierrez-Angoa, L. E.
   Castillo-Duran, L. C.
   Gomez-Castelo, B. E.
   Acatzi-Silva, A. I.
TI Quantification of genetically modified maize with qPCR and dPCR
   techniques.
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SO Agrociencia (Montecillo)
VL 49
IS 4
PS 373-394
PY 2015
AB In 2009 in Mexico, permission was given to release genetically modified
   maize ( Zea mays L.) into the environment. This made it necessary to
   detect, identify and quantify genetically modified organisms (GMO) in
   the country's crops. The objective of this study was to validate the
   technique of absolute quantification of leaf mixtures in mass fraction
   of GM maize using real time (qPCR) and digital (dPCR) polymerase chain
   reaction (PCR) technique. Mixed leaves of maize modified with the MON810
   event were prepared with conventional maize and analyzed with the qPCR
   technique. A certified reference plasmid and DNA obtained from a leaf
   with the MON810 modification were used as calibrants; besides, the dPCR
   technique was utilized since it allows a precise measurement of the
   number of DNA initial copies in the samples and does not require the
   utilization of calibrants. The test in qPCR complied with validation
   criteria, such as quantification limit, dynamic interval, amplification
   efficiency, correlation coefficient and estimation of uncertainty.
   Moreover, the dPCR technique was validated prior to quantification of
   the mixtures with the certified reference materials (CRM). Once the dPCR
   technique was validated, the GM material in the mixtures were
   quantified, and the results of the two techniques were comparable,
   indicating that they can be applied in quantifying genetic modification
   in crops and emit the results in mass fraction or copy number. The
   results show that quantification of genetically modified crop material
   in Mexico is possible with reliable results.
UT CABI:20153259471
SN 1405-3195
ER

PT J
AU Whiting, S. A.
   Lydy, M. J.
TI A site-specific ecological risk assessment for corn-associated
   insecticides.
SO Integrated Environmental Assessment and Management (IEAM)
VL 11
IS 3
PS 445-458
PY 2015
AB A site-specific ecological risk assessment (ERA) was conducted to
   examine the simultaneous use of genetically modified corn (Bt corn) with
   a neonicotinoid seed coating, clothianidin, and use of a granular
   insecticide, tefluthrin, to protect crops from pest damage. A field
   study was conducted on site, and exposure data from the literature were
   summarized to determine the matrices and exposure concentrations that
   nontarget species could typically experience within an agricultural
   ecosystem. To determine ecological effects on nontarget species, acute
   toxicity bioassays were conducted on earthworms ( Eisenia fetida),
   amphipods ( Hyalella azteca), and Elmid riffle beetle larvae ( Ancyronyx
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   spp.) in which the test species were exposed to single insecticides as
   well as the mixture of the 3 insecticides. In the risk characterization
   section of the ERA, stressor-response profiles for each species tested
   were compared with field distributions of the insecticides, and a margin
   of safety at the 10th percentile (MOS10) was calculated to estimate
   risk. No acute toxicity was observed in any of the 3 nontarget species
   after exposure to senescent Bt corn leaf tissue. Large MOS10 values were
   calculated for clothianidin to the nontarget species. When bioassays
   were compared with tefluthrin field distributions, very low MOS10 values
   were calculated for earthworms (0.06) and  H. azteca (0.08) because the
   environmental concentrations often exceeded the stressor-response
   profile. No increased toxicity was observed when nontarget species were
   exposed to a mixture of the 3 insecticides. In summary, the genetically
   modified corn insecticidal proteins and clothianidin were not found at
   environmental concentrations exceeding benchmark values for ecological
   effects, but tefluthrin was consistently detected in the environment at
   levels that could be causing toxicity to nontarget species, especially
   if this pyrethroid is able to travel off site.
UT CABI:20153261937
SN 1551-3777
DI 10.1002/ieam.1613
ER

PT S
AU Shinoyama, H.
   Mitsuhara, I.
   Ichikawa, H.
   Kato, K.
   Mochizuki, A.
BE Huylenbroeck, J. van
   Dhooghe, E.
TI Transgenic chrysanthemums ( Chrysanthemum morifolium Ramat.) carrying
   both insect and disease resistance.
SO Acta Horticulturae
IS 1087
PS 485-497
PY 2015
AB The chrysanthemum ( Chrysanthemum morifolium Ramat.) is a very important
   ornamental flower worldwide. Damage due to both harmful insects and
   pathogenic microbes results in a loss of quality and leads to high
   control costs. To reduce the likelihood of such damage, we have
   developed genetically modified chrysanthemums by introducing a modified
   cry1Ab gene of  Bacillus thuringiensis var.  kurstaki HD-1 ( mcbt) and a
   modified  sarcotoxin IA gene of  Sarcophaga peregrina ( msar) with or
   without the 5′-untranslated region of the  alcohol dehydrogenase gene of
   Arabidopsis thaliana ( AtADH-5′UTR, as  ADH). The leaf discs were
   transformed using a disarmed strain of  Agrobacterium tumefaciens,
   EHA105, carrying the binary vectors pBIK201BPS or pBIK201ABPS, which
   contain the  mcbt and  msar genes. The  mcbt and  msar genes were
   detected in all regenerated plantlets by Southern blot analysis, with a
   transformation frequency of 6.8%. Northern blot analysis revealed that
   the amount of the  mcbt transcription was influenced by the transgene
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   copy number in the genetically modified (GM) chrysanthemum. However,
   that of the  msar transcript was influenced by the presence of the  HSP
   terminator, regardless of the gene copy number. The GM chrysanthemums
   accumulated more than 1.31 g of Cry1Ab per mg of total soluble protein
   and showed a strong resistance against 4 species of lepidopteran larvae
   ( Helicoverpa armigera and others). All larvae died during the first
   instar stage. A strong resistance against white rust by  Puccinia
   horiana was observed especially in the  ADH::msar-transgenic
   chrysanthemum in which the expression level of sarcotoxin IA peptide was
   more than 19.5 g per g fresh weight of leaves. These GM chrysanthemums
   will be useful in reducing control costs for lepidopteran insects and
   white rust disease.
UT CABI:20153254827
CT XXV International EUCARPIA Symposium Section Ornamentals: Crossing
   Borders, Melle, Belgium.
SN 0567-7572
BN 978-94-62610-78-1
ER

PT J
AU Taverniers, I.
   Meyer, L. de
   Droogenbroeck, B. van
   Messens, K.
   Loose, M. de
TI Influence of plant developmental stage on DNA yield and extractability
   in MON810 maize.
SO Agricultural and Food Science
VL 24
IS 2
PS 128-138
PY 2015
AB The amount and extractability of DNA in different parts of MON810 GM
   hybrid was studied during different developmental stages. To quantify GM
   contents, an evaluation was performed of the effect of plant development
   stage on DNA density. To this end, the evolution of weights, absolute
   DNA yields, DNA densities and ratios of endosperm and embryo relative to
   total maize kernel were studied. Sampling at four stages during the
   growth shows an influence on relative GM quantification based on haploid
   genome equivalents, due to the specific maize seed composition and
   differences in DNA extractability from different seed tissues. During
   plant growth, plant parts with potential GM genes (embryo in kernel and
   cob on total plant) increase in importance on weight and DNA
   concentration level, while the endosperm drops in relative importance.
   Expected % GM maize values are calculated for a whole field harvest of
   grain maize.
UT CABI:20153249425
OI Taverniers, Isabel/0000-0003-0515-3412
SN 1459-6067
ER

PT J
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AU Jalali, S. K.
   Lalitha Yadavalli
   Rakshit Ojha
   Pradyumn Kumar
   Sulaikhabeevi, S. B.
   Reema Sharma
   Rupa Nair
   Kadanur, R. C.
   Kamath, S. P.
   Komarlingam, M. S.
TI Baseline sensitivity of maize borers in India to the  Bacillus
   thuringiensis insecticidal proteins Cry1A.105 and Cry2Ab2.
SO Pest Management Science
VL 71
IS 8
PS 1082-1090
PY 2015
AB BACKGROUND: Among the major pests of maize in India are two stem borers,
   Chilo partellus (Swinhoe) and  Sesamia inferens (Walker), and an
   earworm,  Helicoverpa armigera (Hubner). As a pest control strategy,
   transgenic  Bacillus thuringiensis ( Bt) maize hybrids are undergoing
   regulatory trials in India. We have determined the sensitivity of the
   target lepidopterans to the insecticidal  Bt proteins expressed in  Bt
   maize, as this determines product efficacy and the resistance management
   strategy to be adopted. Maize hybrids with event MON89034 express two
   insecticidal  Bt proteins, Cry1A.105 and Cry2Ab2. RESULTS: Sensitivity
   profiles of 53 populations of  C. partellus, 21 populations of  S.
   inferens and 21 populations of  H. armigera, collected between 2008 and
   2013 from maize-growing areas in India, to Cry1A.105 and Cry2Ab2
   proteins were generated through dose-response assays. Cry1A.105 protein
   was the most effective to neonates of  C. partellus (mean MIC 90 range
   0.30-1.0 g mL -1) and  H. armigera (mean MIC 90 range 0.71-8.22 g mL
   -1), whereas Cry2Ab2 (mean MIC 90 range 0.65-1.70 g mL -1) was the most
   effective to  S. inferens. CONCLUSION: Populations of  C. partellus,  S.
   inferens and  H. armigera were susceptible to the  Bt proteins Cry1A.105
   and Cry2Ab2. The  Bt sensitivity data will serve as precommercialisation
   benchmarks for resistance monitoring purposes.
UT CABI:20153247303
SN 1526-498X
DI 10.1002/ps.3888
ER

PT J
AU Frank, D. L.
   Kurtz, R.
   Tinsley, N. A.
   Gassmann, A. J.
   Meinke, L. J.
   Moellenbeck, D.
   Gray, M. E.
   Bledsoe, L. W.
   Krupke, C. H.
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   Estes, R. E.
   Weber, P.
   Hibbard, B. E.
TI Effect of seed blends and soil-insecticide on western and northern corn
   rootworm emergence from mCry3A+eCry3.1Ab Bt maize.
SO Journal of Economic Entomology
VL 108
IS 3
PS 1260-1270
PY 2015
AB Seed blends containing various ratios of transgenic Bt maize ( Zea mays
   L.) expressing the mCry3A+eCry3.1Ab proteins and non-Bt maize
   (near-isoline maize) were deployed alone and in combination with a soil
   applied pyrethroid insecticide (Force CS) to evaluate the emergence of
   the western corn rootworm,  Diabrotica virgifera virgifera LeConte, in a
   total of nine field environments across the Midwestern United States in
   2010 and 2011. Northern corn rootworm,  Diabrotica barberi Smith &
   Lawrence emergence was also evaluated in four of these environments.
   Both western and northern corn rootworm beetle emergence from all Bt
   treatments was significantly reduced when compared with beetle emergence
   from near-isoline treatments. Averaged across all environments, western
   corn rootworm beetle emergence from 95:5, 90:10, and 80:20 seed blend
   ratios of mCry3A+eCry3.1Ab: near-isoline were 2.6-, 4.2-, and 6.7-fold
   greater than that from the 100:0 ratio treatment. Northern corn rootworm
   emergence from the same seed blend treatments resulted in 2.8-, 3.2-,
   and 4.2-fold more beetles than from the 100:0 treatment. The addition of
   Force CS (tefluthrin) significantly reduced western corn rootworm beetle
   emergence for each of the three treatments to which it was applied.
   Force CS also significantly delayed the number of days to 50% beetle
   emergence in western corn rootworms. Time to 50% beetle emergence in the
   100% mCry3A+eCry3.1Ab treatment with Force CS was delayed 13.7 d when
   compared with western corn rootworm beetle emergence on near-isoline
   corn. These data are discussed in terms of rootworm resistance
   management.
UT CABI:20153238738
SN 0022-0493
DI 10.1093/jee/tov081
ER

PT J
AU Zhong RuQing
   Chen Liang
   Gao LiXiang
   Huang QingHua
   Liu Lei
   Zhang HongFu
TI Evaluation of enzymatic hydrolysate gross energy of glyphosate-tolerant
   corn and transgenic  Bt corn using simulative digestion system.
SO Chinese Journal of Animal Nutrition
VL 27
IS 5
PS 1468-1476
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PY 2015
AB The objective of the present study was to evaluate the energy value of
   the glyphosate-tolerant corn and transgenic  Bt corn or the
   glyphosate-tolerant corn diet and transgenic  Bt corn diet comparing to
   the isogenic non-transgenic corn or diet using an  in vitro digestion
   method with computer-controlled simulated digestion system (SDS). It
   would provide a reference to develop  in vitro method for evaluating the
   nutritional substantial equivalence of genetically modified crops using
   the SDS. A single factorial completely randomized design with 3 corn
   ingredients (isogenic non-transgenic corn, glyphosate-tolerant corn, and
   transgenic  Bt corn) and corresponding 3 corn diets (isogenic
   non-transgenic corn diet, glyphosate-tolerant corn diet, and transgenic
   Bt corn diet) was adapted. The digestion in the stomach and total tract
   were simulated respectively. The  in vitro dry matter digestibility
   (DMD),  in vitro gross energy digestibility (GED), and enzymatic
   hydrolysate gross energy (EHGE) were determined of corn ingredients and
   diets. The results showed that the nutrient concentration was similar
   between the corn ingredients and diets. As a whole, the gastric and
   total tract DMD, the gastric and total tract GED and the EHGH were not
   affected by the corn ingredient treatments ( P>0.05). However, the GED
   of transgenic Bt corn were lower than the GED of isogenic non-transgenic
   corn ( P=0.03, coefficient of variation=0.50%), when the EHGE of
   transgenic Bt corn diet were greater than the EHGE of isogenic
   non-transgenic corn diet ( P=0.02, coefficient of variation=1.12%). But,
   above two coefficient of variations were all less than the coefficient
   of variation of feed ingredients using the SDS (coefficient of variation
   ≤1.64%). These results suggest that  in vitro gastric and total tract
   digestibility of dry matter and gross energy for glyphosate-tolerant
   corn is similar to that for isogenic non-transgenic corn, with
   transgenic  Bt corn has some statistical differences. These differences
   are all within the test error of the SDS, via next animal testing test
   and verify. The SDS may supply a new method for evaluating the
   nutritional substantial equivalence of genetically modified crops.
UT CABI:20153232370
SN 1006-267X
ER

PT J
AU Czerwinski, J.
   Bogacki, M.
   Jalali, B. M.
   Konieczka, P.
   Smulikowska, S.
TI The use of genetically modified Roundup Ready soyabean meal and
   genetically modified MON 810 maize in broiler chicken diets. Part 1.
   Effects on performance and blood lymphocyte subpopulations.
SO Journal of Animal and Feed Sciences
VL 24
IS 2
PS 134-143
PY 2015
AB The effects of genetically modified (GM) soyabean meal (SBM) and GM
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   maize (MON 810) on the performance and immunological response of broiler
   chickens were studied. Eight diets were prepared based on conventional
   or GM SBM (GTS 40-3-2) combined with non-modified maize cvs. Clarica or
   PR39 F58 or their isogenic GM counterparts, cvs. Bacilla or PR39 F56.
   Diets were fed in mash form from day one of age to 192 Ross 308 broiler
   females, allocated to 8 groups, 24 birds per group. From day 8 to 28 of
   age, 18 chickens per group were kept in individual cages and performance
   parameters were measured. After slaughter the shares of T helper and T
   cytotoxic cells in the blood were determined in 8 birds per group. The
   feed conversion ratio (FCR) of birds fed GM SBM was better by 3.2% than
   in birds fed conventional SBM ( P<0.01). The performance of birds fed GM
   maize did not differ from those fed conventional maize, but body weight
   gain was lower and FCR worse by 3.3% in birds fed diets with
   Clarica/Bacilla compared with the PR 39 cultivar. The shares of
   circulating lymphocytes in their entire population averaged 10% to 17%
   and 6.5 to 12.2% (T helper and T cytotoxic, respectively) for all groups
   except the group fed conventional cv. Clarica maize and non-modified SBM
   (31% and 20.6%, respectively). It may be concluded that the use of GM
   GTS 40-3-2 soyabean meal and GM MON 810 maize in broiler diets did not
   negatively affect the feed efficiency and blood lymphocyte
   subpopulations of broilers.
UT CABI:20153232468
SN 1230-1388
ER

PT J
AU Czerwinski, J.
   Slupecka-Ziemilska, M.
   Wolinski, J.
   Barszcz, M.
   Konieczka, P.
   Smulikowska, S.
TI The use of genetically modified Roundup Ready soyabean meal and
   genetically modified MON 810 maize in broiler chicken diets. Part 2.
   Functional status of the small intestine.
SO Journal of Animal and Feed Sciences
VL 24
IS 2
PS 144-152
PY 2015
AB The effects of genetically modified (GM) soyabean meal (SBM) and GM
   maize on the functional status of the small intestine of broiler
   chickens was studied. Eight diets were prepared, based on conventional
   or GM SBM (GTS 40-3-2) combined with non-modified maize cvs. Clarica and
   PR39 F58 or their isogenic GM (MON 810) counterparts cvs. Bacilla or
   PR39 F56. Diets were fed in mash form from days 1 to 30 of age to 192
   Ross 308 broiler females, assigned to 8 groups and kept in individual
   cages from day 8 of life. The functional status of the small intestine
   was studied in 8 birds per group after slaughter. The investigation
   included morphological evaluation of jejunum and ileum sections,
   calculation of apoptotic and mitotic indices, and measurement of DNA
   damage in jejunal epithelial cells. There were no statistically
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   significant differences in morphological parameters of the jejunum and
   ileum except the width of the tunica mucosa in the jejunum, which was
   greater in birds fed GM than in those given conventional maize. GM SBM
   had no effect on the apoptotic and mitotic indices in the crypt area or
   in villi tips, while GM maize did not affect these indices in the crypt
   area, but increased the apoptotic index in the villi tips of the
   jejunum. Neither substituting conventional SBM by GM SBM, nor
   conventional maize by GM maize induced significant DNA damage in the
   epithelial cells of the jejunum. Our results indicate that the
   functional development and maturation of the small intestinal epithelium
   is not greatly modified by the use of GM SBM and GM maize in broiler
   diets.
UT CABI:20153232469
SN 1230-1388
ER

PT J
AU Hoffmann, A. M.
   French, B. W.
   Hellmich, R. L.
   Lauter, N.
   Gassmann, A. J.
BE Kuhlmann, U.
   Sappington, T. W.
   Wang, Z.
TI Fitness costs of resistance to Cry3Bb1 maize by western corn rootworm.
SO Journal of Applied Entomology
VL 139
IS 6
PS 403-415
PY 2015
AB Crops producing toxins derived from the bacterium  Bacillus
   thuringiensis (Bt) are widely planted to manage insect pests including
   western corn rootworm,  Diabrotica virgifera virgifera LeConte
   (Coleoptera: Chrysomelidae), which is a significant pest of maize in the
   United States and Europe. However, the widespread use of Bt maize places
   intense selection pressure on pest populations to evolve resistance, and
   field-evolved resistance to Bt maize by western corn rootworm has been
   documented in the United States. In conjunction with non-Bt refuges,
   fitness costs of Bt resistance can delay resistance evolution. Fitness
   costs arise in the absence of Bt toxin when individuals with resistance
   alleles have lower fitness than Bt-susceptible genotypes. We quantified
   the level of resistance and fitness costs of resistance for a strain of
   western corn rootworm with laboratory-selected resistance to transgenic
   maize ( Zea mays L.) producing Bt toxin Cry3Bb1. Survival to adulthood
   on Cry3Bb1 maize was more than twofold higher for resistant insects vs.
   susceptible insects, which is similar to the magnitude of resistance
   first observed in the field. Fitness costs were measured in two
   experiments; the first used maize hybrids and the second used inbred
   lines. The experiment with maize hybrids compared resistant and
   susceptible strains while the experiment with maize inbreds compared
   resistant, susceptible and heterozygous genotypes. The only
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   non-recessive fitness cost detected (i.e. cost affecting heterozygotes)
   was for adult size. Recessive fitness costs (i.e. costs affecting the
   resistant strain) were observed for developmental rate, female survival
   and egg viability. However, when reared on non-Bt maize, the resistant
   strain also displayed higher fecundity, higher survival for males and
   greater adult longevity compared to the susceptible strain. These
   results suggest that resistance to Bt maize by western corn rootworm may
   not impose substantial fitness costs, and consequently, may evolve
   quickly and persist once present.
UT CABI:20153230354
CT 25th IWGO Conference, Chicago, USA, 13-17 April 2014.
SN 0931-2048
DI 10.1111/jen.12209
ER

PT J
AU Monnerat, R.
   Martins, E.
   Macedo, C.
   Queiroz, P.
   Praca, L.
   Soares, C. M.
   Moreira, H.
   Grisi, I.
   Silva, J.
   Soberon, M.
   Bravo, A.
TI Evidence of field-evolved resistance of  Spodoptera frugiperda to Bt
   corn expressing Cry1F in Brazil that is still sensitive to modified Bt
   toxins.
SO PLoS ONE
VL 10
IS 4
PS e0119544
PY 2015
AB Brazil ranked second only to the United States in hectares planted to
   genetically modified crops in 2013. Recently corn producers in the
   Cerrado region reported that the control of  Spodoptera frugiperda with
   Bt corn expressing Cry1Fa has decreased, forcing them to use chemicals
   to reduce the damage caused by this insect pest. A colony of  S.
   frugiperda was established from individuals collected in 2013 from
   Cry1Fa corn plants (SfBt) in Brazil and shown to have at least more than
   ten-fold higher resistance levels compared with a susceptible colony
   (Sflab). Laboratory assays on corn leaves showed that in contrast to
   SfLab population, the SfBt larvae were able to survive by feeding on
   Cry1Fa corn leaves. The SfBt population was maintained without selection
   for eight generations and shown to maintain high levels of resistance to
   Cry1Fa toxin. SfBt showed higher cross-resistance to Cry1Aa than to
   Cry1Ab or Cry1Ac toxins. As previously reported, Cry1A toxins competed
   the binding of Cry1Fa to brush border membrane vesicles (BBMV) from
   SfLab insects, explaining cross-resistance to Cry1A toxins. In contrast
   Cry2A toxins did not compete Cry1Fa binding to SfLab-BBMV and no
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   cross-resistance to Cry2A was observed, although Cry2A toxins show low
   toxicity to  S. frugiperda. Bioassays with Cry1AbMod and Cry1AcMod show
   that they are highly active against both the SfLab and the SfBt
   populations. The bioassay data reported here show that insects collected
   from Cry1Fa corn in the Cerrado region were resistant to Cry1Fa
   suggesting that resistance contributed to field failures of Cry1Fa corn
   to control  S. frugiperda.
UT CABI:20153222813
OI Queiroz, Paulo/0000-0002-4672-8123
SN 1932-6203
DI 10.1371/journal.pone.0119544
ER

PT J
AU Trtikova, M.
   Wikmark, O. G.
   Zemp, N.
   Widmer, A.
   Hilbeck, A.
TI Transgene expression and Bt protein content in transgenic Bt maize
   (MON810) under optimal and stressful environmental conditions.
SO PLoS ONE
VL 10
IS 4
PS e0123011
PY 2015
AB Bt protein content in transgenic insect resistant (Bt) maize may vary
   between tissues within plants and between plants growing under different
   environmental conditions. However, it is unknown whether and how Bt
   protein content correlates with transgene expression, and whether this
   relationship is influenced by stressful environmental conditions. Two Bt
   maize varieties containing the same transgene cassette (MON 810) were
   grown under optimal and stressful conditions. Before and during stress
   exposure, the upper leaves were analysed for transgene expression using
   quantitative RT-PCR and for Bt content using ELISA. Under optimal
   conditions there was no significant difference in the transgene
   expression between the two investigated Bt maize varieties whereas Bt
   protein content differed significantly. Transgene expression was
   correlated with Bt protein content in only one of the varieties. Under
   stressful environmental conditions we found similar transgene
   expressions as under optimal conditions but Bt content responded
   differently. These results suggest that Bt content is not only
   controlled by the transgene expression but is also dependent on the
   genetic background of the maize variety. Under stressful conditions the
   concentration of Bt protein is even more difficult to predict.
UT CABI:20153223146
RI Widmer, Alex/B-6841-2009
OI Widmer, Alex/0000-0001-8253-5137
SN 1932-6203
DI 10.1371/journal.pone.0123011
ER
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PT J
AU Gomez, I.
   Flores, B.
   Bravo, A.
   Soberon, M.
BE Nachman, R. J.
TI Bacillus thuringiensis Cry1AbMod toxin counters tolerance associated
   with low cadherin expression but not that associated with low alkaline
   phosphatase expression in  Manduca sexta.
SO Peptides
VL 68
PS 130-133
PY 2015
AB To exert their toxic effect,  Bacillus thuringiensis Cry1Ab toxin
   undergoes a sequential binding mechanism with different larval gut
   proteins including glycosyl-phosphatidyl-inositol anchored proteins like
   aminopeptidase-N (APN) or alkaline-phosphatase (ALP) and a transmembrane
   cadherin to form pre-pore structures that insert into the membrane.
   Cadherin binding induces oligomerization of the toxin by facilitating
   removal of the N-terminal region, while APN/ALP binding helps in
   oligomer membrane insertion. Cry1AbMod toxin was engineered to lack
   N-terminal region of the toxin and shown to counter resistance linked to
   cadherin mutations. In this manuscript we determined the toxicity of
   Cry1AbMod to  Manduca sexta larvae silenced in the expression of
   cadherin, ALP or APN receptors. As previously reported Cry1Ab toxicity
   relied principally in ALP and cadherin in comparison to APN. Our data
   shows that Cry1AbMod counters resistance associated with low cadherin
   expression but was not effective against ALP silenced larvae. These
   results show that Cry1AbMod could be effective against resistance
   insects linked to mutations on binding molecules involved in toxin
   oligomerization but not against resistant insects linked to mutations on
   binding molecules involved in oligomer membrane insertion.
UT CABI:20153211191
SN 0196-9781
ER

PT J
AU Chavez, C.
   Recio-Totoro, B.
   Flores-Escobar, B.
   Lanz-Mendoza, H.
   Sanchez, J.
   Soberon, M.
   Bravo, A.
BE Nachman, R. J.
TI Nitric oxide participates in the toxicity of  Bacillus thuringiensis
   Cry1Ab toxin to kill  Manduca sexta larvae.
SO Peptides
VL 68
PS 134-139
PY 2015
AB Nitric oxide (NO) produced by the nitric oxide synthase (NOS) enzyme is
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   a reactive oxygen molecule widely considered as important participant in
   the immune system of different organisms to confront microbial
   infections. In insects the NO molecule has also been implicated in
   immune response against microbial pathogens.  Bacillus thuringiensis
   (Bt) is an insect-pathogenic bacterium that produces insecticidal
   proteins such as Cry toxins. These proteins kill insects because they
   form pores in the larval-midgut cells. Here we show that intoxication of
   Manduca sexta larvae with Cry1Ab activates expression of NOS with a
   corresponding increase in NO. This effect is not observed with a
   non-toxic mutant toxin Cry1Ab-E129K that is affected in pore formation.
   The increased production of NO triggered by intoxication with LC 50 dose
   of Cry1Ab toxin is not associated with higher expression of
   antimicrobial peptides. NO participates in Cry1Ab toxicity since
   inhibition of NOS by selective l-NAME inhibitor prevented NO production
   and resulted in reduced mortality of the larvae. The fact that mortality
   was not completely abolished by L-NAME indicates that other processes
   participate in toxin action and induction of NO production upon Cry1Ab
   toxin administration accounts only for a part of the toxicity of this
   protein to  M. sexta larvae.
UT CABI:20153211192
SN 0196-9781
ER

PT J
AU Sushil Kumar
   Renu Kumari
TI Occurrence of molecularly diverse  Bt Cry toxin-resistant mutations in
   insect pests of  Bt+ corn and cotton crops and remedial approaches.
SO Current Science
VL 108
IS 8
PS 1483-1490
PY 2015
AB Cultivation of  Bt+ genotypes has dispensed with insecticidal sprays and
   thereby corn and cotton farmers have hugely benefited worldwide. Recent
   recordings of genetically diverse Cry-resistance in insect pests of  Bt+
   corn and cotton fields have raised grave concern. Curiously, bulk of
   Cry-resistant pink bollworms found in certain  Bt+ cotton fields in
   India proved homozygous for multiple linked mutations. Besides,
   dominantly inheritable Cry-resistance and cross resistance between
   different Cry-proteins have also been noted. To stem evolution of
   resistance against anti-insect protein-toxins, new nematology research
   on IPM procedures, complementary to refuge and Cry stacking technologies
   is imminently needed.
UT CABI:20153203151
SN 0011-3891
ER

PT J
AU Bhoge, R. K.
   Rashmi Chhabra
   Gurinderjit Randhawa
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   Muthukrishnan Sathiyabama
   Monika Singh
TI Event-specific analytical methods for six genetically modified maize
   events using visual and real-time loop-mediated isothermal
   amplification.
SO Food Control
VL 55
PS 18-30
PY 2015
AB Currently 138 genetically modified (GM) maize events have been
   authorized for commercial cultivation, comprising more than 65 per cent
   stacked events. With the increase in number of GM maize events globally,
   cost- and time-efficient diagnostics with on-site applicability are
   required to check for authorized GM events. Six GM maize events, namely,
   Bt11, GA21, MON810, MON89034, NK603 and TC1507, also present in 89
   stacked events, are being widely commercialized in more than 17
   countries. Visual and real-time loop-mediated isothermal amplification
   (LAMP) assays targeting these six GM maize events are being reported in
   the present study. Specificity of the developed LAMP assays was
   confirmed using fourteen commercialized GM maize events. Limit of
   detection of visual and real-time LAMP assays targeting  Bt11, GA21,
   MON810, MON89034 and TC1507, was up to 0.01%, detecting 8 target copies,
   and for NK603 event-specific assays, was up to 0.1% detecting 73 target
   copies. Practical applicability of developed LAMP assays was verified
   using a set of five stacked GM maize events, namely,  Bt11 * GA21,
   MON89034 * NK603, MON89034 * NK603 * TC1507, TC1507 * NK603 and TC1507 *
   MON810; and six powdered maize samples of proficiency testing. The
   reported LAMP assays can be efficiently employed for screening for
   presence of selected GM maize events in single or stacked form.
UT CABI:20153200179
SN 0956-7135
DI 10.1016/j.foodcont.2015.02.016
ER

PT J
AU Strain, K. E.
   Lydy, M. J.
TI The fate and transport of the Cry1Ab protein in an agricultural field
   and laboratory aquatic microcosms.
SO Chemosphere
VL 132
PS 94-100
PY 2015
AB Genetically engineered crops expressing insecticidal crystalline
   proteins derived from  Bacillus thuringiensis (Bt), were commercialized
   almost two decades ago as a means to manage agricultural pests. The Bt
   proteins are highly specific and only lethal upon ingestion, limiting
   the scope of toxicity to target insects. However, concern of exposure to
   non-target organisms and negative public perceptions regarding Bt crops
   has caused controversy surrounding their use. The objective of this
   research was to monitor the fate and transport of a Bt protein, Cry1Ab,
   in a large-scale agricultural field containing maize expressing the
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   Cry1Ab protein and a non-Bt near isoline, and in aquatic microcosms. The
   highest environmental concentrations of the Cry1Ab protein were found in
   runoff water and sediment, up to 130 ng L -1 and 143 ng g -1 dry weight,
   respectively, with the Cry1Ab protein detected in both Bt and non-Bt
   maize fields. As surface runoff and residual crop debris can transport
   Bt proteins to waterways adjacent to agricultural fields, a series of
   laboratory experiments were conducted to determine the potential fate of
   the Cry1Ab protein under different conditions. The results showed that
   sediment type and temperature can influence the degradation of the
   Cry1Ab protein in an aquatic system and that the Cry1Ab protein can
   persist for up to two months. Although Cry1Ab protein concentrations
   measured in the field soil indicate little exposure to terrestrial
   organisms, the consistent input of Bt-contaminated runoff and crop
   debris into agricultural waterways is relevant to understanding
   potential consequences to aquatic species.
UT CABI:20153191459
SN 0045-6535
DI 10.1016/j.chemosphere.2015.03.005
ER

PT J
AU Keweshan, R. S.
   Head, G. P.
   Gassmann, A. J.
TI Effects of pyramided Bt corn and blended refuges on western corn
   rootworm and northern corn rootworm (Coleoptera: Chrysomelidae).
SO Journal of Economic Entomology
VL 108
IS 2
PS 720-729
PY 2015
AB The western corn rootworm,  Diabrotica virgifera virgifera LeConte, and
   the northern corn rootworm,  Diabrotica barberi Smith & Lawrence
   (Coleoptera: Chrysomelidae), are major pests of corn ( Zea mays L).
   Several transgenic corn events producing insecticidal toxins derived
   from the bacterium  Bacillus thuringiensis (Bt) kill corn rootworm
   larvae and reduce injury to corn roots. However, planting of Bt corn
   imposes selection on rootworm populations to evolve Bt resistance. The
   refuge strategy and pyramiding of multiple Bt toxins can delay
   resistance to Bt crops. In this study, we assessed the impact of four
   treatments - (1) non-Bt corn, (2) Cry3Bb1 corn, (3) corn pyramided with
   Cry3Bb1 and Cry34/35Ab1, and (4) pyramided corn with a blended refuge -
   on survival, time of adult emergence, and size of western and northern
   corn rootworm. All treatments with Bt corn led to significant reductions
   in the number of adults that emerged per plot. However, at one location,
   we identified Cry3Bb1-resistant western corn rootworm. In some cases Bt
   treatments reduced size of adults and delayed time of adult emergence,
   with effects most pronounced for pyramided corn. For both species, the
   number of adults that emerged from pyramided corn with a blended refuge
   was significantly lower than expected, based solely on emergence
   frompure stands of pyramided corn and non-Bt corn. The results of this
   study indicate that pyramided corn with a blended refuge substantially
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   reduces survival of both western and northern corn rootworm, and as
   such, should be a useful tool within the context of a broader integrated
   pestmanagement strategy.
UT CABI:20153191861
SN 0022-0493
DI 10.1093/jee/tov005
ER

PT J
AU Wangila, D. S.
   Gassmann, A. J.
   Petzold-Maxwell, J. L.
   French, B. W.
   Meinke, L. J.
TI Susceptibility of Nebraska western corn rootworm (Coleoptera:
   Chrysomelidae) populations to Bt corn events.
SO Journal of Economic Entomology
VL 108
IS 2
PS 742-751
PY 2015
AB Transgenic plants have been widely adopted by growers to manage the
   western corn rootworm,  Diabrotica virgifera virgifera LeConte, in field
   corn. Because of reduced efficacy in some Nebraska fields after repeated
   use of Cry3Bb1-expressing hybrids, single plant bioassays were conducted
   in 2012 and 2013 to characterize the susceptibility of western corn
   rootworm populations to the rootwormactive proteins Cry3Bb1, mCry3A, and
   Cry34/35Ab1. Results demonstrate that there are heritable differences in
   susceptibility of Nebraska western corn rootworm populations to
   rootworm-active Bt traits. Proportional survival and corrected survival
   data coupled with field histories collectively support the conclusion
   that a level of field resistance to Cry3Bb1 has evolved in some Nebraska
   populations in response to selection pressure and that cross-resistance
   exists between Cry3Bb1 and mCry3A. There was no apparent
   cross-resistance between Cry34/35Ab1 and either Cry3Bb1 or mCry3A. The
   potential implications of these results on current and future corn
   rootworm management strategies are discussed.
UT CABI:20153191864
SN 0022-0493
DI 10.1093/jee/tou063
ER

PT J
AU Davolos, C. C.
   Hernandez-Martinez, P.
   Crialesi-Legori, P. C. B.
   Desiderio, J. A.
   Ferre, J.
   Escriche, B.
   Lemos, M. V. F.
TI Binding analysis of  Bacillus thuringiensis Cry1 proteins in the
   sugarcane borer,  Diatraea saccharalis (Lepidoptera: Crambidae).
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SO Journal of Invertebrate Pathology
VL 127
PS 32-34
PY 2015
AB Sugarcane borer ( Diatraea saccharalis, F.) is an important corn pest in
   South America and United States. The aim of the present study was to
   analyze the susceptibility and binding interactions of three Cry1A
   proteins and Cry1Fa in a Brazilian  D. saccharalis population. The
   results showed that Cry1Ab was the most active, followed by Cry1Ac,
   Cry1Fa and Cry1Aa. All Cry1-biotinylated proteins tested bound
   specifically to the  D. saccharalis brush border membrane vesicles
   (BBMV). Heterologous competition assays showed shared binding sites for
   all Cry1A proteins and another one shared by Cry1Fa and Cry1Ab. Thus,
   pyramiding Cry1Aa/Cry1Ac and Cry1F proteins would be a recommended
   strategy for managing this pest.
UT CABI:20153190294
RI Ferre, Juan/L-9426-2014;
OI Ferre, Juan/0000-0001-5535-0612; Escriche, Baltasar/0000-0003-4889-793X
SN 0022-2011
DI 10.1016/j.jip.2015.01.013
ER

PT J
AU Dangal, V.
   Huang, F. N.
TI Fitness costs of Cry1F resistance in two populations of fall armyworm,
   Spodoptera frugiperda (J.E. Smith), collected from Puerto Rico and
   Florida.
SO Journal of Invertebrate Pathology
VL 127
PS 81-86
PY 2015
AB The development of resistance in target pest populations is a threat to
   the sustainability of transgenic crops expressing  Bacillus
   thuringiensis (Bt) proteins. Fall armyworm,  Spodoptera frugiperda (J.E.
   Smith), is a major target pest of Bt maize in North and South America.
   This insect is the first target pest that has developed field resistance
   to Bt maize at multiple locations in these regions. The objective of
   this study was to assess the fitness costs associated with the Cry1F
   resistance in two populations of  S. frugiperda collected from Puerto
   Rico (RR-PR) and Florida (RR-FL). In the study, fitness costs were
   evaluated by comparing survival, growth, and developmental time of seven
   populations of  S. frugiperda on (1) non-Bt meridic diet and (2) non-Bt
   maize leaf tissue and non-Bt diet. The seven populations were RR-PR,
   RR-FL, a Bt-susceptible strain (Bt-SS), and four F 1 populations
   developed from reciprocal crosses between Bt-SS and the two resistant
   populations. Biological parameters measured were neonate-to-adult
   survivorship, neonate-to-adult developmental time, 10 day larval weight
   on non-Bt maize leaf tissue, pupal weight, and sex ratios. Results of
   the study show that the Cry1F resistance in both RR-PR and RR-FL was
   associated with considerable fitness costs, especially for the Florida
   population. Compared to the Bt-susceptible population, RR-PR showed an
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   average of 61.1% reduction in larval weight, 20.4% less in
   neonate-to-adult survivorship, and 3.7 days delay in neonate-to-adult
   developmental time. These fitness costs for RR-FL were 66.9%, 31.7% and
   4.4 days, respectively. The fitness costs of RR-PR and RR-FL appeared to
   be non-recessive. The results indicate that a diversified genetic basis
   may exist for the Cry1F resistance in  S. frugiperda.
UT CABI:20153190302
SN 0022-2011
DI 10.1016/j.jip.2015.03.004
ER

PT J
AU Binning, R. R.
   Coats, J.
   Kong, X. X.
   Hellmich, R. L.
TI Susceptibility to  Bt proteins is not required for  Agrotis ipsilon
   aversion to  Bt maize.
SO Pest Management Science
VL 71
IS 4
PS 601-606
PY 2015
AB BACKGROUND: Although  Bacillus thuringiensis ( Bt) maize has been widely
   adopted in diverse regions around the world, relatively little is known
   about the susceptibility and behavioral response of certain insect pests
   to  Bt maize in countries where this maize is not currently cultivated.
   These are important factors to consider as management plans are
   developed. These factors were investigated for  Agrotis ipsilon, a
   global pest of maize, with Cry1F and Cry34Ab1/Cry35Ab1 maize. RESULTS:
   Agrotis ipsilon demonstrated an initial, post-ingestive aversive
   response to Cry1F maize. Development and mortality were also affected -
   survival on Cry1F maize tissue was 40% and weight gain of survivors of
   Cry1F exposure was significantly reduced. A post-ingestive aversive
   response was also seen for Cry34Ab1/Cry35Ab1 maize; however, longer-term
   feeding, weight gain and survival were not affected. CONCLUSION: Agrotis
   ipsilon showed aversion to both  Bt treatments. Aversion to
   Cry34Ab1/Cry35Ab1 maize was unexpected because these proteins have no
   known insecticidal effect against Lepidoptera; however, results confirm
   that this aversion was temporary and did not affect growth or
   development. The Cry1F results suggest that  A. ipsilon will abandon
   Cry1F maize in the field before any selection for resistance. These data
   support the use of refuge to delay Cry1F resistance development in  A.
   ipsilon populations.
UT CABI:20153189349
SN 1526-498X
DI 10.1002/ps.3901
ER

PT J
AU Bortolotto, O. C.
   Bueno, A. de F.
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   Queiroz, A. P. de
   Silva, G. V.
   Barbosa, G. C.
TI Larval development of  Spodoptera eridania (Cramer) fed on leaves of  Bt
   maize expressing Cry1F and Cry1F+Cry1A.105+Cry2Ab2 proteins and its non-
   Bt isoline.
SO Revista Brasileira de Entomologia
VL 59
IS 1
PS 7-11
PY 2015
AB This study aimed to evaluate, in controlled laboratory conditions
   (temperature of 252 °C, relative humidity of 6010%, and 14/10 h L/D
   photoperiod), the larval development of  Spodoptera eridania (Cramer,
   1784) (Lepidoptera, Noctuidae) fed with leaves of  Bt maize expressing
   Cry1F and Cry1F+Cry1A.105+Cry2Ab2 insecticide proteins and its non- Bt
   isoline. Maize leaves triggered 100% of mortality on  S. eridania larvae
   independently of being  Bt or non- Bt plants. However, it was observed
   that in overall  Bt maize (expressing a single or pyramided protein)
   slightly affects the larval development of  S. eridania, even under
   reduced leaf consumption. Therefore, these results showed that Cry1F and
   Cry1F+Cry1A.105+Cry2Ab2 can affect the larval development of  S.
   eridania, although it is not a target pest of this plant; however, more
   research is needed to better understand this evidence. Finally, this
   study confirms that non- Bt maize leaves are unsuitable food source to
   S. eridania larvae, suggesting that they are not a potential pest in
   maize fields.
UT CABI:20153188482
SN 0085-5626
DI 10.1016/j.rbe.2014.12.001
ER

PT J
AU Hodgson, E. W.
   Wright, R.
   Gray, M.
   Hunt, T.
   Ostlie, K.
   Andow, D. A.
TI Farmer responses to resistance issues in corn rootworm to Bt corn:
   qualitative analysis of focus groups.
SO Journal of Extension
VL 53
IS 2
PS 2RIB7
PY 2015
AB Western corn rootworm is an important corn pest in the U.S. Some farmers
   noted unexpected corn rootworm injury of transgenic hybrids as early as
   2008; however, the full extent of product performance is still not fully
   understood. We conducted telephone focus groups with farmers in 2013 to
   gain their perspective of current and future issues for corn rootworm.
   Respondents were surprised how quickly corn rootworm injury escalated in
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   their fields and were disappointed with incorrect diagnoses from
   consultants and seed companies. Most participating farmers saw
   university Extension as an unbiased source of information.
UT CABI:20153165872
SN 1077-5315
ER

PT J
AU Cheeke, T. E.
   Schutte, U. M.
   Hemmerich, C. M.
   Cruzan, M. B.
   Rosenstiel, T. N.
   Bever, J. D.
TI Spatial soil heterogeneity has a greater effect on symbiotic arbuscular
   mycorrhizal fungal communities and plant growth than genetic
   modification with  Bacillus thuringiensis toxin genes.
SO Molecular Ecology
VL 24
IS 10
PS 2580-2593
PY 2015
AB Maize, genetically modified with the insect toxin genes of  Bacillus
   thuringiensis ( Bt), is widely cultivated, yet its impacts on soil
   organisms are poorly understood. Arbuscular mycorrhizal fungi (AMF) form
   symbiotic associations with plant roots and may be uniquely sensitive to
   genetic changes within a plant host. In this field study, the effects of
   nine different lines of  Bt maize and their corresponding non- Bt
   parental isolines were evaluated on AMF colonization and community
   diversity in plant roots. Plants were harvested 60 days after sowing,
   and data were collected on plant growth and per cent AMF colonization of
   roots. AMF community composition in roots was assessed using 454
   pyrosequencing of the 28S rRNA genes, and spatial variation in
   mycorrhizal communities within replicated experimental field plots was
   examined. Growth responses, per cent AMF colonization of roots and AMF
   community diversity in roots did not differ between  Bt and non- Bt
   maize, but root and shoot biomass and per cent colonization by
   arbuscules varied by maize cultivar. Plot identity had the most
   significant effect on plant growth, AMF colonization and AMF community
   composition in roots, indicating spatial heterogeneity in the field.
   Mycorrhizal fungal communities in maize roots were autocorrelated within
   approximately 1 m, but at greater distances, AMF community composition
   of roots differed between plants. Our findings indicate that spatial
   variation and heterogeneity in the field has a greater effect on the
   structure of AMF communities than host plant cultivar or modification by
    Bt toxin genes.
UT CABI:20153163517
SN 0962-1083
DI 10.1111/mec.13178
ER

PT J
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AU Aguirre, L. A.
   Hernandez, A.
   Flores, M.
   Perez-Zubiri, R.
   Cerna, E.
   Landeros, J.
   Frias, G. A.
TI Comparison of the level of damage by  Spodoptera frugiperda
   (Lepidoptera: Noctuidae) on genetically-modified and conventional maize
   plants in Northern Mexico.
TI Comparacion del nivel de dano de  Spodoptera frugiperda (Lepidoptera:
   Noctuidae) en plantas de maiz geneticamente modificado y convencional en
   el norte de Mexico.
SO Southwestern Entomologist
VL 40
IS 1
PS 171-178
PY 2015
AB The level of damage caused by the fall armyworm,  Spodoptera frugiperda
   (J.E. Smith), was evaluated under field conditions in three
   genetically-modified (GM) maize hybrids with and without application of
   insecticide, and a conventional hybrid used as control. The GM varieties
   Agrisure 3110, expressing the  Bacillus thuringiensis proteins Cry1Ab
   and Vip3Aa20, and Agrisure Viptera 3111 expressing the Cry1Ab, Vip3Aa20,
   and mCry3A, with or without insecticide, showed a high level of
   resistance against the fall armyworm with values of 1 on the Davis
   Scale. Agrisure 3000 GT that expresses Cry1Ab and mCry3A had 2.3 and 3.3
   foliar damage with and without insecticide, whereas foliar damage was
   higher on the control check with values of 7.2 and 9 with and without
   insecticide application, respectively. These results show that the
   technology is highly effective to control this key pest and could bring
   considerable benefits to the farmers of Mexico.
UT CABI:20153161204
SN 0147-1724
ER

PT J
AU Cerevkova, A.
   Cagan, L'.
TI Effect of transgenic insect-resistant maize to the community structure
   of soil nematodes in two field trials.
SO Helminthologia
VL 52
IS 1
PS 41-49
PY 2015
AB The aim of this study was to determine the effects of Bt maize hybrid
   cultivation on soil nematode communities in two field trials, as well as
   to analyse other factors (fertilisation and moisture) responsible for
   the community structure of soil nematodes. Nematode communities were
   studied in maize plots at the locality of Borovce in western Slovakia.
   During 2012 and 2013, hybrids DK440 and DKC3871 (conventional) or
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   DKC4442YG and DKC3872YG (Bt maize, event MON810) were sown in 10
   repetitions each. Nematodes were extracted from soil samples collected
   at the maize flowering (July 11, 2012 and July 30, 2013). Altogether, 39
   nematode species belonged to 35 genera were identified in two maize
   variants. The dominant taxa in both variants were  Acrobeloides nanus,
   Cephalobus persegnis,  Aphelenchoides composticola,  Aphelenchus avenae,
   Eudorylaimus carteri and  Filenchus vulgaris. Calculation of the
   maturity index, plant parasitic index, enrichment index and structure
   index did not confirm any clear influence of year or hybrid type on soil
   nematode communities. The proportional representation of cp-1, cp-2 and
   cp-3-5 groups of nematode fauna indicated conditions of low stability
   and high stress. Faunal profiles representing the structure and
   enrichment conditions of the soil food web showed an environment with a
   high C:N ratio and high levels of fungal feeders. Based on the
   calculation of the metabolic footprint of nematodes in the soil food
   web, a difference between the isoline maize variant and Bt maize variant
   in 2012 was found, but this difference was not readily apparent in 2013.
   The occurrence of nematodes, their abundance, proportion of feeding
   types and selected ecological indices did not depend on the type of
   maize hybrid (Bt or non-Bt). Thus, the cultivation of genetically
   modified maize did not directly influence nematode populations. The
   application of fertiliser at certain periods does not influence the
   nematode community. The observed significant higher abundance of
   nematodes was correlated with soil moisture.
UT CABI:20153154625
SN 0440-6605
ER

PT J
AU Zhang YuWen
   Liu Yan
   Zhang Jie
   Wang GuoYing
   Wang JianHua
   Liu YunJun
TI Assessment of transgene copy number and zygosity of transgenic maize
   overexpressing  Cry1Ie gene with SYBR Green qRT-PCR.
SO In Vitro Cellular & Developmental Biology - Plant
VL 51
IS 2
PS 125-134
PY 2015
AB Transgenic maize expressing the  Cry1Ie gene was shown to efficiently
   kill susceptible and Cry1Ac-resistant insects, indicating that  Cry1Ie
   might be a good candidate for the development of a new Bt-maize variety
   in China. As transgenic maize events with potential commercial usage are
   required to have one copy of a transgene, it is important to develop
   high-throughput methods to determine the transgene copy number initially
   and zygosity during subsequent breeding. In this study, a SYBR Green
   quantitative real-time PCR (qRT-PCR) method was established and used to
   estimate the transgene copy number in  Agrobacterium-derived transgenic
   maize lines expressing  Cry1Ie gene. The amplification efficiencies of
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   Cry1Ie,  bar, and  Adh1 with specific primers were calculated as 0.987,
   1.194, and 0.992, respectively. The transgene copy number was calculated
   using the formula Ratio=2 Ct_reference-Ct_transgene , where a calibrator
   line with a single copy of the transgene was not required. Six
   homozygous transgenic maize lines were initially analyzed using this
   calculation method, and the results were as accurate as those obtained
   using 2 DeltaDeltaCt , a common method for calculation of relative
   expression levels. More T 0 generation transgene lines were compared
   using both the SYBR Green qRT-PCR and TaqMan qRT-PCR methods, and the
   results showed a high correlation ( R2=0.8942) between SYBR Green
   qRT-PCR and TaqMan qRT-PCR values, confirming the reliability of the
   SYBR Green qRT-PCR method. Using this method, we successfully determined
   the transgene copy number and zygosity in transgenic maize lines
   expressing  Cry1Ie.
UT CABI:20153151998
SN 1054-5476
DI 10.1007/s11627-014-9658-5
ER

PT J
AU Zhu HaoJun
   Chen Yi
   Li YunHe
   Wang JiaMei
   Ding JiaTong
   Chen XiuPing
   Peng YuFa
TI A 90 day safety assessment of genetically modified rice expressing
   Cry1Ab/1Ac protein using an aquatic animal model.
SO Journal of Agricultural and Food Chemistry
VL 63
IS 14
PS 3627-3633
PY 2015
AB In fields of transgenic  Bt rice, frogs are exposed to Bt proteins
   through consumption of both target and nontarget insects. In the present
   study, we assessed the risk posed by transgenic rice expressing a
   Cry1Ab/1Ac fusion protein (Huahui 1, HH1) on the development of  Xenopus
   laevis. For 90 days, froglets were fed a diet with 30% HH1 rice, 30%
   parental rice (Minghui 63, MH63), or no rice as a control. Body weight
   and length were measured every 15 days. After sacrificing the froglets,
   we performed a range of biological, clinical, and pathological
   assessments. No significant differences were found in body weight (on
   day 90: 27.72.17, 27.42.40, and 27.91.67 g for HH1, MH63, and control,
   respectively), body length (on day 90: 60.21.55, 59.32.33, and 59.71.64
   mm for HH1, MH63, and control, respectively), animal behavior, organ
   weight, liver and kidney function, or the microstructure of some tissues
   between the froglets fed on the HH1-containing diet and those fed on the
   MH63-containing or control diets. This indicates that frog development
   was not adversely affected by dietary intake of Cry1Ab/1Ac protein.
UT CABI:20153157405
SN 0021-8561
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PT J
AU Shera, P. S.
   Ramesh Arora
   Pritpal Singh
TI Comparative susceptibility of transgenic Bt cotton hybrids to  Earias
   spp. and other non-target insects.
SO Crop Protection
VL 71
PS 51-59
PY 2015
AB Four Bt cotton ( Gossypium hirsutum L.) 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 evaluated along with
   their respective isogenic non-Bt genotypes against  Earias spp., sucking
   insect pests, and predators in 2010 and 2011. Female oviposition was not
   significantly different between Bt and non-Bt cotton hybrids. All Bt
   cotton hybrids recorded significantly reduced damage of  Earias spp. in
   shoots, squares, green bolls and freshly shed fruiting bodies as
   compared to the isogenic non-Bt genotypes. In 2010, the incidence of
   Earias spp. was observed only on 136 day old crop or later. MRC 7017
   Bollgard II had the lowest damage followed by NCEH 6R Bt, MRC 6301 Bt
   and JKCH 1947 Bt. However, no damage was observed in any of the Bt
   hybrids throughout the cropping season in 2011. The time of first
   appearance of  Earias spp. on Bt cotton differed from non-Bt genotypes,
   whereas, first appearance of sucking insects and predators did not
   differ between Bt and their isogenic non-Bt genotypes. Populations of
   sucking insect pests { Amrasca biguttula biguttula (Ishida),  Bemisia
   tabaci (Gen.) and  Thrips tabaci (Lindemann)} varied significantly among
   different cotton genotypes. Nevertheless, their incidence on Bt cotton
   hybrids did not differ significantly from the respective isogenic non-Bt
   genotypes. No significant differences were observed with respect to
   relative abundance of predators,  viz., spiders, chrysopids and
   coccinellids on Bt and non-Bt cotton genotypes. All Bt cotton hybrids
   out-yielded their isogenic non-Bt genotypes during both years. The yield
   was significantly higher in MRC 7017 Bollgard II followed by MRC 6301
   Bt, NCEH 6R Bt and JKCH 1947 Bt. The selection of superior genotypes
   with better yield characteristics is thus vital for developing high
   yielding transgenic cotton.
UT CABI:20153149093
SN 0261-2194
DI 10.1016/j.cropro.2015.01.022
ER

PT J
AU Chandni Mathur
   Kathuria, P. C.
   Pushpa Dahiya
   Singh, A. B.
TI Lack of detectable allergenicity in genetically modified maize
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   containing "Cry" proteins as compared to native maize based on  in
   silico &  in vitro analysis.
SO PLoS ONE
VL 10
IS 2
PS e0117340
PY 2015
AB Background: Genetically modified, (GM) crops with potential allergens
   must be evaluated for safety and endogenous IgE binding pattern compared
   to native variety, prior to market release. Objective: To compare
   endogenous IgE binding proteins of three GM maize seeds containing Cry
   1Ab, 1Ac, 1C transgenic proteins with non GM maize. Methods: An
   integrated approach of  in silico &  in vitro methods was employed. Cry
   proteins were tested for presence of allergen sequence by FASTA in
   allergen databases. Biochemical assays for maize extracts were
   performed. Specific IgE (sIgE) and Immunoblot using food sensitized
   patients sera (n=39) to non GM and GM maize antigens was performed.
   Results: In  silico approaches, confirmed for non sequence similarity of
   stated transgenic proteins in allergen databases. An insignificant
   (p>0.05) variation in protein content between GM and non GM maize was
   observed. Simulated Gastric Fluid (SGF) revealed reduced number of
   stable protein fractions in GM then non GM maize which might be due to
   shift of constituent protein expression. Specific IgE values from
   patients showed insignificant difference in non GM and GM maize
   extracts. Five maize sensitized cases, recognized same 7 protein
   fractions of 88-28 kD as IgE bindng in both GM and non-GM maize,
   signifying absence of variation. Four of the reported IgE binding
   proteins were also found to be stable by SGF. Conclusion: Cry proteins
   did not indicate any significant similarity of >35% in allergen
   databases. Immunoassays also did not identify appreciable differences in
   endogenous IgE binding in GM and non GM maize.
UT CABI:20153145988
SN 1932-6203
DI 10.1371/journal.pone.0117340
ER

PT J
AU Gulli, M.
   Salvatori, E.
   Fusaro, L.
   Pellacani, C.
   Manes, F.
   Marmiroli, N.
TI Comparison of drought stress response and gene expression between a GM
   maize variety and a near-isogenic non-GM variety.
SO PLoS ONE
VL 10
IS 2
PS e0117073
PY 2015
AB Maize MON810, grown and commercialised worldwide, is the only cultivated
   GM event in the EU. Maize MON810, variety DKC6575, and the corresponding
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   near-isogenic line Tietar were studied in different growth conditions,
   to compare their behaviour in response to drought. Main photosynthetic
   parameters were significantly affected by drought stress in both GM and
   non-GM varieties to a similar extent. Though DKC6575 (GM) had a greater
   sensitivity in the early phase of stress response as compared with
   Tietar (non-GM), after six days of stress they behaved similarly, and
   both varieties recovered from stress damage. Profiling gene expression
   in water deficit regimes and in a generalised drought stress condition
   showed an up-regulation of many stress-responsive genes, but a greater
   number of differentially expressed genes was observed in Tietar, with
   genes belonging to transcription factor families and genes encoding heat
   shock proteins, late embryogenesis abundant proteins and detoxification
   enzymes. Since induction of these genes have been indicated from the
   literature as typical of stress responses, their activation in Tietar
   rather than in DKC6575 may be reminiscent of a more efficient response
   to drought. DKC6575 was also analysed for the expression of the
   transgene  CryIAb (encoding the delta-endotoxin insecticidal protein) in
   water deficit conditions. In all the experiments, the  CryIAb transcript
   was not influenced by drought stress, but was expressed at a constant
   level. This suggests that though possessing a different pattern of
   sensitivity to stress, the GM variety maintains the same expression
   level for the transgene.
UT CABI:20153145862
RI Gulli, Mariolina/G-9759-2011
OI Pellacani, Claudia/0000-0002-2853-3429; Gulli,
   Mariolina/0000-0001-8326-4965
SN 1932-6203
ER

PT J
AU Vanhie, M.
   Deen, W.
   Lauzon, J. D.
   Hooker, D. C.
TI Effect of increasing levels of maize ( Zea mays L.) residue on no-till
   soybean ( Glycine max Merr.) in Northern production regions: a review.
SO Soil & Tillage Research
VL 150
PS 201-210
PY 2015
AB In northern temperate regions, such as the northern mid-west, USA and
   the province of Ontario, Canada, soybean is a common annual row crop for
   which no-till production has been encouraged for environmental benefit.
   Soybean is commonly grown in rotation following maize. Increasing maize
   yield has been implicated as the primary reason why the practice of
   no-till soybean is declining relative to conventional and reduced
   tillage systems. In these regions, maize yield has substantially
   increased during the last decade resulting in greater maize residue. In
   the following review, we provide evidence that maize residue levels at
   soybean planting may be increasing, not just due to increasing maize
   yields, but to changes in the cropping system of these regions. Maize
   residue levels may increase due to reductions in decomposition before
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   soybean planting because of higher adoption of full-season maize and
   soybean cultivars, potential limitations in nitrogen available for
   decomposition, and changes in maize residue quality such as the
   introduction of  Bt maize hybrids. A further review of the literature
   demonstrates that greater amounts of maize residue could negatively
   affect no-till soybean production in Northern regions by impacting soil
   nitrogen and soybean nodulation, soybean emergence, growth and
   development, as well as impacting soil physical properties such as
   moisture and temperature. Finally, we review potential strategies that
   could be employed to address high levels of maize residues for soybean
   planted with no-till.
UT CABI:20153144716
SN 0167-1987
DI 10.1016/j.still.2015.01.011
ER

PT J
AU Ostry, V.
   Malir, F.
   Pfohl-Leszkowicz, A.
TI Comparative data concerning aflatoxin contents in Bt maize and non-Bt
   isogenic maize in relation to human and animal health - a review.
SO Acta Veterinaria Brno
VL 84
IS 1
PS 47-53
PY 2015
AB Transgenic Bt maize is a potentially important tool against insect pest
   in the EU and other countries. Bt maize (e.g. MON 810, Bt 11) which
   carries the Bt gene is highly resistant to larval feeding of European
   corn borer, stalk borer, and Southwestern corn borer, depending on Bt
   toxin (delta toxin) production. Effective measures used to fight pests
   may often have positive side-effects in that they may also contribute to
   reducing mycotoxin concentrations. A systematic review has been used for
   the purposes of evaluating the studies on the reduction of aflatoxins in
   Bt maize. According to five studies, Bt maize has significantly lower
   concentrations of aflatoxins than non-Bt maize hybrids, only one study
   has shown no significant effect of Bt maize. Other studies have shown
   mixed results (four studies). The results of these studies were
   influenced by the year of sampling or by using maize breeding lines
   selected for resistance to aflatoxin accumulation.
UT CABI:20153137916
SN 0001-7213
ER

PT B
AU Tabashnik, B. E.
   Carriere, Y.
BE Soberon, M.
   Gao, A.
   Bravo, A.
TI Successes and failures of transgenic Bt crops: global patterns of
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   field-evolved resistance.
SO Bt resistance: characterization and strategies for GM crops producing
   Bacillus thuringiensis toxins
PS 1-14
PY 2015
AB Farmers planted genetically engineered crops that produce insecticidal
   proteins from the bacterium  Bacillus thuringiensis (Bt) on a cumulative
   total of 570 million ha worldwide from 1996 to 2013. These Bt crops kill
   some key insect pests, yet they are not toxic to most other organisms,
   including people. Bt crops can suppress pests, reduce the use of
   insecticide sprays and increase farmer profits, but their benefits are
   diminished or lost when pests evolve resistance. Here we review data
   monitoring resistance to seven Bt proteins in 13 major pest species
   targeting Bt maize and Bt cotton on six continents. Of the 27 sets of
   monitoring data analysed, seven show severe field-evolved resistance in
   2 to 8 years with practical consequences for pest control (i.e.
   practical resistance), eight show statistically significant but less
   severe field evolved resistance and 12 show no evidence of decreased
   susceptibility after 2 to 15 years. The surge in cases of practical
   resistance since 2005 is associated with increased planting of Bt crops,
   increased cumulative exposure of pests to Bt crops and increased
   monitoring. In addition, practical resistance to Bt crops is associated
   with a scarcity of refuges, which consist of host plants that do not
   produce Bt proteins. To maximize the benefits of Bt crops, we encourage
   collaboration between growers and scientists in industry, academia and
   government to implement large refuges of non-Bt host plants,
   particularly when the inheritance of resistance is not recessive and
   alleles conferring resistance are not rare.
UT CABI:20153137244
BN 978-1-78064-437-0
DI 10.1079/9781780644370.0001
ER

PT B
AU Berg, J. van den
   Campagne, P.
BE Soberon, M.
   Gao, A.
   Bravo, A.
TI Resistance of  Busseola fusca to Cry1Ab Bt maize plants in South Africa
   and challenges to insect resistance management in Africa.
SO Bt resistance: characterization and strategies for GM crops producing
   Bacillus thuringiensis toxins
PS 36-48
PY 2015
AB The evolution of resistance to  Bacillus thuringiensis (Bt) maize by the
   African stem borer,  Busseola fusca, in South Africa highlighted the
   importance of the development of appropriate integrated resistance
   management (IRM) strategies for stem borers in Africa. Landscape
   heterogeneity is characteristic of African agroecosystems. This
   heterogeneity, in addition to between field and within-field spatial
   mosaics resulting from variable gene expression in Bt maize, will
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   provide challenges to managing resistance evolution of the lepidopteran
   stem borers that attack maize. Adding to this landscape heterogeneity is
   the cultivation of open-pollinated maize varieties (OPVs) and bimodal
   rainfall patterns that allow two maize cropping seasons each year in
   many subtropical and tropical areas. The role that these factors, as
   well as aspects such as low-dose expression events, refuge compliance,
   the genetic bases of resistance, pest behaviour, host plant range and
   farming practices, may play in the evolution of stem borers to Bt maize
   in Africa are addressed in this chapter.
UT CABI:20153137247
BN 978-1-78064-437-0
DI 10.1079/9781780644370.0036
ER

PT B
AU Soberon, M.
   Garcia-Gomez, B. I.
   Pacheco, S.
   Sanchez, J.
   Tabashnik, B. E.
   Bravo, A.
BE Soberon, M.
   Gao, A.
   Bravo, A.
TI Countering pest resistance with genetically modified Bt toxins.
SO Bt resistance: characterization and strategies for GM crops producing
   Bacillus thuringiensis toxins
PS 150-161
PY 2015
AB Insecticidal crystalline (Cry) toxins from the bacterium  Bacillus
   thuringiensis (Bt) used in sprays and transgenic crop plants have
   provided major benefits for pest control, including decreased reliance
   on broad-spectrum chemical insecticides. However, extensive use of Bt
   toxins has selected for resistance, thus reducing or eliminating these
   benefits against some populations of at least seven species of major
   crop pests. This chapter reviews efforts to counter pest resistance to
   native Bt toxins with genetically engineered toxins called Cry1AbMod and
   Cry1AcMod. We generated these modified toxins by trimming the genes
   encoding the native toxins Cry1Ab and Cry1Ac so they lack the
   nucleotides that code for a portion of the amino-terminal end of the
   protein, including helix alpha-1 and part of helix alpha-2. Consistent
   with the sequential binding model for the mode of action of the toxins,
   the Cry1AMod toxins formed oligomers without binding to cadherin, but
   the native toxins required cadherin for oligomer formation. The modified
   toxins were more potent than the corresponding native toxins in 13 of 19
   pairwise comparisons with 12 resistant strains of nine species of
   Lepidoptera, including field-selected strains of  Plutella xylostella,
   Trichoplusia ni and  Spodoptera frugiperda. The potency of modified
   toxins relative to native toxins in these resistant strains did not
   depend on the resistance mechanism. Against susceptible strains, the
   modified toxins were less effective than their native counterparts in
   nearly all cases. Transgenic tobacco plants producing Cry1AbMod killed
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   larvae of  Manduca sexta, which represents progress towards commercial
   use of the modified toxins for pest management.
UT CABI:20153137257
BN 978-1-78064-437-0
DI 10.1079/9781780644370.0150
ER

PT B
AU Huang, F. N.
BE Soberon, M.
   Gao, A.
   Bravo, A.
TI Resistance management for Bt maize and above-ground lepidopteran targets
   in the USA: from single gene to pyramided traits.
SO Bt resistance: characterization and strategies for GM crops producing
   Bacillus thuringiensis toxins
PS 173-185
PY 2015
AB Since first being commercialized in 1996, transgenic maize expressing
   Bacillus thuringiensis (Bt) proteins has gained widespread acceptance in
   the world. In 2013, nearly 50 Mha of Bt maize were planted in 15
   countries. In the same year, growers in the USA alone planted  c.30 Mha
   of Bt maize, which accounted for 76% of the total Bt maize area of the
   country. Up to now, Bt maize technology can be classified into two
   generations. The first generation of Bt maize contains only a single Bt
   gene for a target. In 2010, the second generation of Bt maize became
   commercially available and this expresses two or more pyramided Bt
   proteins. Currently, the pyramided products are predominant in the USA.
   The major lepidopteran targets of Bt maize in the USA are corn borers
   (Crambidae), the corn earworm,  Helicoverpa zea, and the fall armyworm,
   Spodoptera frugiperda. To counter the threat of insect resistance, two
   resistance management strategies for Bt maize, 'high dose/refuge' and
   gene pyramiding, have been implemented. The long-term use of Bt maize
   against the major agricultural pests in North America provides a good
   opportunity to analyse the effectiveness of the adopted insect
   resistance management (IRM) plans. Analysis of the available data shows
   that all corn borer species remain susceptible to Bt proteins and that
   no field resistance has occurred after nearly two decades of intensive
   use of Bt maize in the continent. Pyramided Bt maize is effective in
   controlling corn earworm and fall armyworm, although recent studies
   indicate that field resistance to single-gene Cry1F maize in the fall
   armyworm has occurred in the south-east coastal areas of the US
   mainland. Knowledge of the resistance management gained from the USA
   should be useful for other countries in their sustainable use of Bt crop
   technology.
UT CABI:20153137259
BN 978-1-78064-437-0
DI 10.1079/9781780644370.0173
ER

PT J
GA EFSA Panel on Genetically Modified Organisms
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TI Scientific opinion on the annual post-market environmental monitoring
   (PMEM) report from Monsanto Europe S.A. on the cultivation of
   genetically modified maize MON 810 in 2013.
SO EFSA Journal
VL 13
IS 3
PS 4039
PY 2015
AB Following a request from the European Commission, the Panel on
   Genetically Modified Organisms of the European Food Safety Authority
   (EFSA GMO Panel) assessed the post-market environmental monitoring
   (PMEM) report for the 2013 growing season of maize MON 810 provided by
   Monsanto Europe S.A. The EFSA GMO Panel concludes that the data related
   to insect resistance monitoring does not indicate a significant and
   consistent decrease in susceptibility of the target pest field
   populations to Cry1Ab protein in Spain over the 2013 growing season.
   However, considering that the methodology for insect resistance
   monitoring remained unchanged compared to previous PMEM reports, the
   EFSA GMO Panel reiterates its previous recommendations for improvement
   of the insect resistance management plan of maize MON 810. The EFSA GMO
   Panel also recommends, as part of general surveillance, the continuation
   of the screening and discussion of literature on possible adverse
   effects of maize MON 810 on rove beetles. In the absence of information
   on the general surveillance of maize MON 810 in 2013, the EFSA GMO Panel
   cannot conclude on potential unanticipated adverse effects due to the
   cultivation of maize MON 810 in 2013, or on possible changes to the
   methodology as compared to previous growing seasons.
UT CABI:20153133414
SN 1831-4732
ER

PT J
AU Andreassen, M.
   Rocca, E.
   Bohn, T.
   Wikmark, O. G.
   Berg, J. van den
   Lovik, M.
   Traavik, T.
   Nygaard, U. C.
TI Humoral and cellular immune responses in mice after airway
   administration of  Bacillus thuringiensis Cry1Ab and MON810
   cry1Ab-transgenic maize.
SO Food and Agricultural Immunology
VL 26
IS 4
PS 521-537
PY 2015
AB Genetically modified (GM) crops may bring new proteins with immunogenic
   and allergenic properties into the food and feed chains. The most
   commonly grown GM maize, MON810, expresses a modified version of the
   insecticidal Cry1Ab protein originating in the soil bacterium  Bacillus
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   thuringiensis (Bt). Immune reactions following inhalation of pollen and
   debris from such plants have been scarcely studied. We exposed BALB/c
   mice to purified Cry1Ab proteins and Cry1Ab-containing MON810 plant
   materials by intranasal installation. No anti-Cry1Ab antibodies were
   detected following exposure to the plant materials. Exposure to purified
   Cry1Ab resulted in specific anti-Cry1Ab IgG1 and IgE production,
   indicating inherent immunogenicity and allergenicity. Mice exposed to
   leaf extracts from both MON810 and unmodified maize demonstrated influx
   of lymphocytes and eosinophils in the broncho-alveolar lavage, and
   increased cytokine release in mediastinal lymph node cells. The results
   indicate that the airway exposure to Cry1Ab proteins may be a route of
   practical relevance.
UT CABI:20153133662
SN 0954-0105
DI 10.1080/09540105.2014.988128
ER

PT J
AU Zhu Xun
   Lei YanYuan
   Yang YanJv
   Baxter, S. W.
   Li JianHong
   Wu QingJun
   Wang ShaoLi
   Xie Wen
   Guo ZhaoJiang
   Fu Wei
   Zhang YouJun
TI Construction and characterisation of near-isogenic  Plutella xylostella
   (Lepidoptera: Plutellidae) strains resistant to Cry1Ac toxin.
SO Pest Management Science
VL 71
IS 2
PS 225-233
PY 2015
AB BACKGROUND: Resistance to insecticidal  Bacillus thuringiensis ( Bt)
   toxins has arisen in multiple populations of the worldwide Brassica pest
   Plutella xylostella (L.). To help elucidate the mechanism of resistance
   to  Bt Cry1Ac toxin in a population from Florida, two pairs of
   near-isogenic lines (NILs) were developed. RESULTS: NILs were generated
   using either backcross or recombinant inbred line methodologies and
   evaluated for near-isogenicity with inter-simple-sequence-repeat (ISSR)
   markers. Backcross line BC6F4 maintained a similar level of Cry1Ac
   resistance to parental strain DBM1Ac-R (>5000-fold) yet showed 98.24%
   genetic similarity to the susceptible parental strain DBM1Ac-S.
   Single-pair backcrosses between DBM1Ac-S and BC6F4 revealed that Cry1Ac
   resistance was controlled by one recessive autosomal locus. BC6F4
   exhibited high levels of cross-resistance to Cry1Ab and Cry1Ah but not
   to Cry1Ca or Cry1Ie. CONCLUSION: Near-isogenic strains were constructed
   to provide a reliable biological system to investigate the mechanism of
   Cry1Ac resistance in  P. xylostella. These data suggest that resistance
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   to Cry1Ac, Cry1Ab and Cry1Ah is probably caused by the alteration of a
   common receptor not recognised by Cry1Ca or Cry1Ie. Understanding  Bt
   toxin cross-resistance provides valuable information to consider when
   developing pest control strategies to delay resistance evolution.
UT CABI:20153142117
SN 1526-498X
ER

PT J
AU Xu LiNa
   Wang YueQin
   Wang ZhenYing
   Hu BenJin
   Ling YingHui
   He KangLai
TI Transcriptome differences between Cry1Ab resistant and susceptible
   strains of Asian corn borer.
SO BMC Genomics
VL 16
IS 173
PS (12 March 2015)
PY 2015
AB Background: Asian corn borer (ACB), Ostrinia furnacalis (Guenee), is the
   major insect pest of maize in China and countries of East and Southeast
   Asia, the Pacific and Australasia. ACB can develop strong resistance to
   the transgenic Bt maize expressing Cry1Ab, the most widely
   commercialized Bt maize worldwide. However, the molecular basis for the
   resistance mechanisms of ACB to Cry1Ab remained unclear. Two biological
   replicates of the transcriptome of Bt susceptible (ACB-BtS) and Cry1Ab
   resistant (ACB-AbR) strains of ACB were sequenced using Solexa/Illumina
   RNA-Seq technology to identify Cry1Ab resistance-relevant genes.
   Results: The numbers of unigenes for two biological replications were
   63,032 and 53,710 for ACB-BtS and 57,770 and 54,468 for ACB-AbR. There
   were 35,723 annotated unigenes from ACB reads found by BLAST searching
   NCBI non-redundant, NCBI non-redundant nucleotide, Swiss-prot protein,
   Kyoto Encyclopedia of Genes and Genomes, Cluster of Orthologous Groups
   of proteins, and Gene Ontology databases. Based on the NOISeq method,
   3,793 unigenes were judged to be differentially expressed between
   ACB-BtS and ACB-AbR. Cry1Ab resistance appeared to be associated with
   change in the transcription level of enzymes involved in growth
   regulation, detoxification and metabolic/catabolic process. Among
   previously described Bt toxin receptors, the differentially expressed
   unigenes associated with aminopeptidase N and chymotrypsin/trypsin were
   up-regulated in ACB-AbR. Whereas, other putative Cry receptors,
   cadherin-like protein, alkaline phosphatase, glycolipid, actin, V-type
   proton ATPase vatalytic, heat shock protein, were under-transcripted.
   Finally, GPI-anchor biosynthesis was found to be involved in the
   significantly enriched pathway, and all genes mapped to the pathway were
   substantially down-regulated in ACB-AbR. Conclusion: To our knowledge,
   this is the first comparative transcriptome study to discover candidate
   genes involved in ACB Bt resistance. This study identified
   differentially expressed unigenes related to general Bt resistance in
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   ACB. The assembled, annotated transcriptomes provides a valuable genomic
   resource for further understanding of the molecular basis of ACB Bt
   resistance mechanisms.
UT CABI:20153127822
SN 1471-2164
ER

PT J
AU Furgal-Dierzuk, I.
   Strzetelski, J.
   Twardowska, M.
   Kwiatek, K.
   Mazur, M.
TI The effect of genetically modified feeds on productivity, milk
   composition, serum metabolite profiles and transfer of tDNA into milk of
   cows.
SO Journal of Animal and Feed Sciences
VL 24
IS 1
PS 19-30
PY 2015
AB The experiment was performed to determine whether transgenic maize
   containing the  Bt gene (MON 810) and soyabean meal produced from
   glyphosate-tolerant plants (Roundup Ready, MON 40-3-2) compared with
   nontransgenic plants can affect the performance parameters, milk
   composition, blood serum metabolite profiles and transfer of tDNA into
   milk of cows. The experiment was carried out from the third week before
   parturition to the 305th day of lactation on 40 Polish Holstein-Friesian
   cows, which were allotted to 4 groups of 10 animals according to body
   weight, milk yield and parity. The cows in all groups were fed a total
   mixed ration (TMR) formulated according to IZ-INRA (2009). The
   concentrate mixtures added to TMR contained: nonmodified (traditional)
   maize and soyabean meal (group TM G/TS); traditional maize and
   genetically modified (GM) soyabean meal (group TMG/MS); GM maize and
   traditional soyabean meal (group MM G/TS); or GM maize and GM soyabean
   meal (group MM G/MS). There were no significant differences between
   transgenic and non-transgenic feeds in productivity, milk composition
   and blood metabolite profiles such as: beta-hydroxybutyric acid (BHBA),
   free fatty acids (FFA), glucose, insulin and progesterone. The
   transgenic DNA sequences of MON 810 and RR soyabean meal were not
   detectable by PCR in milk.
UT CABI:20153127492
SN 1230-1388
ER

PT J
AU Hughson, S. A.
   Spencer, J. L.
TI Emergence and abundance of western corn rootworm (Coleoptera:
   Chrysomelidae) in Bt cornfields with structured and seed blend refuges.
SO Journal of Economic Entomology
VL 108
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IS 1
PS 114-125
PY 2015
AB To slow evolution of western corn rootworm ( Diabrotica virgifera
   virgifera LeConte) resistance to Bt ( Bacillus thuringiensis Berliner)
   corn hybrids, non-Bt "refuges" must be planted within or adjacent to Bt
   cornfields, allowing susceptible insects to develop without exposure to
   Bt toxins. Btsusceptible adults from refuges are expected to find and
   mate with resistant adults that have emerged from Bt corn, reducing the
   likelihood that Bt-resistant offspring are produced. The spatial and
   temporal distribution of adults in four refuge treatments (20, 5, and 0%
   structured refuges and 5% seed blend) and adjacent soybean fields was
   compared from 2010 to 2012. Adult emergence (adults/trap/day) from
   refuge corn in structured refuge treatments was greater than that from
   Bt corn, except during the post-pollination period of corn phenology
   when emergence from refuge and Bt plants was often the same. Abundance
   of free-moving adults was greatest in and near refuge rows in structured
   refuge treatments during vegetative and pollination periods. By
   post-pollination, adult abundance became evenly distributed. In
   contrast, adult abundance in 5% seed blends and 0% refuges was evenly
   distributed, or nearly so, across plots throughout the season. The
   persistent concentration of adults in refuge rows suggests that
   structured refuge configurations may not facilitate the expected mixing
   of adults from refuge and Bt corn. Seed blends produce uniform
   distributions of adults across the field that may facilitate mating
   between Bt and refuge adults and ultimately delay the evolution of Bt
   resistance.
UT CABI:20153124686
SN 0022-0493
DI 10.1093/jee/tou029
ER

PT J
AU Reisig, D. D.
   Akin, D. S.
   All, J. N.
   Bessin, R. T.
   Brewer, M. J.
   Buntin, D. G.
   Catchot, A. L.
   Cook, D.
   Flanders, K. L.
   Huang, F. N.
   Johnson, D. W.
   Leonard, B. R.
   Mcleod, P. J.
   Porter, R. P.
   Reay-Jones, F. P. F.
   Tindall, K. V.
   Stewart, S. D.
   Troxclair, N. N.
   Youngman, R. R.
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   Rice, M. E.
TI Lepidoptera (Crambidae, Noctuidae, and Pyralidae) injury to corn
   Containing single and pyramided Bt traits, and blended or block refuge,
   in the southern United States.
SO Journal of Economic Entomology
VL 108
IS 1
PS 157-165
PY 2015
AB Fall armyworm,  Spodoptera frugiperda (J. E. Smith) (Lepidoptera:
   Noctuidae); corn earworm,  Helicoverpa zea Boddie (Lepidoptera:
   Noctuidae); southwestern corn borer,  Diatraeagrandiosella Dyar
   (Lepidoptera: Crambidae); sugarcane borer,  Diatraea saccharalis F.
   (Lepidoptera: Crambidae); and lesser cornstalk borer,  Elasmopalpus
   lignosellus Zeller (Lepidoptera: Pyralidae), are lepidopteran pests of
   corn,  Zea mays L., in the southern United States. Blended refuge for
   transgenic plants expressing the insecticidal protein derivative from
   Bacillus thuringiensis (Bt) has recently been approved as an alternative
   resistance management strategy in the northern United States. We
   conducted a two-year study with 39 experiments across 12 states in the
   southern United States to evaluate plant injury from these five species
   of Lepidoptera to corn expressing Cry1F and Cry1Ab, as both single and
   pyramided traits, a pyramid of Cry1Ab * Vip3Aa20, and a pyramid of Cry1F
   * Cry1Ab plus non-Bt in a blended refuge. Leaf injury and kernel damage
   from corn earworm and fall armyworm, and stalking tunneling by
   southwestern corn borer, were similar in Cry1Fx * Cry1Ab plants compared
   with the Cry1F * Cry1Ab plus non-Bt blended refuge averaged across
   five-plant clusters. When measured on an individual plant basis, leaf
   injury, kernel damage, stalk tunneling (southwestern corn borer), and
   dead or injured plants (lesser cornstalk borer) were greater in the
   blended non-Bt refuge plants compared to Cry1F * Cry1Ab plants in the
   non-Bt and pyramided Cry1F * Cry1Ab blended refuge treatment. When
   non-Bt blended refuge plants were compared to a structured refuge of
   non-Bt plants, no significant difference was detected in leaf injury,
   kernel damage, or stalk tunneling (southwestern corn borer). Plant
   stands in the non-Bt and pyramided Cry1F * Cry1Ab blended refuge
   treatment had more stalk tunneling from sugarcane borer and plant death
   from lesser cornstalk borer compared to a pyramided Cry1F * Cry1Ab
   structured refuge treatment. Hybrid plants containing Cry1F * Cry1Ab
   within the pyramided Cry1F * Cry1Ab blended refuge treatment had
   significantly less kernel damage than non-Bt structured refuge
   treatments. Both single and pyramided Bt traits were effective against
   southwestern corn borer, sugarcane borer, and lesser cornstalk borer.
UT CABI:20153124691
SN 0022-0493
DI 10.1093/jee/tou009
ER

PT J
AU Vidal, N.
   Barbosa, H.
   Jacob, S.
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   Arruda, M.
TI Comparative study of transgenic and non-transgenic maize ( Zea mays)
   flours commercialized in Brazil, focussing on proteomic analyses.
SO Food Chemistry
VL 180
PS 288-294
PY 2015
AB Genetically modified foods are a major concern around the world due to
   the lack of information concerning their safety and health effects. This
   work evaluates differences, at the proteomic level, between two types of
   crop samples: transgenic (MON810 event with the Cry1Ab gene, which
   confers resistance to insects) and non-transgenic maize flour
   commercialized in Brazil. The 2-D DIGE technique revealed 99
   differentially expressed spots, which were collected in 2-D PAGE gels
   and identified via mass spectrometry (nESI-QTOF MS/MS). The abundance of
   protein differences between the transgenic and non-transgenic samples
   could arise from genetic modification or as a result of an environmental
   influence pertaining to the commercial sample. The major functional
   category of proteins identified was related to disease/defense and,
   although differences were observed between samples, no toxins or
   allergenic proteins were found.
UT CABI:20153115874
RI Barbosa, Herbert/N-9284-2014
SN 0308-8146
DI 10.1016/j.foodchem.2015.02.051
ER

PT J
AU Monika Singh
   Randhawa, G. J.
   Payal Sood
   Bhoge, R. K.
TI Loop-mediated isothermal amplification targeting insect resistant and
   herbicide tolerant transgenes: monitoring for GM contamination in supply
   chain.
SO Food Control
VL 51
PS 283-292
PY 2015
AB Efficient detection strategies for genetically modified (GM) crops are
   required to effectively address some of the biosafety and post-release
   monitoring issues, as global adoption of GM crops has been unprecedently
   increased. Herbicide tolerance and insecticide resistance are the major
   traits in commercialized GM food crops. Visual as well as real-time
   detection system based on loop-mediated isothermal amplification (LAMP)
   targeting lepidopteron insect resistant  cry1Ac,  cry2Ab2 and glyphosate
   tolerant  cp4-epsps genes has been reported. Specificity of LAMP assays
   were confirmed using fourteen GM events of four crops, namely, corn
   (MON810, NK603,  Bt11,  Bt176, MON89034), cotton (MON531, MON15985, GFM-
   cry1A, Event1, MLS9124, MON1445, MON15985 * MON88913), eggplant (EE1)
   and soybean (GTS40-3-2). Real-time LAMP was found sensitive enough to
   detect as low as 2 copies for  cry1Ac and 4 copies for  cry2Ab2 and
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   cp4-epsps within 35 min using a calibration curve. The limit of
   detection (LOD) of visual LAMP assays was down to 0.01% (4 copies of GM
   content) which is lower than conventional PCR (detecting 40-400 copies
   depending on target). LAMP assays are faster and more user-friendly than
   conventional PCR and could be efficiently utilized for monitoring of GM
   contamination in food and feed supply chain, with high specificity and
   sensitivity. The developed assays, when combined with a fast DNA
   extraction method, will facilitate on-site detection to check the GM
   status of a sample or product at ports of entry and in farmers' fields.
UT CABI:20153116852
SN 0956-7135
DI 10.1016/j.foodcont.2014.11.045
ER

PT J
AU Curran, K. L.
   Festa, A. R.
   Goddard, S. D.
   Harrigan, G. G.
   Taylor, M. L.
TI Kernel compositions of glyphosate-tolerant and corn rootworm-protected
   MON 88017 sweet corn and insect-protected MON 89034 sweet corn are
   equivalent to that of conventional sweet corn ( Zea mays).
SO Journal of Agricultural and Food Chemistry
VL 63
IS 11
PS 3046-3052
PY 2015
AB Monsanto Co. has developed two sweet corn hybrids, MON 88017 and MON
   89034, that contain biotechnology-derived (biotech) traits designed to
   enhance sustainability and improve agronomic practices. MON 88017
   confers benefits of glyphosate tolerance and protection against corn
   rootworm. MON 89034 provides protection against European corn borer and
   other lepidopteran insect pests. The purpose of this assessment was to
   compare the kernel compositions of MON 88017 and MON 89034 sweet corn
   with that of a conventional control that has a genetic background
   similar to the biotech sweet corn but does not express the
   biotechnology-derived traits. The sweet corn samples were grown at five
   replicated sites in the United States during the 2010 growing season and
   the conventional hybrid and 17 reference hybrids were grown concurrently
   to provide an estimate of natural variability for all assessed
   components. The compositional analysis included proximates, fibers,
   amino acids, sugars, vitamins, minerals, and selected metabolites.
   Results highlighted that MON 88017 and MON 89034 sweet corns were
   compositionally equivalent to the conventional control and that levels
   of the components essential to the desired properties of sweet corn,
   such as sugars and vitamins, were more affected by growing environment
   than the biotech traits. In summary, the benefits of biotech traits can
   be incorporated into sweet corn with no adverse effects on nutritional
   quality.
UT CABI:20153119195
SN 0021-8561
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DI 10.1021/jf505687s
ER

PT J
AU Andreassen, M.
   Bohn, T.
   Wikmark, O. G.
   Berg, J. van den
   Lovik, M.
   Traavik, T.
   Nygaard, U. C.
TI Cry1Ab protein from  Bacillus thuringiensis and MON810
   cry1Ab-transgenic maize exerts no adjuvant effect after airway exposure.

SO Scandinavian Journal of Immunology
VL 81
IS 3
PS 192-200
PY 2015
AB The genetically modified (GM) maize event MON810 has been inserted with
   a processed version of the transgene,  cry1Ab, derived from the soil
   bacterium  Bacillus thuringiensis (Bt) to express proteins with
   insecticidal properties. Such proteins may introduce new allergens and
   also act as adjuvants that promote allergic responses. While focus has
   been on safe consumption and hence the oral exposure to GM food and
   feed, little is known regarding inhalation of pollen and desiccated
   airborne plant material from GM crops. The aim of this study was to
   investigate whether plant material from the Cry1Ab-expressing maize
   variety MON810, or trypsin-activated Cry1Ab (trypCry1Ab) protein
   produced in recombinant bacteria, may act as adjuvants against the
   allergen ovalbumin (OVA) in a mouse model of airway allergy. A clear
   proallergic adjuvant effect of the mucosal adjuvant cholera toxin (CT)
   was demonstrated, determined as increased specific IgE, eosinophils and
   Th2 cytokines in MLN cell supernates, while no elevation in OVA-specific
   antibodies or cytokine release from MLN cells after stimulation with OVA
   were observed in mice receiving Cry1Ab-containing plant materials or the
   trypCry1Ab protein. Our data suggest that Cry1Ab proteins had no
   detectable systemic adjuvant effect in mice after airway exposure.
   Further experiments with purified plant proteins, as well as long-term
   exposures needs be conducted to further evaluate exposures experienced
   in real-life situations.
UT CABI:20153119967
SN 0300-9475
DI 10.1111/sji.12269
ER

PT J
AU Barroso, M. F.
   Freitas, M.
   Oliveira, M. B. P. P.
   de-los-Santos-Alvarez, N.
   Lobo-Castanon, M. J.
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   Delerue-Matos, C.
TI 3D-nanostructured Au electrodes for the event-specific detection of
   MON810 transgenic maize.
SO Talanta
VL 134
PS 158-164
PY 2015
AB In the present work, the development of a genosensor for the
   event-specific detection of MON810 transgenic maize is proposed. Taking
   advantage of nanostructuration, a cost-effective three dimensional
   electrode was fabricated and a ternary monolayer containing a dithiol, a
   monothiol and the thiolated capture probe was optimized to minimize the
   unspecific signals. A sandwich format assay was selected as a way of
   precluding inefficient hybridization associated with stable secondary
   target structures. A comparison between the analytical performance of
   the Au nanostructured electrodes and commercially available
   screen-printed electrodes highlighted the superior performance of the
   nanostructured ones. Finally, the genosensor was effectively applied to
   detect the transgenic sequence in real samples, showing its potential
   for future quantitative analysis.
UT CABI:20153121345
RI de-los-Santos-Alvarez, Noemi/F-1427-2011; Freitas, Maria/L-1529-2014;
   Delerue-Matos, Cristina/D-4990-2013; Lobo-Castanon, Maria
   Jesus/E-8757-2011
OI de-los-Santos-Alvarez, Noemi/0000-0002-5216-6825; Freitas,
   Maria/0000-0002-0628-2753; Delerue-Matos, Cristina/0000-0002-3924-776X;
   Lobo-Castanon, Maria Jesus/0000-0002-2964-9490
SN 0039-9140
ER

PT J
AU Li YongXin
   Su Ning
   Zheng Bo
   Ruan Jia
   Li Yang
   Luo ChunYing
   Li YuanQian
TI Detection of GM soybean by multiplex-touchdown PCR-microchip capillary
   electrophoresis with response surface methodology optimization.
SO Journal of Chromatographic Science
VL 53
IS 2
PS 345-352
PY 2015
AB The combination of the molecular technique, the multivariate strategy
   and microchip capillary electrophoresis (MCE) was applied to rapid and
   sensitive analysis of genetically modified (GM) soybean in food samples.
   A multiplex-touchdown polymerase chain reaction (PCR) system was
   developed for simultaneously amplifying three target sequences in
   Roundup Ready soybean (RRS). Response surface methodology was introduced
   to determine the optimal separation condition in MCE with good
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   resolution and short analytical time. The detection of the PCR products
   of RRS was completed within 4 min under the optimal conditions. The
   specificity of the method was evaluated by testing non-GM soybean
   materials and three GM maize varieties (MON810, Bt176 and Bt11). A
   sensitivity of 0.1% GM organisms content was obtained, which was
   remarkably lower than the labeling threshold for transgenic food defined
   as 0.9% in the European regulation. The relative standard deviation of
   migration time was in the range of 0.17-0.95%. The proposed method was
   rapid, sensitive and specific and can be used to identify and detect GM
   soybean in food samples.
UT CABI:20153109329
SN 0021-9665
ER

PT J
AU Liu Yu'e
   Lu ZengBin
   Ye GongYin
TI Effects of transgenic  cry1Ab japonica rice lines on the oviposition
   behavior of adult rice leaffolder,  Cnaphalocrocis medinalis (Guenee)
   (Lepidoptera: Pyralidae).
SO Acta Phytophylacica Sinica
VL 42
IS 1
PS 17-24
PY 2015
AB The widely planted  Bacillus thuringiensis (Bt) crops pose risks that
   target insect pests may evolve resistance to Bt crops. Non-Bt crop
   refuges play important roles in delaying the resistance development of
   target insect pests. However, the oviposition behavior of target insect
   pests may impact establishment of refuges for resistance management of
   crops transformed with Bt insecticidal protein genes. In the current
   study, the effects of two transgenic  japonica rice lines, KMD1 and
   KMD2, both expressing Cry1Ab protein, and their non-transgenic rice line
   (Xiushui 11) on the oviposition behavior of adult rice leaf folder,
   Cnaphalocrocis medinalis (Guenee) under laboratory and field conditions.
   "Y"-tube olfactometer and cages were used to compare the oviposition
   behaviors of  C. medinalis among different rice types in the laboratory.
   In addition, the volatiles emitted from Bt and non-Bt rice plants were
   also compared by using solid phase microextraction (SPME) and linked gas
   chromatography-mass spectrometry (GS-MS). The results showed that  C.
   medinalis adults did not significantly prefer Bt or non-Bt rice in
   "Y"-tube olfactometer and small cages. However,  C. medinalis adults
   significantly preferred non-Bt rice compared with Bt rice in the large
   cages and under field conditions. The numbers of eggs laid by  C.
   medinalis on KMD1, KMD2, and non-Bt rice plots were 2.201.28, 1.000.77
   and 5.602.16 per 100 leaves, respectively. The components and relative
   contents of the volatiles emitted from Bt and control plants were also
   similar.  C. medinalis adults prefer to lay eggs on non-Bt rice plants
   compared with Bt rice under field conditions. The differences in the
   oviposition behavior of  C. medinalis adults were unlikely directly
   caused by changes of the volatiles between Bt and non-Bt rice plants.
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UT CABI:20153077916
SN 0577-7518
ER

PT J
AU Rayan, A. M.
   Abbott, L. C.
TI Compositional analysis of genetically modified corn events (NK603,
   MON88017 * MON810 and MON89034 * MON88017) compared to conventional
   corn.
SO Food Chemistry
VL 176
PS 99-105
PY 2015
AB Compositional analysis of genetically modified (GM) crops continues to
   be an important part of the overall evaluation in the safety assessment
   for these materials. The present study was designed to detect the
   genetic modifications and investigate the compositional analysis of GM
   corn containing traits of multiple genes (NK603, MON88017 * MON810 and
   MON89034 * MON88017) compared with non-GM corn. Values for most
   biochemical components assessed for the GM corn samples were similar to
   those of the non-GM control or were within the literature range.
   Significant increases were observed in protein, fat, fiber and fatty
   acids of the GM corn samples. The observed increases may be due to the
   synergistic effect of new traits introduced into corn varieties.
   Furthermore, SDS-PAGE analysis showed high similarity among the protein
   fractions of the investigated corn samples. These data indicate that GM
   corn samples were compositionally equivalent to, and as nutritious as,
   non-GM corn.
UT CABI:20153078621
SN 0308-8146
DI 10.1016/j.foodchem.2014.12.044
ER

PT J
AU Kolm, C.
   Mach, R. L.
   Krska, R.
   Brunner, K.
TI A rapid DNA lateral flow test for the detection of transgenic maize by
   isothermal amplification of the 35S promoter.
SO Analytical Methods
VL 7
IS 1
PS 129-134
PY 2015
AB The present study describes an isothermal DNA amplification method
   combined with a rapid visual signal read-out for the detection of the
   35S promoter, a regulatory element commonly found in GM plants and often
   used for screening of genetically modified crops. The amplification of
   the target sequence is accomplished by helicase-dependent amplification
   (HDA), which can be entirely performed on a simple heating block, within
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   60 min reaction time and without costly instrumentation. For
   visualisation of the amplified products, a nucleic acid lateral flow
   immunostrip is applied, which enables the detection of the formed
   products within 5-10 min and simply by naked eye. The specificity and
   sensitivity of the developed assay were tested and determined by
   analysing certified reference materials of MON810, Bt11 and NK603. The
   obtained limit of detection is 0.5% GM content, which fulfils the
   European demands for mandatory labelling of any food and feed that
   contains more than 0.9% GM components.
UT CABI:20153069671
SN 1759-9660
DI 10.1039/C4AY01997K
ER

PT J
AU Yang, F.
   Kerns, D. L.
   Leonard, B. R.
   Oyediran, I.
   Burd, T.
   Niu, Y.
   Huang, F. N.
TI Performance of AgrisureViptera TM 3111 corn against  Helicoverpa zea
   (Lepidoptera: Noctuidae) in seed mixed plantings.
SO Crop Protection
VL 69
PS 77-82
PY 2015
AB Corn earworm,  Helicoverpa zea (Boddie), is a major target of pyramided
   Bacillus thuringiensis (Bt) corn. In the U.S. Corn Belt, a
   refuge-in-the-bag (RIB) strategy has been adopted to provide susceptible
   populations for insect resistance management (IRM) in planting pyramided
   Bt corn. In this study, eight field trials were conducted to evaluate
   occurrence and injury of  H. zea in three planting patterns of non-Bt
   and Bt corn containing the Agrisure Viptera TM 3111 trait. Viptera 3111
   corn possesses two Bt genes, Vip3A and Cry1Ab, targeting above-ground
   lepidopteran pests. Occurrence of  H. zea eggs was similar between
   non-Bt and Bt corn ears. Eggs of  H. zea were distributed either
   randomly or uniformly in all three planting patterns. Field trials
   consistently showed that Viptera 3111 corn was extremely effective in
   H. zea control in both structured and RIB plantings. Across all the
   trials, there were very little or no larval survival and damage on Bt
   corn ears. Ear damage and larval occurrence at the peak of 3rd to 4th
   instars on refuge ears in the RIB plantings were not less than those
   observed in the structured non-Bt corn plantings. However, larval
   development on RIB refuge ears was significantly delayed relative to
   that on ears of structured non-Bt corn plantings. Information generated
   from this study should provide useful information to improve IRM
   modeling for Bt corn.
UT CABI:20153072039
SN 0261-2194
DI 10.1016/j.cropro.2014.12.002
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ER

PT J
AU Xing FuGuo
   Zhang Wei
   Selvaraj, J. N.
   Liu Yang
TI DNA degradation in genetically modified rice with  Cry1Ab by food
   processing methods: implications for the quantification of genetically
   modified organisms.
SO Food Chemistry
VL 174
PS 132-138
PY 2015
AB Food processing methods contribute to DNA degradation, thereby affecting
   genetically modified organism detection and quantification. This study
   evaluated the effect of food processing methods on the relative
   transgenic content of genetically modified rice with  Cry1Ab. In steamed
   rice and rice noodles, the levels of  Cry1Ab were ≥100% and <83%,
   respectively. Frying and baking in rice crackers contributed to a
   reduction in  Pubi and  Cry1Ab, while microwaving caused a decrease in
   Pubi and an increase in  Cry1Ab. The processing methods of sweet rice
   wine had the most severe degradation effects on  Pubi and  Cry1Ab. In
   steamed rice and rice noodles,  Cry1Ab was the most stable, followed by
   SPS and  Pubi. However, in rice crackers and sweet rice wine,  SPS was
   the most stable, followed by  Cry1Ab and  Pubi. Therefore,  Cry1Ab is a
   better representative of transgenic components than is  Pubi because the
   levels of  Cry1Ab were less affected compared to  Pubi.
UT CABI:20153058993
SN 0308-8146
ER

PT J
AU Su, H. H.
   Tian, J. C.
   Naranjo, S. E.
   Romeis, J.
   Hellmich, R. L.
   Shelton, A. M.
TI Bacillus thuringiensis plants expressing Cry1Ac, Cry2Ab and Cry1F are
   not toxic to the assassin bug,  Zelus renardii.
SO Journal of Applied Entomology
VL 139
IS 1/2
PS 23-30
PY 2015
AB Cotton- and maize-producing insecticidal crystal (Cry) proteins from the
   bacterium,  Bacillus thuringiensis (Bt), have been commercialized since
   1996. Bt plants are subjected to environmental risk assessments for
   non-target organisms, including natural enemies that suppress pest
   populations. Here, we used Cry1F-resistant  Spodoptera frugiperda (J.E.
   Smith) and Cry1Ac and Cry2Ab-resistant  Trichoplusia ni (Hubner) as prey
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   for the assassin bug,  Zelus renardii (Kolenati), a common predator in
   maize and cotton fields. In tritrophic studies, we assessed several
   fitness parameters of  Z. renardii when it fed on resistant  S.
   frugiperda that had fed on Bt maize expressing Cry1F or on resistant  T.
   ni that had fed on Bt cotton expressing Cry1Ac and Cry2Ab. Survival,
   nymphal duration, adult weight, adult longevity and female fecundity of
   Z. renardii were not different when they were fed resistant-prey larvae
   ( S. frugiperda or  T. ni) reared on either a Bt crop or respective
   non-Bt crops. ELISA tests demonstrated that the Cry proteins were
   present in the plant at the highest levels, at lower levels in the prey
   and at the lowest levels in the predator. While  Z. renardii was exposed
   to Cry1F and Cry1Ac and Cry2Ab when it fed on hosts that consumed
   Bt-transgenic plants, the proteins did not affect important fitness
   parameters in this common and important predator.
UT CABI:20153057785
SN 0931-2048
ER

PT J
AU Habustova, O. S.
   Svobodova, Z.
   Spitzer, L.
   Dolezal, P.
   Hussein, H. M.
   Sehnal, F.
TI Communities of ground-dwelling arthropods in conventional and transgenic
   maize: background data for the post-market environmental monitoring.
SO Journal of Applied Entomology
VL 139
IS 1/2
PS 31-45
PY 2015
AB To verify the validity of concerns about environmental safety of maize
   expressing insecticidal Cry toxins (referred to as Bt maize), we
   compared communities of ground beetles (Carabidae), rove beetles
   (Staphylinidae) and spiders (Araneae) in plots planted either with Bt
   maize cultivar YieldGard or with the non-transgenic parental cultivar
   Monumental. Each cultivar was grown on 5 plots of 0.5 ha for three
   consecutive years. To increase the field load of Cry toxin, the fully
   grown maize of the first study year was shredded to small pieces that
   were ploughed into the soil. Arthropods were collected in pitfall traps
   and determined to the species level. The abundance and species richness
   of all studied groups greatly varied over the season and between the
   seasons but without statistically significant differences between the Bt
   and non-Bt plots. A single spider species and three ground beetle
   species dominated in the catches every year, whereas a set of 1-4 most
   abundant rove beetle species changed every year. Frequently occurring
   species were typical for most of Europe. The total counts of ground
   beetles, rove beetles and spiders collected once or twice per season are
   proposed to serve as bioindicators in the post-market environmental
   monitoring (PMEM).
UT CABI:20153057786
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RI Dolezal, Petr/G-8822-2014; Svobodova, Zdenka/L-2361-2015;
OI hussein, Hany/0000-0002-4618-0874
SN 0931-2048
ER

PT J
AU Tinsley, N. A.
   Spencer, J. L.
   Estes, R. E.
   Prasifka, J. R.
   Schrader, P. M.
   French, B. W.
   Gray, M. E.
TI Larval mortality and development for rotation-resistant and
   rotation-susceptible populations of western corn rootworm on Bt corn.
SO Journal of Applied Entomology
VL 139
IS 1/2
PS 46-54
PY 2015
AB The western corn rootworm,  Diabrotica virgifera virgifera LeConte, is
   one of the most economically important insect pests threatening the
   production of corn,  Zea mays (L.), in the United States. Throughout its
   history, this insect has displayed considerable adaptability by
   overcoming a variety of pest management tactics, including the cultural
   practice of annual crop rotation. Since first reported in Illinois in
   the late 1980s, populations of the rotation-resistant western corn
   rootworm have spread over a wide area of the eastern Corn Belt.
   Currently, little information is available concerning the interaction of
   rotation resistance with the use of genetically modified corn expressing
   insecticidal toxins from  Bacillus thuringiensis Berliner (Bt), a
   popular tactic for preventing larval injury and its associated yield
   loss. The goal of this greenhouse experiment was to determine whether
   rotation-resistant and rotation-susceptible western corn rootworm larvae
   differ with respect to survival or development when exposed to single-
   or dual-toxin (pyramided) Bt corn. Individual corn plants were infested
   with 225 near-hatch eggs at the V5 (five leaf collar) growth stage.
   Larvae developed undisturbed on the root systems for 17 days, after
   which they were recovered using Berlese-Tullgren funnels. Surviving
   larvae were counted to estimate mortality, and head capsule widths were
   measured to assess development. Rotation-resistant and
   rotation-susceptible larvae had statistically similar mean levels of
   mortality and head capsule widths when exposed to both single-toxin
   (Cry3Bb1 or Cry34/35Ab1) and pyramided (Cry3Bb1+Cry34/35Ab1) Bt corn,
   suggesting that these two populations do not differ with respect to
   survival or development when exposed to Bt corn. Additionally, the
   statistically similar mean levels of mortality for larvae exposed to
   single-toxin and pyramided Bt corn suggest that pyramided Bt hybrids
   containing the Cry3Bb1 and Cry34/35Ab1 toxins do not result in additive
   mortality for western corn rootworm larvae. Implications for management
   of this economically important pest are discussed.
UT CABI:20153057787
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SN 0931-2048
ER

PT J
AU Yang Jing
   Zheng QiuYue
   Wang HongWei
   Han Hui
   Zhang GongLiang
   Cao JiJuan
TI Detection of genetically modified potato lattice.
SO Journal of Food Safety and Quality
VL 6
IS 1
PS 107-112
PY 2015
AB Objective: To establish a method for rapid detection of the import and
   export genetically modified foods. Methods: The DNA of potato chips was
   quickly extract using DNA extraction kit, and the basic ingredients of
   the potato chips were identified by real-time PCR. Results: Unmarked GMO
   was found in its identity component by preliminary screening of food
   labels. The potato chips with corn flour wrapped contained a variety of
   genetically modified ingredients, including transgenic strains TC1507,
   NK603, MON810, 59122, and MON89034,  etc. Conclusion: This method can be
   used for the qualitative detection of ingredients and strains of
   transgenic corn in processed food and as a confirmatory test methods
   qualitative for the conventional PCR methods.
UT CABI:20153060513
SN 2095-0381
ER

PT J
AU Sun YuanDong
   Liu YuFang
   Li Fei
   Xiao Lu
   Tan ShuHua
   Gui FangYan
   Mo ShuYin
   Sun LiChuan
   Liu WenHai
   Ge Feng
TI Responses of growth and activities of antioxidant and detoxification
   enzymes of  Misgurnus anguillicaudatus to transgenic  Cry1Ab/Ac rice
   residues in water.
SO Zhongguo Shengtai Nongye Xuebao / Chinese Journal of Eco-Agriculture
VL 23
IS 1
PS 95-101
PY 2015
AB A loach ( Misgurnus anguillicaudatus) aquaculture experiment was
   conducted in phytotron with aquatic water added with straw power in
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   different concentrations (10 mg.L -1, 50 mg.L -1, 100 mg.L -1, 200 mg.L
   -1) of different rice varieties, which were transgenic  Cry1Ab/Ac rice
   variety of 'Huahui 1' (HH1) and non- Bt control rice variety of 'Minghui
   63' (MH63). In the experiment, the loach basal fed without rice straw
   powder was set as the blank control. The specific growth rate, condition
   factor, and viscera somatic index as well as activities of antioxidant
   enzymes of superoxide dismutase (SOD) and catalase (CAT), and
   detoxification enzyme of glutathione-s-transferase (GST) of loach were
   investigated after culture for 100 days. The aim of the study was to
   explore effects of transgenic  Bt rice on aquatic animal through
   simulating rice residues in paddy water. The results showed no
   significant differences ( P>0.05) in specific growth rate, condition
   factor, viscera somatic, and activities of SOD, CAT and GST between
   loaches cultured in aquatic water added with HH1 and MH63 straw powders
   with four concentrations. Compared with the blank control, the growth
   performance gradually decreased with increasing concentration of rice
   straw powder of both varieties. Furthermore, the specific growth rate,
   viscera somatic index and CAT activity of loach decreased obviously when
   loach was cultured in aquatic water with 200 mg.L -1 of HH1 and MH63
   straw powder. These results indicated that aquatic water with lower
   concentration of transgenic  Cry1Ab/Ac rice straw powder had no obvious
   effect on growth performance and activities of antioxidant and
   detoxification enzymes of loach. When the concentration of rice straw
   powder was up to 200 mg.L -1, the growth performance and activities of
   physiologic enzymes of loach decreased significantly, regardless of rice
   variety. It was suggested that higher level of rice straw powder in
   water hindered breathing of loach. In addition, the decomposition of
   rice straw powder in water induced decreasing of pH and dissolved
   oxygen.
UT CABI:20153061351
SN 1671-3990
ER

PT J
AU Bottger, R.
   Schaller, J.
   Lintow, S.
   Dudel, E. G.
TI Aquatic degradation of Cry1Ab protein and decomposition dynamics of
   transgenic corn leaves under controlled conditions.
SO Ecotoxicology and Environmental Safety
VL 113
PS 454-459
PY 2015
AB The increasing cultivation of genetically modified corn plants (Zea
   mays) during the last decades is suggested as a potential risk to the
   environment. One of these genetically modified variety expressed the
   insecticidal Cry1Ab protein originating from  Bacillus thuringiensis
   (Bt), resulting in resistance against  Ostrinia nubilalis, the European
   corn borer. Transgenic litter material is extensively studied regarding
   the decomposition in soils. However, only a few field studies analyzed
   the fate of the Cry1Ab protein and the impact of green and senescent
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   leaf litter from corn on the decomposition rate and related ecosystem
   functions in aquatic environments. Consequently, a microbial litter
   decomposition experiment was conducted under controlled semi-natural
   conditions in batch culture using two maize varieties: one variety with
   Cry1Ab and another one with the appertaining Iso-line as control
   treatment. The results showed no significant differences between the
   treatment with Cry1Ab and the Iso-line regarding loss of total mass in
   dry weight of 43% for Iso-line and 45% for Bt-corn litter, lignin
   content increased to 137.5% (Iso-line) and 115.7% (Bt-corn), and phenol
   loss decreased by 53.6% (Iso-line), 62.2% (Bt-corn) during three weeks
   of the experiment. At the end of the experiment Cry1Ab protein was still
   detected with 6% of the initial concentration. A slightly but
   significant lower cellulose content was found for the Cry1Ab treatment
   compared to the Iso-line litter at the end of the experiment. The
   significant higher total protein (25%) and nitrogen (25%) content in Bt
   corn, most likely due to the additionally expression of the transgenic
   protein, may increase the microbial cellulose degradation and decrease
   microbial lignin degradation. In conclusion a relevant year by year
   input of protein and therefore nitrogen rich Bt corn litter into aquatic
   environments may affect the balanced nutrient turnover in aquatic
   ecosystems.
UT CABI:20153045684
SN 0147-6513
DI 10.1016/j.ecoenv.2014.12.034
ER

PT J
AU Wang XiuMin
   Teng Da
   Guan QingFeng
   Tian Fang
   Wang JianHua
TI Detection of genetically modified crops using multiplex asymmetric
   polymerase chain reaction and asymmetric hyperbranched rolling circle
   amplification coupled with reverse dot blot.
SO Food Chemistry
VL 173
PS 1022-1029
PY 2015
AB To meet the ever-increasing demand for detection of genetically modified
   crops (GMCs), low-cost, high-throughput and high-accuracy detection
   assays are needed. The new multiplex asymmetric polymerase chain
   reaction and asymmetric hyper-branched rolling circle amplification
   coupled with reverse dot blot (RDB) systems were developed to detect
   GMCs. Thirteen oligonucleotide probes were designed to identify
   endogenous targets ( Lec1,  Hmg and  Sad1), event-specific targets (
   RRS-5C,  RRS-3C,  Bt176-3C and  MON810-3C), screening targets ( 35S
   promoter and  NOS terminator), and control targets ( 18S and  PLX).
   Optimised conditions were as follows: tailed hybridization probes (1-2
   pmol/l) were immobilized on a membrane by baking for 2 h, and a 10:1
   ratio of forward to reverse primers was used. The detection limits were
   0.1 g/l of 2% RRS and 0.5 ng/l of DNA from genetically modified (GM)
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   soybean. These results indicate that the RDB assay could be used to
   detect multiplex target genes of GMCs rapidly and inexpensively.
UT CABI:20153014209
SN 0308-8146
ER

PT J
AU Ming HuaMi
   Wang ManLi
   Yin HongZong
TI Detection of  Bacillus thuringiensis Cry1Ab protein based on surface
   plasmon resonance immunosensor.
SO Analytical Biochemistry
VL 468
PS 59-65
PY 2015
AB Two novel surface plasmon resonance immunosensors were fabricated for
   detection of the  Bacillus thuringiensis Cry1Ab protein and to
   demonstrate their performance in analyzing Cry1Ab protein in crop
   samples. Sensor 2 was modified by 1,6-hexanedithiol, Au/Ag alloy
   nanoparticles, 3-mercaptopropionic acid, and protein A (or not [sensor
   1]), with Cry1Ab monoclonal antibody. As a result, both of the
   immunosensors exhibited satisfactory linear responses in the Cry1Ab
   protein concentration ranges of 10 to 500 ng ml -1 and 8 to 1000 ng ml
   -1, and the detection limits were 5.0 and 4.8 ng ml -1, respectively.
   The immunosensors possessed good specificity and acceptable
   reproducibility. In addition, crop samples could be analyzed after a
   simple treatment. The transgenic crops could be easily identified from
   the conventional ones by the two immunosensors.
UT CABI:20143423286
SN 0003-2697
DI 10.1016/j.ab.2014.09.014
ER

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